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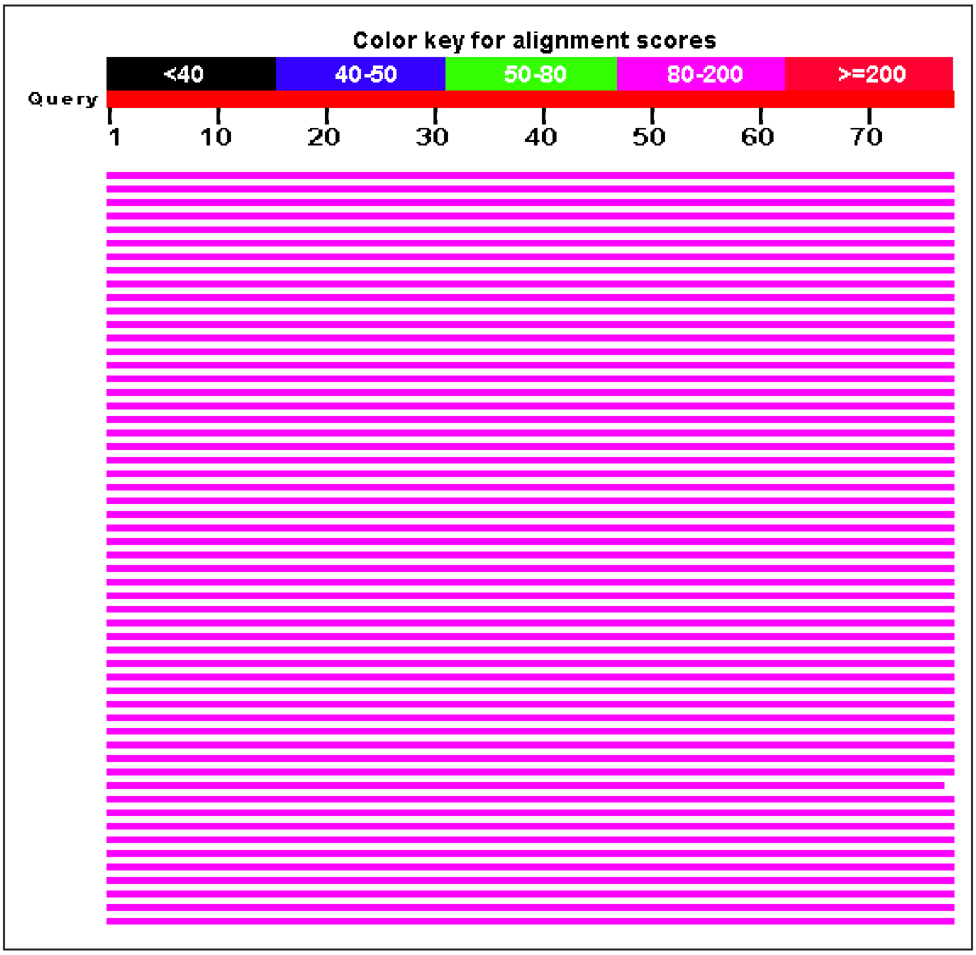
Blast report description

c2

RID	BT5KXG9C015 (Expires on 02-12 21:11 pm)		
Query ID	lcl|Query_21457	**Database Name**	nr
Description	c2	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	77		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Vicia faba isolate 7612 tRNA-Leu (trnL) gene, partial sequence; chloroplast	134	134	100%	1e-28	99%	KJ787213.1
Vicia faba plastid, complete genome	134	134	100%	1e-28	99%	KF042344.1
Vicia faba isolate HS879 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	134	134	100%	1e-28	99%	JX505737.1
Vicia faba var. minor tRNA-Leu (trnL) gene, partial sequence; chloroplast	134	134	100%	1e-28	99%	JN617168.1
Vicia faba var. major tRNA-Leu (trnL) gene, partial sequence; chloroplast	134	134	100%	1e-28	99%	JN617167.1
Vicia faba chloroplast transfer RNA-Leu(CAA)	134	134	100%	1e-28	99%	M55084.1
Vicia faba chloroplast tRNA-Leu, tRNA-Phe, tRNA-His, ORFX, NADH-deydrogenase genes & partial sequence ORFx & psbA genes	134	134	100%	1e-28	99%	X51471.1
Broad bean chloroplast genes for tRNA-Leu(CAA) and (UAA) and tRNA-Phe	134	134	100%	1e-28	99%	X02444.1
Melilotus albus isolate xt_plant115 tRNA-Leu (trnL) gene, intron; chloroplast	122	122	100%	8e-25	95%	KJ746436.1
Tracheophyta environmental sample clone N-11 tRNA-Leu (trnL) gene, partial sequence; chloroplast	122	122	100%	8e-25	95%	KF616419.1
Tracheophyta environmental sample clone N-3 tRNA-Leu (trnL) gene, partial sequence; chloroplast	122	122	100%	8e-25	95%	KF616411.1
Tracheophyta environmental sample clone N-6 tRNA-Leu (trnL) gene, partial sequence; chloroplast	122	122	100%	8e-25	95%	KF616414.1
Tracheophyta environmental sample clone N-5 tRNA-Leu (trnL) gene, partial sequence; chloroplast	122	122	100%	8e-25	95%	KF616413.1
Tracheophyta environmental sample clone N-4 tRNA-Leu (trnL) gene, partial sequence; chloroplast	122	122	100%	8e-25	95%	KF616412.1
Melilotus alba tRNA-Leu (trnL) gene, intron; chloroplast	122	122	100%	8e-25	95%	DQ311713.1
Melilotus alba chloroplast tRNA-Leu (trnL) gene, intron sequence	122	122	100%	8e-25	95%	AF124232.1
Tracheophyta environmental sample clone N-1 tRNA-Leu (trnL) gene, partial sequence; chloroplast	120	120	100%	3e-24	94%	KF616409.1
Tracheophyta environmental sample clone N-2 tRNA-Leu (trnL) gene, partial sequence; chloroplast	116	116	100%	4e-23	94%	KF616410.1
Vicia cypria isolate HS866 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	113	113	100%	4e-22	92%	JX505734.1
Vicia koeieana isolate 7619 tRNA-Leu (trnL) gene, partial sequence; chloroplast	111	111	100%	1e-21	91%	KJ787256.1
Vicia lunata isolate V25 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	111	111	100%	1e-21	89%	JX505749.1
Ononis hirta tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	111	111	100%	1e-21	93%	GQ488565.1
Ononis dentata tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	111	111	100%	1e-21	89%	GQ488559.1

Trigonella suavissima isolate EC 583624 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	109	109	100%	5e-21	88%	JX274187.1
Trigonella suavissima isolate EC 583623 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	109	109	100%	5e-21	88%	JX274186.1
Ononis varelae tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	109	109	100%	5e-21	91%	GQ488605.1
Astragalus pectinatus isolate CP18 tRNA-Leu (trnL) gene, partial sequence; chloroplast	107	107	100%	2e-20	90%	KP208342.1
Astragalus hemsleyi chloroplast gene for tRNA-Leu and trnL-trnF intergenic spacer, specimen_voucher: TARI:69578, partial sequence	107	107	100%	2e-20	90%	AB485940.1
Astragalus polaris tRNA-Leu (trnL) gene, partial sequence; chloroplast	107	107	100%	2e-20	90%	GQ244622.1
Astragalus polaris tRNA-Leu (trnL) gene, intron	107	107	100%	2e-20	90%	DQ860525.1
Astragalus layneae voucher ASLA-4 tRNA-Leu (trnL) gene, partial sequence; and trnL-trnF intergenic spacer, complete sequence; chloroplast	107	107	100%	2e-20	90%	DQ403850.1
Astragalus layneae voucher ASLA-1 tRNA-Leu (trnL) gene, partial sequence; and trnL-trnF intergenic spacer, complete sequence; chloroplast	107	107	100%	2e-20	90%	DQ403849.1
Astragalus didymocarpus voucher ASDI-16 tRNA-Leu (trnL) gene, partial sequence; and trnL-trnF intergenic spacer, complete sequence; chloroplast	107	107	100%	2e-20	90%	DQ403848.1
Astragalus didymocarpus voucher ASDI-2 tRNA-Leu (trnL) gene, partial sequence; and trnL-trnF intergenic spacer, complete sequence; chloroplast	107	107	100%	2e-20	90%	DQ403847.1
Astragalus didymocarpus voucher ASDI-1 tRNA-Leu (trnL) gene, partial sequence; and trnL-trnF intergenic spacer, complete sequence; chloroplast	107	107	100%	2e-20	90%	DQ403846.1
Nicotiana trigonophylla chloroplast partial tRNA-Leu gene, IGS and partial tRNA-Phe gene	107	107	100%	2e-20	91%	AJ577438.2
Nicotiana bigelovii chloroplast partial tRNA-Leu gene, IGS and partial tRNA-Phe gene	107	107	100%	2e-20	91%	AJ577437.1
Nicotiana palmeri chloroplast partial tRNA-Leu gene, IGS and partial tRNA-Phe gene	107	107	100%	2e-20	91%	AJ577406.1
Astragalus linifolius chloroplast tRNA-Leu (trnL) gene, intron sequence	107	107	100%	2e-20	90%	AF126978.1
Astragalus bodinii chloroplast tRNA-Leu (trnL) gene, intron sequence	107	107	100%	2e-20	90%	AF126977.1
Astragalus gilviflorus chloroplast tRNA-Leu (trnL) gene, intron sequence	107	107	100%	2e-20	90%	AF126976.1
Astragalus douglasii chloroplast tRNA-Leu (trnL) gene, intron sequence	107	107	100%	2e-20	90%	AF126974.1
Astragalus palanae var. palanae chloroplast tRNA-Leu (trnL) gene, intron sequence	107	107	100%	2e-20	90%	AF126971.1
Astragalus sabulonum chloroplast tRNA-Leu (trnL) gene, intron sequence	107	107	100%	2e-20	90%	AF126969.1
Melilotus officinalis isolate CP46 tRNA-Leu (trnL) gene, partial sequence; chloroplast	105	105	100%	6e-20	85%	KP208370.1
Astragalus flexuosus isolate CP17 tRNA-Leu (trnL) gene, partial sequence; chloroplast	105	105	98%	6e-20	90%	KP208341.1
Melilotus officinalis isolate xt_plant51 tRNA-						

Leu (trnL) gene, intron; chloroplast	105	105	100%	6e-20	85%	KJ746435.1
Trigonella balansae isolate EC 546586 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	JX274188.1
Trigonella maritima isolate EC 583601 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	86%	JX274171.1
Trigonella cretica isolate EC 583577 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	JX274153.1
Trigonella cretica isolate EC 583576 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	JX274152.1
Trigonella cretica isolate EC 583575 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	JX274151.1
Trigonella coerulescens isolate EC 583574 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	JX274150.1
Trigonella coerulescens isolate EC 583573 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	JX274149.1
Trigonella caerulea isolate EC 583569 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	JX274147.1
Trigonella caerulea isolate EC 583567 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	JX274145.1
Trigonella balansae isolate EC 583507 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	JX274137.1
Trigonella anguina isolate EC 583495 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	JX274134.1
Melilotus officinalis voucher personal collection:I. Hiiesalu 47 tRNA-Leu (trnL) gene, partial sequence; chloroplast	105	105	100%	6e-20	85%	HM590318.1
Trigonella caerulea tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	GQ488615.1
Ononis speciosa tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	86%	GQ488593.1
Ononis reclinata subsp. reclinata tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	88%	GQ488586.1
Ononis filicaulis tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	88%	GQ488561.1
Ononis cristata subsp. cristata tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	90%	GQ488558.1
Melilotus albus chloroplast DNA, tRNA-Leu (trnL) and trnL-trnF intergenic spacer, partial sequence, specimen_voucher: TUH:19700	105	105	100%	6e-20	85%	AB546813.1
Melilotus officinalis chloroplast DNA, tRNA-Leu (trnL) and trnL-trnF intergenic spacer, partial sequence, specimen_voucher: TUH:7346	105	105	100%	6e-20	85%	AB546812.1
Melilotus officinalis tRNA-Leu (trnL) gene, intron; chloroplast	105	105	100%	6e-20	85%	DQ311714.1

Melilotus officinalis chloroplast tRNA-Leu (trnL) gene, intron sequence	105	105	100%	6e-20	85%	AF124233.1
Trigonella strangulata isolate EC 583622 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	84%	JX274185.1
Trigonella stellata isolate EC 583621 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	JX274184.1
Trigonella filipes isolate EC 583584 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	84%	JX274158.1
Ononis natrix tRNA-Leu (trnL) gene, intron; chloroplast	104	104	100%	2e-19	85%	HQ323975.1
Ononis zygantha tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488611.1
Ononis viscosa subsp. breviflora tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488609.1
Ononis tazaensis tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488600.1
Ononis sicula tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488591.1
Ononis serotina tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488589.1
Ononis pubescens tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488582.1
Ononis pseudoserotina tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488581.1
Ononis polysperma tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488580.1
Ononis ornithopodioides tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488576.1
Ononis natrix subsp. arganietorum tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488574.1
Ononis megalostachys tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488570.1
Ononis hebecarpa tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488563.1
Ononis biflora tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488555.1
Ononis aurasiaca tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488553.1
Ononis atlantica tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488552.1
Ononis angustissima subsp. longifolia tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488550.1
Ononis angustissima subsp. angustissima tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488549.1
Astragalus ophiocarpus chloroplast gene for tRNA-Leu and trnL-trnF intergenic spacer, specimen_voucher: TARI:55143,	104	104	100%	2e-19	89%	AB485941.1

partial sequence						
Astragalus jaegerianus voucher ASJA-1 tRNA-Leu (trnL) gene, partial sequence; and trnL-trnF intergenic spacer, complete sequence; chloroplast	104	104	100%	2e-19	88%	DQ403845.1
Lycium ruthenicum chloroplast trnL (UAA) gene, intron sequence	104	104	100%	2e-19	90%	AB036585.1
Astragalus nothoxys chloroplast tRNA-Leu (trnL) gene, intron sequence	104	104	100%	2e-19	89%	AF126979.1
Astragalus arizonicus chloroplast tRNA-Leu (trnL) gene, intron sequence	104	104	100%	2e-19	89%	AF126973.1
Astragalus pehuenches chloroplast tRNA-Leu (trnL) gene, intron sequence	104	104	100%	2e-19	89%	AF126972.1
Medicago papillosa chloroplast, complete genome	102	102	100%	8e-19	84%	KJ850241.1
Medicago hybrida chloroplast, complete genome	102	102	100%	8e-19	84%	KJ850240.1
Lathyrus inconspicuus chloroplast, complete genome	102	102	100%	8e-19	84%	KJ850236.1
Ipomoea batatas cultivar Xushu 18 chloroplast, complete genome	102	102	100%	8e-19	90%	KP212149.1
Lathyrus crassipes isolate P025 tRNA-Leu (trnL) gene, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP057648.1

Alignments

Vicia faba isolate 7612 tRNA-Leu (trnL) gene, partial sequence; chloroplast
Sequence ID: **gb|KJ787213.1|** Length: 487 Number of Matches: 1
Range 1: 83 to 159

Score	Expect	Identities	Gaps	Strand	Frame
134 bits(148)	1e-28()	76/77(99%)	0/77(0%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCaaaaacaaaaaactaaaagttcagaaaaaaaG  60
            |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  83   GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAG  142

Query  61   GATAGGTGCAGAGACTC  77
            |||||||||||||||||
Sbjct  143  GATAGGTGCAGAGACTC  159
```

Vicia faba plastid, complete genome
Sequence ID: **gb|KF042344.1|** Length: 123722 Number of Matches: 1
Range 1: 118542 to 118618

Score	Expect	Identities	Gaps	Strand	Frame
134 bits(148)	1e-28()	76/77(99%)	0/77(0%)	Plus/Plus	

Features:

```
Query  1       GGCAATCCTGAGCCAAATCCTTCTTTCCaaaaacaaaaaactaaaagttcagaaaaaaaG  60
               |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  118542  GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAG  118601

Query  61      GATAGGTGCAGAGACTC  77
               |||||||||||||||||
Sbjct  118602  GATAGGTGCAGAGACTC  118618
```

Vicia faba isolate HS879 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|JX505737.1|** Length: 604 Number of Matches: 1
Range 1: 66 to 142

Score	Expect	Identities	Gaps	Strand	Frame
134 bits(148)	1e-28()	76/77(99%)	0/77(0%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCaaaaacaaaaaactaaaagttcagaaaaaaaG  60
            |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  66   GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAG  125
```

```
Query  61   GATAGGTGCAGAGACTC  77
            |||||||||||||||||
Sbjct  126  GATAGGTGCAGAGACTC  142
```

Vicia faba var. minor tRNA-Leu (trnL) gene, partial sequence; chloroplast
Sequence ID: **gb|JN617168.1|** Length: 938 Number of Matches: 1
Range 1: 554 to 630

Score	Expect	Identities	Gaps	Strand	Frame
134 bits(148)	1e-28()	76/77(99%)	0/77(0%)	Plus/Minus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCaaaaacaaaaaactaaaagttcagaaaaaaaG  60
            |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  630  GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAG  571

Query  61   GATAGGTGCAGAGACTC  77
            |||||||||||||||||
Sbjct  570  GATAGGTGCAGAGACTC  554
```

Vicia faba var. major tRNA-Leu (trnL) gene, partial sequence; chloroplast
Sequence ID: **gb|JN617167.1|** Length: 949 Number of Matches: 1
Range 1: 558 to 634

Score	Expect	Identities	Gaps	Strand	Frame
134 bits(148)	1e-28()	76/77(99%)	0/77(0%)	Plus/Minus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCaaaaacaaaaaactaaaagttcagaaaaaaaG  60
            |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  634  GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAG  575

Query  61   GATAGGTGCAGAGACTC  77
            |||||||||||||||||
Sbjct  574  GATAGGTGCAGAGACTC  558
```

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Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BSMG674J014**
Formatting options
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Blast report description

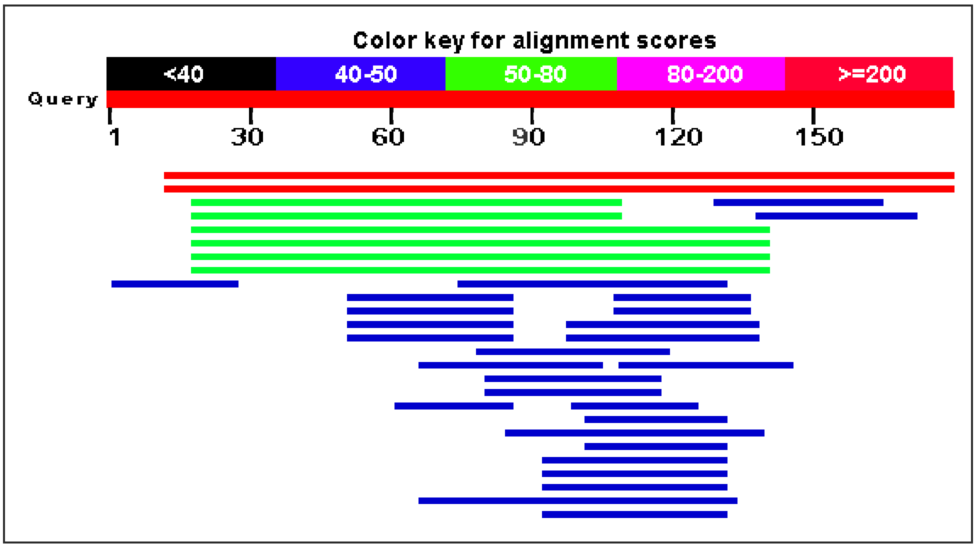
HMF1EA_S2S_Clone1

RID BSMG674J014 (Expires on 02-12 16:19 pm)

Query ID	lcl|Query_209549	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	179		

Graphic Summary

Distribution of 35 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Burkholderia xenovorans LB400 chromosome 1, complete sequence	297	297	93%	6e-77	99%	CP008760.1
Burkholderia xenovorans LB400 chromosome 1, complete sequence	297	297	93%	6e-77	99%	CP000270.1
Burkholderia sp. YI23 chromosome 3, complete sequence	78.8	78.8	50%	3e-11	79%	CP003089.1
Burkholderia sp. RPE67 DNA, complete genome, chromosome: 3	69.8	69.8	50%	2e-08	77%	AP014578.1
Pandoraea apista strain DSM 16535, complete genome	59.0	59.0	68%	3e-05	70%	CP013481.1
Pandoraea apista strain AU2161, complete genome	59.0	59.0	68%	3e-05	70%	CP011501.1
Pandoraea apista strain TF80G25, complete genome	59.0	59.0	68%	3e-05	70%	CP011279.1
Pandoraea apista strain TF81F4, complete genome	59.0	59.0	68%	3e-05	70%	CP010518.3
Paenibacillus naphthalenovorans strain 32O-Y, complete genome	44.6	44.6	31%	0.61	77%	CP013652.1
Anaplasma marginale str. Dawn genome	44.6	44.6	19%	0.61	89%	CP006847.1
Anaplasma marginale str. Gypsy Plains genome	44.6	44.6	19%	0.61	89%	CP006846.1
Anaplasma marginale hypothetical protein AM1108s gene, complete cds	44.6	44.6	19%	0.61	89%	KF053047.1
Anaplasma marginale str. Florida, complete genome	44.6	44.6	19%	0.61	89%	CP001079.1
Cyprinus carpio genome assembly common carp genome, scaffold: LG11, chromosome: 11	42.8	42.8	16%	2.1	93%	LN590705.1
Ctenopharyngodon idella microsatellite CID-12 sequence	42.8	42.8	16%	2.1	93%	KJ854952.1
Emiliania huxleyi CCMP1516 hypothetical protein partial mRNA	42.8	42.8	22%	2.1	83%	XM_005761800.1
Mycobacterium gilvum Spyr1, complete genome	42.8	42.8	22%	2.1	83%	CP002385.1
Desulfarculus baarsii DSM 2075, complete genome	42.8	42.8	20%	2.1	86%	CP002085.1
Mycobacterium gilvum PYR-GCK, complete genome	42.8	42.8	22%	2.1	83%	CP000656.1
Rheinheimera sp. F8 genome	41.0	41.0	18%	7.4	88%	CP013656.1
Azospirillum brasilense strain Sp7, complete sequence	41.0	41.0	21%	7.4	85%	CP012914.1
Bordetella hinzii strain H568, complete genome	41.0	41.0	20%	7.4	86%	CP012077.1
Bordetella hinzii strain F582, complete genome	41.0	41.0	20%	7.4	86%	CP012076.1
Uncultured fungus clone 2168_676 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence	41.0	41.0	15%	7.4	96%	KP897765.1
Sandaracinus amylolyticus strain DSM 53668, complete genome	41.0	41.0	15%	7.4	93%	CP011125.1
PREDICTED: Eucalyptus grandis uncharacterized LOC104444097 (LOC104444097), mRNA	41.0	41.0	16%	7.4	90%	XM_010057698.1

Paenibacillus stellifer strain DSM 14472, complete genome	41.0	41.0	30%	7.4	76%	CP009286.1
Rhizobium sp. LPU83 main chrosome complete genome	41.0	41.0	16%	7.4	90%	HG916852.1
Cordyceps militaris CM01 Fungal specific transcription factor (CCM_02166), partial mRNA	41.0	41.0	13%	7.4	96%	XM_006667319.1
PREDICTED: Pantholops hodgsonii long-chain specific acyl-CoA dehydrogenase, mitochondrial-like (LOC102340858), mRNA	41.0	41.0	21%	7.4	85%	XM_005975426.1
Variovorax paradoxus B4 chromosome 1, complete sequence	41.0	41.0	21%	7.4	85%	CP003911.1
Desulfomonile tiedjei DSM 6799, complete genome	41.0	41.0	20%	7.4	85%	CP003360.1
Acidovorax avenae subsp. avenae ATCC 19860, complete genome	41.0	41.0	21%	7.4	85%	CP002521.1
Gordonia bronchialis DSM 43247, complete genome	41.0	41.0	37%	7.4	73%	CP001802.1
Variovorax paradoxus S110 chromosome 1, complete sequence	41.0	41.0	21%	7.4	85%	CP001635.1

Alignments

Burkholderia xenovorans LB400 chromosome 1, complete sequence
Sequence ID: **gb|CP008760.1|** Length: 4868129 Number of Matches: 1
Range 1: 401861 to 402027

Score	Expect	Identities	Gaps	Strand	Frame
297 bits(328)	6e-77()	166/167(99%)	0/167(0%)	Plus/Plus	

Features:
citrate synthase family protein

```
Query  13      CCTACCTGAGATCCGATTGCGGTTGCCACGCAGTTGAAAAGATCAGCGTTTGTAGACGCC  72
               ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  401861  CCTTCCTGAGATCCGATTGCGGTTGCCACGCAGTTGAAAAGATCAGCGTTTGTAGACGCC  401920

Query  73      GCAATACGCGCTGCAAACGTTGCGGGCGCGAGCTCGTGATCAGCGAGGAGAACAAGGGCC  132
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  401921  GCAATACGCGCTGCAAACGTTGCGGGCGCGAGCTCGTGATCAGCGAGGAGAACAAGGGCC  401980

Query  133     GAATTCATGATCCGCGTGCTGTCCGGCCGGCTTTGTCCCCCACCCGC  179
               |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  401981  GAATTCATGATCCGCGTGCTGTCCGGCCGGCTTTGTCCCCCACCCGC  402027
```

Burkholderia xenovorans LB400 chromosome 1, complete sequence
Sequence ID: **gb|CP000270.1|** Length: 4895836 Number of Matches: 1
Range 1: 1942171 to 1942337

Score	Expect	Identities	Gaps	Strand	Frame
297 bits(328)	6e-77()	166/167(99%)	0/167(0%)	Plus/Minus	

Features:

```
Query  13       CCTACCTGAGATCCGATTGCGGTTGCCACGCAGTTGAAAAGATCAGCGTTTGTAGACGCC  72
                ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1942337  CCTTCCTGAGATCCGATTGCGGTTGCCACGCAGTTGAAAAGATCAGCGTTTGTAGACGCC  1942278

Query  73       GCAATACGCGCTGCAAACGTTGCGGGCGCGAGCTCGTGATCAGCGAGGAGAACAAGGGCC  132
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1942277  GCAATACGCGCTGCAAACGTTGCGGGCGCGAGCTCGTGATCAGCGAGGAGAACAAGGGCC  1942218

Query  133      GAATTCATGATCCGCGTGCTGTCCGGCCGGCTTTGTCCCCCACCCGC  179
                |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1942217  GAATTCATGATCCGCGTGCTGTCCGGCCGGCTTTGTCCCCCACCCGC  1942171
```

Burkholderia sp. YI23 chromosome 3, complete sequence
Sequence ID: **gb|CP003089.1|** Length: 1569570 Number of Matches: 1
Range 1: 636610 to 636700

Score	Expect	Identities	Gaps	Strand	Frame
78.8 bits(86)	3e-11()	72/91(79%)	0/91(0%)	Plus/Plus	

Features:

```
Query  19      TGAGATCCGATTGCGGTTGCCACGCAGTTGAAAAGATCAGCGTTTGTAGACGCCGCAATA  78
               ||||| ||||| || |  ||||||||  |||| | ||| ||||| || |||||||| |
Sbjct  636610  TGAGAGCCGATCGCCGCCGCCACGCAACTGAACACATCTGCGTTGGTCGACGCCGCCACG  636669

Query  79      CGCGCTGCAAACGTTGCGGGCGCGAGCTCGT  109
               ||||| | ||| |||||||||||||| ||||
Sbjct  636670  CGCGCCGAAAAGGTTGCGGGCGCGAGTTCGT  636700
```

Burkholderia sp. RPE67 DNA, complete genome, chromosome: 3

Sequence ID: **dbj|AP014578.1|** Length: 1680600 Number of Matches: 1
Range 1: 669090 to 669180

Score	Expect	Identities	Gaps	Strand	Frame
69.8 bits(76)	2e-08()	70/91(77%)	0/91(0%)	Plus/Minus	

Features:

```
Query  19      TGAGATCCGATTGCGGTTGCCACGCAGTTGAAAAGATCAGCGTTTGTAGACGCCGCAATA  78
               || || ||||| || |  ||||||||  |||| | ||| ||||| || ||||| || |
Sbjct  669180  TGCGACCCGATCGCCGCCGCCACGCAACTGAACACATCTGCGTTGGTCGACGCGGCCACG  669121

Query  79      CGCGCTGCAAACGTTGCGGGCGCGAGCTCGT  109
               ||||| | ||| |||||||||||||| ||||
Sbjct  669120  CGCGCCGAAAAGGTTGCGGGCGCGAGTTCGT  669090
```

Pandoraea apista strain DSM 16535, complete genome

Sequence ID: **gb|CP013481.1|** Length: 5507928 Number of Matches: 1
Range 1: 1995107 to 1995228

Score	Expect	Identities	Gaps	Strand	Frame
59.0 bits(64)	3e-05()	86/122(70%)	0/122(0%)	Plus/Plus	

Features:
citrate synthase

```
Query  19       TGAGATCCGATTGCGGTTGCCACGCAGTTGAAAAGATCAGCGTTTGTAGACGCCGCAATA  78
                || || ||||| || |  ||||| ||    || ||||| || || |||||||||||||
Sbjct  1995107  TGCGAGCCGATGGCCGCCGCCACACAACCAAACAGATCCGCATTGGTAGACGCCGCAACG  1995166

Query  79       CGCGCTGCAAACGTTGCGGGCGCGAGCTCGTGATCAGCGAGGAGAACAAGGGCCGAATTC  138
                ||||| | ||| || || || || || ||||  || ||||| |  || || || |  |||
Sbjct  1995167  CGCGCCGAAAAAGTGGCCGGGGCCAGTTCGTTGTCGGCGAGCACGACGAGCGCGGCGTTC  1995226

Query  139      AT  140
                ||
Sbjct  1995227  AT  1995228
```

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NCBI/ BLAST/ blastn suite/ **Formatting Results - BSMJJETB014**
Formatting options
Download
Blast report description

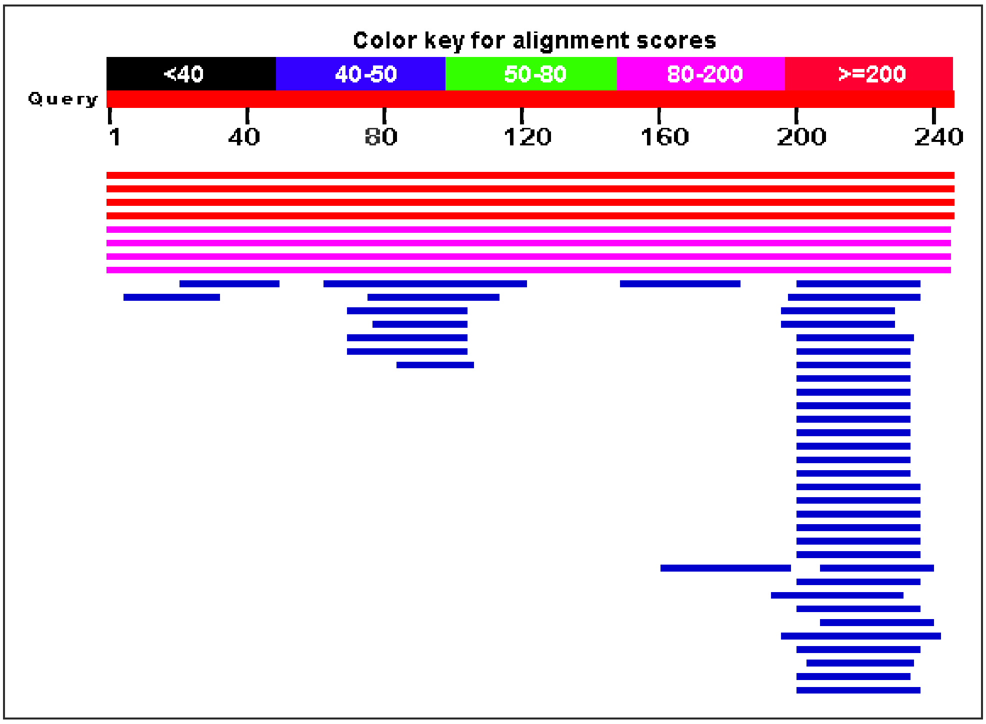
HMF1EA_S2S_Clone2

RID BSMJJETB014 (Expires on 02-12 16:20 pm)

Query ID	lcl|Query_238417	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	246		

Graphic Summary

Distribution of 50 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Burkholderia xenovorans LB400 chromosome 3, complete sequence	430	430	100%	6e-117	99%	CP008761.1
Burkholderia xenovorans LB400 chromosome 3, complete sequence	430	430	100%	6e-117	99%	CP000272.1
Burkholderia phytofirmans PsJN chromosome 1, complete sequence	322	322	100%	2e-84	89%	CP001052.1
Burkholderia gladioli strain ATCC 10248 chromosome 1, complete sequence	282	282	100%	2e-72	85%	CP009323.1
Burkholderia cenocepacia MC0-3 chromosome 2, complete sequence	158	158	99%	6e-35	74%	CP000959.1
Burkholderia cenocepacia J2315 chromosome 2, complete genome	154	154	99%	7e-34	74%	AM747721.1
Burkholderia cepacia strain DDS 7H-2 chromosome 2, complete sequence	149	149	99%	3e-32	73%	CP007786.1
Burkholderia cenocepacia strain ST32 chromosome 2, complete sequence	136	136	99%	2e-28	72%	CP011918.1
Streptomyces fulvissimus DSM 40593, complete genome	48.2	48.2	14%	0.073	89%	CP005080.1
Kibdelosporangium phytohabitans strain KLBMP1111, complete genome	46.4	46.4	15%	0.25	87%	CP012752.1
Eggerthella sp. YY7918 DNA, complete genome	46.4	46.4	14%	0.25	89%	AP012211.1
Ralstonia pickettii DTP0602 chromosome 1, complete sequence	44.6	44.6	23%	0.89	78%	CP006667.1
Streptomyces ahygroscopicus subsp. wuzhouensis tetramycin biosynthetic gene cluster, complete sequence	44.6	44.6	13%	0.89	91%	JX827252.1
Streptomyces hygrospinosus strain beijingensis tetramycin gene cluster, complete sequence	44.6	44.6	13%	0.89	91%	JN688154.1
Gordonibacter pamelaeae 7-10-1-b draft genome	44.6	44.6	13%	0.89	88%	FP929047.1
Thioalkalivibrio sulfidophilus HL-EbGr7, complete genome	44.6	44.6	15%	0.89	87%	CP001339.1
Mus musculus chromosome 7, clone RP23-285C18, complete sequence	44.6	44.6	11%	0.89	93%	AC158749.5
Ralstonia solanacearum genome assembly 9 genomes, chromosome : IV	42.8	42.8	13%	3.1	88%	LN899822.1
Ralstonia solanacearum genome assembly 9 genomes, chromosome : II	42.8	42.8	13%	3.1	88%	LN899820.1
Ralstonia solanacearum genome assembly 9 genomes, chromosome : IX	42.8	42.8	13%	3.1	88%	LN899827.1
Ralstonia solanacearum genome assembly 9 genomes, chromosome : VIII	42.8	42.8	13%	3.1	88%	LN899826.1
Ralstonia solanacearum genome assembly 9 genomes, chromosome : VII	42.8	42.8	13%	3.1	88%	LN899825.1
Ralstonia solanacearum genome assembly 9 genomes, chromosome : VI	42.8	42.8	13%	3.1	88%	LN899824.1
Ralstonia solanacearum genome assembly 9 genomes, chromosome : V	42.8	42.8	13%	3.1	88%	LN899823.1

Ralstonia solanacearum genome assembly 9 genomes, chromosome : III	42.8	42.8	13%	3.1	88%	LN899821.1
Ralstonia solanacearum strain YC45, complete genome	42.8	42.8	13%	3.1	88%	CP011997.1
Azoarcus sp. CIB, complete genome	42.8	42.8	13%	3.1	88%	CP011072.1
Enterobacter cloacae strain GGT036, complete genome	42.8	42.8	14%	3.1	89%	CP009756.1
Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei, scaffold SPER_scaffold0195741	42.8	42.8	11%	3.1	93%	LN247851.1
Spathaspora passalidarum NRRL Y-27907 hypothetical protein (SPAPADRAFT_63283), mRNA	42.8	42.8	11%	3.1	93%	XM_007377357.1
Kutzneria albida DSM 43870, complete genome	42.8	42.8	14%	3.1	86%	CP007155.1
Amycolatopsis mediterranei RB, complete genome	42.8	42.8	14%	3.1	86%	CP003777.1
Streptomyces rapamycinicus NRRL 5491 genome	42.8	42.8	14%	3.1	86%	CP006567.1
Mycobacterium smegmatis JS623, complete genome	42.8	42.8	14%	3.1	86%	CP003078.1
Amycolatopsis mediterranei S699, complete genome	42.8	42.8	14%	3.1	86%	CP003729.1
Enterobacter cloacae subsp. dissolvens SDM, complete genome	42.8	42.8	14%	3.1	89%	CP003678.1
Amycolatopsis mediterranei S699, complete genome	42.8	42.8	14%	3.1	86%	CP002896.1
Delftia sp. Cs1-4, complete genome	42.8	42.8	13%	3.1	88%	CP002735.1
Amycolatopsis mediterranei U32, complete genome	42.8	42.8	14%	3.1	86%	CP002000.1
Hyphomicrobium denitrificans ATCC 51888, complete genome	42.8	42.8	15%	3.1	84%	CP002083.1
Enterobacter cloacae subsp. cloacae ATCC 13047, complete genome	42.8	42.8	14%	3.1	89%	CP001918.1
Citrobacter rodentium ICC168, complete genome	42.8	42.8	9%	3.1	100%	FN543502.1
Streptomyces griseus subsp. griseus NBRC 13350 DNA, complete genome	42.8	42.8	14%	3.1	86%	AP009493.1
Delftia acidovorans SPH-1, complete genome	42.8	42.8	13%	3.1	88%	CP000884.1
Anopheles gambiae str. PEST AGAP008667-PA (AgaP_AGAP008667) mRNA, complete cds	42.8	42.8	18%	3.1	80%	XM_314766.4
Streptomyces avermitilis MA-4680 = NBRC 14893 DNA, complete genome	42.8	42.8	14%	3.1	86%	BA000030.3
Monosiga brevicollis clone JGIACYI-117E12, complete sequence	42.8	42.8	12%	3.1	90%	AC198956.1
Ralstonia solanacearum GMI1000 chromosome complete sequence	42.8	42.8	13%	3.1	88%	AL646052.1
Ralstonia eutropha JMP134 chromosome 1, complete sequence	42.8	42.8	15%	3.1	87%	CP000090.1
Streptomyces avermitilis oligomycin biosynthetic gene cluster	42.8	42.8	14%	3.1	86%	AB070940.1

Alignments

Burkholderia xenovorans LB400 chromosome 3, complete sequence

Sequence ID: **gb|CP008761.1|** Length: 1471816 Number of Matches: 1

Range 1: 607400 to 607645

Score	Expect	Identities	Gaps	Strand	Frame
430 bits(476)	6e-117()	243/246(99%)	0/246(0%)	Plus/Plus	

Features:

```
Query  1       ACGGTATCGTCGGTAAGGTCATTGTTGTTGGTTACCCTTTCATACTGGAGATAGAGCTTC  60
               ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  607400  ACGGTATCGTCGGTAAGGTCATTGTTGTTGGTTACCCTTTCGTACTGGAGATAGAGCTTC  607459
Query  61      ACCGCCTGCAGGCGATACGCCGCACCAGCCAGCCACGCCGTCTGCTCCGTGGCGCCGTTG  120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  607460  ACCGCCTGCAGGCGATACGCCGCACCAGCCAGCCACGCCGTCTGCTCCGTGGCGCCGTTG  607519
Query  121     AGGAAAAGCGACGCAGTGTGAAGACTCTGGATTGCGGCGGTCGCCGAGAACAGTCCCGCG  180
               ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  607520  AGGAAAAGCGACGCAGTGTGAAGACTCTGGATTGCGGCGGTCGCCGAGAACGGTCCCGCG  607579
Query  181     AAGTAGAGCACGTTCACACTGTAGTTCGCCTGCCCGGCGTGGCCCGCGATGCCCGCATTG  240
               ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  607580  AAGTAGAGCACGTTCGCACTGTAGTTCGCCTGCCCGGCGTGGCCCGCGATGCCCGCATTG  607639
Query  241     CTGTAC  246
               ||||||
Sbjct  607640  CTGTAC  607645
```

Burkholderia xenovorans LB400 chromosome 3, complete sequence
Sequence ID: **gb|CP000272.1|** Length: 1471779 Number of Matches: 1
Range 1: 461620 to 461865

Score	Expect	Identities	Gaps	Strand	Frame
430 bits(476)	6e-117()	243/246(99%)	0/246(0%)	Plus/Minus	

Features:

```
Query  1       ACGGTATCGTCGGTAAGGTCATTGTTGTTGGTTACCCTTTCATACTGGAGATAGAGCTTC  60
               ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  461865  ACGGTATCGTCGGTAAGGTCATTGTTGTTGGTTACCCTTTCGTACTGGAGATAGAGCTTC  461806
Query  61      ACCGCCTGCAGGCGATACGCCGCACCAGCCAGCCACGCCGTCTGCTCCGTGGCGCCGTTG  120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  461805  ACCGCCTGCAGGCGATACGCCGCACCAGCCAGCCACGCCGTCTGCTCCGTGGCGCCGTTG  461746
Query  121     AGGAAAAGCGACGCAGTGTGAAGACTCTGGATTGCGGCGGTCGCCGAGAACAGTCCCGCG  180
               ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  461745  AGGAAAAGCGACGCAGTGTGAAGACTCTGGATTGCGGCGGTCGCCGAGAACGGTCCCGCG  461686
Query  181     AAGTAGAGCACGTTCACACTGTAGTTCGCCTGCCCGGCGTGGCCCGCGATGCCCGCATTG  240
               ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  461685  AAGTAGAGCACGTTCGCACTGTAGTTCGCCTGCCCGGCGTGGCCCGCGATGCCCGCATTG  461626
Query  241     CTGTAC  246
               ||||||
Sbjct  461625  CTGTAC  461620
```

Burkholderia phytofirmans PsJN chromosome 1, complete sequence
Sequence ID: **gb|CP001052.1|** Length: 4467537 Number of Matches: 1
Range 1: 170181 to 170426

Score	Expect	Identities	Gaps	Strand	Frame
322 bits(356)	2e-84()	219/246(89%)	0/246(0%)	Plus/Minus	

Features:

```
Query  1       ACGGTATCGTCGGTAAGGTCATTGTTGTTGGTTACCCTTTCATACTGGAGATAGAGCTTC  60
               |||||||||||||| || || ||||||||||| ||||  ||||||||||||||||||||
Sbjct  170426  ACGGTATCGTCGGTGAGCTCGTTGTTGTTGGTCACCCGCTCATACTGGAGATAGAGCTTT  170367
Query  61      ACCGCCTGCAGGCGATACGCCGCACCAGCCAGCCACGCCGTCTGCTCCGTGGCGCCGTTG  120
               |||||||||||||||||||| || ||  |||||||||| ||||| ||||||||||||||
Sbjct  170366  ACCGCCTGCAGGCGATACGCGGCGCCGACCAGCCACGCTGTCTGTTCCGTGGCGCCGTTC  170307
Query  121     AGGAAAAGCGACGCAGTGTGAAGACTCTGGATTGCGGCGGTCGCCGAGAACAGTCCCGCG  180
               |||||||||||||| ||||| || ||||||| |||||| ||||| || ||| | |||||
Sbjct  170306  AGGAAAAGCGACGCGGTGTGCAGGCTCTGGACTGCGGCCGTCGCAGAAAACGGCCCCGCA  170247
Query  181     AAGTAGAGCACGTTCACACTGTAGTTCGCCTGCCCGGCGTGGCCCGCGATGCCCGCATTG  240
               ||||||||||||||| |||||||||| |||||||||||||||||||||| ||||||||||
Sbjct  170246  AAGTAGAGCACGTTCGCACTGTAGTTTGCCTGCCCGGCGTGGCCCGCGACGCCCGCATTG  170187
Query  241     CTGTAC  246
               ||||||
Sbjct  170186  CTGTAC  170181
```

Burkholderia gladioli strain ATCC 10248 chromosome 1, complete sequence
Sequence ID: **gb|CP009323.1|** Length: 4668573 Number of Matches: 1
Range 1: 78469 to 78714

Score	Expect	Identities	Gaps	Strand	Frame
282 bits(312)	2e-72()	210/246(85%)	0/246(0%)	Plus/Plus	

Features:
gram-negative porin family protein

```
Query  1      ACGGTATCGTCGGTAAGGTCATTGTTGTTGGTTACCCTTTCATACTGGAGATAGAGCTTC  60
              ||||||||||||||||| |||||||||||||| || |  || |||| || |||||||||
Sbjct  78469  ACGGTATCGTCGGTAAGCTCATTGTTGTTGGTCACACGCTCGTACTCGAAATAGAGCTTT  78528

Query  61     ACCGCCTGCAGGCGATACGCCGCACCAGCCAGCCACGCCGTCTGCTCCGTGGCGCCGTTG  120
              ||||||||||| |||||||| || ||  | |||||||||||||| ||||||||||| ||
Sbjct  78529  ACCGCCTGCAGACGATACGCGGCTCCGACGAGCCACGCCGTCTGTTCCGTGGCGCCATTC  78588

Query  121    AGGAAAAGCGACGCAGTGTGAAGACTCTGGATTGCGGCGGTCGCCGAGAACAGTCCCGCG  180
              || ||||||||||| ||||| || ||||||| |||| |||| || || ||| | ||||||
Sbjct  78589  AGAAAAAGCGACGCCGTGTGGAGGCTCTGGACTGCTGCGGTTGCGGAAAACGGCCCCGCG  78648

Query  181    AAGTAGAGCACGTTCACACTGTAGTTCGCCTGCCCGGCGTGGCCCGCGATGCCCGCATTG  240
              ||||| ||||||||| | ||||||||||||||||| || || ||||||| ||||||||||
Sbjct  78649  AAGTAAAGCACGTTCGCGCTGTAGTTCGCCTGCCCTGCATGCCCCGCGACGCCCGCATTG  78708

Query  241    CTGTAC  246
              ||||||
Sbjct  78709  CTGTAC  78714
```

Burkholderia cenocepacia MC0-3 chromosome 2, complete sequence
Sequence ID: **gb|CP000959.1|** Length: 3213911 Number of Matches: 1
Range 1: 1213614 to 1213858

Score	Expect	Identities	Gaps	Strand	Frame
158 bits(174)	6e-35()	182/245(74%)	0/245(0%)	Plus/Plus	

Features:

```
Query  1        ACGGTATCGTCGGTAAGGTCATTGTTGTTGGTTACCCTTTCATACTGGAGATAGAGCTTC  60
                ||||| |||||||| | ||   | |||| | | ||||  || |||||||    |||||||
Sbjct  1213614  ACGGTGTCGTCGGTCACGTTGCTATTGTCGCTCACCCGCTCGTACTGGAACATGAGCTTC  1213673

Query  61       ACCGCCTGCAGGCGATACGCCGCACCAGCCAGCCACGCCGTCTGCTCCGTGGCGCCGTTG  120
                   || || |  ||||| ||  | ||  | ||||| ||||| ||  |||| || || ||
Sbjct  1213674  GTTGCGTGGATCCGATAGGCACCGCCGACAAGCCATGCCGTTTGTGCCGTCGCACCATTC  1213733

Query  121      AGGAAAAGCGACGCAGTGTGAAGACTCTGGATTGCGGCGGTCGCCGAGAACAGTCCCGCG  180
                || ||||||||||| ||||| ||||| || | |||||| || ||||| |||   || |||
Sbjct  1213734  AGAAAAAGCGACGCTGTGTGCAGACTTTGCACTGCGGCCGTTGCCGAAAACGCACCGGCG  1213793

Query  181      AAGTAGAGCACGTTCACACTGTAGTTCGCCTGCCCGGCGTGGCCCGCGATGCCCGCATTG  240
                ||||| ||||||||  |||| |||||||||||||| | |||||| || |  |||||||||
Sbjct  1213794  AAGTAAAGCACGTTGGCACTATAGTTCGCCTGCCCAGTGTGGCCGGCCACACCCGCATTG  1213853

Query  241      CTGTA  245
                || ||
Sbjct  1213854  CTATA  1213858
```

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NCBI/ BLAST/ blastn suite/ **Formatting Results - BSMKKHTD014**
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Blast report description

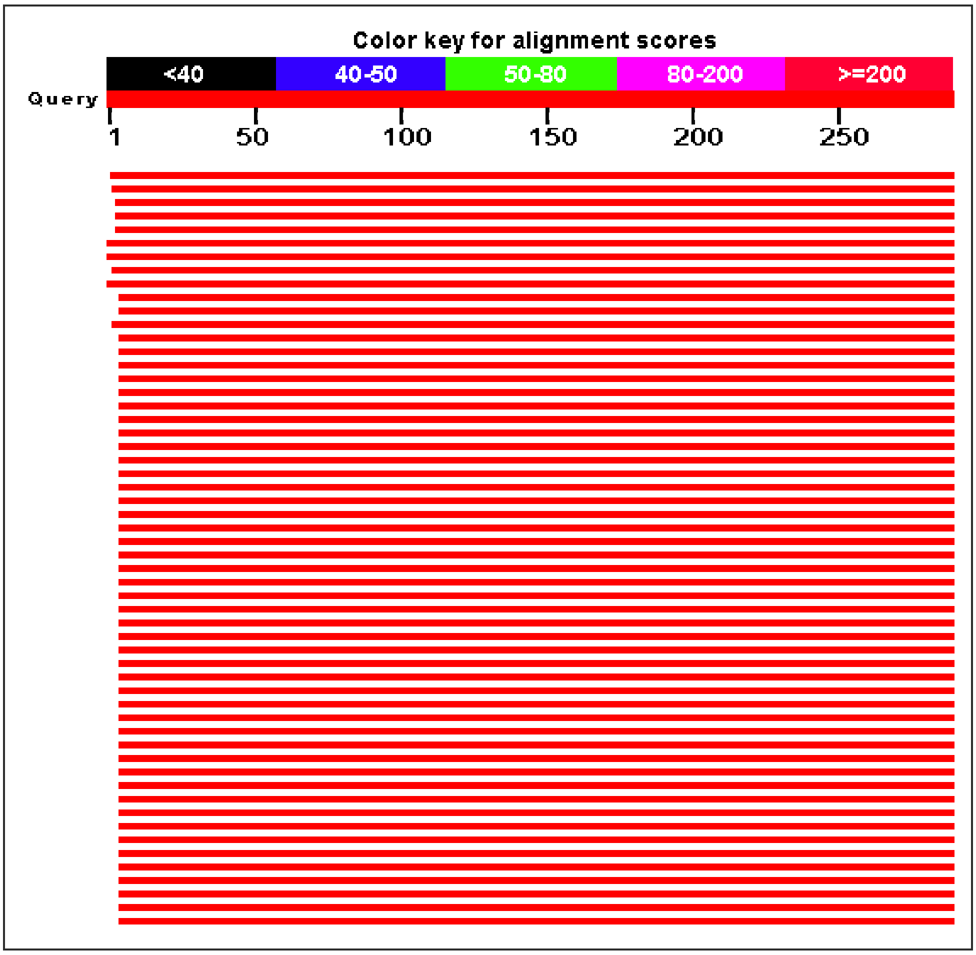
HMF1EA_S2S_Clone3

RID BSMKKHTD014 (Expires on 02-12 16:20 pm)

Query ID	lcl|Query_31119	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	289		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Burkholderia fungorum strain ATCC BAA-463 chromosome 2, complete sequence	493	493	99%	7e-136	98%	CP010027.1
Burkholderia phytofirmans PsJN chromosome 2, complete sequence	410	410	99%	7e-111	92%	CP001053.1
Burkholderia sp. HB1, complete sequence	408	408	98%	2e-110	92%	CP012193.1
Burkholderia xenovorans LB400 chromosome 2, complete sequence	408	408	98%	2e-110	92%	CP008762.1
Burkholderia xenovorans LB400 chromosome 2, complete sequence	408	408	98%	2e-110	92%	CP000271.1
Burkholderia phenoliruptrix BR3459a chromosome 2, complete sequence	405	405	100%	3e-109	91%	CP003864.1
Burkholderia sp. CCGE1001 chromosome 2, complete sequence	405	405	100%	3e-109	91%	CP002520.1
Burkholderia sp. CCGE1003 chromosome 2, complete sequence	401	401	99%	3e-108	91%	CP002218.1
Burkholderia ubonensis MSMB22 chromosome I, complete sequence	399	399	100%	1e-107	91%	CP009488.1
Burkholderia oklahomensis C6786 chromosome I, complete sequence	379	379	98%	1e-101	89%	CP009555.1
Burkholderia oklahomensis strain EO147 chromosome 1, complete sequence	379	379	98%	1e-101	89%	CP008726.1
Burkholderia caribensis MBA4 chromosome 1, complete sequence	374	374	99%	5e-100	89%	CP012746.1
Burkholderia pseudomallei strain Bp1651 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP012041.1
Burkholderia pseudomallei strain 982 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP012576.1
Burkholderia pseudomallei strain vgh16W chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP012517.1
Burkholderia pseudomallei strain vgh16R chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP012515.1
Burkholderia mallei strain 2002721276 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP010065.1
Burkholderia mallei strain KC_1092 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP009942.1
Burkholderia mallei strain 2002734306 chromosome I, complete sequence	370	370	98%	6e-99	89%	CP009707.1
Burkholderia mallei strain India86-567-2 chromosome I, complete sequence	370	370	98%	6e-99	89%	CP009642.1
Burkholderia mallei strain 11 chromosome I, complete sequence	370	370	98%	6e-99	89%	CP009587.1
Burkholderia pseudomallei strain PHLS 112 chromosome I, complete sequence	370	370	98%	6e-99	89%	CP009585.1
Burkholderia pseudomallei PB08298010 chromosome I, complete sequence	370	370	98%	6e-99	89%	CP009551.1
Burkholderia pseudomallei K96243 chromosome I, complete sequence	370	370	98%	6e-99	89%	CP009538.1
Burkholderia pseudomallei 7894 chromosome I, complete sequence	370	370	98%	6e-99	89%	CP009535.1
Burkholderia pseudomallei MSHR2543 chromosome I, complete sequence	370	370	98%	6e-99	89%	CP009478.1
Burkholderia pseudomallei MSHR491 chromosome I, complete sequence	370	370	98%	6e-99	89%	CP009485.1
Burkholderia pseudomallei MSHR840 chromosome I, complete sequence	370	370	98%	6e-99	89%	CP009474.1

Burkholderia mallei strain 2002734299 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP009337.1
Burkholderia pseudomallei 406e chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP009298.1
Burkholderia pseudomallei 1026b chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP004379.1
Burkholderia pseudomallei strain vgh07 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP010973.1
Burkholderia mallei strain 2000031063 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP008732.2
Burkholderia pseudomallei TSV 48 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP009161.1
Burkholderia pseudomallei B03 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP009151.1
Burkholderia pseudomallei A79A chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP009165.1
Burkholderia pseudomallei MSHR3965 chromosome 1 sequence	370	370	98%	6e-99	89%	CP009153.1
Burkholderia pseudomallei MSHR62 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP009235.1
Burkholderia pseudomallei MSHR2243 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP009270.1
Burkholderia pseudomallei MSHR1153 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP009271.1
Burkholderia pseudomallei NAU35A-3 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP004377.1
Burkholderia sp. BGK chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP008916.1
Burkholderia mallei NCTC 10247 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP007802.1
Burkholderia mallei strain FMH 23344 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP009148.1
Burkholderia pseudomallei strain BSR chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP009128.1
Burkholderia pseudomallei HBPUB10134a chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP008911.1
Burkholderia pseudomallei MSHR5848 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP008909.1
Burkholderia pseudomallei MSHR5855 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP008784.1
Burkholderia pseudomallei strain BGR chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP008834.1
Burkholderia pseudomallei strain Mahidol-1106a chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP008781.1
Burkholderia pseudomallei strain MSHR346, complete sequence	370	370	98%	6e-99	89%	CP008764.1
Burkholderia pseudomallei strain MSHR1655 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP008780.1
Burkholderia pseudomallei 576 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP008777.1
Burkholderia pseudomallei strain 1106a chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP008758.1
Burkholderia mallei strain BMQ chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP008723.1
Burkholderia mallei strain 6 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP008711.1
Burkholderia mallei strain 23344 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP008704.1
Burkholderia pseudomallei genome assembly BP_3921g, chromosome : 1	370	370	98%	6e-99	89%	LK936442.1
Burkholderia pseudomallei MSHR146 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP004042.1
Burkholderia pseudomallei MSHR511	370	370	98%	6e-99	89%	CP004023.1

chromosome 1, complete sequence						
Burkholderia pseudomallei NAU20B-16 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP004003.1
Burkholderia pseudomallei NCTC 13179 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP003976.1
Burkholderia thailandensis MSMB121 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP004095.1
Burkholderia pseudomallei BPC006 chromosome I, complete sequence	370	370	98%	6e-99	89%	CP003781.1
Burkholderia pseudomallei 1026b chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP002833.1
Burkholderia pseudomallei MSHR346 chromosome I, complete sequence	370	370	98%	6e-99	89%	CP001408.1
Burkholderia mallei NCTC 10247 chromosome I, complete sequence	370	370	98%	6e-99	89%	CP000548.1
Burkholderia pseudomallei 1106a chromosome I, complete sequence	370	370	98%	6e-99	89%	CP000572.1
Burkholderia mallei NCTC 10229 chromosome I, complete sequence	370	370	98%	6e-99	89%	CP000546.1
Burkholderia mallei SAVP1 chromosome I, complete sequence	370	370	98%	6e-99	89%	CP000526.1
Burkholderia mallei ATCC 23344 chromosome 1, complete sequence	370	370	98%	6e-99	89%	CP000010.1
Burkholderia pseudomallei 1710b chromosome I, complete sequence	370	370	98%	6e-99	89%	CP000124.1
Burkholderia pseudomallei strain K96243, chromosome 1, complete sequence	370	370	98%	6e-99	89%	BX571965.1
Burkholderia sp. Bp5365 strain MSMB43 chromosome 1, complete sequence	365	365	98%	3e-97	88%	CP013380.1
Burkholderia pseudomallei strain 350105 chromosome 1 sequence	365	365	98%	3e-97	88%	CP012094.1
Burkholderia sp. 2002721687 chromosome I, complete sequence	365	365	98%	3e-97	88%	CP009549.1
Burkholderia thailandensis 34 chromosome 1, complete sequence	365	365	98%	3e-97	88%	CP010017.1
Burkholderia pseudomallei Pasteur 52237 chromosome 1, complete sequence	365	365	98%	3e-97	88%	CP009899.1
Burkholderia thailandensis 2002721643 chromosome I, complete sequence	365	365	98%	3e-97	88%	CP009601.1
Burkholderia pseudomallei strain MSHR668 chromosome I, complete sequence	365	365	98%	3e-97	88%	CP009545.1
Burkholderia thailandensis strain 2003015869 chromosome 1, complete sequence	365	365	98%	3e-97	88%	CP008914.2
Burkholderia pseudomallei K42 chromosome 1, complete sequence	365	365	98%	3e-97	88%	CP009162.1
Burkholderia sp. TSV202 chromosome 1, complete sequence	365	365	98%	3e-97	88%	CP009157.1
Burkholderia thailandensis E254 chromosome 1, complete sequence	365	365	98%	3e-97	88%	CP004381.1
Burkholderia thailandensis MSMB59 chromosome 1, complete sequence	365	365	98%	3e-97	88%	CP004385.1
Burkholderia pseudomallei strain BDP chromosome 1, complete sequence	365	365	98%	3e-97	88%	CP009209.1
Burkholderia pseudomallei HBPUB10303a chromosome 1, complete sequence	365	365	98%	3e-97	88%	CP008894.1
Burkholderia pseudomallei MSHR5858 chromosome 1, complete sequence	365	365	98%	3e-97	88%	CP008892.1
Burkholderia thailandensis E264 chromosome 1, complete sequence	365	365	98%	3e-97	88%	CP008785.1
Burkholderia pseudomallei strain 9 chromosome 1, complete sequence	365	365	98%	3e-97	88%	CP008755.1
Burkholderia thailandensis USAMRU Malaysia #20 chromosome 1, complete	365	365	98%	3e-97	88%	CP004383.1

sequence						
Burkholderia pseudomallei MSHR520 chromosome 1, complete sequence	365	365	98%	3e-97	88%	CP004368.1
Burkholderia thailandensis E444 chromosome 1, complete sequence	365	365	98%	3e-97	88%	CP004117.1
Burkholderia thailandensis 2002721723 chromosome 1, complete sequence	365	365	98%	3e-97	88%	CP004097.1
Burkholderia thailandensis H0587 chromosome 1, complete sequence	365	365	98%	3e-97	88%	CP004089.1
Burkholderia pseudomallei NCTC 13178 chromosome 1, complete sequence	365	365	98%	3e-97	88%	CP004001.1
Burkholderia pseudomallei MSHR305 chromosome 1, complete sequence	365	365	98%	3e-97	88%	CP006470.1
Burkholderia pseudomallei 668 chromosome I, complete sequence	365	365	98%	3e-97	88%	CP000570.1
Burkholderia thailandensis E264 chromosome I, complete sequence	365	365	98%	3e-97	88%	CP000086.1
Achromobacter denitrificans strain USDA-ARS-USMARC-56712, complete genome	360	360	99%	1e-95	88%	CP013923.1

Alignments

Burkholderia fungorum strain ATCC BAA-463 chromosome 2, complete sequence
Sequence ID: **gb|CP010027.1|** Length: 3508455 Number of Matches: 1
Range 1: 477005 to 477292

Score	Expect	Identities	Gaps	Strand	Frame
493 bits(546)	7e-136()	282/288(98%)	0/288(0%)	Plus/Plus	

Features:
methylmalonate-semialdehyde dehydrogenase

```
Query  2       CTTACTTCGCAACCGGCATCGTGAACTCCGCACCCTTCGCGATGCTGTCCGGCCAACGCT  61
               |||||||||| ||||||||||||||||||||||||||||||||||| |||||||| ||||
Sbjct  477005  CTTACTTCGCGACCGGCATCGTGAACTCCGCACCCTTCGCGATGCTATCCGGCCAGCGCT  477064

Query  62      GCATGATGCTCTTGTAGCGCGTATAGAAACGCACGCCTTCTTCGCCGTACGCGTGGTGGT  121
               ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  477065  GCATGATGCTCTTGTAGCGCGTATAGAAACGCACGCCTTCTTCGCCGTATGCGTGGTGGT  477124

Query  122     CGCCGAACAGCGAGCGCTTCCAGCCGCCGAACGAGTGCCATGCCATCGGCACCGGAATCG  181
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  477125  CGCCGAACAGCGAGCGCTTCCAGCCGCCGAACGAGTGCCATGCCATCGGCACCGGAATCG  477184

Query  182     GTACGTTGATACCGACCATACCCACCTGAATCTGCCGGCCGAATACGCGCGCCACGCCGC  241
               |||||||||||||||||||||||||||||||||| ||||||||| |||||||||||||||
Sbjct  477185  GTACGTTGATACCGACCATACCCACCTGAATCTGTCGGCCGAATGCGCGCGCCACGCCGC  477244

Query  242     CGTCCGACGTGAAGAGGGACACGCCGTTGCCGAACTCGTGCGCGTTGA  289
               ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  477245  CGTCCGACGTGAAGAGGGACACGCCGTTGCCGAACTCGTGCGCGTTGA  477292
```

Burkholderia phytofirmans PsJN chromosome 2, complete sequence
Sequence ID: **gb|CP001053.1|** Length: 3625999 Number of Matches: 1
Range 1: 2017055 to 2017341

Score	Expect	Identities	Gaps	Strand	Frame
410 bits(454)	7e-111()	263/287(92%)	0/287(0%)	Plus/Plus	

Features:

```
Query  3        TTACTTCGCAACCGGCATCGTGAACTCCGCACCCTTCGCGATGCTGTCCGGCCAACGCTG  62
                ||||||||| ||||||||||| || || |||||||| || ||||| |||||||| |||||
Sbjct  2017055  TTACTTCGCCACCGGCATCGTAAATTCGGCACCCTTGGCAATGCTATCCGGCCAGCGCTG  2017114

Query  63       CATGATGCTCTTGTAGCGCGTATAGAAACGCACGCCTTCTTCGCCGTACGCGTGGTGGTC  122
                ||||||||||||||||||||||||||| |||||||| ||||||||||| ||||| || ||
Sbjct  2017115  CATGATGCTCTTGTAGCGCGTATAGAAGCGCACGCCCTCTTCGCCGTAAGCGTGATGATC  2017174

Query  123      GCCGAACAGCGAGCGCTTCCAGCCGCCGAACGAGTGCCATGCCATCGGCACCGGAATCGG  182
                |||||||||||| |||||||||||||||||||| ||||| ||||||||||||||||||||
Sbjct  2017175  GCCGAACAGCGAACGCTTCCAGCCGCCGAACGAATGCCACGCCATCGGCACCGGAATCGG  2017234

Query  183      TACGTTGATACCGACCATACCCACCTGAATCTGCCGGCCGAATACGCGCGCCACGCCGCC  242
                 |||||||| |||||||| |||||||||||||||||||||||  |||||||||| |||||
Sbjct  2017235  CACGTTGATGCCGACCATGCCCACCTGAATCTGCCGGCCGAACGCGCGCGCCACACCGCC  2017294

Query  243      GTCCGACGTGAAGAGGGACACGCCGTTGCCGAACTCGTGCGCGTTGA  289
                |||||| |||||||| |||||||||||||||||||||||||||||||
Sbjct  2017295  GTCCGAGGTGAAGAGCGACACGCCGTTGCCGAACTCGTGCGCGTTGA  2017341
```

Burkholderia sp. HB1, complete sequence

Sequence ID: **gb|CP012193.1|** Length: 3124497 Number of Matches: 1
Range 1: 743400 to 743685

Score	Expect	Identities	Gaps	Strand	Frame
408 bits(452)	2e-110()	262/286(92%)	0/286(0%)	Plus/Plus	

Features:
methylmalonate-semialdehyde dehydrogenase

```
Query  4       TACTTCGCAACCGGCATCGTGAACTCCGCACCCTTCGCGATGCTGTCCGGCCAACGCTGC  63
               ||||||||||| ||||||||||| ||||| ||||||||||||||||| ||||||||||||
Sbjct  743400  TACTTCGCAACAGGCATCGTGAATTCCGCGCCCTTCGCGATGCTGTCGGGCCAACGCTGC  743459

Query  64      ATGATGCTCTTGTAGCGCGTATAGAAACGCACGCCTTCTTCGCCGTACGCGTGGTGGTCG  123
               |||||||||||||||||||||||||| |||||||| |||||||||||||| ||||| |||
Sbjct  743460  ATGATGCTCTTGTAGCGCGTATAGAAGCGCACGCCCTCTTCGCCGTACGCATGGTGATCG  743519

Query  124     CCGAACAGCGAGCGCTTCCAGCCGCCGAACGAGTGCCATGCCATCGGCACCGGAATCGGT  183
               ||||||||||| |||||||||||||| ||||| ||||||||||||||||||||||| ||
Sbjct  743520  CCGAACAGCGACCGCTTCCAGCCGCCAAACGAATGCCATGCCATCGGCACCGGAATGGGC  743579

Query  184     ACGTTGATACCGACCATACCCACCTGAATCTGCCGGCCGAATACGCGCGCCACGCCGCCG  243
               |||||||| |||||||| || ||||||||||||||||||||  ||||||| |||||||||
Sbjct  743580  ACGTTGATGCCGACCATGCCGACCTGAATCTGCCGGCCGAACGCGCGCGCGACGCCGCCG  743639

Query  244     TCCGACGTGAAGAGGGACACGCCGTTGCCGAACTCGTGCGCGTTGA  289
               || ||||||||||| ||||||||||||||||| || || |||||||
Sbjct  743640  TCGGACGTGAAGAGCGACACGCCGTTGCCGAATTCATGTGCGTTGA  743685
```

Burkholderia xenovorans LB400 chromosome 2, complete sequence

Sequence ID: **gb|CP008762.1|** Length: 3363006 Number of Matches: 1
Range 1: 3252114 to 3252399

Score	Expect	Identities	Gaps	Strand	Frame
408 bits(452)	2e-110()	262/286(92%)	0/286(0%)	Plus/Plus	

Features:
methylmalonate-semialdehyde dehydrogenase

```
Query  4        TACTTCGCAACCGGCATCGTGAACTCCGCACCCTTCGCGATGCTGTCCGGCCAACGCTGC  63
                |||||||| ||||||||||| || || ||||| || |||||||| |||||||| ||||||
Sbjct  3252114  TACTTCGCCACCGGCATCGTAAATTCAGCACCTTTGGCGATGCTATCCGGCCAGCGCTGC  3252173

Query  64       ATGATGCTCTTGTAGCGCGTATAGAAACGCACGCCTTCTTCGCCGTACGCGTGGTGGTCG  123
                |||||||||||||||||||||||||| |||||||| ||||||||||| ||||| ||||||
Sbjct  3252174  ATGATGCTCTTGTAGCGCGTATAGAAGCGCACGCCCTCTTCGCCGTAAGCGTGATGGTCG  3252233

Query  124      CCGAACAGCGAGCGCTTCCAGCCGCCGAACGAGTGCCATGCCATCGGCACCGGAATCGGT  183
                ||||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  3252234  CCGAACAGCGAACGCTTCCAGCCGCCGAACGAATGCCATGCCATCGGCACCGGAATCGGC  3252293

Query  184      ACGTTGATACCGACCATACCCACCTGAATCTGCCGGCCGAATACGCGCGCCACGCCGCCG  243
                |||||||| |||||||| |||||||||||||||||||||||  |||||||||| |||||
Sbjct  3252294  ACGTTGATGCCGACCATGCCCACCTGAATCTGCCGGCCGAACGCGCGCGCCACCCCGCCA  3252353

Query  244      TCCGACGTGAAGAGGGACACGCCGTTGCCGAACTCGTGCGCGTTGA  289
                |||||||||||||| ||||||||||| ||||| |||||||||||||
Sbjct  3252354  TCCGACGTGAAGAGCGACACGCCGTTACCGAATTCGTGCGCGTTGA  3252399
```

Burkholderia xenovorans LB400 chromosome 2, complete sequence

Sequence ID: **gb|CP000271.1|** Length: 3363523 Number of Matches: 1
Range 1: 1142304 to 1142589

Score	Expect	Identities	Gaps	Strand	Frame
408 bits(452)	2e-110()	262/286(92%)	0/286(0%)	Plus/Minus	

Features:

```
Query  4        TACTTCGCAACCGGCATCGTGAACTCCGCACCCTTCGCGATGCTGTCCGGCCAACGCTGC  63
                |||||||| ||||||||||| || || ||||| || |||||||| |||||||| ||||||
Sbjct  1142589  TACTTCGCCACCGGCATCGTAAATTCAGCACCTTTGGCGATGCTATCCGGCCAGCGCTGC  1142530

Query  64       ATGATGCTCTTGTAGCGCGTATAGAAACGCACGCCTTCTTCGCCGTACGCGTGGTGGTCG  123
                |||||||||||||||||||||||||| |||||||| ||||||||||| ||||| ||||||
Sbjct  1142529  ATGATGCTCTTGTAGCGCGTATAGAAGCGCACGCCCTCTTCGCCGTAAGCGTGATGGTCG  1142470

Query  124      CCGAACAGCGAGCGCTTCCAGCCGCCGAACGAGTGCCATGCCATCGGCACCGGAATCGGT  183
                ||||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  1142469  CCGAACAGCGAACGCTTCCAGCCGCCGAACGAATGCCATGCCATCGGCACCGGAATCGGC  1142410

Query  184      ACGTTGATACCGACCATACCCACCTGAATCTGCCGGCCGAATACGCGCGCCACGCCGCCG  243
                |||||||| |||||||| |||||||||||||||||||||||  |||||||||| |||||
Sbjct  1142409  ACGTTGATGCCGACCATGCCCACCTGAATCTGCCGGCCGAACGCGCGCGCCACCCCGCCA  1142350

Query  244      TCCGACGTGAAGAGGGACACGCCGTTGCCGAACTCGTGCGCGTTGA  289
                |||||||||||||| ||||||||||| ||||| |||||||||||||
Sbjct  1142349  TCCGACGTGAAGAGCGACACGCCGTTACCGAATTCGTGCGCGTTGA  1142304
```

BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BSMMWWZW014**
Formatting options
Download
Blast report description

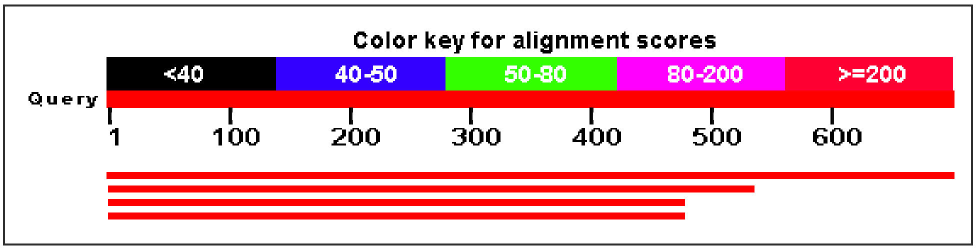
HMF1EA_S2S_Clone4

RID BSMMWWZW014 (Expires on 02-12 16:21 pm)

Query ID	lcl|Query_55877	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	697		

Graphic Summary

Distribution of 4 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Burkholderia fungorum strain ATCC BAA-463 chromosome 2, complete sequence	1178	1178	100%	0.0	98%	CP010027.1
Burkholderia sp. CCGE1002 chromosome 2, complete sequence	408	408	76%	6e-110	77%	CP002014.1
Burkholderia phenoliruptrix BR3459a chromosome 2, complete sequence	324	324	67%	2e-84	76%	CP003864.1
Burkholderia sp. CCGE1001 chromosome 2, complete sequence	324	324	67%	2e-84	76%	CP002520.1

Alignments

Burkholderia fungorum strain ATCC BAA-463 chromosome 2, complete sequence
Sequence ID: **gb|CP010027.1|** Length: 3508455 Number of Matches: 1
Range 1: 2138852 to 2139546

Score	Expect	Identities	Gaps	Strand	Frame
1178 bits(1306)	0.0()	680/697(98%)	2/697(0%)	Plus/Plus	

Features:
glycosyl transferases group 1 family proteinO-Antigen ligase family protein

```
Query  1        CGTATAAGCGCATCGATCTGATCGTGCGGGCCTTTTCACAGACACCTGAGCGCCGTCTTG  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2138852  CGTATAAGCGCATCGATCTGATCGTGCGGGCCTTTTCACAGACACCTGAGCGCCGTCTTG  2138911
Query  61       TCGTGATTGGCGACGGCCCTGAGATGAAGAAGATCAGGGCAGCGGCCGGCGAGAACGTCA  120
                |||||||||||||||| || ||||||||||||||||||||||||||||||||||||||||
Sbjct  2138912  TCGTGATTGGCGACGGTCCCGAGATGAAGAAGATCAGGGCAGCGGCCGGCGAGAACGTCA  2138971
Query  121      CGATCCTGGGTCATCAACCGTTCGATACGCTGGTCGATCATTTAAGGCGCGCGCGTGCGT  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2138972  CGATCCTGGGTCATCAACCGTTCGATACGCTGGTCGATCATTTAAGGCGCGCGCGTGCGT  2139031
Query  181      TCGTGTTTGCTGCAGAAGAAGACTTCGGTATCTCGGTGGTGGAGGCGCAGGCATGCGGAA  240
                ||||||||||||||||||||||||||||||| ||||| ||||||||||||||||||||||
Sbjct  2139032  TCGTGTTTGCTGCAGAAGAAGACTTCGGTATTTCGGTTGTGGAGGCGCAGGCATGCGGAA  2139091
Query  241      CGCCGGTGATCGCATTCGGCAGAGGCGGTGCGCTCGAATCCGTTATCGGCCTGCCACTTG  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2139092  CGCCGGTGATCGCATTCGGCAGAGGCGGTGCGCTCGAATCCGTTATCGGCCTGCCACTTG  2139151
Query  301      AACGGCCCACGGGCGTGTTCTTCGGGGAACAGACGCCAGAGTCATTGCTGGCCGCGGTAG  360
                ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2139152  AACGGCCTACGGGCGTGTTCTTCGGGGAACAGACGCCAGAGTCATTGCTGGCCGCGGTAG  2139211
Query  361      ACCGGTTTGAGCGCAACGCCGGCCTGTTCGATCCGCGGGCGTGCCGTAGAAACGCAGAGC  420
                 |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2139212  GCCGGTTTGAGCGGAACGCCGGCCTGTTCGATCCGCGGGCGTGCCGTAGAAACGCAGAGC  2139271
Query  421      GCTTTTCGTCGGAGAACTTCAAGACGGCGCTAACCAGCTTTATCGACTCACGACTCCCAT  480
                | |||||||||||||||||||||||||||||||||||||| ||||||||||| |||||||
Sbjct  2139272  GTTTTTCGTCGGAGAACTTCAAGACGGCGCTAACCAGCTTCATCGACTCACGGCTCCCAT  2139331
Query  481      ACGGAGGACTCGAACACTTCCTGCCGTATCCGGTGGCGAGCCAGCAACTGCCTGTCAATC  540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2139332  ACGGAGGACTCGAACACTTCCTGCCGTATCCGGTGGCGAGCCAGCAACTGCCTGTCAATC  2139391
Query  541      AGCGCCAGCATGCTGATGTGGTGTCGTGAGTACGAATGTGTGCGCCGGCGAATCTGATCT  600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2139392  AGCGCCAGCATGCTGATGTGGTGTCGTGAGTACGAATGTGTGCGCCGGCGAATCTGATCT  2139451
Query  601      AGGACGGAGTTCGCCGACGCCCGCCAGCAATCAGAGCAGCGNNNNGCNNNTTTTGACTTC  660
                |||||||||||||||||||||||||||||||||||||||||    ||   ||||||||||
Sbjct  2139452  AGGACGGAGTTCGCCGACGCCCGCCAGCAATCAGAGCAGCG-CGTGC-TCTTTTGACTTC  2139509
Query  661      TGCTGAAGATGATCGATCGCGGCATTGTTGACTGATC  697
                |||||||||||||||||||||||||||||||||||||
Sbjct  2139510  TGCTGAAGATGATCGATCGCGGCATTGTTGACTGATC  2139546
```

Burkholderia sp. CCGE1002 chromosome 2, complete sequence
Sequence ID: **gb|CP002014.1|** Length: 2593966 Number of Matches: 1
Range 1: 136722 to 137248

Score	Expect	Identities	Gaps	Strand	Frame
408 bits(452)	6e-110()	409/530(77%)	3/530(0%)	Plus/Plus	

Features:

```
Query  3       TATAAGCGCATCGATCTGATCGTGCGGGCCTTTTCACAGACACCTGAGCGCCGTCTTGTC  62
               |||||||| || ||||||||||| | ||| |||||||| || |||||||||   || |||
Sbjct  136722  TATAAGCGTATTGATCTGATCGTTCAGGCTTTTTCACAAACGCCTGAGCGCAAGCTGGTC  136781

Query  63      GTGATTGGCGACGGCCCTGAGATGAAGAAGATCAGGGCAGCGGCCGGCGAGAACGTCACG  122
               ||||| |||||||| || |||||||||||||||| ||| |  |||||||| ||||| | |
Sbjct  136782  GTGATCGGCGACGGTCCCGAGATGAAGAAGATCAAGGCGGTCGCCGGCGACAACGTGAAG  136841

Query  123     ATCCTGGGTCATCAACCGTTCGATACGCTGGTCGATCATTTAAGGCGCGCGCGTGCGTTC  182
               ||||| || ||||| |||| |||   ||||||||||||  |  | ||||||||||| |||
Sbjct  136842  ATCCTTGGGCATCAGCCGTCCGACGTGCTGGTCGATCACCTGCGTCGCGCGCGTGCATTC  136901

Query  183     GTGTTTGCTGCAGAAGAAGACTTCGGTATCTCGGTGGTGGAGGCGCAGGCATGCGGAACG  242
               |||||||| || |||||||| ||||| || || ||||| || |||||||||||||| |||
Sbjct  136902  GTGTTTGCGGCGGAAGAAGATTTCGGCATTTCCGTGGTCGAAGCGCAGGCATGCGGCACG  136961

Query  243     CCGGTGATCGCATTCGGCAGAGGCGGTGCGCTCGAATCCGTTATCGGCCTGCCACTTGAA  302
               |||||||| || |||||| | ||||| ||||| ||||| ||  | |   |||| || || 
Sbjct  136962  CCGGTGATAGCCTTCGGCCGCGGCGGCGCGCTTGAATCGGTGGTGGGATTGCCGCTCGAG  137021

Query  303     CGGCCCACGGGCGTGTTCTTCGGGGAACAGACGCCAGAGTCATTGCTGGCCGCGGTAGAC  362
               |||||||| || || |||||||| || || |   | | |||  |||| |  || ||   |
Sbjct  137022  CGGCCCACCGGGGTATTCTTCGGCGAGCAAAGCACCGCGTCCCTGCTCGAAGCCGTTATC  137081

Query  363     CGGTTTGAGCGCAACGCCGGCCTGTTCGATCCGCGGGCGTGCCGTAGAAACGCAGAGCGC  422
               || || ||  ||||||||| | | |||||| | ||||||||||| |  || || ||||||
Sbjct  137082  CGTTTCGAAAGCAACGCCGCCTTATTCGATGCACGGGCGTGCCGCAAGAATGCCGAGCGC  137141

Query  423     TTTTCGTCGGAGAACTTCAAGACGGCGCTAACCAGCTTTATCGACTCACGACTCCCATAC  482
               |||||||||||||||||||||| |||||| |   ||||  ||||  | || ||||| || 
Sbjct  137142  TTTTCGTCGGAGAACTTCAAGAAGGCGCTGATGGGCTTCGTCGATGCGCGGCTCCCTTAT  137201

Query  483     GGAGGACTCGAACACTTCCTGCCGTATCCGGTGGCGAGCCAGCAACTGCC  532
               |   |  ||||||| || || ||||||   | | ||||||||   |||||
Sbjct  137202  GCGTGCGTCGAACAGTTTCTTCCGTAT---GCGCCGAGCCAGTCGCTGCC  137248
```

Burkholderia phenoliruptrix BR3459a chromosome 2, complete sequence
Sequence ID: **gb|CP003864.1|** Length: 2713495 Number of Matches: 1
Range 1: 2131722 to 2132194

Score	Expect	Identities	Gaps	Strand	Frame
324 bits(358)	2e-84()	360/476(76%)	6/476(1%)	Plus/Plus	

Features:

```
Query  3        TATAAGCGCATCGATCTGATCGTGCGGGCCTTTTCACAGACACCTGAGCGCCGTCTTGTC  62
                |||||||||||||||||||||||||||||||| || ||||| ||||||||| | || || 
Sbjct  2131722  TATAAGCGCATCGATCTGATCGTGCGGGCCTTCTCGCAGACGCCTGAGCGCAGGCTCGTG  2131781

Query  63       GTGATTGGCGACGGCCCTGAGATGAAGAAGATCAGGGCAGCGGCCGGCGAGAACGTCACG  122
                ||||| ||||||||||| || ||||||    | |  ||    || ||   ||| || || 
Sbjct  2131782  GTGATCGGCGACGGCCCGGAAATGAAGCGCGTAAAAGCGCTTGCGGGGCCGAATGTGACC  2131841

Query  123      ATCCTGGGTCATCAACCGTTCGATACGCTGGTCGATCATTTAAGGCGCGCGCGTGCGTTC  182
                || || || ||||| ||  | ||   ||| || || || ||  | ||||| || || |||
Sbjct  2131842  ATACTCGGCCATCAGCCTCTGGACGTGCTCGTTGACCACTTGCGCCGCGCCCGCGCATTC  2131901

Query  183      GTGTTTGCTGCAGAAGAAGACTTCGGTATCTCGGTGGTGGAGGCGCAGGCATGCGGAACG  242
                || ||||| || ||||| |||||||| || || || || ||||||||||| ||||| |||
Sbjct  2131902  GTTTTTGCGGCGGAAGAGGACTTCGGGATTTCCGTCGTCGAGGCGCAGGCGTGCGGCACG  2131961

Query  243      CCGGTGATCGCATTCGGCAGAGGCGGTGCGCTCGAATCCGTTATCGGCCTGCCACTTGAA  302
                |||||||| ||||||||||| || || || ||||| ||||||||||||||||| || || 
Sbjct  2131962  CCGGTGATTGCATTCGGCAGGGGAGGCGCACTCGAGTCCGTTATCGGCCTGCCTCTCGAG  2132021

Query  303      CGGCCCACGGGCGTGTTCTTCGGGGAACAGACGCCAGAGTCATTGCTGGCCGCGGTAGAC  362
                | ||| |||||||| |||||||| || |||||  | |||||  ||||||  || || |||
Sbjct  2132022  CAGCCTACGGGCGTCTTCTTCGGCGAGCAGACAGCGGAGTCGCTGCTGGAGGCCGT-GAC  2132080

Query  363      -CGGTTTGAGCGCAACGCCGGCC--TGTTCGATCCGCGGGCGTGCCGTAGAAACGCAGAG  419
                 || || |||||||| ||  |||  | |||||||||  |   |||||    ||||| || 
Sbjct  2132081  GCGCTTCGAGCGCAATGC--GCCATTATTCGATCCGGTGAATTGCCGCCAGAACGCCGAA  2132138

Query  420      CGCTTTTCGTCGGAGAACTTCAAGACGGCGCTAACCAGCTTTATCGACTCACGACT  475
                || || ||| | |||||||||||||||||  | ||   ||| |||||| | || ||
Sbjct  2132139  CGATTCTCGACCGAGAACTTCAAGACGGCATTGACGGACTTCATCGACGCGCGGCT  2132194
```

Burkholderia sp. CCGE1001 chromosome 2, complete sequence
Sequence ID: **gb|CP002520.1|** Length: 2770302 Number of Matches: 1
Range 1: 2084245 to 2084717

Score	Expect	Identities	Gaps	Strand	Frame
324 bits(358)	2e-84()	360/476(76%)	6/476(1%)	Plus/Plus	

Features:

```
Query  3        TATAAGCGCATCGATCTGATCGTGCGGGCCTTTTCACAGACACCTGAGCGCCGTCTTGTC  62
                |||||||||||||||||||||||||||||||| || ||||| ||||||||| | || || 
Sbjct  2084245  TATAAGCGCATCGATCTGATCGTGCGGGCCTTCTCGCAGACGCCTGAGCGCAGGCTCGTG  2084304

Query  63       GTGATTGGCGACGGCCCTGAGATGAAGAAGATCAGGGCAGCGGCCGGCGAGAACGTCACG  122
                ||||| ||||||||||| || ||||||    | |  ||    || ||   ||| || || 
Sbjct  2084305  GTGATCGGCGACGGCCCGGAAATGAAGCGCGTAAAAGCGCTTGCGGGGCCGAATGTGACC  2084364

Query  123      ATCCTGGGTCATCAACCGTTCGATACGCTGGTCGATCATTTAAGGCGCGCGCGTGCGTTC  182
```

```
                || || || ||||| ||  | ||   ||| || || || ||  | ||||| || || |||
Sbjct  2084365  ATACTCGGCCATCAGCCTCTGGACGTGCTCGTTGACCACTTGCGCCGCGCCCGCGCATTC  2084424

Query  183      GTGTTTGCTGCAGAAGAAGACTTCGGTATCTCGGTGGTGGAGGCGCAGGCATGCGGAACG  242
                || ||||| || ||||| |||||||| || || || || ||||||||||| ||||| |||
Sbjct  2084425  GTTTTTGCGGCGGAAGAGGACTTCGGGATTTCCGTCGTCGAGGCGCAGGCGTGCGGCACG  2084484

Query  243      CCGGTGATCGCATTCGGCAGAGGCGGTGCGCTCGAATCCGTTATCGGCCTGCCACTTGAA  302
                |||||||| ||||||||||| || || || ||||| ||||||||||||||||| || ||
Sbjct  2084485  CCGGTGATTGCATTCGGCAGGGGAGGCGCACTCGAGTCCGTTATCGGCCTGCCTCTCGAG  2084544

Query  303      CGGCCCACGGGCGTGTTCTTCGGGGAACAGACGCCAGAGTCATTGCTGGCCGCGGTAGAC  362
                | ||| |||||||| |||||||| || |||||  | |||||  ||||||  || || |||
Sbjct  2084545  CAGCCTACGGGCGTCTTCTTCGGCGAGCAGACAGCGGAGTCGCTGCTGGAGGCCGT-GAC  2084603

Query  363      -CGGTTTGAGCGCAACGCCGGCC--TGTTCGATCCGCGGGCGTGCCGTAGAAACGCAGAG  419
                 || || |||||||| ||  |||  | |||||||||  |   |||||    ||||| ||
Sbjct  2084604  GCGCTTCGAGCGCAATGC--GCCATTATTCGATCCGGTGAATTGCCGCCAGAACGCCGAA  2084661

Query  420      CGCTTTTCGTCGGAGAACTTCAAGACGGCGCTAACCAGCTTTATCGACTCACGACT  475
                || || ||| | |||||||||||||||||  | ||   ||| |||||| | |  ||
Sbjct  2084662  CGATTCTCGACCGAGAACTTCAAGACGGCATTGACGGACTTCATCGACGCGCGGCT  2084717
```

BLAST ®

Basic Local Alignment Search Tool

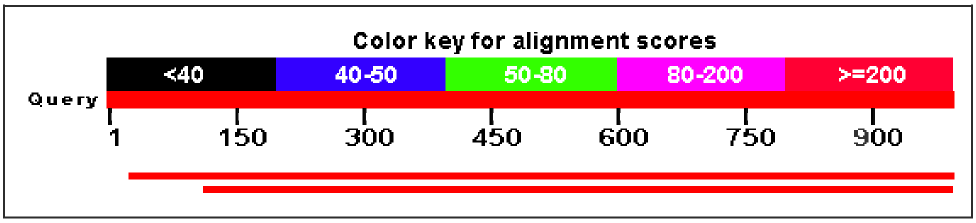
NCBI/ BLAST/ blastn suite/ **Formatting Results - BSMPTJUJ015**
 Formatting options
 Download
Blast report description

HMF1EA_S2S_Clone5

RID	BSMPTJUJ015 (Expires on 02-12 16:22 pm)		
Query ID	lcl|Query_91393	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	996		

Graphic Summary

Distribution of 2 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Burkholderia fungorum strain ATCC BAA-463 chromosome 2, complete sequence	1472	1472	97%	0.0	95%	CP010027.1
Burkholderia sp. CCGE1002 chromosome 2, complete sequence	304	304	88%	3e-78	69%	CP002014.1

Alignments

Burkholderia fungorum strain ATCC BAA-463 chromosome 2, complete sequence

Sequence ID: **gb|CP010027.1|** Length: 3508455 Number of Matches: 1

Range 1: 2138844 to 2139795

Score	Expect	Identities	Gaps	Strand	Frame
1472 bits(1632)	0.0()	919/971(95%)	19/971(1%)	Plus/Plus	

Features:

glycosyl transferases group 1 family proteinO-Antigen ligase family protein

```
Query  26       CATGGTGCCCGTATANGNGCATCGATCTGAATCGTGCGGGCCCTTTTCCNCCAGACAACT  85
                ||||||||| ||||| | |||||||||||| ||||||||||| |||||   |||||| ||
Sbjct  2138844  CATGGTGCC-GTATAAGCGCATCGATCTGA-TCGTGCGGGCC-TTTTCA--CAGACACCT  2138898

Query  86       TNNNNCGCCGTCCTTGTCGTGATTTNNCGGACGNCCCTGAGATGAAGAAGAATCAAGAGC  145
                     ||||||| |||||||||||     ||||  ||| ||||||||||||| ||| | ||
Sbjct  2138899  --GAGCGCCGTC-TTGTCGTGATTGGC--GACGGTCCCGAGATGAAGAAGA-TCAGG-GC  2138951

Query  146      AGCGGCCGGCGNGAACGTCACGATCCTGGGTCATCAACCGTTCGATAACGCTGGTCGATC  205
                ||||||||||| ||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  2138952  AGCGGCCGGCGAGAACGTCACGATCCTGGGTCATCAACCGTTCGATA-CGCTGGTCGATC  2139010

Query  206      ATTTATAGGCGCGCGCGTGGCGTTCGTGTTTTGCTGCAGAAGAAGACTATCAGTATCTCG  265
                ||||| ||||||||||||| ||||||||||| |||||||||||||||| || |||| |||
Sbjct  2139011  ATTTA-AGGCGCGCGCGTG-CGTTCGTGTTT-GCTGCAGAAGAAGACT-TCGGTATTTCG  2139066

Query  266      GTGGTGGAGGGGCAGGCATGCGGAACGCCGGTGATCGCATTCGGCAGAGGCGGTGCGCTC  325
                || ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2139067  GTTGTGGAGGCGCAGGCATGCGGAACGCCGGTGATCGCATTCGGCAGAGGCGGTGCGCTC  2139126

Query  326      GAATCCGTTATCGGCCTGCCACTTGAACGGCCCACGGGCGTGTTCTTTCGNGTGAACAGA  385
                |||||||||||||||||||||||||||||||| |||||||||||||| || | |||||||
Sbjct  2139127  GAATCCGTTATCGGCCTGCCACTTGAACGGCCTACGGGCGTGTTCTT-CGGG-GAACAGA  2139184

Query  386      CGCCAGAGTCATTGCTGGCCGCGGTAGGCCGGTTTGAGCGCAACGCCGGCCTGTTCGATC  445
                |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  2139185  CGCCAGAGTCATTGCTGGCCGCGGTAGGCCGGTTTGAGCGGAACGCCGGCCTGTTCGATC  2139244

Query  446      CGCGGGCGTGCCGTAGAAACGCAGAGCGCTTTTCGTCGGAGAACTTCAAGACGGCGCTAA  505
                |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  2139245  CGCGGGCGTGCCGTAGAAACGCAGAGCGTTTTTCGTCGGAGAACTTCAAGACGGCGCTAA  2139304

Query  506      CCAGCTTTATCGACTCACGACTCCCATACGGAGGACTCGAACACTTCCTGCCGTATCCGG  565
                ||||||| ||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  2139305  CCAGCTTCATCGACTCACGGCTCCCATACGGAGGACTCGAACACTTCCTGCCGTATCCGG  2139364

Query  566      TGGCGAGGCAGCAACTGCCTGTCAATCAGCGCCAGCATGCTGATGTGGTGTCGTGAGTAC  625
                ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2139365  TGGCGAGCCAGCAACTGCCTGTCAATCAGCGCCAGCATGCTGATGTGGTGTCGTGAGTAC  2139424

Query  626      GAATGTGTGCGCCGGCGAATCTGATCTAGGACGGAGTTCGCCGACGCCCGCCAGCAATCA  685
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2139425  GAATGTGTGCGCCGGCGAATCTGATCTAGGACGGAGTTCGCCGACGCCCGCCAGCAATCA  2139484

Query  686      GAGCAGCGCGTGCTCTTTTGACTTCTGCTGAAGATGATCGATCGCGGCATTGTTGACTGA  745
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2139485  GAGCAGCGCGTGCTCTTTTGACTTCTGCTGAAGATGATCGATCGCGGCATTGTTGACTGA  2139544

Query  746      TCGCGCGGCCAGCAACAGGGAAATGACTAGCGCAAGGATCAGCACATTCGATGGCGAGAC  805
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2139545  TCGCGCGGCCAGCAACAGGGAAATGACTAGCGCAAGGATCAGCACATTCGATGGCGAGAC  2139604

Query  806      CAGACGATGTTCGGTCGCTGCCATGACAAGCAGGCAAACGGATGAAATCTCAACGAACCT  865
                |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  2139605  CAGACGATGTTCGGTCGCTGCCATGACAAGTAGGCAAACGGATGAAATCTCAACGAACCT  2139664

Query  866      GAAGGCGGCGAAGTTCTGTCCGCCACCAAATAGTGCAGCGGCGGCCGCGCCGTGTTTGCA  925
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2139665  GAAGGCGGCGAAGTTCTGTCCGCCACCAAATAGTGCAGCGGCGGCCGCGCCGTGTTTGCA  2139724

Query  926      CCACTCAATCAGTCTCCAGTAGAAGCCCAGCATCTTAACAAGTCCCATTACNCCGAGCTC  985
                ||||||||||||||||||||||||||||||||||    ||||||||| ||| ||||||||
Sbjct  2139725  CCACTCAATCAGTCTCCAGTAGAAGCCCAGCATCAGGGCAAGTCCCACTACGCCGAGCTC  2139784

Query  986      CGCAAGAATGT  996
                |||||||||||
Sbjct  2139785  CGCAAGAATGT  2139795
```

Burkholderia sp. CCGE1002 chromosome 2, complete sequence
Sequence ID: **gb|CP002014.1|** Length: 2593966 Number of Matches: 1
Range 1: 136791 to 137632

Score	Expect	Identities	Gaps	Strand	Frame
304 bits(336)	3e-78()	607/886(69%)	50/886(5%)	Plus/Plus	

Features:

```
Query  115     GACGNCCCTGAGATGAAGAAGAATCAAGAGCAGCGGCCGGCGNGAACGTCACGATCCTGG  174
               ||||  || ||||||||||||| ||||| || |  |||||||  ||||| | |||||| |
Sbjct  136791  GACGGTCCCGAGATGAAGAAGA-TCAAG-GCGGTCGCCGGCGACAACGTGAAGATCCTTG  136848

Query  175     GTCATCAACCGTTCGATAACGCTGGTCGATCATTTATAGGCGCGCGCGTGGCGTTCGTGT  234
               | ||||| |||| |||    ||||||||||||  |   | |||||||||| | |||||||
Sbjct  136849  GGCATCAGCCGTCCGACGT-GCTGGTCGATCACCTGC-GTCGCGCGCGTG-CATTCGTGT  136905

Query  235     TTTGCTGCAGAAGAAGACTATCAGTATCTCGGTGGTGGAGGGGCAGGCATGCGGAACGCC  294
               || || || |||||||| | || | || || ||||| || | |||||||||||| |||||
Sbjct  136906  TT-GCGGCGGAAGAAGATT-TCGGCATTTCCGTGGTCGAAGCGCAGGCATGCGGCACGCC  136963

Query  295     GGTGATCGCATTCGGCAGAGGCGGTGCGCTCGAATCCGTTATCGGCCTGCCACTTGAACG  354
               |||||| || |||||| | ||||| ||||| ||||| ||  | ||  |||| || || ||
Sbjct  136964  GGTGATAGCCTTCGGCCGCGGCGGCGCGCTTGAATCGGTGGTGGGATTGCCGCTCGAGCG  137023

Query  355     GCCCACGGGCGTGTTCTTTCGNGTGAACAGACGCCAGAGTCATTGCTGGCCGCGGTAGGC  414
               |||||| || || |||||  | | | | || | || | |||  |||| |  || ||   |
Sbjct  137024  GCCCACCGGGGTATTCTTCGGCGAGCAAAG-CACC-GCGTCCCTGCTCGAAGCCGTTATC  137081

Query  415     CGGTTTGAGCGCAACGCCGGCCTGTTCGATCCGCGGGCGTGCCGTAGAAACGCAGAGCGC  474
               || || ||  ||||||||| | | |||||| | ||||||||||| |  || || ||||||
Sbjct  137082  CGTTTCGAAAGCAACGCCGCCTTATTCGATGCACGGGCGTGCCGCAAGAATGCCGAGCGC  137141

Query  475     TTTTCGTCGGAGAACTTCAAGACGGCGCTAACCAGCTTTATCGACTCACGACTCCCATAC  534
               |||||||||||||||||||||| |||||| |   ||||  ||||  | || ||||| || 
Sbjct  137142  TTTTCGTCGGAGAACTTCAAGAAGGCGCTGATGGGCTTCGTCGATGCGCGGCTCCCTTAT  137201

Query  535     GGAGGACTCGAACACTTCCTGCCGTATCCGGTGGCGAGGCAGCAACTGCCTGTCAATCAG  594
               |   |  ||||||| || || ||||||   | | |||| |||   ||||| | | |  | 
Sbjct  137202  GCGTGCGTCGAACAGTTTCTTCCGTAT---GCGCCGAGCCAGTCGCTGCCGGCCGAAGAA  137258

Query  595     CGCCAGCATGCTGATGTGGTGTCGTGAGTACGAATGTGTGCGCCGGCGAA--TCTGATCT  652
               || || |  || || || | | | |||||        | ||||||| | |     | | |
Sbjct  137259  CGTCATCTGGCCGACGTTGCGCCCTGAGT-------CGGGCGCCGGGGCACGGGCGGTGT  137311

Query  653     AGGACGGAGTTCGCCGACGCCCGCC---AGCAATCAGAGCAGCGCGTGCTCTTTTGACTT  709
               ||  ||     |  ||| |||||||    ||  || | || |  || ||           
Sbjct  137312  AGCTCGCGCGCCCACGATGCCCGCCTTGCGCGCTCCGCGCGGGCCGGGC-----------  137360

Query  710     CTGCTGAAGATGATCGATCGCGGCATTGTTGACTGATCGCGCGGCCAGCAACAGGGAAAT  769
                  ||||  |||  || | || ||       |  |  |||||||| |||| ||| || ||
Sbjct  137361  ---CTGA--ATG--CGGTGGCCGC------CAGCGGACGCGCGGCTAGCAGCAGCGAGAT  137407

Query  770     GACTAGCGCAAGGATCAGCACATTCGATGGCGAGACCAGACGATGTTCGGTCGCTGCCAT  829
                || || | ||| ||||  |||||||| |||| |||||| ||||| ||||| || | |||
Sbjct  137408  CACCAGAGAAAGAATCAATACATTCGACGGCGTGACCAGCCGATGCTCGGTTGCCGACAT  137467

Query  830     GACAAGCAGGCAAACGGATGAAATCTCAACGAACCTGAAGGCGGCGAAGTTCTGTCCGCC  889
                || |||||||| || || |||||||| ||||| | ||| || ||||| |   | || ||
Sbjct  137468  CACCAGCAGGCATACCGACGAAATCTCGACGAAGCGGAACGCCGCGAACTGGCGGCCCCC  137527

Query  890     ACCAAATAGTGCAGCGGCGGCCGCGCCGTGTTTGCACCACTCAATCAGTCTCCAGTAGAA  949
                 | |  |  || ||    ||||| || ||||||| |||||| | |||| ||||| ||||
Sbjct  137528  CTCGACCAACGCGGCATATGCCGCTCCCTGTTTGCTCCACTCGACCAGTTTCCAGAAGAA  137587

Query  950     GCCCAGCATC-TTAACAAGTCCCATTACNCCGAGCTCCGCAAGAAT  994
                 | || |||     |||| ||||  || |||||||| || || ||
Sbjct  137588  CGCGAGGATCAGCGTCAAG-CCCACGACGCCGAGCTCGGCGAGGAT  137632
```

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NCBI/ BLAST/ blastn suite/ **Formatting Results - BSNWSBHA014**
Formatting options
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Blast report description

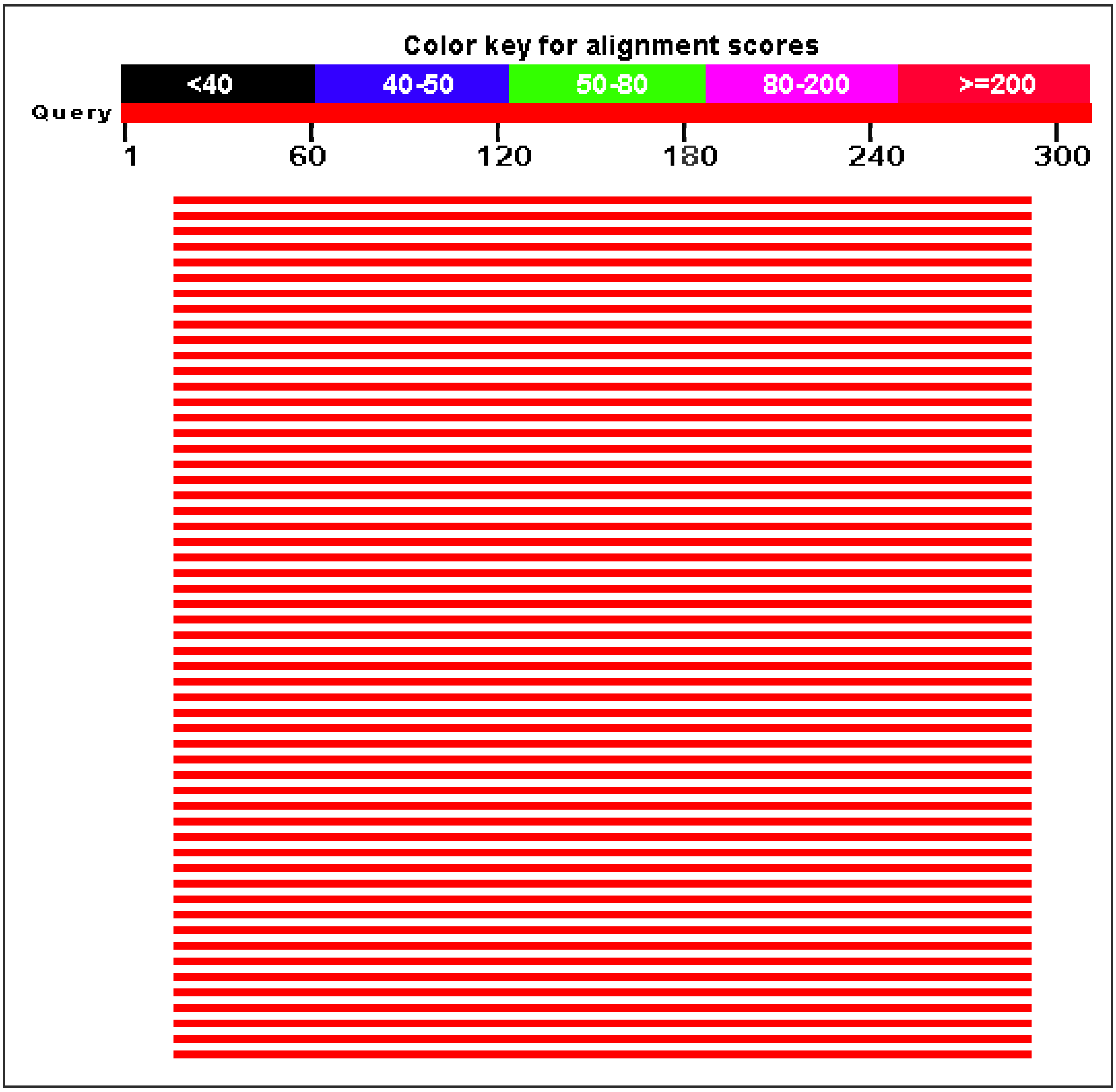
mc_5992_1e_1c_trnL_Clone8

RID BSNWSBHA014 (Expires on 02-12 16:42 pm)

Query ID	lcl|Query_117831	**Database Name**	nr
Description	Clone8	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	311		

Graphic Summary

Distribution of 101 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Variovorax sp. LMR331 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KU182837.1**
Variovorax sp. E37 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KR703575.1**
Variovorax sp. GLT-Slr-56 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KT343856.1**
Variovorax sp. GLT-Slr-51 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KT343851.1**
Variovorax paradoxus strain PDD-59b-55 16S ribosomal RNA gene, complete sequence	497	497	88%	6e-137	100%	**KR922177.1**
Uncultured bacterium clone HF77 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KR188953.1**
Variovorax paradoxus strain 11-4(2) 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KT369961.1**
Variovorax sp. YN34 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KR051070.1**
Variovorax sp. 369 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KT461877.1**
Variovorax sp. 110 16S						

ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KT461839.1
Variovorax sp. 48 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KT461830.1
Variovorax sp. NB24 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KP844880.1
Variovorax sp. AB30 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KP844879.1
Variovorax sp. EECC-613 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KP860659.1
Variovorax sp. EECC-546 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KP860654.1
Variovorax paradoxus strain hca0013 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KP834437.1
Variovorax paradoxus strain KAR44 16S ribosomal RNA gene, complete sequence	497	497	88%	6e-137	100%	KR055005.1
Variovorax sp. CC4W1 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KM187269.1
Variovorax sp. StTD764 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025495.1
Variovorax sp. StTD761 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025494.1
Variovorax sp. StTD755 gene for 16S rRNA, partial	497	497	88%	6e-137	100%	LC025488.1

sequence						
Variovorax sp. StTD752 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025485.1
Variovorax sp. StTD751 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025484.1
Variovorax sp. StTD746 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025480.1
Variovorax sp. StTD741 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025475.1
Variovorax sp. StTD740 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025474.1
Variovorax sp. StTD487 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025345.1
Variovorax sp. StTD473 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025332.1
Variovorax sp. StTD472 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025331.1
Variovorax sp. StTD461 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025320.1
Variovorax sp. StTD460 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025319.1
Variovorax sp. StTD396 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025261.1
Variovorax sp. StTD372 gene for 16S rRNA,	497	497	88%	6e-137	100%	LC025238.1

partial sequence						
Variovorax sp. StRD768 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025141.1
Variovorax sp. StRD470 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC024961.1
Variovorax sp. StRD421 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC024912.1
Variovorax sp. StRD416 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC024907.1
Variovorax sp. StRD404 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC024896.1
Variovorax sp. 285P1R 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KR611635.1
Variovorax boronicumulans strain LR 2-10 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KP407102.1
Variovorax boronicumulans strain LR 1-13 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KP407094.1
Variovorax boronicumulans strain LR 1-6B 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KP407089.1
Variovorax sp. RC3.3 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KP267842.1
Variovorax						

paradoxus strain S12A6 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KF975363.1
Variovorax sp. S12P10 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KF975359.1
Variovorax sp. S13P8 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KF975358.1
Variovorax paradoxus strain S12S4 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KF975336.1
Bacillaceae bacterium x8-9 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KP230463.1
Variovorax paradoxus gene for 16S ribosomal RNA, partial sequence, strain: AF90	497	497	88%	6e-137	100%	LC015538.1
Variovorax paradoxus strain IHB B 12181 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KJ767382.1
Variovorax boronicumulans strain E2B5_13 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KM604967.1
Variovorax boronicumulans strain E2B5_5 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KM604959.1
Variovorax sp. ML3-12 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KM411504.1

Variovorax sp. IDSBO-4 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KM199761.1**
Bacterium NCr-7 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KJ792863.1**
Variovorax sp. MR-I14 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KJ811555.1**
Uncultured bacterium clone PhyMu0012 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KC746053.1**
Uncultured bacterium clone ncd266e10c1 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KF070930.1**
Uncultured Variovorax sp. clone PIPOManured06 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KF590885.1**
Variovorax paradoxus strain SL37 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KJ529023.1**
Variovorax sp. TA_EF partial 16S rRNA gene, strain TA_EF	497	497	88%	6e-137	100%	**HG942167.1**
Variovorax paradoxus strain ZR 1-3 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KJ472791.1**
Variovorax boronicumulans strain ZR 1-1 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KJ472790.1**
Variovorax sp.						

CV50Nov 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KJ482855.1**
Variovorax sp. CO8Nov 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KJ482792.1**
Variovorax sp. MM43Nov 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KJ482749.1**
Variovorax paradoxus strain 11709033 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KF981560.1**
Variovorax sp. BvORHM081 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	**AB851216.1**
Variovorax sp. BvORHM030 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	**AB851165.1**
Variovorax sp. BvIRR112 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	**AB851079.1**
Variovorax sp. BvIRHM077 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	**AB850959.1**
Variovorax sp. b49 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KF733334.1**
Variovorax sp. 613 partial 16S rRNA gene, isolate 613	497	497	88%	6e-137	100%	**HG737356.1**
Variovorax paradoxus strain ZY-173s 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KF580876.1**
Uncultured Variovorax sp. clone Cb1 16S ribosomal RNA,	497	497	88%	6e-137	100%	**KF704360.1**

partial sequence						
Variovorax sp. 231-FB gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	**AB566088.1**
Uncultured bacterium gene for 16S rRNA, partial sequence, clone: SBG-U_F05	497	497	88%	6e-137	100%	**AB810907.1**
Uncultured bacterium gene for 16S rRNA, partial sequence, clone: SU_E07	497	497	88%	6e-137	100%	**AB810809.1**
Variovorax paradoxus B4 chromosome 1, complete sequence	497	994	88%	6e-137	100%	**CP003911.1**
Variovorax paradoxus partial 16S rRNA gene, strain BD12OL2-R01	497	497	88%	6e-137	100%	**FR877674.1**
Variovorax sp. NAS2(11) 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**JX154309.1**
Variovorax paradoxus strain MOSEL-ES1 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KF307662.1**
Uncultured Variovorax sp. clone BC0195 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KC166847.1**
Uncultured Variovorax sp. clone BC059 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	**KC166765.1**
Uncultured Variovorax sp. clone BC003 16S ribosomal RNA gene,	497	497	88%	6e-137	100%	**KC166740.1**

partial sequence						
Uncultured Variovorax sp. clone BC095 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KC166723.1
Variovorax sp. Zs13 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	JQ977458.1
Variovorax sp. Azb3 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	JQ977354.1
Uncultured bacterium gene for 16S ribosomal RNA, partial sequence, clone: SZ3-1039	497	497	88%	6e-137	100%	AB769480.1
Bacterium LW 181_159 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	GQ288950.1
Bacterium LW 181_158 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	GQ288866.1
Bacterium LW 181_121 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	GQ288853.1
Uncultured bacterium clone PsppD06 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	JX644382.1
Uncultured bacterium clone DC2ROB04 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	JX644220.1
Variovorax sp. SMX332 partial 16S rRNA gene, strain SMX332	497	497	88%	6e-137	100%	HF571534.1
Bacterium 58-L049616-122-						

011-B08 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	JX228569.1
Variovorax paradoxus S110 strain S110 16S ribosomal RNA, complete sequence	497	497	88%	6e-137	100%	NR_074654.1
Variovorax paradoxus EPS strain EPS 16S ribosomal RNA, complete sequence	497	497	88%	6e-137		

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NCBI/ BLAST/ blastn suite/ **Formatting Results - BT5P15GS014**
Formatting options
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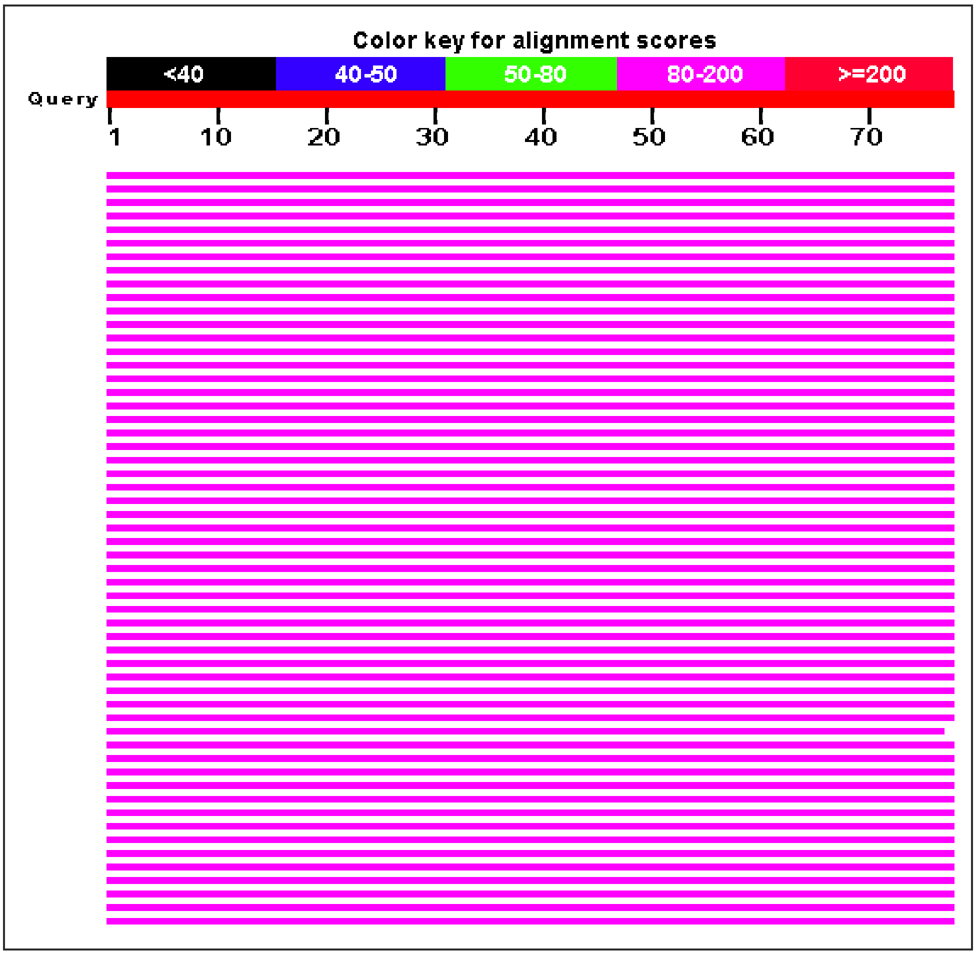
MM745.1C_trnL_Clone3,4

RID BT5P15GS014 (Expires on 02-12 21:12 pm)

Query ID	lcl|Query_58851	**Database Name**	nr
Description	c4	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	77		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Vicia faba isolate 7612 tRNA-Leu (trnL) gene, partial sequence; chloroplast	140	140	100%	3e-30	100%	KJ787213.1
Vicia faba plastid, complete genome	140	140	100%	3e-30	100%	KF042344.1
Vicia faba isolate HS879 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	140	140	100%	3e-30	100%	JX505737.1
Vicia faba var. minor tRNA-Leu (trnL) gene, partial sequence; chloroplast	140	140	100%	3e-30	100%	JN617168.1
Vicia faba var. major tRNA-Leu (trnL) gene, partial sequence; chloroplast	140	140	100%	3e-30	100%	JN617167.1
Vicia faba chloroplast transfer RNA-Leu(CAA)	140	140	100%	3e-30	100%	M55084.1
Vicia faba chloroplast tRNA-Leu, tRNA-Phe, tRNA-His, ORFX, NADH-deydrogenase genes & partial sequence ORFx & psbA genes	140	140	100%	3e-30	100%	X51471.1
Broad bean chloroplast genes for tRNA-Leu(CAA) and (UAA) and tRNA-Phe	140	140	100%	3e-30	100%	X02444.1
Melilotus albus isolate xt_plant115 tRNA-Leu (trnL) gene, intron; chloroplast	127	127	100%	2e-26	96%	KJ746436.1
Tracheophyta environmental sample clone N-11 tRNA-Leu (trnL) gene, partial sequence; chloroplast	127	127	100%	2e-26	96%	KF616419.1
Tracheophyta environmental sample clone N-3 tRNA-Leu (trnL) gene, partial sequence; chloroplast	127	127	100%	2e-26	96%	KF616411.1
Tracheophyta environmental sample clone N-6 tRNA-Leu (trnL) gene, partial sequence; chloroplast	127	127	100%	2e-26	96%	KF616414.1
Tracheophyta environmental sample clone N-5 tRNA-Leu (trnL) gene, partial sequence; chloroplast	127	127	100%	2e-26	96%	KF616413.1
Tracheophyta environmental sample clone N-4 tRNA-Leu (trnL) gene, partial sequence; chloroplast	127	127	100%	2e-26	96%	KF616412.1
Melilotus alba tRNA-Leu (trnL) gene, intron; chloroplast	127	127	100%	2e-26	96%	DQ311713.1
Melilotus alba chloroplast tRNA-Leu (trnL) gene, intron sequence	127	127	100%	2e-26	96%	AF124232.1
Tracheophyta environmental sample clone N-1 tRNA-Leu (trnL) gene, partial sequence; chloroplast	125	125	100%	7e-26	95%	KF616409.1
Tracheophyta environmental sample clone N-2 tRNA-Leu (trnL) gene, partial sequence; chloroplast	120	120	100%	3e-24	95%	KF616410.1
Vicia cypria isolate HS866 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	118	118	100%	1e-23	94%	JX505734.1
Vicia koeieana isolate 7619 tRNA-Leu (trnL) gene, partial sequence; chloroplast	116	116	100%	4e-23	93%	KJ787256.1
Ononis hirta tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	116	116	100%	4e-23	94%	GQ488565.1
Vicia lunata isolate V25 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	114	114	100%	1e-22	90%	JX505749.1
Ononis varelae tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	114	114	100%	1e-22	93%	GQ488605.1

Ononis dentata tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	114	114	100%	1e-22	90%	GQ488559.1
Astragalus pectinatus isolate CP18 tRNA-Leu (trnL) gene, partial sequence; chloroplast	113	113	100%	4e-22	91%	KP208342.1
Trigonella suavissima isolate EC 583624 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	113	113	100%	4e-22	89%	JX274187.1
Trigonella suavissima isolate EC 583623 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	113	113	100%	4e-22	89%	JX274186.1
Astragalus polaris tRNA-Leu (trnL) gene, partial sequence; chloroplast	113	113	100%	4e-22	91%	GQ244622.1
Astragalus polaris tRNA-Leu (trnL) gene, intron	113	113	100%	4e-22	91%	DQ860525.1
Astragalus layneae voucher ASLA-4 tRNA-Leu (trnL) gene, partial sequence; and trnL-trnF intergenic spacer, complete sequence; chloroplast	113	113	100%	4e-22	91%	DQ403850.1
Astragalus layneae voucher ASLA-1 tRNA-Leu (trnL) gene, partial sequence; and trnL-trnF intergenic spacer, complete sequence; chloroplast	113	113	100%	4e-22	91%	DQ403849.1
Astragalus didymocarpus voucher ASDI-16 tRNA-Leu (trnL) gene, partial sequence; and trnL-trnF intergenic spacer, complete sequence; chloroplast	113	113	100%	4e-22	91%	DQ403848.1
Astragalus didymocarpus voucher ASDI-2 tRNA-Leu (trnL) gene, partial sequence; and trnL-trnF intergenic spacer, complete sequence; chloroplast	113	113	100%	4e-22	91%	DQ403847.1
Astragalus didymocarpus voucher ASDI-1 tRNA-Leu (trnL) gene, partial sequence; and trnL-trnF intergenic spacer, complete sequence; chloroplast	113	113	100%	4e-22	91%	DQ403846.1
Astragalus linifolius chloroplast tRNA-Leu (trnL) gene, intron sequence	113	113	100%	4e-22	91%	AF126978.1
Astragalus bodinii chloroplast tRNA-Leu (trnL) gene, intron sequence	113	113	100%	4e-22	91%	AF126977.1
Astragalus gilviflorus chloroplast tRNA-Leu (trnL) gene, intron sequence	113	113	100%	4e-22	91%	AF126976.1
Astragalus douglasii chloroplast tRNA-Leu (trnL) gene, intron sequence	113	113	100%	4e-22	91%	AF126974.1
Astragalus palanae var. palanae chloroplast tRNA-Leu (trnL) gene, intron sequence	113	113	100%	4e-22	91%	AF126971.1
Astragalus sabulonum chloroplast tRNA-Leu (trnL) gene, intron sequence	113	113	100%	4e-22	91%	AF126969.1
Melilotus officinalis isolate CP46 tRNA-Leu (trnL) gene, partial sequence; chloroplast	111	111	100%	1e-21	86%	KP208370.1
Astragalus flexuosus isolate CP17 tRNA-Leu (trnL) gene, partial sequence; chloroplast	111	111	98%	1e-21	91%	KP208341.1
Melilotus officinalis isolate xt_plant51 tRNA-Leu (trnL) gene, intron; chloroplast	111	111	100%	1e-21	86%	KJ746435.1
Trigonella balansae isolate EC 546586 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	111	111	100%	1e-21	86%	JX274188.1
Trigonella cretica isolate EC 583577 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	111	111	100%	1e-21	86%	JX274153.1
Trigonella cretica isolate EC 583576 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	111	111	100%	1e-21	86%	JX274152.1
Trigonella cretica isolate EC 583575 tRNA-Leu (trnL) gene and trnL-trnF intergenic	111	111	100%	1e-21	86%	JX274151.1

spacer, partial sequence; chloroplast						
Trigonella coerulescens isolate EC 583574 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	111	111	100%	1e-21	86%	JX274150.1
Trigonella coerulescens isolate EC 583573 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	111	111	100%	1e-21	86%	JX274149.1
Trigonella caerulea isolate EC 583569 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	111	111	100%	1e-21	86%	JX274147.1
Trigonella caerulea isolate EC 583567 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	111	111	100%	1e-21	86%	JX274145.1
Trigonella balansae isolate EC 583507 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	111	111	100%	1e-21	86%	JX274137.1
Trigonella anguina isolate EC 583495 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	111	111	100%	1e-21	86%	JX274134.1
Melilotus officinalis voucher personal collection:I. Hiiesalu 47 tRNA-Leu (trnL) gene, partial sequence; chloroplast	111	111	100%	1e-21	86%	HM590318.1
Trigonella caerulea tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	111	111	100%	1e-21	86%	GQ488615.1
Ononis reclinata subsp. reclinata tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	111	111	100%	1e-21	89%	GQ488586.1
Ononis filicaulis tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	111	111	100%	1e-21	89%	GQ488561.1
Melilotus albus chloroplast DNA, tRNA-Leu (trnL) and trnL-trnF intergenic spacer, partial sequence, specimen_voucher: TUH:19700	111	111	100%	1e-21	86%	AB546813.1
Melilotus officinalis chloroplast DNA, tRNA-Leu (trnL) and trnL-trnF intergenic spacer, partial sequence, specimen_voucher: TUH:7346	111	111	100%	1e-21	86%	AB546812.1
Melilotus officinalis tRNA-Leu (trnL) gene, intron; chloroplast	111	111	100%	1e-21	86%	DQ311714.1
Nicotiana trigonophylla chloroplast partial tRNA-Leu gene, IGS and partial tRNA-Phe gene	111	111	100%	1e-21	92%	AJ577438.2
Nicotiana bigelovii chloroplast partial tRNA-Leu gene, IGS and partial tRNA-Phe gene	111	111	100%	1e-21	92%	AJ577437.1
Nicotiana palmeri chloroplast partial tRNA-Leu gene, IGS and partial tRNA-Phe gene	111	111	100%	1e-21	92%	AJ577406.1
Melilotus officinalis chloroplast tRNA-Leu (trnL) gene, intron sequence	111	111	100%	1e-21	86%	AF124233.1
Trigonella strangulata isolate EC 583622 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	109	109	100%	5e-21	85%	JX274185.1
Trigonella maritima isolate EC 583601 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	109	109	100%	5e-21	87%	JX274171.1
Trigonella filipes isolate EC 583584 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	109	109	100%	5e-21	85%	JX274158.1
Ononis speciosa tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial	109	109	100%	5e-21	87%	GQ488593.1

sequence; chloroplast						
Ononis cristata subsp. cristata tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	109	109	100%	5e-21	91%	GQ488558.1
Ipomoea batatas cultivar Xushu 18 chloroplast, complete genome	107	107	100%	2e-20	91%	KP212149.1
Ipomoea purpurea chloroplast DNA, trnL-trnF intergenic spacer, partial sequence	107	107	100%	2e-20	91%	AB889433.1
Operculina macrocarpa chloroplast, partial genome	107	107	100%	2e-20	91%	KF242502.1
Ipomoea cordatotriloba chloroplast, partial genome	107	107	100%	2e-20	91%	KF242497.1
Ipomoea trifida chloroplast, partial genome	107	107	100%	2e-20	91%	KF242496.1
Ipomoea splendor-sylvae chloroplast, partial genome	107	107	100%	2e-20	91%	KF242493.1
Ipomoea setosa chloroplast, partial genome	107	107	100%	2e-20	91%	KF242492.1
Ipomoea polpha chloroplast, partial genome	107	107	100%	2e-20	91%	KF242491.1
Ipomoea pes-caprae chloroplast, partial genome	107	107	100%	2e-20	91%	KF242490.1
Ipomoea orizabensis chloroplast, partial genome	107	107	100%	2e-20	91%	KF242488.1
Ipomoea nil chloroplast, partial genome	107	107	100%	2e-20	91%	KF242487.1
Ipomoea murucoides chloroplast, partial genome	107	107	100%	2e-20	91%	KF242486.1
Ipomoea hederifolia chloroplast, partial genome	107	107	100%	2e-20	91%	KF242484.1
Ipomoea dumetorum chloroplast, partial genome	107	107	100%	2e-20	91%	KF242482.1
Ipomoea diamantinensis chloroplast, partial genome	107	107	100%	2e-20	91%	KF242481.1
Ipomoea argillicola chloroplast, partial genome	107	107	100%	2e-20	91%	KF242479.1
Ipomoea amnicola chloroplast, partial genome	107	107	100%	2e-20	91%	KF242478.1
Ipomoea trifida chloroplast, partial genome	107	107	100%	2e-20	91%	KF242476.1
Ipomoea batatas chloroplast, partial genome	107	107	100%	2e-20	91%	KF242475.1
Ipomoea batatas chloroplast, partial genome	107	107	100%	2e-20	91%	KF242474.1
Ipomoea batatas chloroplast, partial genome	107	107	100%	2e-20	91%	KF242473.1
Trigonella stellata isolate EC 583621 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	107	107	100%	2e-20	86%	JX274184.1
Trigonella schlumbergeri isolate EC 583609 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	107	107	100%	2e-20	87%	JX274177.1
Trigonella arabica isolate EC 583496 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	107	107	100%	2e-20	87%	JX274135.1
Ipomoea pes-caprae chloroplast trnL gene, intron, partial sequence, isolate: OGA0263	107	107	100%	2e-20	91%	AB817485.1
Convolvulus lineatus voucher LIN01 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	107	107	100%	2e-20	91%	KC786127.1
Convolvulus althaeoides voucher AT01 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene,	107	107	100%	2e-20	91%	KC786128.1

partial sequence; chloroplast						
Convolvulus compactus voucher COMP01 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	107	107	100%	2e-20	91%	KC786126.1
Convolvulus boissieri voucher PTO01 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	107	107	100%	2e-20	91%	KC786124.1
Convolvulus boissieri voucher TRE01 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	107	107	100%	2e-20	91%	KC786089.1
Convolvulus cneorum tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	107	107	100%	2e-20	91%	HQ412972.1

Alignments

Vicia faba isolate 7612 tRNA-Leu (trnL) gene, partial sequence; chloroplast
Sequence ID: **gb|KJ787213.1|** Length: 487 Number of Matches: 1
Range 1: 83 to 159

Score	Expect	Identities	Gaps	Strand	Frame
140 bits(154)	3e-30()	77/77(100%)	0/77(0%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCGaaaacaaaaaactaaaagttcagaaaaaaaG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  83   GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAG  142

Query  61   GATAGGTGCAGAGACTC  77
            |||||||||||||||||
Sbjct  143  GATAGGTGCAGAGACTC  159
```

Vicia faba plastid, complete genome
Sequence ID: **gb|KF042344.1|** Length: 123722 Number of Matches: 1
Range 1: 118542 to 118618

Score	Expect	Identities	Gaps	Strand	Frame
140 bits(154)	3e-30()	77/77(100%)	0/77(0%)	Plus/Plus	

Features:

```
Query  1       GGCAATCCTGAGCCAAATCCTTCTTTCCGaaaacaaaaaactaaaagttcagaaaaaaaG  60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  118542  GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAG  118601

Query  61      GATAGGTGCAGAGACTC  77
               |||||||||||||||||
Sbjct  118602  GATAGGTGCAGAGACTC  118618
```

Vicia faba isolate HS879 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|JX505737.1|** Length: 604 Number of Matches: 1
Range 1: 66 to 142

Score	Expect	Identities	Gaps	Strand	Frame
140 bits(154)	3e-30()	77/77(100%)	0/77(0%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCGaaaacaaaaaactaaaagttcagaaaaaaaG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  66   GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAG  125

Query  61   GATAGGTGCAGAGACTC  77
            |||||||||||||||||
Sbjct  126  GATAGGTGCAGAGACTC  142
```

Vicia faba var. minor tRNA-Leu (trnL) gene, partial sequence; chloroplast
Sequence ID: **gb|JN617168.1|** Length: 938 Number of Matches: 1
Range 1: 554 to 630

Score	Expect	Identities	Gaps	Strand	Frame
140 bits(154)	3e-30()	77/77(100%)	0/77(0%)	Plus/Minus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCGaaaacaaaaaactaaaagttcagaaaaaaaG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  630  GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAG  571

Query  61   GATAGGTGCAGAGACTC  77
            |||||||||||||||||
Sbjct  570  GATAGGTGCAGAGACTC  554
```

Vicia faba var. major tRNA-Leu (trnL) gene, partial sequence; chloroplast
Sequence ID: **gb|JN617167.1|** Length: 949 Number of Matches: 1
Range 1: 558 to 634

Score	Expect	Identities	Gaps	Strand	Frame
140 bits(154)	3e-30()	77/77(100%)	0/77(0%)	Plus/Minus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCGaaaacaaaaaactaaaagttcagaaaaaaaG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  634  GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAG  575

Query  61   GATAGGTGCAGAGACTC  77
            |||||||||||||||||
Sbjct  574  GATAGGTGCAGAGACTC  558
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Basic Local Alignment Search Tool

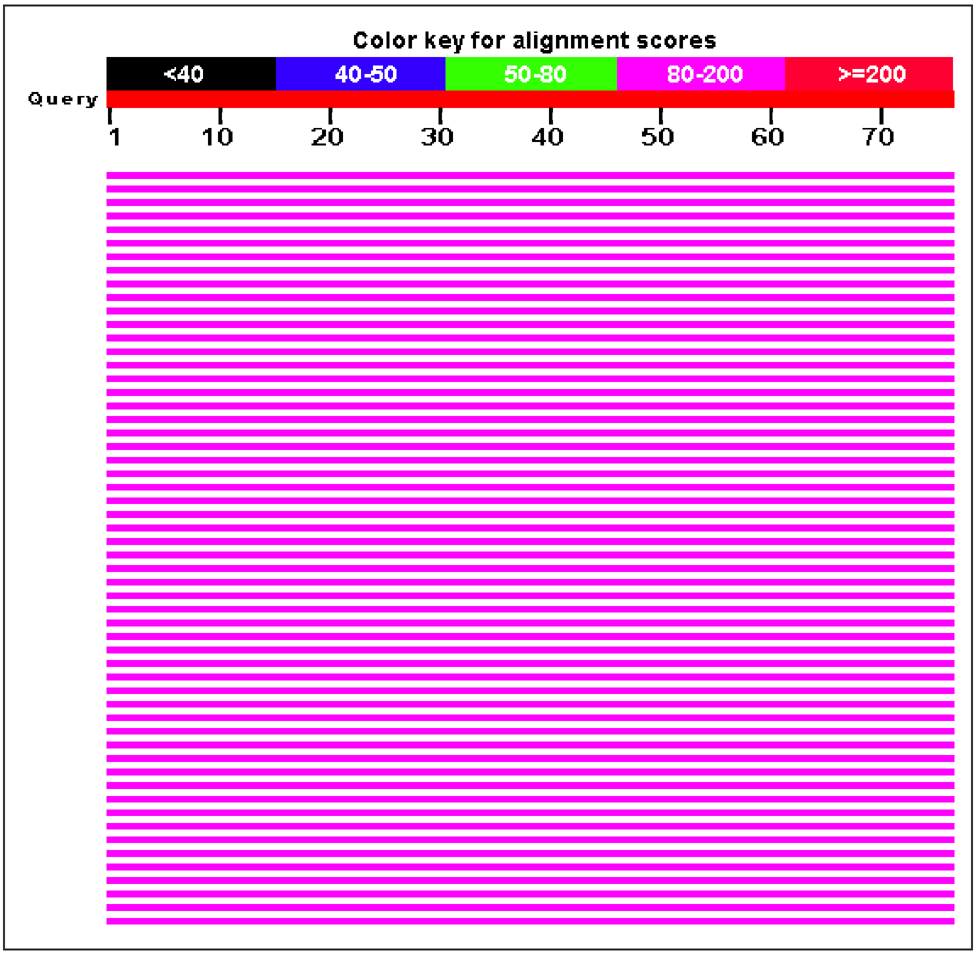
NCBI/ BLAST/ blastn suite/ **Formatting Results - BT6H50AT015**
Formatting options
Download
Blast report description

MM745.1D_trnL_Clone3

RID	BT6H50AT015 (Expires on 02-12 21:26 pm)		
Query ID	lcl|Query_192505	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	76		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Vicia faba isolate 7612 tRNA-Leu (trnL) gene, partial sequence; chloroplast	122	122	100%	8e-25	96%	KJ787213.1
Vicia faba plastid, complete genome	122	122	100%	8e-25	96%	KF042344.1
Vicia faba isolate HS879 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	122	122	100%	8e-25	96%	JX505737.1
Vicia faba var. minor tRNA-Leu (trnL) gene, partial sequence; chloroplast	122	122	100%	8e-25	96%	JN617168.1
Vicia faba var. major tRNA-Leu (trnL) gene, partial sequence; chloroplast	122	122	100%	8e-25	96%	JN617167.1
Vicia faba chloroplast transfer RNA-Leu(CAA)	122	122	100%	8e-25	96%	M55084.1
Vicia faba chloroplast tRNA-Leu, tRNA-Phe, tRNA-His, ORFX, NADH-deydrogenase genes & partial sequence ORFx & psbA genes	122	122	100%	8e-25	96%	X51471.1
Broad bean chloroplast genes for tRNA-Leu(CAA) and (UAA) and tRNA-Phe	122	122	100%	8e-25	96%	X02444.1
Melilotus albus isolate xt_plant115 tRNA-Leu (trnL) gene, intron; chloroplast	114	114	100%	1e-22	92%	KJ746436.1
Tracheophyta environmental sample clone N-11 tRNA-Leu (trnL) gene, partial sequence; chloroplast	114	114	100%	1e-22	92%	KF616419.1
Tracheophyta environmental sample clone N-3 tRNA-Leu (trnL) gene, partial sequence; chloroplast	114	114	100%	1e-22	92%	KF616411.1
Tracheophyta environmental sample clone N-6 tRNA-Leu (trnL) gene, partial sequence; chloroplast	114	114	100%	1e-22	92%	KF616414.1
Tracheophyta environmental sample clone N-5 tRNA-Leu (trnL) gene, partial sequence; chloroplast	114	114	100%	1e-22	92%	KF616413.1
Tracheophyta environmental sample clone N-4 tRNA-Leu (trnL) gene, partial sequence; chloroplast	114	114	100%	1e-22	92%	KF616412.1
Melilotus alba tRNA-Leu (trnL) gene, intron; chloroplast	114	114	100%	1e-22	92%	DQ311713.1
Melilotus alba chloroplast tRNA-Leu (trnL) gene, intron sequence	114	114	100%	1e-22	92%	AF124232.1
Tracheophyta environmental sample clone N-1 tRNA-Leu (trnL) gene, partial sequence; chloroplast	113	113	100%	4e-22	91%	KF616409.1
Vicia cypria isolate HS866 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	109	109	100%	5e-21	91%	JX505734.1
Vicia koeieana isolate 7619 tRNA-Leu (trnL) gene, partial sequence; chloroplast	107	107	100%	2e-20	90%	KJ787256.1
Tracheophyta environmental sample clone N-2 tRNA-Leu (trnL) gene, partial sequence; chloroplast	107	107	100%	2e-20	91%	KF616410.1
Ononis hirta tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	107	107	100%	2e-20	91%	GQ488565.1
Ononis varelae tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	90%	GQ488605.1
Porana volubilis tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe	105	105	100%	6e-20	92%	AY101137.1

(trnF) gene, partial sequence; chloroplast genes for chloroplast products						
Vicia lunata isolate V25 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	87%	JX505749.1
Ononis dentata tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	87%	GQ488559.1
Evolvulus alsinoides trnL-trnF intergenic spacer, partial sequence; chloroplast	100	100	100%	3e-18	91%	KR738653.1
Evolvulus alsinoides trnL-trnF intergenic spacer, partial sequence; chloroplast	100	100	100%	3e-18	91%	KR738561.1
Evolvulus alsinoides trnL-trnF intergenic spacer, partial sequence; chloroplast	100	100	100%	3e-18	91%	KR738174.1
Evolvulus alsinoides trnL-trnF intergenic spacer, partial sequence; chloroplast	100	100	100%	3e-18	91%	KR737964.1
Astragalus pectinatus isolate CP18 tRNA-Leu (trnL) gene, partial sequence; chloroplast	100	100	100%	3e-18	88%	KP208342.1
Ipomoea tricolor chloroplast, partial genome	100	100	100%	3e-18	91%	KF242495.1
Trigonella suavissima isolate EC 583624 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	100	100	100%	3e-18	86%	JX274187.1
Trigonella suavissima isolate EC 583623 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	100	100	100%	3e-18	86%	JX274186.1
Convolvulus arvensis voucher AV01 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	100	100	100%	3e-18	91%	KC786130.1
Datura stramonium isolate NN003 chloroplast, complete genome	100	100	100%	3e-18	91%	JN662489.1
Mandragora chinghaiensis voucher T. Tu Tu521-1 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	100	100	100%	3e-18	91%	JX067474.1
Evolvulus pilosus tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	100	100	100%	3e-18	91%	HQ412973.1
Solanum abutiloides isolate UPG0083 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	100	100	100%	3e-18	91%	HM006829.1
Astragalus polaris tRNA-Leu (trnL) gene, partial sequence; chloroplast	100	100	100%	3e-18	88%	GQ244622.1
Solandra brachycalyx voucher Plowman & Gentry 2957 (MO) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	100	100	100%	3e-18	91%	EU581062.1
Sclerophylax gilliesii voucher Bartlett s.n. (UC) tRNA-Leu (trnL) gene, partial sequence; chloroplast	100	100	100%	3e-18	91%	EU581059.1
Nicandra physalodes voucher Olmstead S-38 (WTU) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	100	100	100%	3e-18	91%	EU581032.1
Astragalus polaris tRNA-Leu (trnL) gene, intron	100	100	100%	3e-18	88%	DQ860525.1
Convolvulus arvensis trnL gene, intron; chloroplast	100	100	100%	3e-18	91%	AY558832.1
Solanum abutiloides RGO259 tRNA-Thr (trnT) gene, partial sequence; tRNA-Leu (trnL) gene, complete sequence; and tRNA-Phe (trnF) gene, partial sequence;	100	100	100%	3e-18	91%	AY266236.1

chloroplast genes for chloroplast products						
Astragalus layneae voucher ASLA-4 tRNA-Leu (trnL) gene, partial sequence; and trnL-trnF intergenic spacer, complete sequence; chloroplast	100	100	100%	3e-18	88%	DQ403850.1
Astragalus layneae voucher ASLA-1 tRNA-Leu (trnL) gene, partial sequence; and trnL-trnF intergenic spacer, complete sequence; chloroplast	100	100	100%	3e-18	88%	DQ403849.1
Astragalus didymocarpus voucher ASDI-16 tRNA-Leu (trnL) gene, partial sequence; and trnL-trnF intergenic spacer, complete sequence; chloroplast	100	100	100%	3e-18	88%	DQ403848.1
Astragalus didymocarpus voucher ASDI-2 tRNA-Leu (trnL) gene, partial sequence; and trnL-trnF intergenic spacer, complete sequence; chloroplast	100	100	100%	3e-18	88%	DQ403847.1
Astragalus didymocarpus voucher ASDI-1 tRNA-Leu (trnL) gene, partial sequence; and trnL-trnF intergenic spacer, complete sequence; chloroplast	100	100	100%	3e-18	88%	DQ403846.1
Astragalus jaegerianus voucher ASJA-1 tRNA-Leu (trnL) gene, partial sequence; and trnL-trnF intergenic spacer, complete sequence; chloroplast	100	100	100%	3e-18	88%	DQ403845.1
Maripa paniculata tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast genes for chloroplast products	100	100	100%	3e-18	91%	AY101155.1
Neuropeltis acuminata tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast genes for chloroplast products	100	100	100%	3e-18	91%	AY101142.1
Breweria rotundifolia tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast genes for chloroplast products	100	100	100%	3e-18	91%	AY101123.1
Evolvulus nuttalianus tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast genes for chloroplast products	100	100	100%	3e-18	91%	AY101122.1
Evolvulus glomeratus tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast genes for chloroplast products	100	100	100%	3e-18	91%	AY101121.1
Seddera hirsuta tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast genes for chloroplast products	100	100	100%	3e-18	91%	AY101119.1
Convolvulus arvensis tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast genes for chloroplast products	100	100	100%	3e-18	91%	AY101102.1
Calystegia sepium tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast genes for chloroplast products	100	100	100%	3e-18	91%	AY101101.1
Calystegia macrostegia tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast genes for chloroplast products	100	100	100%	3e-18	91%	AY101100.1
Operculina turpethum tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe	100	100	100%	3e-18	91%	AY101097.1

(trnF) gene, partial sequence; chloroplast genes for chloroplast products						
Ipomoea alba tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast genes for chloroplast products	100	100	100%	3e-18	91%	AY101072.1
Nicandra physalodes chloroplast tRNA-Leu gene (partial), trnL-F intergenic spacer and tRNA-Phe gene (partial)	100	100	100%	3e-18	91%	AJ492268.1
Lycium ruthenicum chloroplast trnL (UAA) gene, intron sequence	100	100	100%	3e-18	90%	AB036585.1
Astragalus linifolius chloroplast tRNA-Leu (trnL) gene, intron sequence	100	100	100%	3e-18	88%	AF126978.1
Astragalus bodinii chloroplast tRNA-Leu (trnL) gene, intron sequence	100	100	100%	3e-18	88%	AF126977.1
Astragalus gilviflorus chloroplast tRNA-Leu (trnL) gene, intron sequence	100	100	100%	3e-18	88%	AF126976.1
Astragalus douglasii chloroplast tRNA-Leu (trnL) gene, intron sequence	100	100	100%	3e-18	88%	AF126974.1
Astragalus palanae var. palanae chloroplast tRNA-Leu (trnL) gene, intron sequence	100	100	100%	3e-18	88%	AF126971.1
Astragalus sabulonum chloroplast tRNA-Leu (trnL) gene, intron sequence	100	100	100%	3e-18	88%	AF126969.1
Ipomoea cairica trnL-trnF intergenic spacer, partial sequence; chloroplast	98.7	98.7	100%	9e-18	91%	KR738692.1
Ipomoea cairica trnL-trnF intergenic spacer, partial sequence; chloroplast	98.7	98.7	100%	9e-18	91%	KR738278.1
Ipomoea cairica trnL-trnF intergenic spacer, partial sequence; chloroplast	98.7	98.7	100%	9e-18	91%	KR738161.1
Ipomoea cairica trnL-trnF intergenic spacer, partial sequence; chloroplast	98.7	98.7	100%	9e-18	91%	KR737877.1
Melilotus officinalis isolate CP46 tRNA-Leu (trnL) gene, partial sequence; chloroplast	98.7	98.7	100%	9e-18	83%	KP208370.1
Astragalus flexuosus isolate CP17 tRNA-Leu (trnL) gene, partial sequence; chloroplast	98.7	98.7	98%	9e-18	88%	KP208341.1
Melilotus officinalis isolate xt_plant51 tRNA-Leu (trnL) gene, intron; chloroplast	98.7	98.7	100%	9e-18	83%	KJ746435.1
Ebenus armitagei chloroplast DNA, tRNA-Leu (trnL) and trnL-trnF intergenic spacer, complete sequence, specimen_voucher: MSB:1015	98.7	98.7	100%	9e-18	88%	AB854523.1
Ipomoea cairica chloroplast, partial genome	98.7	98.7	100%	9e-18	91%	KF242480.1
Trigonella balansae isolate EC 546586 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	98.7	98.7	100%	9e-18	83%	JX274188.1
Trigonella cretica isolate EC 583577 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	98.7	98.7	100%	9e-18	83%	JX274153.1
Trigonella cretica isolate EC 583576 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	98.7	98.7	100%	9e-18	83%	JX274152.1
Trigonella cretica isolate EC 583575 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	98.7	98.7	100%	9e-18	83%	JX274151.1
Trigonella coerulescens isolate EC 583574 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	98.7	98.7	100%	9e-18	83%	JX274150.1
Trigonella coerulescens isolate EC 583573 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	98.7	98.7	100%	9e-18	83%	JX274149.1
Trigonella caerulea isolate EC 583569 tRNA-Leu (trnL) gene and trnL-trnF						

intergenic spacer, partial sequence; chloroplast	98.7	98.7	100%	9e-18	83%	JX274147.1
Trigonella caerulea isolate EC 583567 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	98.7	98.7	100%	9e-18	83%	JX274145.1
Trigonella balansae isolate EC 583507 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	98.7	98.7	100%	9e-18	83%	JX274137.1
Trigonella anguina isolate EC 583495 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	98.7	98.7	100%	9e-18	83%	JX274134.1
Melilotus officinalis voucher personal collection:I. Hiiesalu 47 tRNA-Leu (trnL) gene, partial sequence; chloroplast	98.7	98.7	100%	9e-18	83%	HM590318.1
Trigonella caerulea tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	98.7	98.7	100%	9e-18	83%	GQ488615.1
Ononis reclinata subsp. reclinata tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	98.7	98.7	100%	9e-18	86%	GQ488586.1
Ononis filicaulis tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	98.7	98.7	100%	9e-18	86%	GQ488561.1
Ononis macrosperma tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	98.7	98.7	100%	9e-18	86%	GQ488554.1
Melilotus albus chloroplast DNA, tRNA-Leu (trnL) and trnL-trnF intergenic spacer, partial sequence, specimen_voucher: TUH:19700	98.7	98.7	100%	9e-18	83%	AB546813.1
Melilotus officinalis chloroplast DNA, tRNA-Leu (trnL) and trnL-trnF intergenic spacer, partial sequence, specimen_voucher: TUH:7346	98.7	98.7	100%	9e-18	83%	AB546812.1
Lycianthes shanesii voucher Bohs 2721 (UT) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	98.7	98.7	100%	9e-18	90%	EU581021.1
Lycianthes multiflora voucher Bohs 2902 (UT) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	98.7	98.7	100%	9e-18	90%	EU581019.1
Lycianthes glandulosa voucher BIRM S.1616/75 (BIRM) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	98.7	98.7	100%	9e-18	90%	EU581017.1
Ononis cristata subsp. cristata tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	96.9	96.9	100%	3e-17	87%	GQ488558.1

Alignments

Vicia faba isolate 7612 tRNA-Leu (trnL) gene, partial sequence; chloroplast
Sequence ID: **gb|KJ787213.1|** Length: 487 Number of Matches: 1
Range 1: 83 to 159

Score	Expect	Identities	Gaps	Strand	Frame
122 bits(134)	8e-25()	74/77(96%)	1/77(1%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCTGAAAACAGAAAACTAAAAGTTCAG-AAAAAAG  59
            ||||||||||||||||||||||||||| ||||||| |||||||||||||||| |||||||
Sbjct  83   GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAG  142

Query  60   GATAGGTGCAGAGACTC  76
            |||||||||||||||||
Sbjct  143  GATAGGTGCAGAGACTC  159
```

Vicia faba plastid, complete genome

Sequence ID: **gb|KF042344.1|** Length: 123722 Number of Matches: 1
Range 1: 118542 to 118618

Score	Expect	Identities	Gaps	Strand	Frame
122 bits(134)	8e-25()	74/77(96%)	1/77(1%)	Plus/Plus	

Features:

```
Query  1       GGCAATCCTGAGCCAAATCCTTCTTTCTGAAAACAGAAAACTAAAAGTTCAG-AAAAAAG  59
               ||||||||||||||||||||||||||| ||||||| |||||||||||||||| |||||||
Sbjct  118542  GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAG  118601

Query  60      GATAGGTGCAGAGACTC  76
               |||||||||||||||||
Sbjct  118602  GATAGGTGCAGAGACTC  118618
```

Vicia faba isolate HS879 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast

Sequence ID: **gb|JX505737.1|** Length: 604 Number of Matches: 1
Range 1: 66 to 142

Score	Expect	Identities	Gaps	Strand	Frame
122 bits(134)	8e-25()	74/77(96%)	1/77(1%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCTGAAAACAGAAAACTAAAAGTTCAG-AAAAAAG  59
            ||||||||||||||||||||||||||| ||||||| |||||||||||||||| |||||||
Sbjct  66   GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAG  125

Query  60   GATAGGTGCAGAGACTC  76
            |||||||||||||||||
Sbjct  126  GATAGGTGCAGAGACTC  142
```

Vicia faba var. minor tRNA-Leu (trnL) gene, partial sequence; chloroplast

Sequence ID: **gb|JN617168.1|** Length: 938 Number of Matches: 1
Range 1: 554 to 630

Score	Expect	Identities	Gaps	Strand	Frame
122 bits(134)	8e-25()	74/77(96%)	1/77(1%)	Plus/Minus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCTGAAAACAGAAAACTAAAAGTTCAGAA-AAAAG  59
            ||||||||||||||||||||||||||| ||||||| |||||||||||||||||| |||||
Sbjct  630  GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAG  571

Query  60   GATAGGTGCAGAGACTC  76
            |||||||||||||||||
Sbjct  570  GATAGGTGCAGAGACTC  554
```

Vicia faba var. major tRNA-Leu (trnL) gene, partial sequence; chloroplast

Sequence ID: **gb|JN617167.1|** Length: 949 Number of Matches: 1
Range 1: 558 to 634

Score	Expect	Identities	Gaps	Strand	Frame
122 bits(134)	8e-25()	74/77(96%)	1/77(1%)	Plus/Minus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCTGAAAACAGAAAACTAAAAGTTCAGAA-AAAAG  59
            ||||||||||||||||||||||||||| ||||||| |||||||||||||||||| |||||
Sbjct  634  GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAG  575

Query  60   GATAGGTGCAGAGACTC  76
            |||||||||||||||||
Sbjct  574  GATAGGTGCAGAGACTC  558
```

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Basic Local Alignment Search Tool

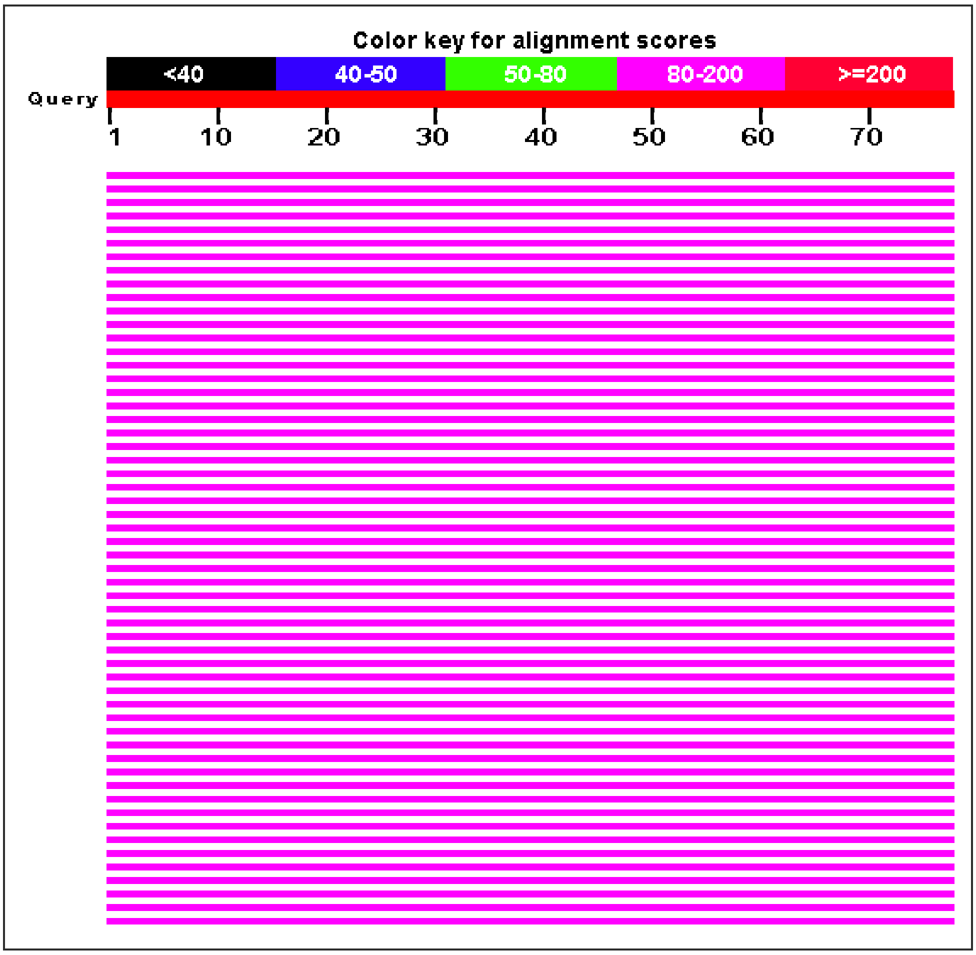
NCBI/ BLAST/ blastn suite/ **Formatting Results - BT6E900N014**
  Formatting options
  Download
Blast report description

MM745.1D_trnL_Clone2,5,6

RID	BT6E900N014 (Expires on 02-12 21:25 pm)		
Query ID	lcl|Query_195251	**Database Name**	nr
Description	c2	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	77		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Vicia faba isolate 7612 tRNA-Leu (trnL) gene, partial sequence; chloroplast	134	134	100%	1e-28	99%	KJ787213.1
Vicia faba plastid, complete genome	134	134	100%	1e-28	99%	KF042344.1
Vicia faba isolate HS879 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	134	134	100%	1e-28	99%	JX505737.1
Vicia faba var. minor tRNA-Leu (trnL) gene, partial sequence; chloroplast	134	134	100%	1e-28	99%	JN617168.1
Vicia faba var. major tRNA-Leu (trnL) gene, partial sequence; chloroplast	134	134	100%	1e-28	99%	JN617167.1
Vicia faba chloroplast transfer RNA-Leu(CAA)	134	134	100%	1e-28	99%	M55084.1
Vicia faba chloroplast tRNA-Leu, tRNA-Phe, tRNA-His, ORFX, NADH-deydrogenase genes & partial sequence ORFx & psbA genes	134	134	100%	1e-28	99%	X51471.1
Broad bean chloroplast genes for tRNA-Leu(CAA) and (UAA) and tRNA-Phe	134	134	100%	1e-28	99%	X02444.1
Melilotus albus isolate xt_plant115 tRNA-Leu (trnL) gene, intron; chloroplast	122	122	100%	8e-25	95%	KJ746436.1
Tracheophyta environmental sample clone N-11 tRNA-Leu (trnL) gene, partial sequence; chloroplast	122	122	100%	8e-25	95%	KF616419.1
Tracheophyta environmental sample clone N-3 tRNA-Leu (trnL) gene, partial sequence; chloroplast	122	122	100%	8e-25	95%	KF616411.1
Tracheophyta environmental sample clone N-6 tRNA-Leu (trnL) gene, partial sequence; chloroplast	122	122	100%	8e-25	95%	KF616414.1
Tracheophyta environmental sample clone N-5 tRNA-Leu (trnL) gene, partial sequence; chloroplast	122	122	100%	8e-25	95%	KF616413.1
Tracheophyta environmental sample clone N-4 tRNA-Leu (trnL) gene, partial sequence; chloroplast	122	122	100%	8e-25	95%	KF616412.1
Melilotus alba tRNA-Leu (trnL) gene, intron; chloroplast	122	122	100%	8e-25	95%	DQ311713.1
Melilotus alba chloroplast tRNA-Leu (trnL) gene, intron sequence	122	122	100%	8e-25	95%	AF124232.1
Tracheophyta environmental sample clone N-1 tRNA-Leu (trnL) gene, partial sequence; chloroplast	120	120	100%	3e-24	94%	KF616409.1
Tracheophyta environmental sample clone N-2 tRNA-Leu (trnL) gene, partial sequence; chloroplast	116	116	100%	4e-23	94%	KF616410.1
Vicia cypria isolate HS866 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	113	113	100%	4e-22	92%	JX505734.1
Vicia lunata isolate V25 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	111	111	100%	1e-21	89%	JX505749.1
Ononis hirta tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	111	111	100%	1e-21	93%	GQ488565.1
Ononis dentata tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	111	111	100%	1e-21	89%	GQ488559.1
Trigonella suavissima isolate EC 583624 tRNA-Leu (trnL) gene and trnL-trnF	109	109	100%	5e-21	88%	JX274187.1

intergenic spacer, partial sequence; chloroplast						
Trigonella suavissima isolate EC 583623 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	109	109	100%	5e-21	88%	JX274186.1
Ononis varelae tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	109	109	100%	5e-21	91%	GQ488605.1
Melilotus officinalis isolate CP46 tRNA-Leu (trnL) gene, partial sequence; chloroplast	105	105	100%	6e-20	85%	KP208370.1
Melilotus officinalis isolate xt_plant51 tRNA-Leu (trnL) gene, intron; chloroplast	105	105	100%	6e-20	85%	KJ746435.1
Trigonella balansae isolate EC 546586 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	JX274188.1
Trigonella maritima isolate EC 583601 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	86%	JX274171.1
Trigonella cretica isolate EC 583577 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	JX274153.1
Trigonella cretica isolate EC 583576 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	JX274152.1
Trigonella cretica isolate EC 583575 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	JX274151.1
Trigonella coerulescens isolate EC 583574 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	JX274150.1
Trigonella coerulescens isolate EC 583573 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	JX274149.1
Trigonella caerulea isolate EC 583569 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	JX274147.1
Trigonella caerulea isolate EC 583567 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	JX274145.1
Trigonella balansae isolate EC 583507 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	JX274137.1
Trigonella anguina isolate EC 583495 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	JX274134.1
Melilotus officinalis voucher personal collection:I. Hiiesalu 47 tRNA-Leu (trnL) gene, partial sequence; chloroplast	105	105	100%	6e-20	85%	HM590318.1
Trigonella caerulea tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	GQ488615.1
Ononis speciosa tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	86%	GQ488593.1
Ononis filicaulis tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	88%	GQ488561.1
Ononis cristata subsp. cristata tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	90%	GQ488558.1
Melilotus albus chloroplast DNA, tRNA-Leu						

(trnL) and trnL-trnF intergenic spacer, partial sequence, specimen_voucher: TUH:19700	105	105	100%	6e-20	85%	AB546813.1
Melilotus officinalis chloroplast DNA, tRNA-Leu (trnL) and trnL-trnF intergenic spacer, partial sequence, specimen_voucher: TUH:7346	105	105	100%	6e-20	85%	AB546812.1
Melilotus officinalis tRNA-Leu (trnL) gene, intron; chloroplast	105	105	100%	6e-20	85%	DQ311714.1
Melilotus officinalis chloroplast tRNA-Leu (trnL) gene, intron sequence	105	105	100%	6e-20	85%	AF124233.1
Trigonella strangulata isolate EC 583622 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	84%	JX274185.1
Trigonella stellata isolate EC 583621 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	JX274184.1
Trigonella filipes isolate EC 583584 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	84%	JX274158.1
Ononis natrix tRNA-Leu (trnL) gene, intron; chloroplast	104	104	100%	2e-19	85%	HQ323975.1
Ononis zygantha tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488611.1
Ononis viscosa subsp. breviflora tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488609.1
Ononis tazaensis tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488600.1
Ononis sicula tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488591.1
Ononis serotina tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488589.1
Ononis pubescens tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488582.1
Ononis pseudoserotina tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488581.1
Ononis polysperma tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488580.1
Ononis ornithopodioides tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488576.1
Ononis natrix subsp. arganietorum tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488574.1
Ononis megalostachys tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488570.1
Ononis hebecarpa tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488563.1
Ononis biflora tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488555.1
Ononis aurasiaca tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488553.1
Ononis atlantica tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488552.1
Ononis angustissima subsp. longifolia						

tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488550.1
Ononis angustissima subsp. angustissima tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488549.1
Medicago papillosa chloroplast, complete genome	102	102	100%	8e-19	84%	KJ850241.1
Medicago hybrida chloroplast, complete genome	102	102	100%	8e-19	84%	KJ850240.1
Lathyrus inconspicuus chloroplast, complete genome	102	102	100%	8e-19	84%	KJ850236.1
Lathyrus clymenum chloroplast, complete genome	102	102	100%	8e-19	84%	KJ850235.1
Lathyrus venosus chloroplast, complete genome	102	102	100%	8e-19	84%	KJ806202.1
Lathyrus pubescens chloroplast, complete genome	102	102	100%	8e-19	84%	KJ806200.1
Lathyrus palustris chloroplast, complete genome	102	102	100%	8e-19	84%	KJ806199.1
Lathyrus ochroleucus chloroplast, complete genome	102	102	100%	8e-19	84%	KJ806198.1
Lathyrus ochroleucus chloroplast, complete genome	102	102	100%	8e-19	84%	KJ806197.1
Lathyrus japonicus chloroplast, complete genome	102	102	100%	8e-19	84%	KJ806195.1
Lathyrus japonicus chloroplast, complete genome	102	102	100%	8e-19	84%	KJ806194.1
Lathyrus graminifolius chloroplast, complete genome	102	102	100%	8e-19	84%	KJ806193.1
Vicia unijuga isolate L-F_WTC5 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699023.1
Vicia unijuga isolate L-F_WTC4 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699022.1
Vicia unijuga isolate L-F_WTC3 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699021.1
Vicia unijuga isolate L-F_WTC2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699020.1
Vicia unijuga isolate L-F_WTC1 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699019.1
Vicia amoena isolate L-F_SY5 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699018.1
Vicia amoena isolate L-F_SY4 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699017.1
Vicia amoena isolate L-F_SY3 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699016.1
Vicia amoena isolate L-F_SY2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699015.1
Vicia amoena isolate L-F_SY1 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699014.1
Vicia amurensis isolate L-F_HLJ5 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699013.1
Vicia amurensis isolate L-F_HLJ4 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699012.1
Vicia amurensis isolate L-F_HLJ3 tRNA-						

Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699011.1
Vicia amurensis isolate L-F_HLJ2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699010.1
Vicia amurensis isolate L-F_HLJ1 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699009.1
Vicia pseudo-orobus isolate L-F_DY5 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699003.1
Vicia pseudo-orobus isolate L-F_DY4 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699002.1
Vicia pseudo-orobus isolate L-F_DY3 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699001.1
Vicia pseudo-orobus isolate L-F_DY2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699000.1
Lathyrus crassipes isolate P025 tRNA-Leu (trnL) gene, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP057648.1

Alignments

Vicia faba isolate 7612 tRNA-Leu (trnL) gene, partial sequence; chloroplast
Sequence ID: **gb|KJ787213.1|** Length: 487 Number of Matches: 1
Range 1: 83 to 159

Score	Expect	Identities	Gaps	Strand	Frame
134 bits(148)	1e-28()	76/77(99%)	0/77(0%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCaaaaacaaaaaactaaaagttcagaaaaaaaG  60
            |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  83   GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAG  142

Query  61   GATAGGTGCAGAGACTC  77
            |||||||||||||||||
Sbjct  143  GATAGGTGCAGAGACTC  159
```

Vicia faba plastid, complete genome
Sequence ID: **gb|KF042344.1|** Length: 123722 Number of Matches: 1
Range 1: 118542 to 118618

Score	Expect	Identities	Gaps	Strand	Frame
134 bits(148)	1e-28()	76/77(99%)	0/77(0%)	Plus/Plus	

Features:

```
Query  1       GGCAATCCTGAGCCAAATCCTTCTTTCCaaaaacaaaaaactaaaagttcagaaaaaaaG  60
               |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  118542  GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAG  118601

Query  61      GATAGGTGCAGAGACTC  77
               |||||||||||||||||
Sbjct  118602  GATAGGTGCAGAGACTC  118618
```

Vicia faba isolate HS879 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|JX505737.1|** Length: 604 Number of Matches: 1
Range 1: 66 to 142

Score	Expect	Identities	Gaps	Strand	Frame
134 bits(148)	1e-28()	76/77(99%)	0/77(0%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCaaaaacaaaaaactaaaagttcagaaaaaaaG  60
            |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  66   GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAG  125

Query  61   GATAGGTGCAGAGACTC  77
            |||||||||||||||||
Sbjct  126  GATAGGTGCAGAGACTC  142
```

Vicia faba var. minor tRNA-Leu (trnL) gene, partial sequence; chloroplast
Sequence ID: **gb|JN617168.1|** Length: 938 Number of Matches: 1
Range 1: 554 to 630

Score	**Expect**	**Identities**	**Gaps**	**Strand**	**Frame**
134 bits(148)	1e-28()	76/77(99%)	0/77(0%)	Plus/Minus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCaaaaacaaaaaactaaaagttcagaaaaaaaG  60
            |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  630  GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAG  571

Query  61   GATAGGTGCAGAGACTC  77
            |||||||||||||||||
Sbjct  570  GATAGGTGCAGAGACTC  554
```

Vicia faba var. major tRNA-Leu (trnL) gene, partial sequence; chloroplast
Sequence ID: **gb|JN617167.1|** Length: 949 Number of Matches: 1
Range 1: 558 to 634

Score	**Expect**	**Identities**	**Gaps**	**Strand**	**Frame**
134 bits(148)	1e-28()	76/77(99%)	0/77(0%)	Plus/Minus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCaaaaacaaaaaactaaaagttcagaaaaaaaG  60
            |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  634  GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAG  575

Query  61   GATAGGTGCAGAGACTC  77
            |||||||||||||||||
Sbjct  574  GATAGGTGCAGAGACTC  558
```

BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BT5RJK6K014**
  Formatting options
  Download
Blast report description

MM745.1C_trnL_Clone8

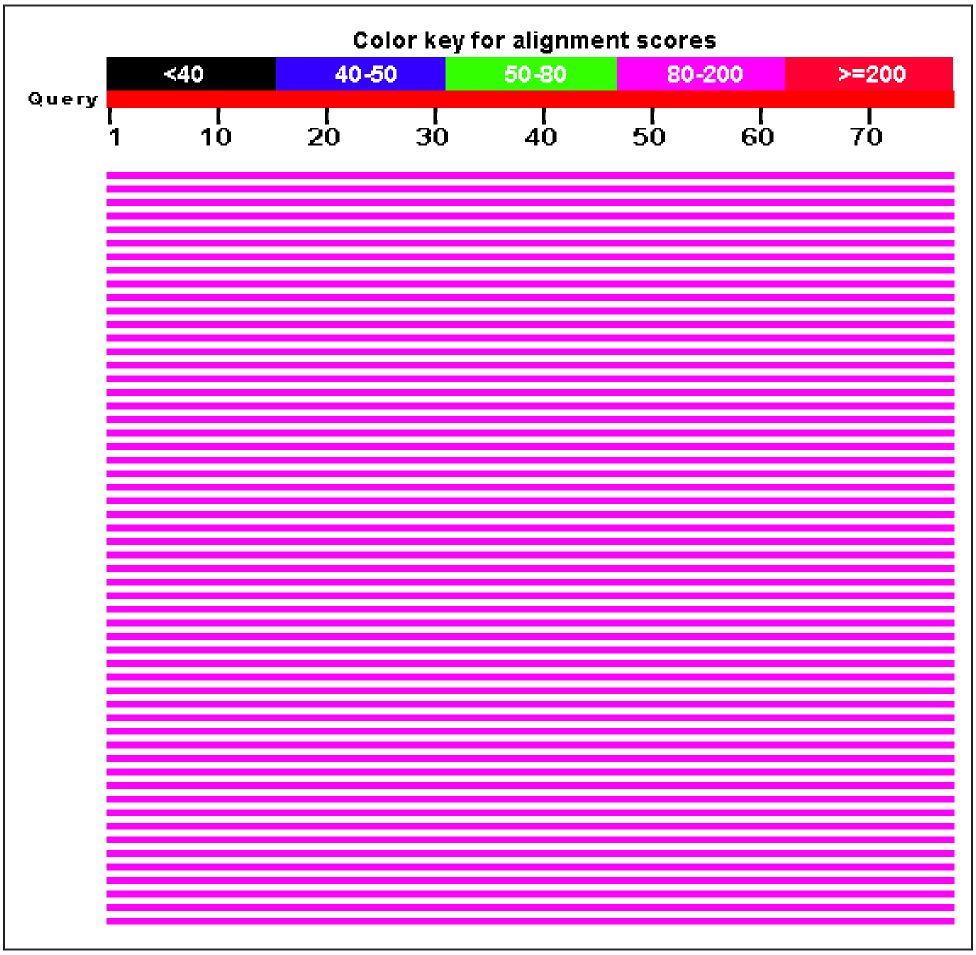
RID BT5RJK6K014 (Expires on 02-12 21:13 pm)

Query ID lcl|Query_121199
Description c8
Molecule type nucleic acid
Query Length 77

Database Name nr
Description Nucleotide collection (nt)
Program BLASTN 2.3.1+

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Vicia faba isolate 7612 tRNA-Leu (trnL) gene, partial sequence; chloroplast	134	134	100%	1e-28	99%	KJ787213.1
Vicia faba plastid, complete genome	134	134	100%	1e-28	99%	KF042344.1
Vicia faba isolate HS879 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	134	134	100%	1e-28	99%	JX505737.1
Vicia faba var. minor tRNA-Leu (trnL) gene, partial sequence; chloroplast	134	134	100%	1e-28	99%	JN617168.1
Vicia faba var. major tRNA-Leu (trnL) gene, partial sequence; chloroplast	134	134	100%	1e-28	99%	JN617167.1
Vicia faba chloroplast transfer RNA-Leu(CAA)	134	134	100%	1e-28	99%	M55084.1
Vicia faba chloroplast tRNA-Leu, tRNA-Phe, tRNA-His, ORFX, NADH-deydrogenase genes & partial sequence ORFx & psbA genes	134	134	100%	1e-28	99%	X51471.1
Broad bean chloroplast genes for tRNA-Leu(CAA) and (UAA) and tRNA-Phe	134	134	100%	1e-28	99%	X02444.1
Melilotus albus isolate xt_plant115 tRNA-Leu (trnL) gene, intron; chloroplast	122	122	100%	8e-25	95%	KJ746436.1
Tracheophyta environmental sample clone N-11 tRNA-Leu (trnL) gene, partial sequence; chloroplast	122	122	100%	8e-25	95%	KF616419.1
Tracheophyta environmental sample clone N-3 tRNA-Leu (trnL) gene, partial sequence; chloroplast	122	122	100%	8e-25	95%	KF616411.1
Tracheophyta environmental sample clone N-6 tRNA-Leu (trnL) gene, partial sequence; chloroplast	122	122	100%	8e-25	95%	KF616414.1
Tracheophyta environmental sample clone N-5 tRNA-Leu (trnL) gene, partial sequence; chloroplast	122	122	100%	8e-25	95%	KF616413.1
Tracheophyta environmental sample clone N-4 tRNA-Leu (trnL) gene, partial sequence; chloroplast	122	122	100%	8e-25	95%	KF616412.1
Melilotus alba tRNA-Leu (trnL) gene, intron; chloroplast	122	122	100%	8e-25	95%	DQ311713.1
Melilotus alba chloroplast tRNA-Leu (trnL) gene, intron sequence	122	122	100%	8e-25	95%	AF124232.1
Tracheophyta environmental sample clone N-1 tRNA-Leu (trnL) gene, partial sequence; chloroplast	120	120	100%	3e-24	94%	KF616409.1
Vicia cypria isolate HS866 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	118	118	100%	1e-23	94%	JX505734.1
Tracheophyta environmental sample clone N-2 tRNA-Leu (trnL) gene, partial sequence; chloroplast	116	116	100%	4e-23	94%	KF616410.1
Ononis hirta tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	116	116	100%	4e-23	94%	GQ488565.1
Ononis varelae tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	114	114	100%	1e-22	93%	GQ488605.1
Vicia lunata isolate V25 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	111	111	100%	1e-21	89%	JX505749.1
Ononis dentata tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial	111	111	100%	1e-21	89%	GQ488559.1

sequence; chloroplast						
Trigonella suavissima isolate EC 583624 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	109	109	100%	5e-21	88%	**JX274187.1**
Trigonella suavissima isolate EC 583623 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	109	109	100%	5e-21	88%	**JX274186.1**
Melilotus officinalis isolate CP46 tRNA-Leu (trnL) gene, partial sequence; chloroplast	105	105	100%	6e-20	85%	**KP208370.1**
Melilotus officinalis isolate xt_plant51 tRNA-Leu (trnL) gene, intron; chloroplast	105	105	100%	6e-20	85%	**KJ746435.1**
Trigonella balansae isolate EC 546586 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	**JX274188.1**
Trigonella maritima isolate EC 583601 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	86%	**JX274171.1**
Trigonella cretica isolate EC 583577 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	**JX274153.1**
Trigonella cretica isolate EC 583576 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	**JX274152.1**
Trigonella cretica isolate EC 583575 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	**JX274151.1**
Trigonella coerulescens isolate EC 583574 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	**JX274150.1**
Trigonella coerulescens isolate EC 583573 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	**JX274149.1**
Trigonella caerulea isolate EC 583569 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	**JX274147.1**
Trigonella caerulea isolate EC 583567 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	**JX274145.1**
Trigonella balansae isolate EC 583507 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	**JX274137.1**
Trigonella anguina isolate EC 583495 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	**JX274134.1**
Melilotus officinalis voucher personal collection:I. Hiiesalu 47 tRNA-Leu (trnL) gene, partial sequence; chloroplast	105	105	100%	6e-20	85%	**HM590318.1**
Trigonella caerulea tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	85%	**GQ488615.1**
Ononis speciosa tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	86%	**GQ488593.1**
Ononis filicaulis tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	88%	**GQ488561.1**
Ononis cristata subsp. cristata tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	6e-20	90%	**GQ488558.1**
Melilotus albus chloroplast DNA, tRNA-Leu						

(trnL) and trnL-trnF intergenic spacer, partial sequence, specimen_voucher: TUH:19700	105	105	100%	6e-20	85%	AB546813.1
Melilotus officinalis chloroplast DNA, tRNA-Leu (trnL) and trnL-trnF intergenic spacer, partial sequence, specimen_voucher: TUH:7346	105	105	100%	6e-20	85%	AB546812.1
Melilotus officinalis tRNA-Leu (trnL) gene, intron; chloroplast	105	105	100%	6e-20	85%	DQ311714.1
Melilotus officinalis chloroplast tRNA-Leu (trnL) gene, intron sequence	105	105	100%	6e-20	85%	AF124233.1
Trigonella strangulata isolate EC 583622 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	84%	JX274185.1
Trigonella stellata isolate EC 583621 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	JX274184.1
Trigonella filipes isolate EC 583584 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	84%	JX274158.1
Ononis natrix tRNA-Leu (trnL) gene, intron; chloroplast	104	104	100%	2e-19	85%	HQ323975.1
Ononis zygantha tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488611.1
Ononis viscosa subsp. breviflora tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488609.1
Ononis tazaensis tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488600.1
Ononis sicula tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488591.1
Ononis serotina tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488589.1
Ononis pubescens tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488582.1
Ononis pseudoserotina tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488581.1
Ononis polysperma tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488580.1
Ononis ornithopodioides tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488576.1
Ononis natrix subsp. arganietorum tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488574.1
Ononis megalostachys tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488570.1
Ononis hebecarpa tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488563.1
Ononis biflora tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488555.1
Ononis aurasiaca tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488553.1
Ononis atlantica tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	GQ488552.1
Ononis angustissima subsp. longifolia						

tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	**GQ488550.1**
Ononis angustissima subsp. angustissima tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	85%	**GQ488549.1**
Medicago papillosa chloroplast, complete genome	102	102	100%	8e-19	84%	**KJ850241.1**
Medicago hybrida chloroplast, complete genome	102	102	100%	8e-19	84%	**KJ850240.1**
Lathyrus inconspicuus chloroplast, complete genome	102	102	100%	8e-19	84%	**KJ850236.1**
Lathyrus clymenum chloroplast, complete genome	102	102	100%	8e-19	84%	**KJ850235.1**
Lathyrus venosus chloroplast, complete genome	102	102	100%	8e-19	84%	**KJ806202.1**
Lathyrus pubescens chloroplast, complete genome	102	102	100%	8e-19	84%	**KJ806200.1**
Lathyrus palustris chloroplast, complete genome	102	102	100%	8e-19	84%	**KJ806199.1**
Lathyrus ochroleucus chloroplast, complete genome	102	102	100%	8e-19	84%	**KJ806198.1**
Lathyrus ochroleucus chloroplast, complete genome	102	102	100%	8e-19	84%	**KJ806197.1**
Lathyrus japonicus chloroplast, complete genome	102	102	100%	8e-19	84%	**KJ806195.1**
Lathyrus japonicus chloroplast, complete genome	102	102	100%	8e-19	84%	**KJ806194.1**
Lathyrus graminifolius chloroplast, complete genome	102	102	100%	8e-19	84%	**KJ806193.1**
Vicia unijuga isolate L-F_WTC5 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	**KP699023.1**
Vicia unijuga isolate L-F_WTC4 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	**KP699022.1**
Vicia unijuga isolate L-F_WTC3 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	**KP699021.1**
Vicia unijuga isolate L-F_WTC2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	**KP699020.1**
Vicia unijuga isolate L-F_WTC1 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	**KP699019.1**
Vicia amoena isolate L-F_SY5 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	**KP699018.1**
Vicia amoena isolate L-F_SY4 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	**KP699017.1**
Vicia amoena isolate L-F_SY3 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	**KP699016.1**
Vicia amoena isolate L-F_SY2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	**KP699015.1**
Vicia amoena isolate L-F_SY1 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	**KP699014.1**
Vicia amurensis isolate L-F_HLJ5 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	**KP699013.1**
Vicia amurensis isolate L-F_HLJ4 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	**KP699012.1**
Vicia amurensis isolate L-F_HLJ3 tRNA-						

Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699011.1
Vicia amurensis isolate L-F_HLJ2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699010.1
Vicia amurensis isolate L-F_HLJ1 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699009.1
Vicia pseudo-orobus isolate L-F_DY5 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699003.1
Vicia pseudo-orobus isolate L-F_DY4 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699002.1
Vicia pseudo-orobus isolate L-F_DY3 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699001.1
Vicia pseudo-orobus isolate L-F_DY2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP699000.1
Lathyrus crassipes isolate P025 tRNA-Leu (trnL) gene, partial sequence; chloroplast	102	102	100%	8e-19	84%	KP057648.1

Alignments

Vicia faba isolate 7612 tRNA-Leu (trnL) gene, partial sequence; chloroplast
Sequence ID: **gb|KJ787213.1|** Length: 487 Number of Matches: 1
Range 1: 83 to 159

Score	Expect	Identities	Gaps	Strand	Frame
134 bits(148)	1e-28()	76/77(99%)	0/77(0%)	Plus/Plus	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCGaaaacaaaaaactaaaaGTTCAGAAAATAAG  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  83   GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAG  142

Query  61   GATAGGTGCAGAGACTC  77
            |||||||||||||||||
Sbjct  143  GATAGGTGCAGAGACTC  159
```

Vicia faba plastid, complete genome
Sequence ID: **gb|KF042344.1|** Length: 123722 Number of Matches: 1
Range 1: 118542 to 118618

Score	Expect	Identities	Gaps	Strand	Frame
134 bits(148)	1e-28()	76/77(99%)	0/77(0%)	Plus/Plus	

Features:

```
Query  1       GGCAATCCTGAGCCAAATCCTTCTTTCCGaaaacaaaaaactaaaaGTTCAGAAAATAAG  60
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  118542  GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAG  118601

Query  61      GATAGGTGCAGAGACTC  77
               |||||||||||||||||
Sbjct  118602  GATAGGTGCAGAGACTC  118618
```

Vicia faba isolate HS879 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|JX505737.1|** Length: 604 Number of Matches: 1
Range 1: 66 to 142

Score	Expect	Identities	Gaps	Strand	Frame
134 bits(148)	1e-28()	76/77(99%)	0/77(0%)	Plus/Plus	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCGaaaacaaaaaactaaaaGTTCAGAAAATAAG  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  66   GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAG  125

Query  61   GATAGGTGCAGAGACTC  77
            |||||||||||||||||
Sbjct  126  GATAGGTGCAGAGACTC  142
```

Vicia faba var. minor tRNA-Leu (trnL) gene, partial sequence; chloroplast
Sequence ID: **gb|JN617168.1|** Length: 938 Number of Matches: 1
Range 1: 554 to 630

Score	Expect	Identities	Gaps	Strand	Frame
134 bits(148)	1e-28()	76/77(99%)	0/77(0%)	Plus/Minus	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCGaaaacaaaaaactaaaaGTTCAGAAAATAAG  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  630  GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAG  571

Query  61   GATAGGTGCAGAGACTC  77
            |||||||||||||||||
Sbjct  570  GATAGGTGCAGAGACTC  554
```

Vicia faba var. major tRNA-Leu (trnL) gene, partial sequence; chloroplast
Sequence ID: **gb|JN617167.1|** Length: 949 Number of Matches: 1
Range 1: 558 to 634

Score	Expect	Identities	Gaps	Strand	Frame
134 bits(148)	1e-28()	76/77(99%)	0/77(0%)	Plus/Minus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCGaaaacaaaaaactaaaaGTTCAGAAAATAAG  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  634  GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAG  575

Query  61   GATAGGTGCAGAGACTC  77
            |||||||||||||||||
Sbjct  574  GATAGGTGCAGAGACTC  558
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BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BT5WT93K014**
Formatting options
Download
Blast report description

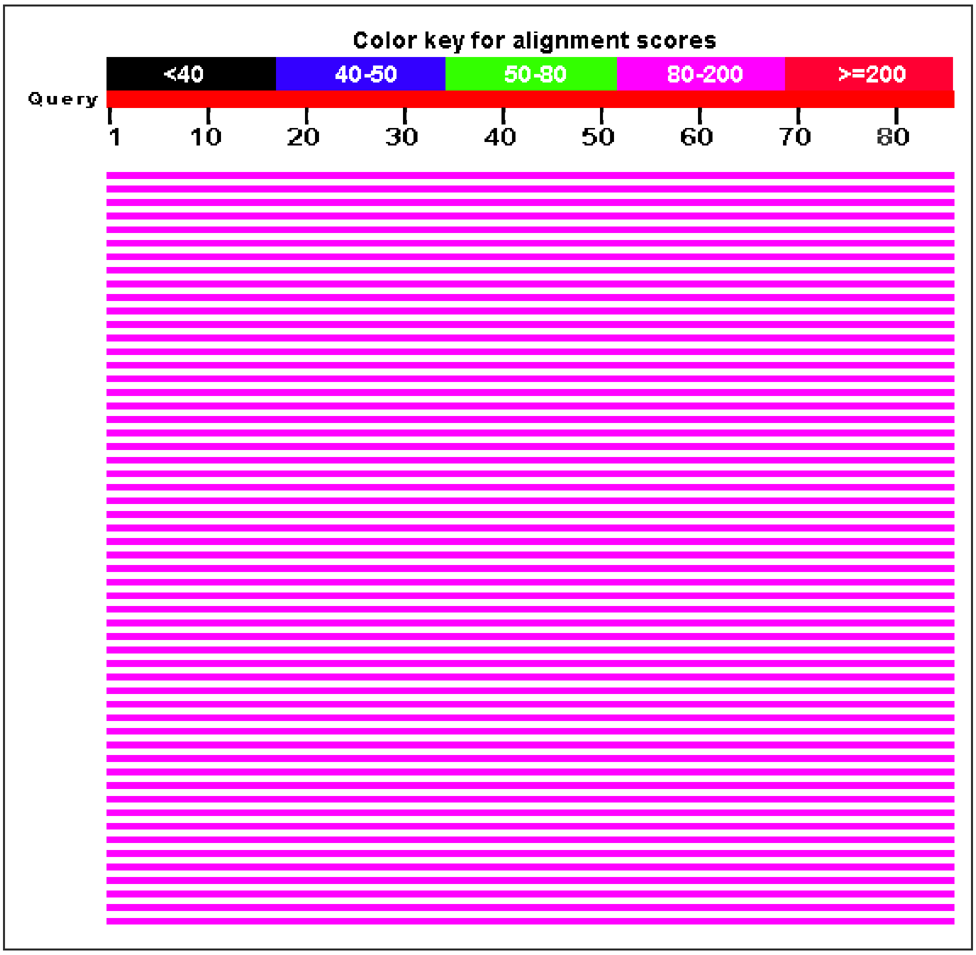
MM745.1C_trnL_Clone10

RID BT5WT93K014 (Expires on 02-12 21:15 pm)

Query ID	lcl|Query_14677	**Database Name**	nr
Description	c10	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	85		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Trigonella schlumbergeri isolate EC 583609 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	149	149	100%	7e-33	99%	JX274177.1
Trigonella arabica isolate EC 583496 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	149	149	100%	7e-33	99%	JX274135.1
Trigonella maritima isolate EC 583601 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	147	147	100%	2e-32	99%	JX274171.1
Trigonella maritima isolate EC 583600 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	147	147	100%	2e-32	99%	JX274170.1
Trigonella suavissima isolate EC 583624 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	145	145	100%	9e-32	99%	JX274187.1
Trigonella suavissima isolate EC 583623 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	145	145	100%	9e-32	99%	JX274186.1
Trigonella stellata isolate EC 583621 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	145	145	100%	9e-32	98%	JX274184.1
Trigonella coelesyriaca isolate EC 583565 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	143	143	100%	3e-31	97%	JX274144.1
Trigonella coelesyriaca isolate EC 583558 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	143	143	100%	3e-31	97%	JX274142.1
Trigonella coelesyriaca isolate EC 583557 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	143	143	100%	3e-31	97%	JX274141.1
Vicia pisiformis isolate Kenicer243 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	143	143	100%	3e-31	97%	JX505770.1
Vicia pisiformis isolate HS643 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	143	143	100%	3e-31	97%	JX505769.1
Vicia minutiflora isolate HV17 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	143	143	100%	3e-31	97%	JX505757.1
Lathyrus saxatilis isolate EDNA09_00968 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	143	143	100%	3e-31	97%	JX505692.1
Lathyrus saxatilis isolate HV39 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	143	143	100%	3e-31	97%	JX505691.1
Vicia unijuga isolate L-F_WTC5 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	KP699023.1
Vicia unijuga isolate L-F_WTC4 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	KP699022.1
Vicia unijuga isolate L-F_WTC3 tRNA-Leu (trnL), trnL-F intergenic spacer, partial	140	140	100%	4e-30	95%	KP699021.1

sequence; chloroplast						
Vicia unijuga isolate L-F_WTC2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	KP699020.1
Vicia unijuga isolate L-F_WTC1 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	KP699019.1
Vicia amoena isolate L-F_SY5 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	KP699018.1
Vicia amoena isolate L-F_SY4 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	KP699017.1
Vicia amoena isolate L-F_SY3 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	KP699016.1
Vicia amoena isolate L-F_SY2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	KP699015.1
Vicia amoena isolate L-F_SY1 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	KP699014.1
Vicia amurensis isolate L-F_HLJ5 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	KP699013.1
Vicia amurensis isolate L-F_HLJ4 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	KP699012.1
Vicia amurensis isolate L-F_HLJ3 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	KP699011.1
Vicia amurensis isolate L-F_HLJ2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	KP699010.1
Vicia amurensis isolate L-F_HLJ1 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	KP699009.1
Vicia pseudo-orobus isolate L-F_DY5 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	KP699003.1
Vicia pseudo-orobus isolate L-F_DY4 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	KP699002.1
Vicia pseudo-orobus isolate L-F_DY3 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	KP699001.1
Vicia pseudo-orobus isolate L-F_DY2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	KP699000.1
Vicia pseudo-orobus isolate L-F_DY1 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	KP698999.1
Vicia multicaulis isolate L-F_DJ4 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	KP698998.1
Vicia multicaulis isolate L-F_DJ3 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	KP698997.1
Vicia multicaulis isolate L-F_DJ2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	KP698996.1
Vicia multicaulis isolate L-F_DJ1 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	KP698995.1
Vicia ramuliflora isolate L-F_BY2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	KP698990.1
Vicia ramuliflora isolate L-F_BY1 tRNA-Leu (trnL), trnL-F intergenic spacer, partial	140	140	100%	4e-30	95%	KP698989.1

sequence; chloroplast						
Melilotus officinalis isolate CP46 tRNA-Leu (trnL) gene, partial sequence; chloroplast	140	140	100%	4e-30	95%	**KP208370.1**
Vicia cassubica isolate 7656 tRNA-Leu (trnL) gene, partial sequence; chloroplast	140	140	100%	4e-30	95%	**KJ787254.1**
Melilotus officinalis isolate xt_plant51 tRNA-Leu (trnL) gene, intron; chloroplast	140	140	100%	4e-30	95%	**KJ746435.1**
Trigonella balansae isolate EC 546586 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	**JX274188.1**
Trigonella cretica isolate EC 583577 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	**JX274153.1**
Trigonella cretica isolate EC 583576 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	**JX274152.1**
Trigonella cretica isolate EC 583575 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	**JX274151.1**
Trigonella caerulea isolate EC 583569 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	**JX274147.1**
Trigonella caerulea isolate EC 583568 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	**JX274146.1**
Trigonella caerulea isolate EC 583567 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	**JX274145.1**
Trigonella balansae isolate EC 583507 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	**JX274137.1**
Trigonella anguina isolate EC 583495 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	**JX274134.1**
Vicia venulosa isolate HS1163 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	**JX505783.1**
Vicia sparsiflora isolate Kenicer240 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	**JX505775.1**
Vicia multicaulis isolate HS1162 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	**JX505761.1**
Vicia montevidensis isolate HV18 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	**JX505760.1**
Vicia dumetorum isolate HS644 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	**JX505736.1**
Vicia costata isolate V23 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	**JX505731.1**
Vicia baicalensis isolate HV06 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	**JX505716.1**
Vicia amurensis isolate HV04 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	**JX505715.1**
Vicia americana isolate HV02 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	**JX505714.1**
Melilotus officinalis voucher personal collection:I. Hiiesalu 47 tRNA-Leu (trnL)	140	140	100%	4e-30	95%	**HM590318.1**

gene, partial sequence; chloroplast						
Melilotus albus chloroplast DNA, tRNA-Leu (trnL) and trnL-trnF intergenic spacer, partial sequence, specimen_voucher: TUH:19700	140	140	100%	4e-30	95%	AB546813.1
Melilotus officinalis chloroplast DNA, tRNA-Leu (trnL) and trnL-trnF intergenic spacer, partial sequence, specimen_voucher: TUH:7346	140	140	100%	4e-30	95%	AB546812.1
Vicia unijuga tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	95%	AY839408.1
Melilotus officinalis tRNA-Leu (trnL) gene, intron; chloroplast	140	140	100%	4e-30	95%	DQ311714.1
Melilotus officinalis chloroplast tRNA-Leu (trnL) gene, intron sequence	140	140	100%	4e-30	95%	AF124233.1
Trigonella strangulata isolate EC 583622 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	138	138	100%	1e-29	94%	JX274185.1
Trigonella filipes isolate EC 583584 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	138	138	100%	1e-29	94%	JX274158.1
Vicia balansae isolate 13048 tRNA-Leu (trnL) gene, partial sequence; chloroplast	136	136	100%	4e-29	94%	KJ787248.1
Ononis natrix tRNA-Leu (trnL) gene, intron; chloroplast	136	136	100%	4e-29	95%	HQ323975.1
Ononis viscosa subsp. breviflora tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	136	136	100%	4e-29	95%	GQ488609.1
Ononis tazaensis tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	136	136	100%	4e-29	95%	GQ488600.1
Ononis sicula tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	136	136	100%	4e-29	95%	GQ488591.1
Ononis serotina tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	136	136	100%	4e-29	95%	GQ488589.1
Ononis pubescens tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	136	136	100%	4e-29	95%	GQ488582.1
Ononis pseudoserotina tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	136	136	100%	4e-29	95%	GQ488581.1
Ononis ornithopodioides tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	136	136	100%	4e-29	95%	GQ488576.1
Ononis natrix subsp. arganietorum tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	136	136	100%	4e-29	95%	GQ488574.1
Ononis megalostachys tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	136	136	100%	4e-29	95%	GQ488570.1
Ononis aurasiaca tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	136	136	100%	4e-29	95%	GQ488553.1
Ononis atlantica tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	136	136	100%	4e-29	95%	GQ488552.1
Ononis angustissima subsp. longifolia tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	136	136	100%	4e-29	95%	GQ488550.1
Ononis angustissima subsp. angustissima tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	136	136	100%	4e-29	95%	GQ488549.1
Medicago papillosa chloroplast, complete	134	134	100%	2e-28	94%	KJ850241.1

genome						
Medicago hybrida chloroplast, complete genome	134	134	100%	2e-28	94%	KJ850240.1
Medicago falcata isolate 02MF tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	134	134	100%	2e-28	94%	KP174819.1
Medicago sativa isolate 01MS tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	134	134	100%	2e-28	94%	KP174818.1
Vicia crocea isolate 18395 tRNA-Leu (trnL) gene, partial sequence; chloroplast	134	134	100%	2e-28	94%	KJ787216.1
Medicago falcata isolate xt_plant82 tRNA-Leu (trnL) gene, intron; chloroplast	134	134	100%	2e-28	94%	KJ746339.1
Trigonella grandiflora isolate EC 583595 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	134	134	100%	2e-28	94%	JX274166.1
Trigonella gladiata isolate EC 583594 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	134	134	100%	2e-28	94%	JX274165.1
Trigonella gladiata isolate EC 583593 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	134	134	100%	2e-28	94%	JX274164.1
Trigonella foenum-graecum isolate EC 583588 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	134	134	100%	2e-28	94%	JX274159.1
Trigonella coerulescens isolate EC 583574 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	134	134	100%	2e-28	94%	JX274150.1
Trigonella coerulescens isolate EC 583573 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	134	134	100%	2e-28	94%	JX274149.1
Vicia monantha isolate HV47 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	134	134	100%	2e-28	94%	JX505758.1
Lathyrus vernus isolate HS917 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	134	134	100%	2e-28	94%	JX505706.1
Medicago sativa tRNA-Leu (trnL) gene, intron; chloroplast	134	134	100%	2e-28	94%	JX874981.1

Alignments

Trigonella schlumbergeri isolate EC 583609 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|JX274177.1|** Length: 506 Number of Matches: 1

See 1 more title(s)
Range 1: 99 to 183

Score	Expect	Identities	Gaps	Strand	Frame
149 bits(164)	7e-33()	84/85(99%)	0/85(0%)	Plus/Plus	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCGaaaacaaaaaaagaaaagttcagaaagttaa  60
            |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  99   GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAAAGAAAAATTCAGAAAGTTAA  158

Query  61   aaaaaaaGGATAGGTGCAGAGACTC  85
            |||||||||||||||||||||||||
Sbjct  159  AAAAAAAGGATAGGTGCAGAGACTC  183
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Trigonella arabica isolate EC 583496 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|JX274135.1|** Length: 506 Number of Matches: 1

See 1 more title(s)
Range 1: 99 to 183

Score	Expect	Identities	Gaps	Strand	Frame
149 bits(164)	7e-33()	84/85(99%)	0/85(0%)	Plus/Plus	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCGaaaacaaaaaaagaaaagttcagaaagttaa  60
            |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  99   GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAAAGAAAAATTCAGAAAGTTAA  158

Query  61   aaaaaaaGGATAGGTGCAGAGACTC  85
            |||||||||||||||||||||||||
Sbjct  159  AAAAAAAGGATAGGTGCAGAGACTC  183
```

Trigonella maritima isolate EC 583601 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|JX274171.1|** Length: 697 Number of Matches: 1
Range 1: 99 to 184

Score	Expect	Identities	Gaps	Strand	Frame
147 bits(162)	2e-32()	85/86(99%)	1/86(1%)	Plus/Plus	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCGaaaacaaaaaaagaaaagttcagaaagtt-a  59
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  99   GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAAAGAAAAGTTCAGAAAGTTAA  158

Query  60   aaaaaaaaGGATAGGTGCAGAGACTC  85
            ||||||||||||||||||||||||||
Sbjct  159  AAAAAAAAGGATAGGTGCAGAGACTC  184
```

Trigonella maritima isolate EC 583600 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|JX274170.1|** Length: 697 Number of Matches: 1
Range 1: 99 to 184

Score	Expect	Identities	Gaps	Strand	Frame
147 bits(162)	2e-32()	85/86(99%)	1/86(1%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCGaaaacaaaaaaagaaaagttcagaaagttaa  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  99   GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAAAGAAAAGTTCAGAAAGTTAA  158

Query  61   aaaaaaa-GGATAGGTGCAGAGACTC  85
            ||||||| ||||||||||||||||||
Sbjct  159  AAAAAAAGGGATAGGTGCAGAGACTC  184
```

Trigonella suavissima isolate EC 583624 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|JX274187.1|** Length: 692 Number of Matches: 1
Range 1: 99 to 182

Score	Expect	Identities	Gaps	Strand	Frame
145 bits(160)	9e-32()	84/85(99%)	1/85(1%)	Plus/Plus	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCGaaaacaaaaaaagaaaagttcagaaagttaa  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  99   GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAAAGAAAAGTTCAGAAAGTT-A  157

Query  61   aaaaaaaGGATAGGTGCAGAGACTC  85
            |||||||||||||||||||||||||
Sbjct  158  AAAAAAAGGATAGGTGCAGAGACTC  182
```

BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BT5TEGUE014**
Formatting options
Download
Blast report description

MM745.1C_trnL_Clone6

RID BT5TEGUE014 (Expires on 02-12 21:14 pm)

Query ID lcl|Query_47037
Description c6
Molecule type nucleic acid
Query Length 71

Database Name nr
Description Nucleotide collection (nt)
Program BLASTN 2.3.1+

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Trigonella stellata isolate EC 583621 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	120	120	100%	2e-24	97%	JX274184.1
Trigonella grandiflora isolate EC 583595 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	118	118	100%	9e-24	97%	JX274166.1
Trigonella maritima isolate EC 583601 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	114	114	95%	1e-22	97%	JX274171.1
Trigonella maritima isolate EC 583600 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	113	113	94%	4e-22	97%	JX274170.1
Trigonella suavissima isolate EC 583624 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	111	111	92%	1e-21	97%	JX274187.1
Trigonella suavissima isolate EC 583623 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	111	111	92%	1e-21	97%	JX274186.1
Trigonella coelesyriaca isolate EC 583565 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	109	109	100%	4e-21	94%	JX274144.1
Trigonella coelesyriaca isolate EC 583558 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	109	109	100%	4e-21	94%	JX274142.1
Trigonella coelesyriaca isolate EC 583557 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	109	109	100%	4e-21	94%	JX274141.1
Vicia pisiformis isolate Kenicer243 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	109	109	100%	4e-21	94%	JX505770.1
Vicia pisiformis isolate HS643 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	109	109	100%	4e-21	94%	JX505769.1
Vicia minutiflora isolate HV17 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	109	109	100%	4e-21	94%	JX505757.1
Lathyrus saxatilis isolate EDNA09_00968 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	109	109	100%	4e-21	94%	JX505692.1
Lathyrus saxatilis isolate HV39 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	109	109	100%	4e-21	94%	JX505691.1
Trigonella strangulata isolate EC 583622 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	107	107	97%	2e-20	94%	JX274185.1
Trigonella schlumbergeri isolate EC 583609 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	107	107	94%	2e-20	96%	JX274177.1
Trigonella filipes isolate EC 583584 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	107	107	97%	2e-20	94%	JX274158.1

Trigonella arabica isolate EC 583496 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	107	107	94%	2e-20	96%	JX274135.1
Vicia balansae isolate 13048 tRNA-Leu (trnL) gene, partial sequence; chloroplast	105	105	100%	5e-20	93%	KJ787248.1
Ononis natrix tRNA-Leu (trnL) gene, intron; chloroplast	105	105	100%	5e-20	93%	HQ323975.1
Ononis viscosa subsp. breviflora tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	5e-20	93%	GQ488609.1
Ononis tazaensis tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	5e-20	93%	GQ488600.1
Ononis sicula tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	5e-20	93%	GQ488591.1
Ononis serotina tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	5e-20	93%	GQ488589.1
Ononis pubescens tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	5e-20	93%	GQ488582.1
Ononis pseudoserotina tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	5e-20	93%	GQ488581.1
Ononis ornithopodioides tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	5e-20	93%	GQ488576.1
Ononis natrix subsp. arganietorum tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	5e-20	93%	GQ488574.1
Ononis megalostachys tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	5e-20	93%	GQ488570.1
Ononis aurasiaca tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	5e-20	93%	GQ488553.1
Ononis atlantica tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	5e-20	93%	GQ488552.1
Ononis angustissima subsp. longifolia tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	5e-20	93%	GQ488550.1
Ononis angustissima subsp. angustissima tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	5e-20	93%	GQ488549.1
Ononis alba subsp. alba tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	105	105	100%	5e-20	93%	GQ488546.1
Vicia unijuga isolate L-F_WTC5 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP699023.1
Vicia unijuga isolate L-F_WTC4 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP699022.1
Vicia unijuga isolate L-F_WTC3 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP699021.1
Vicia unijuga isolate L-F_WTC2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP699020.1
Vicia unijuga isolate L-F_WTC1 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP699019.1
Vicia amoena isolate L-F_SY5 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP699018.1

Vicia amoena isolate L-F_SY4 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP699017.1
Vicia amoena isolate L-F_SY3 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP699016.1
Vicia amoena isolate L-F_SY2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP699015.1
Vicia amoena isolate L-F_SY1 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP699014.1
Vicia amurensis isolate L-F_HLJ5 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP699013.1
Vicia amurensis isolate L-F_HLJ4 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP699012.1
Vicia amurensis isolate L-F_HLJ3 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP699011.1
Vicia amurensis isolate L-F_HLJ2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP699010.1
Vicia amurensis isolate L-F_HLJ1 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP699009.1
Vicia pseudo-orobus isolate L-F_DY5 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP699003.1
Vicia pseudo-orobus isolate L-F_DY4 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP699002.1
Vicia pseudo-orobus isolate L-F_DY3 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP699001.1
Vicia pseudo-orobus isolate L-F_DY2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP699000.1
Vicia pseudo-orobus isolate L-F_DY1 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP698999.1
Vicia multicaulis isolate L-F_DJ4 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP698998.1
Vicia multicaulis isolate L-F_DJ3 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP698997.1
Vicia multicaulis isolate L-F_DJ2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP698996.1
Vicia multicaulis isolate L-F_DJ1 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP698995.1
Vicia ramuliflora isolate L-F_BY2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP698990.1
Vicia ramuliflora isolate L-F_BY1 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP698989.1
Melilotus officinalis isolate CP46 tRNA-Leu (trnL) gene, partial sequence; chloroplast	104	104	100%	2e-19	93%	KP208370.1
Vicia cassubica isolate 7656 tRNA-Leu (trnL) gene, partial sequence; chloroplast	104	104	100%	2e-19	93%	KJ787254.1
Melilotus officinalis isolate xt_plant51 tRNA-Leu (trnL) gene, intron; chloroplast	104	104	100%	2e-19	93%	KJ746435.1
Trigonella balansae isolate EC 546586 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	JX274188.1

Trigonella cretica isolate EC 583577 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	JX274153.1
Trigonella cretica isolate EC 583576 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	JX274152.1
Trigonella cretica isolate EC 583575 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	JX274151.1
Trigonella caerulea isolate EC 583569 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	JX274147.1
Trigonella caerulea isolate EC 583568 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	JX274146.1
Trigonella caerulea isolate EC 583567 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	JX274145.1
Trigonella balansae isolate EC 583507 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	JX274137.1
Trigonella anguina isolate EC 583495 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	JX274134.1
Vicia venulosa isolate HS1163 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	JX505783.1
Vicia sparsiflora isolate Kenicer240 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	JX505775.1
Vicia multicaulis isolate HS1162 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	JX505761.1
Vicia montevidensis isolate HV18 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	JX505760.1
Vicia dumetorum isolate HS644 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	JX505736.1
Vicia costata isolate V23 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	JX505731.1
Vicia baicalensis isolate HV06 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	JX505716.1
Vicia amurensis isolate HV04 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	JX505715.1
Vicia americana isolate HV02 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	JX505714.1
Melilotus officinalis voucher personal collection:I. Hiiesalu 47 tRNA-Leu (trnL) gene, partial sequence; chloroplast	104	104	100%	2e-19	93%	HM590318.1
Ononis villosissima tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	GQ488608.1
Ononis striata tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	GQ488598.1
Ononis pusilla subsp. pusilla tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	GQ488583.1
Ononis diffusa tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial	104	104	100%	2e-19	93%	GQ488560.1

sequence; chloroplast						
Ononis cintrana tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	GQ488557.1
Ononis cephalotes tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	GQ488556.1
Ononis alopecuroides subsp. alopecuroides tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	GQ488548.1
Ononis alba subsp. monophylla tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	GQ488547.1
Melilotus albus chloroplast DNA, tRNA-Leu (trnL) and trnL-trnF intergenic spacer, partial sequence, specimen_voucher: TUH:19700	104	104	100%	2e-19	93%	AB546813.1
Melilotus officinalis chloroplast DNA, tRNA-Leu (trnL) and trnL-trnF intergenic spacer, partial sequence, specimen_voucher: TUH:7346	104	104	100%	2e-19	93%	AB546812.1
Vicia unijuga tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	104	104	100%	2e-19	93%	AY839408.1
Melilotus officinalis tRNA-Leu (trnL) gene, intron; chloroplast	104	104	100%	2e-19	93%	DQ311714.1
Melilotus officinalis chloroplast tRNA-Leu (trnL) gene, intron sequence	104	104	100%	2e-19	93%	AF124233.1
Vicia lutea isolate 3719 tRNA-Leu (trnL) gene, partial sequence; chloroplast	102	102	100%	7e-19	93%	KJ787282.1
Vicia lutea isolate 3720 tRNA-Leu (trnL) gene, partial sequence; chloroplast	102	102	100%	7e-19	93%	KJ787264.1
Vicia lutea isolate V64 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	102	102	100%	7e-19	93%	JX505753.1
Vicia chaetocalyx isolate HS319 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	102	102	100%	7e-19	93%	JX505722.1
Ononis zygantha tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	102	102	100%	7e-19	92%	GQ488611.1

Alignments

Trigonella stellata isolate EC 583621 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|JX274184.1|** Length: 696 Number of Matches: 1
Range 1: 99 to 169

Score	Expect	Identities	Gaps	Strand	Frame
120 bits(132)	2e-24()	69/71(97%)	0/71(0%)	Plus/Plus	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCGAATACaaaaaaagaaaagttcaggaagttaa  60
            ||||||||||||||||||||||||||||||| |||||||||||||||||||| |||||||
Sbjct  99   GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAAAGAAAAGTTCAGAAAGTTAA  158

Query  61   aaaaaaaaaGG  71
            |||||||||||
Sbjct  159  AAAAAAAAAGG  169
```

Trigonella grandiflora isolate EC 583595 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|JX274166.1|** Length: 713 Number of Matches: 1
Range 1: 99 to 170

Score	Expect	Identities	Gaps	Strand	Frame
118 bits(130)	9e-24()	70/72(97%)	1/72(1%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCGAATACaaaaaaagaaaagttcaggaagttaa  60
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  99   GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAAAGAAAAGTTCAGGAAGTTAA  158

Query  61   aa-aaaaaaaGG  71
            || |||||||||
Sbjct  159  AATAAAAAAAGG  170
```

Trigonella maritima isolate EC 583601 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|JX274171.1|** Length: 697 Number of Matches: 1
Range 1: 99 to 166

Score	Expect	Identities	Gaps	Strand	Frame
114 bits(126)	1e-22()	66/68(97%)	0/68(0%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCGAATACaaaaaaagaaaagttcaggaagttaa  60
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||| ||||||
Sbjct  99   GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAAAGAAAAGTTCAGAAAGTTAA  158

Query  61   aaaaaaaa  68
            ||||||||
Sbjct  159  AAAAAAAA  166
```

Trigonella maritima isolate EC 583600 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|JX274170.1|** Length: 697 Number of Matches: 1
Range 1: 99 to 165

Score	Expect	Identities	Gaps	Strand	Frame
113 bits(124)	4e-22()	65/67(97%)	0/67(0%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCGAATACaaaaaaagaaaagttcaggaagttaa  60
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||| ||||||
Sbjct  99   GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAAAGAAAAGTTCAGAAAGTTAA  158

Query  61   aaaaaaa  67
            |||||||
Sbjct  159  AAAAAAA  165
```

Trigonella suavissima isolate EC 583624 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|JX274187.1|** Length: 692 Number of Matches: 1
Range 1: 99 to 164

Score	Expect	Identities	Gaps	Strand	Frame
111 bits(122)	1e-21()	64/66(97%)	0/66(0%)	Plus/Plus	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCGAATACaaaaaaagaaaagttcaggaagttaa  60
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||| ||||||
Sbjct  99   GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAAAGAAAAGTTCAGAAAGTTAA  158

Query  61   aaaaaa  66
            ||||||
Sbjct  159  AAAAAA  164
```

BLAST ®

Basic Local Alignment Search Tool

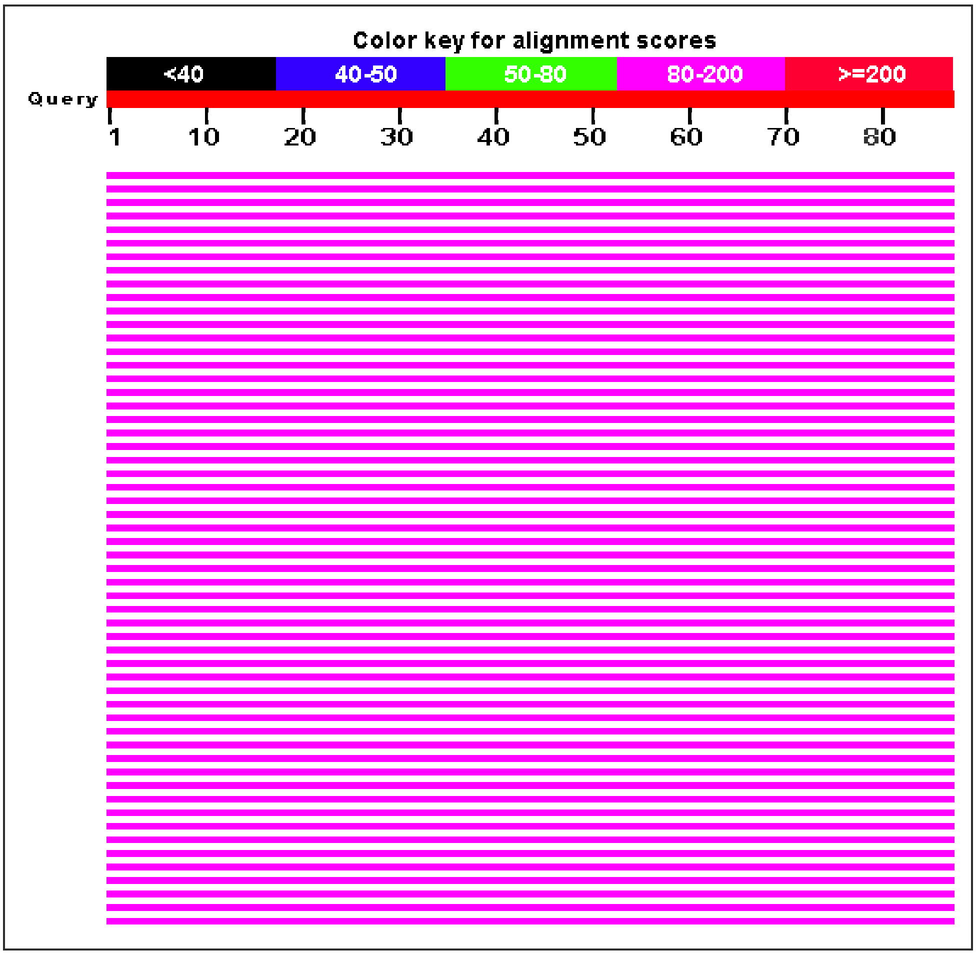
NCBI/ BLAST/ blastn suite/ **Formatting Results - BT5VAV1Y015**
  Formatting options
  Download
Blast report description

MM745.1C_trnL_Clone5

RID	BT5VAV1Y015 (Expires on 02-12 21:15 pm)		
Query ID	LCL | Query_140475	**Database Name**	No.
Description	c5	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	2.3.1+ the BLASTN
Query Length	87		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Trigonella stellata isolate EC 583621 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	149	149	100%	7e-33	98%	JX274184.1
Trigonella grandiflora isolate EC 583595 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	141	141	100%	1e-30	97%	JX274166.1
Trigonella maritima isolate EC 583601 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	140	140	100%	4e-30	97%	JX274171.1
Trigonella coelesyriaca isolate EC 583565 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	138	138	100%	1e-29	95%	JX274144.1
Trigonella coelesyriaca isolate EC 583558 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	138	138	100%	1e-29	95%	JX274142.1
Trigonella coelesyriaca isolate EC 583557 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	138	138	100%	1e-29	95%	JX274141.1
Vicia pisiformis isolate Kenicer243 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	138	138	100%	1e-29	95%	JX505770.1
Vicia pisiformis isolate HS643 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	138	138	100%	1e-29	95%	JX505769.1
Vicia minutiflora isolate HV17 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	138	138	100%	1e-29	95%	JX505757.1
Lathyrus saxatilis isolate EDNA09_00968 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	138	138	100%	1e-29	95%	JX505692.1
Lathyrus saxatilis isolate HV39 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	138	138	100%	1e-29	95%	JX505691.1
Trigonella strangulata isolate EC 583622 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	136	136	100%	5e-29	94%	JX274185.1
Trigonella maritima isolate EC 583600 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	136	136	100%	5e-29	95%	JX274170.1
Trigonella filipes isolate EC 583584 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	136	136	100%	5e-29	94%	JX274158.1
Vicia balansae isolate 13048 tRNA-Leu (trnL) gene, partial sequence; chloroplast	134	134	100%	2e-28	94%	KJ787248.1
Ononis natrix tRNA-Leu (trnL) gene, intron; chloroplast	134	134	100%	2e-28	94%	HQ323975.1
Ononis viscosa subsp. breviflora tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	134	134	100%	2e-28	94%	GQ488609.1
Ononis tazaensis tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	134	134	100%	2e-28	94%	GQ488600.1
Ononis sicula tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial	134	134	100%	2e-28	94%	GQ488591.1

sequence; chloroplast						
Ononis serotina tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	134	134	100%	2e-28	94%	GQ488589.1
Ononis pubescens tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	134	134	100%	2e-28	94%	GQ488582.1
Ononis pseudoserotina tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	134	134	100%	2e-28	94%	GQ488581.1
Ononis ornithopodioides tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	134	134	100%	2e-28	94%	GQ488576.1
Ononis natrix subsp. arganietorum tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	134	134	100%	2e-28	94%	GQ488574.1
Ononis megalostachys tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	134	134	100%	2e-28	94%	GQ488570.1
Ononis aurasiaca tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	134	134	100%	2e-28	94%	GQ488553.1
Ononis atlantica tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	134	134	100%	2e-28	94%	GQ488552.1
Ononis angustissima subsp. longifolia tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	134	134	100%	2e-28	94%	GQ488550.1
Ononis angustissima subsp. angustissima tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	134	134	100%	2e-28	94%	GQ488549.1
Ononis alba subsp. alba tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	134	134	100%	2e-28	94%	GQ488546.1
Vicia unijuga isolate L-F_WTC5 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP699023.1
Vicia unijuga isolate L-F_WTC4 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP699022.1
Vicia unijuga isolate L-F_WTC3 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP699021.1
Vicia unijuga isolate L-F_WTC2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP699020.1
Vicia unijuga isolate L-F_WTC1 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP699019.1
Vicia amoena isolate L-F_SY5 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP699018.1
Vicia amoena isolate L-F_SY4 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP699017.1
Vicia amoena isolate L-F_SY3 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP699016.1
Vicia amoena isolate L-F_SY2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP699015.1
Vicia amoena isolate L-F_SY1 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP699014.1
Vicia amurensis isolate L-F_HLJ5 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP699013.1

Vicia amurensis isolate L-F_HLJ4 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP699012.1
Vicia amurensis isolate L-F_HLJ3 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP699011.1
Vicia amurensis isolate L-F_HLJ2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP699010.1
Vicia amurensis isolate L-F_HLJ1 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP699009.1
Vicia pseudo-orobus isolate L-F_DY5 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP699003.1
Vicia pseudo-orobus isolate L-F_DY4 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP699002.1
Vicia pseudo-orobus isolate L-F_DY3 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP699001.1
Vicia pseudo-orobus isolate L-F_DY2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP699000.1
Vicia pseudo-orobus isolate L-F_DY1 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP698999.1
Vicia multicaulis isolate L-F_DJ4 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP698998.1
Vicia multicaulis isolate L-F_DJ3 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP698997.1
Vicia multicaulis isolate L-F_DJ2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP698996.1
Vicia multicaulis isolate L-F_DJ1 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP698995.1
Vicia ramuliflora isolate L-F_BY2 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP698990.1
Vicia ramuliflora isolate L-F_BY1 tRNA-Leu (trnL), trnL-F intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP698989.1
Melilotus officinalis isolate CP46 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	6e-28	94%	KP208370.1
Vicia cassubica isolate 7656 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	6e-28	94%	KJ787254.1
Melilotus officinalis isolate xt_plant51 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	6e-28	94%	KJ746435.1
Trigonella balansae isolate EC 546586 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	JX274188.1
Trigonella suavissima isolate EC 583624 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	JX274187.1
Trigonella suavissima isolate EC 583623 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	JX274186.1
Trigonella schlumbergeri isolate EC 583609 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	JX274177.1
Trigonella cretica isolate EC 583577 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	JX274153.1

Trigonella cretica isolate EC 583576 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	JX274152.1
Trigonella cretica isolate EC 583575 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	JX274151.1
Trigonella caerulea isolate EC 583569 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	JX274147.1
Trigonella caerulea isolate EC 583568 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	JX274146.1
Trigonella caerulea isolate EC 583567 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	JX274145.1
Trigonella balansae isolate EC 583507 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	JX274137.1
Trigonella arabica isolate EC 583496 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	JX274135.1
Trigonella anguina isolate EC 583495 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	JX274134.1
Vicia venulosa isolate HS1163 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	JX505783.1
Vicia sparsiflora isolate Kenicer240 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	JX505775.1
Vicia multicaulis isolate HS1162 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	JX505761.1
Vicia montevidensis isolate HV18 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	JX505760.1
Vicia dumetorum isolate HS644 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	JX505736.1
Vicia costata isolate V23 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	JX505731.1
Vicia baicalensis isolate HV06 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	JX505716.1
Vicia amurensis isolate HV04 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	JX505715.1
Vicia americana isolate HV02 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	JX505714.1
Melilotus officinalis voucher personal collection:I. Hiiesalu 47 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	6e-28	94%	HM590318.1
Ononis villosissima tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	GQ488608.1
Ononis striata tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	GQ488598.1
Ononis pusilla subsp. pusilla tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	GQ488583.1
Ononis diffusa tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	GQ488560.1

Ononis cintrana tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	GQ488557.1
Ononis cephalotes tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	GQ488556.1
Ononis alopecuroides subsp. alopecuroides tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	GQ488548.1
Ononis alba subsp. monophylla tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	GQ488547.1
Melilotus albus chloroplast DNA, tRNA-Leu (trnL) and trnL-trnF intergenic spacer, partial sequence, specimen_voucher: TUH:19700	132	132	100%	6e-28	94%	AB546813.1
Melilotus officinalis chloroplast DNA, tRNA-Leu (trnL) and trnL-trnF intergenic spacer, partial sequence, specimen_voucher: TUH:7346	132	132	100%	6e-28	94%	AB546812.1
Vicia unijuga tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	132	132	100%	6e-28	94%	AY839408.1
Melilotus officinalis tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	6e-28	94%	DQ311714.1
Melilotus officinalis chloroplast tRNA-Leu (trnL) gene, intron sequence	132	132	100%	6e-28	94%	AF124233.1
Vicia lutea isolate 3719 tRNA-Leu (trnL) gene, partial sequence; chloroplast	131	131	100%	2e-27	94%	KJ787282.1
Vicia lutea isolate 3720 tRNA-Leu (trnL) gene, partial sequence; chloroplast	131	131	100%	2e-27	94%	KJ787264.1
Vicia lutea isolate V64 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	131	131	100%	2e-27	94%	JX505753.1
Vicia chaetocalyx isolate HS319 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	131	131	100%	2e-27	94%	JX505722.1
Ononis zygantha tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	131	131	100%	2e-27	93%	GQ488611.1

Alignments

Trigonella stellata isolate EC 583621 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|JX274184.1|** Length: 696 Number of Matches: 1
Range 1: 99 to 185

Score	Expect	Identities	Gaps	Strand	Frame
149 bits(164)	7e-33()	85/87(98%)	0/87(0%)	More more	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAATAAAAGAAAAGTTCAGGAAGTTaa  60
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Sbjct 99 GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAAAGAAAAGTTCAGAAAGTTAA 158

Query  61   aaaaaaaaaGGATAGGTGCAGAGACTC  87
            |||||||||||||||||||||||||||
Sbjct AAAAAAAAAGGATAGGTGCAGAGACTC 159 185
```

Trigonella grandiflora isolate EC 583595 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|JX274166.1|** Length: 713 Number of Matches: 1
Range 1: 99 to 186

Score	Expect	Identities	Gaps	Strand	Frame
141 bits(156)	1e-30()	85/88(97%)	1/88(1%)	More more	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAATAAAAGAAAAGTTCAGGAAGTTaa  60
            |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct 99 GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAAAGAAAAGTTCAGGAAGTTAA 158

Query  61   aa-aaaaaaaGGATAGGTGCAGAGACTC  87
            || ||||||||||||||||| |||||||
Sbjct AATAAAAAAAGGATAGGTGCGGAGACTC 159 186
```

Trigonella maritima isolate EC 583601 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|JX274171.1|** Length: 697 Number of Matches: 1
Range 1: 99 to 184

Score	Expect	Identities	Gaps	Strand	Frame
140 bits(154)	4e-30()	84/87(97%)	1/87(1%)	More more	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAATAAAAGAAAAGTTCAGGAAGTTaa  60
            |||||||||||||||||||||||||||||||||||| |||||||||||||| |||||| |
Sbjct  99   GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAAAGAAAAGTTCAGAAAGTT-A  157

Query  61   aaaaaaaaaGGATAGGTGCAGAGACTC  87
            |||||||||||||||||||||||||||
Sbjct AAAAAAAAAGGATAGGTGCAGAGACTC 158 184
```

Trigonella coelesyriaca isolate EC 583565 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|JX274144.1|** Length: 713 Number of Matches: 1
Range 1: 99 to 186

Score	Expect	Identities	Gaps	Strand	Frame
138 bits(152)	1e-29()	84/88(95%)	1/88(1%)	More more	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAATAAAAGAAAAGTTCAGGAAGTTaa  60
            |||||||||||||||||||||||||||||||||||| |||||||||||||| ||||||||
Sbjct 99 GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAAAGAAAAGTTCAGAAAGTTAA 158

Query  61   aa-aaaaaaaGGATAGGTGCAGAGACTC  87
            ||  ||||||||||||||||||||||||
Sbjct AATCAAAAAAGGATAGGTGCAGAGACTC 159 186
```

Trigonella coelesyriaca isolate EC 583558 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|JX274142.1|** Length: 714 Number of Matches: 1
Range 1: 99 to 186

Score	Expect	Identities	Gaps	Strand	Frame
138 bits(152)	1e-29()	84/88(95%)	1/88(1%)	More more	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAATAAAAGAAAAGTTCAGGAAGTTaa  60
            |||||||||||||||||||||||||||||||||||| |||||||||||||| ||||||||
Sbjct 99 GGCAATCCTGAGCCAAATCCTTCTTTCCGAAAACAAAAAAAGAAAAGTTCAGAAAGTTAA 158

Query  61   aa-aaaaaaaGGATAGGTGCAGAGACTC  87
            ||  ||||||||||||||||||||||||
Sbjct AATCAAAAAAGGATAGGTGCAGAGACTC 159 186
```

BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BSPJ2D6U014**
  Formatting options
  Download
Blast report description

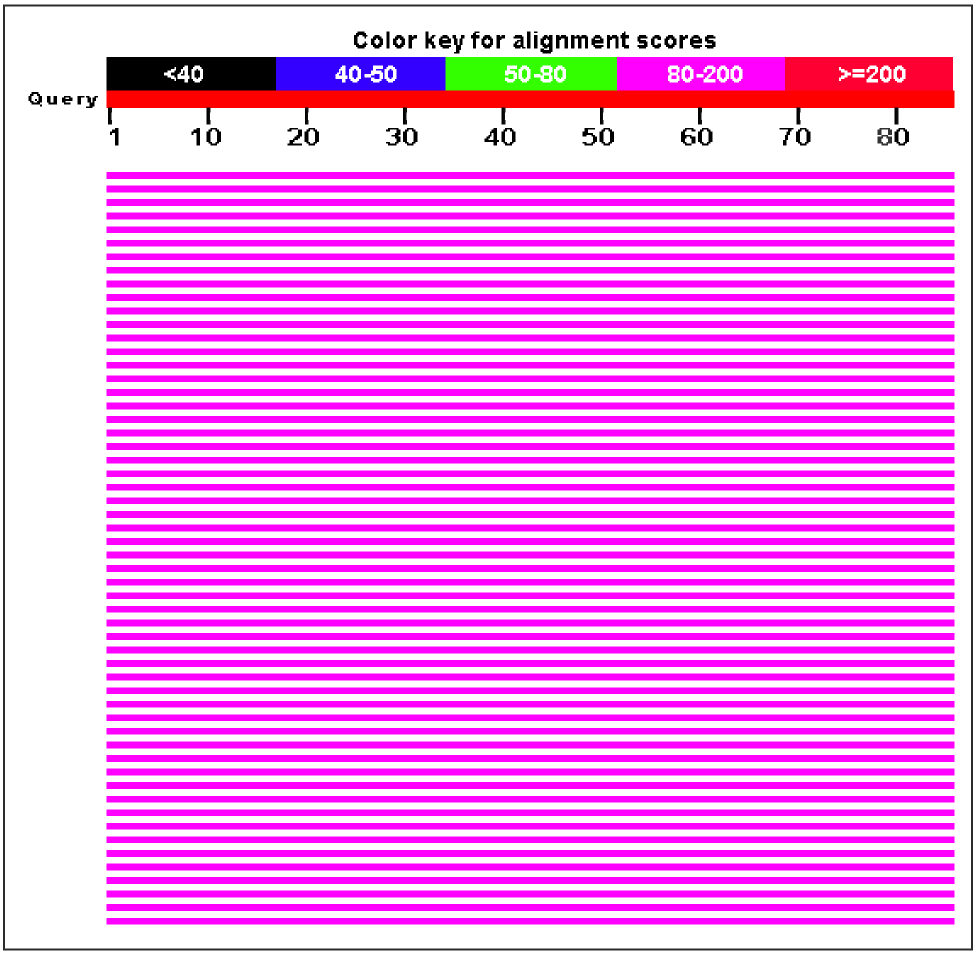
M/C5992.1E-1C_trnL_Clone1,4,6,12

RID BSPJ2D6U014 (Expires on 02-12 16:54 pm)

Query ID	lcl|Query_29089	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	85		

Graphic Summary

Distribution of 102 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Elymus peschkovae voucher 115 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP325400.1
Elymus scandicus voucher 114 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP325399.1
Elymus excelsus voucher 1114 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP325398.1
Elymus pendulinus voucher 113 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP325397.1
Elymus dahuricus var. cylindricus voucher 5509 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP325396.1
Elymus excelsus voucher 5513 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP325395.1
Elymus probatovae voucher 5645 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP325394.1
Elymus ircutensis voucher Alt 10-198 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP325393.1
Elymus vassiljevii voucher 5665 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP325392.1
Elymus peschkovae voucher 5631 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP325391.1
Elymus charkeviczii voucher 5550 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP325390.1
Agropyron cristatum var. pectinatum voucher M.Pinar 4412a trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP723655.1
Agropyron deweyi voucher M.Pinar 4321a trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene, complete	154	154	100%	2e-34	100%	KP723652.1

sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast						
Aegilops geniculata isolate CRF BGE022746 trnL gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	154	154	100%	2e-34	100%	KR559558.1
Aegilops neglecta bio-material USDA:PI170209 trnL gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	154	154	100%	2e-34	100%	KR559557.1
Elymus nevskii voucher Alt 1124 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KJ744043.1
Agropyron cristatum voucher Alt 11-377 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KJ744042.1
Elymus caninus voucher Alt 1031 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KJ744041.1
Campeiostachys dahurica voucher Xa 09-157 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KJ744040.1
Elymus fedtschenkoi voucher Alt 12-133 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KJ755833.1
Agropyron krylovianum voucher Alt 12-264 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KJ755832.1
Elymus subfibrosus tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP257587.1
Elymus lanceolatus subsp. lanceolatus isolate CP3 tRNA-Leu (trnL) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP208327.1
Triticum macha chloroplast DNA, complete genome	154	154	100%	2e-34	100%	LC005978.1
Triticum monococcum subsp. monococcum chloroplast DNA, complete genome	154	154	100%	2e-34	100%	LC005977.1
Triticum turgidum subsp. durum cultivar Langdon chloroplast, complete genome	154	154	100%	2e-34	100%	KM352501.1
Triticum timopheevii chloroplast DNA, complete genome	154	154	100%	2e-34	100%	AB976560.1
Aegilops kotschyi cultivar TA1980 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614420.1
Aegilops sharonensis cultivar TA1995 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614419.1
Aegilops bicornis cultivar Clae57 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614418.1
Aegilops sharonensis cultivar TA1996 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614417.1
Aegilops longissima cultivar TA1924 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614416.1
Aegilops searsii cultivar TA1841 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614415.1
Aegilops searsii cultivar TA1837 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614414.1
Aegilops searsii cultivar TA1926	154	154	100%	2e-34	100%	KJ614413.1

chloroplast, complete genome						
Aegilops tauschii cultivar AL8/78 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614412.1
Triticum urartu cultivar PI428335 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614411.1
Triticum timopheevii cultivar Tim01 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614410.1
Triticum timopheevii cultivar TA944 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614409.1
Triticum timopheevii cultivar TA1485 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614408.1
Triticum timopheevii cultivar TA0941 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614407.1
Aegilops speltoides var. speltoides cultivar PI487232 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614406.1
Aegilops speltoides var. ligustica cultivar TA1796 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614405.1
Aegilops speltoides var. ligustica cultivar AE918 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614404.1
Triticum aestivum cultivar spleta PI384000 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614403.1
Triticum turgidum cultivar TA1133 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614402.1
Triticum turgidum cultivar TA0060 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614401.1
Triticum turgidum cultivar TA0073 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614400.1
Triticum turgidum cultivar TA2801 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614399.1
Triticum turgidum cultivar PI520121 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614398.1
Triticum aestivum cultivar Chinese Spring TA3008 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614396.1
Elymus repens isolate xt_plant145 tRNA-Leu (trnL) gene, intron; chloroplast	154	154	100%	2e-34	100%	KJ746409.1
Triticum aestivum chromosome 3B, genomic scaffold, cultivar Chinese Spring	154	319	100%	2e-34	100%	HG670306.1
Triticum aestivum chloroplast, complete genome	154	154	100%	2e-34	100%	KJ592713.1
Elymus sibiricus isolate EI_201311 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905225.1
Elymus dolichatherus isolate EI_201310 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905224.1
Elymus nutans isolate EI_201309 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905223.1
Elymus sibiricus isolate EI_201307 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905221.1
Elymus tangutorum isolate EI_201305 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905219.1
Elymus nutans isolate EI_201302 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905216.1

Elymus nutans isolate EI_201301 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905215.1
Elymus dolichatherus isolate EI_201228 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905214.1
Elymus tangutorum isolate EI_201226 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905212.1
Elymus tangutorum isolate EI_201216 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905202.1
Elymus nutans isolate EI_201224 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905210.1
Elymus dahuricus var. cylindricus isolate EI_201222 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905208.1
Elymus tangutorum isolate EI_201221 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905207.1
Elymus sibiricus isolate EI_201220 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905206.1
Elymus antiquus isolate EI_201219 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905205.1
Elymus excelsus isolate EI_201218 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905204.1
Elymus nutans isolate EI_201217 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905203.1
Elymus excelsus isolate EI_201214 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905200.1
Elymus tangutorum isolate EI_201213 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905199.1
Elymus dolichatherus isolate EI_201212 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905198.1
Elymus dolichatherus isolate EI_201211 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene,	154	154	100%	2e-34	100%	KF905197.1

partial sequence; chloroplast						
Elymus tangutorum isolate El_201209 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905195.1
Elymus dahuricus isolate El_201208 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905194.1
Elymus tibeticus isolate El_201206 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905192.1
Elymus tangutorum isolate El_201205 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905191.1
Elymus tangutorum isolate El_201204 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905190.1
Elymus dahuricus var. cylindricus isolate El_201202 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905188.1
Elymus nutans isolate El_201102 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905186.1
Elymus sibiricus isolate El_201101 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905185.1
Triticum urartu plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732946.1
Triticum spelta plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732945.1
Triticum monococcum plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732944.1
Triticum durum plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732942.1
Triticum monococcum subsp. aegilopoides plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732941.1
Triticum aestivum plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732940.1
Elymus tsukushiensis plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732933.1
Elymus racemifer plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732932.1
Elymus humidus plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732931.1
Elymus dahuricus plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732930.1

Elymus caninus plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732929.1
Aegilops geniculata chloroplast, complete genome	154	154	100%	2e-34	100%	KF534490.1
Aegilops cylindrica chloroplast, complete genome	154	154	100%	2e-34	100%	KF534489.1
Elymus tauri isolate Psetau3 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu (trnL) gene, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF600705.1
Elymus tauri isolate Psetau2 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu (trnL) gene, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF600704.1
Elymus stipifolius isolate Psesti3 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu (trnL) gene, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF600702.1
Elymus stipifolius isolate Psesti2 trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF600701.1

Alignments

Elymus peschkovae voucher 115 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast

Sequence ID: **gb|KP325400.1|** Length: 1046 Number of Matches: 1
Range 1: 102 to 186

Score	Expect	Identities	Gaps	Strand	Frame
154 bits(170)	2e-34()	85/85(100%)	0/85(0%)	Plus/Minus	

Features:

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Query  1    GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  186  GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  127

Query  61   AACACGGATTTGGCTCAGGATTGCC  85
            |||||||||||||||||||||||||
Sbjct  126  AACACGGATTTGGCTCAGGATTGCC  102
```

Elymus scandicus voucher 114 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast

Sequence ID: **gb|KP325399.1|** Length: 1039 Number of Matches: 1
Range 1: 102 to 186

Score	Expect	Identities	Gaps	Strand	Frame
154 bits(170)	2e-34()	85/85(100%)	0/85(0%)	Plus/Minus	

Features:

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Query  1    GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  186  GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  127

Query  61   AACACGGATTTGGCTCAGGATTGCC  85
            |||||||||||||||||||||||||
Sbjct  126  AACACGGATTTGGCTCAGGATTGCC  102
```

Elymus excelsus voucher 1114 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast

Sequence ID: **gb|KP325398.1|** Length: 1043 Number of Matches: 1
Range 1: 102 to 186

Score	Expect	Identities	Gaps	Strand	Frame
154 bits(170)	2e-34()	85/85(100%)	0/85(0%)	Plus/Minus	

Features:

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Query  1    GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  186  GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  127

Query  61   AACACGGATTTGGCTCAGGATTGCC  85
            |||||||||||||||||||||||||
Sbjct  126  AACACGGATTTGGCTCAGGATTGCC  102
```

Elymus pendulinus voucher 113 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KP325397.1|** Length: 1049 Number of Matches: 1
Range 1: 102 to 186

Score	Expect	Identities	Gaps	Strand	Frame
154 bits(170)	2e-34()	85/85(100%)	0/85(0%)	Plus/Minus	

Features:

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Query  1    GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  186  GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  127

Query  61   AACACGGATTTGGCTCAGGATTGCC  85
            |||||||||||||||||||||||||
Sbjct  126  AACACGGATTTGGCTCAGGATTGCC  102
```

Elymus dahuricus var. cylindricus voucher 5509 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KP325396.1|** Length: 1043 Number of Matches: 1
Range 1: 102 to 186

Score	Expect	Identities	Gaps	Strand	Frame
154 bits(170)	2e-34()	85/85(100%)	0/85(0%)	Plus/Minus	

Features:

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Query  1    GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  186  GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  127

Query  61   AACACGGATTTGGCTCAGGATTGCC  85
            |||||||||||||||||||||||||
Sbjct  126  AACACGGATTTGGCTCAGGATTGCC  102
```

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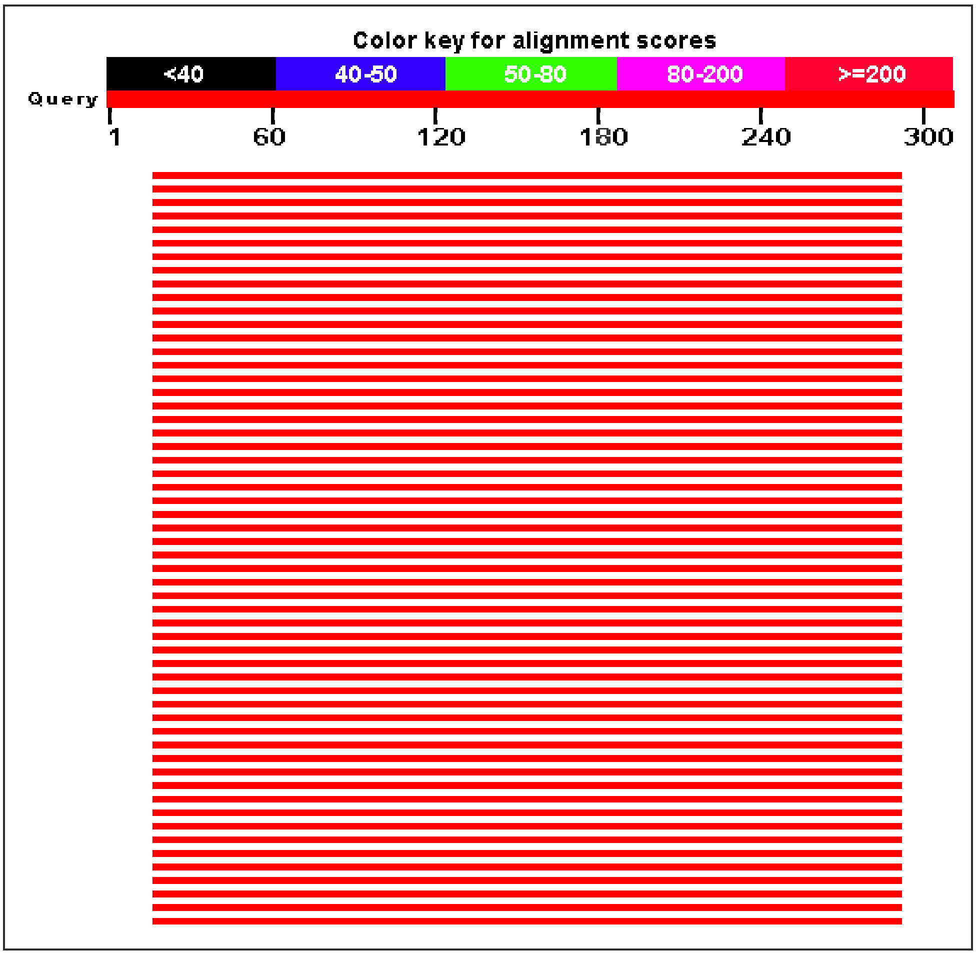
NCBI/ BLAST/ blastn suite/ **Formatting Results - BSP2E7PU014**
Formatting options
Download
Blast report description

M/C5992.1E-1C_trnL_Clone8

RID	BSP2E7PU014 (Expires on 02-12 16:45 pm)		
Query ID	lcl|Query_159469	**Database Name**	nr
Description	Clone8	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	311		

Graphic Summary

Distribution of 101 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Variovorax sp. LMR331 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KU182837.1
Variovorax sp. E37 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KR703575.1
Variovorax sp. GLT-Slr-56 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KT343856.1
Variovorax sp. GLT-Slr-51 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KT343851.1
Variovorax paradoxus strain PDD-59b-55 16S ribosomal RNA gene, complete sequence	497	497	88%	6e-137	100%	KR922177.1
Uncultured bacterium clone HF77 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KR188953.1
Variovorax paradoxus strain 11-4(2) 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KT369961.1
Variovorax sp. YN34 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KR051070.1
Variovorax sp. 369 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KT461877.1
Variovorax sp. 110 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KT461839.1
Variovorax sp. 48 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KT461830.1
Variovorax sp. NB24 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KP844880.1
Variovorax sp. AB30 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KP844879.1
Variovorax sp. EECC-613 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KP860659.1
Variovorax sp. EECC-546 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KP860654.1
Variovorax paradoxus strain hca0013 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KP834437.1
Variovorax paradoxus strain KAR44 16S ribosomal RNA gene, complete sequence	497	497	88%	6e-137	100%	KR055005.1
Variovorax sp. CC4W1 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KM187269.1
Variovorax sp. StTD764 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025495.1
Variovorax sp. StTD761 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025494.1
Variovorax sp. StTD755 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025488.1
Variovorax sp. StTD752 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025485.1
Variovorax sp. StTD751 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025484.1
Variovorax sp. StTD746 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025480.1
Variovorax sp. StTD741 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025475.1
Variovorax sp. StTD740 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025474.1
Variovorax sp. StTD487 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025345.1

Variovorax sp. StTD473 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025332.1
Variovorax sp. StTD472 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025331.1
Variovorax sp. StTD461 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025320.1
Variovorax sp. StTD460 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025319.1
Variovorax sp. StTD396 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025261.1
Variovorax sp. StTD372 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025238.1
Variovorax sp. StRD768 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC025141.1
Variovorax sp. StRD470 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC024961.1
Variovorax sp. StRD421 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC024912.1
Variovorax sp. StRD416 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC024907.1
Variovorax sp. StRD404 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	LC024896.1
Variovorax sp. 285P1R 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KR611635.1
Variovorax boronicumulans strain LR 2-10 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KP407102.1
Variovorax boronicumulans strain LR 1-13 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KP407094.1
Variovorax boronicumulans strain LR 1-6B 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KP407089.1
Variovorax sp. RC3.3 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KP267842.1
Variovorax paradoxus strain S12A6 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KF975363.1
Variovorax sp. S12P10 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KF975359.1
Variovorax sp. S13P8 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KF975358.1
Variovorax paradoxus strain S12S4 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KF975336.1
Bacillaceae bacterium x8-9 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KP230463.1
Variovorax paradoxus gene for 16S ribosomal RNA, partial sequence, strain: AF90	497	497	88%	6e-137	100%	LC015538.1
Variovorax paradoxus strain IHB B 12181 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KJ767382.1
Variovorax boronicumulans strain E2B5_13 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KM604967.1
Variovorax boronicumulans strain E2B5_5 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KM604959.1
Variovorax sp. ML3-12 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KM411504.1
Variovorax sp. IDSBO-4 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KM199761.1
Bacterium NCr-7 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KJ792863.1
Variovorax sp. MR-I14 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KJ811555.1
Uncultured bacterium clone PhyMu0012						

16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KC746053.1
Uncultured bacterium clone ncd266e10c1 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KF070930.1
Uncultured Variovorax sp. clone PIPOManured06 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KF590885.1
Variovorax paradoxus strain SL37 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KJ529023.1
Variovorax sp. TA_EF partial 16S rRNA gene, strain TA_EF	497	497	88%	6e-137	100%	HG942167.1
Variovorax paradoxus strain ZR 1-3 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KJ472791.1
Variovorax boronicumulans strain ZR 1-1 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KJ472790.1
Variovorax sp. CV50Nov 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KJ482855.1
Variovorax sp. CO8Nov 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KJ482792.1
Variovorax sp. MM43Nov 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KJ482749.1
Variovorax paradoxus strain 11709033 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KF981560.1
Variovorax sp. BvORHM081 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	AB851216.1
Variovorax sp. BvORHM030 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	AB851165.1
Variovorax sp. BvIRR112 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	AB851079.1
Variovorax sp. BvIRHM077 gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	AB850959.1
Variovorax sp. b49 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KF733334.1
Variovorax sp. 613 partial 16S rRNA gene, isolate 613	497	497	88%	6e-137	100%	HG737356.1
Variovorax paradoxus strain ZY-173s 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KF580876.1
Uncultured Variovorax sp. clone Cb1 16S ribosomal RNA, partial sequence	497	497	88%	6e-137	100%	KF704360.1
Variovorax sp. 231-FB gene for 16S rRNA, partial sequence	497	497	88%	6e-137	100%	AB566088.1
Uncultured bacterium gene for 16S rRNA, partial sequence, clone: SBG-U_F05	497	497	88%	6e-137	100%	AB810907.1
Uncultured bacterium gene for 16S rRNA, partial sequence, clone: SU_E07	497	497	88%	6e-137	100%	AB810809.1
Variovorax paradoxus B4 chromosome 1, complete sequence	497	994	88%	6e-137	100%	CP003911.1
Variovorax paradoxus partial 16S rRNA gene, strain BD12OL2-R01	497	497	88%	6e-137	100%	FR877674.1
Variovorax sp. NAS2(11) 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	JX154309.1
Variovorax paradoxus strain MOSEL-ES1 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KF307662.1
Uncultured Variovorax sp. clone BC0195 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KC166847.1
Uncultured Variovorax sp. clone BC059 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KC166765.1
Uncultured Variovorax sp. clone BC003 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KC166740.1

Uncultured Variovorax sp. clone BC095 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	KC166723.1
Variovorax sp. Zs13 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	JQ977458.1
Variovorax sp. Azb3 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	JQ977354.1
Uncultured bacterium gene for 16S ribosomal RNA, partial sequence, clone: SZ3-1039	497	497	88%	6e-137	100%	AB769480.1
Bacterium LW 181_159 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	GQ288950.1
Bacterium LW 181_158 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	GQ288866.1
Bacterium LW 181_121 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	GQ288853.1
Uncultured bacterium clone PsppD06 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	JX644382.1
Uncultured bacterium clone DC2ROB04 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	JX644220.1
Variovorax sp. SMX332 partial 16S rRNA gene, strain SMX332	497	497	88%	6e-137	100%	HF571534.1
Bacterium 58-L049616-122-011-B08 16S ribosomal RNA gene, partial sequence	497	497	88%	6e-137	100%	JX228569.1
Variovorax paradoxus S110 strain S110 16S ribosomal RNA, complete sequence	497	497	88%	6e-137	100%	NR_074654.1
Variovorax paradoxus EPS strain EPS 16S ribosomal RNA, complete sequence	497	497	88%	6e-137	100%	NR_074646.1
Variovorax paradoxus partial 16S rRNA gene, isolate 3-RHI-7	497	497	88%	6e-137	100%	HF558412.1
Variovorax sp. EK-CH-I8 16S ribosomal RNA gene, partial sequence	493	493	87%	8e-136	100%	KC809929.1

Alignments

Variovorax sp. LMR331 16S ribosomal RNA gene, partial sequence
Sequence ID: **gb|KU182837.1|** Length: 776 Number of Matches: 1
Range 1: 127 to 401

Score	Expect	Identities	Gaps	Strand	Frame
497 bits(550)	6e-137()	275/275(100%)	0/275(0%)	Plus/Minus	

Features:

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Query  18   TCTTACGGTACCGTCATTAGCCCTCTTTATTAGAAAAGGCCGTTTCGTTCCGTACAAAAG  77
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Sbjct  401  TCTTACGGTACCGTCATTAGCCCTCTTTATTAGAAAAGGCCGTTTCGTTCCGTACAAAAG  342

Query  78   CAGTTTACAACCCGAAGGCCTTCATCCTGCACGCGGCATGGCTGGATCAGGCTTTCGCCC  137
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  341  CAGTTTACAACCCGAAGGCCTTCATCCTGCACGCGGCATGGCTGGATCAGGCTTTCGCCC  282

Query  138  ATTGTCCAAAATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAG  197
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  281  ATTGTCCAAAATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAG  222

Query  198  TGTGGCTGGTCGTCCTCTCAGACCAGCTACAGATCGAAGGCTTGGTGAGCCTTTACCTCA  257
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  221  TGTGGCTGGTCGTCCTCTCAGACCAGCTACAGATCGAAGGCTTGGTGAGCCTTTACCTCA  162

Query  258  CCAACTACCTAATCTGCCATCGGCCGCTCCATTCG  292
            |||||||||||||||||||||||||||||||||||
Sbjct  161  CCAACTACCTAATCTGCCATCGGCCGCTCCATTCG  127
```

Variovorax sp. E37 16S ribosomal RNA gene, partial sequence
Sequence ID: **gb|KR703575.1|** Length: 593 Number of Matches: 1
Range 1: 186 to 460

Score	Expect	Identities	Gaps	Strand	Frame
497 bits(550)	6e-137()	275/275(100%)	0/275(0%)	Plus/Minus	

Features:

```
Query  18   TCTTACGGTACCGTCATTAGCCCTCTTTATTAGAAAAGGCCGTTTCGTTCCGTACAAAAG  77
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  460  TCTTACGGTACCGTCATTAGCCCTCTTTATTAGAAAAGGCCGTTTCGTTCCGTACAAAAG  401

Query  78   CAGTTTACAACCCGAAGGCCTTCATCCTGCACGCGGCATGGCTGGATCAGGCTTTCGCCC  137
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Sbjct  400  CAGTTTACAACCCGAAGGCCTTCATCCTGCACGCGGCATGGCTGGATCAGGCTTTCGCCC  341

Query  138  ATTGTCCAAAATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAG  197
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  340  ATTGTCCAAAATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAG  281

Query  198  TGTGGCTGGTCGTCCTCTCAGACCAGCTACAGATCGAAGGCTTGGTGAGCCTTTACCTCA  257
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  280  TGTGGCTGGTCGTCCTCTCAGACCAGCTACAGATCGAAGGCTTGGTGAGCCTTTACCTCA  221

Query  258  CCAACTACCTAATCTGCCATCGGCCGCTCCATTCG  292
            |||||||||||||||||||||||||||||||||||
Sbjct  220  CCAACTACCTAATCTGCCATCGGCCGCTCCATTCG  186
```

Variovorax sp. GLT-Slr-56 16S ribosomal RNA gene, partial sequence
Sequence ID: **gb|KT343856.1|** Length: 606 Number of Matches: 1
Range 1: 139 to 413

Score	Expect	Identities	Gaps	Strand	Frame
497 bits(550)	6e-137()	275/275(100%)	0/275(0%)	Plus/Minus	

Features:

```
Query  18   TCTTACGGTACCGTCATTAGCCCTCTTTATTAGAAAAGGCCGTTTCGTTCCGTACAAAAG  77
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  413  TCTTACGGTACCGTCATTAGCCCTCTTTATTAGAAAAGGCCGTTTCGTTCCGTACAAAAG  354

Query  78   CAGTTTACAACCCGAAGGCCTTCATCCTGCACGCGGCATGGCTGGATCAGGCTTTCGCCC  137
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Sbjct  353  CAGTTTACAACCCGAAGGCCTTCATCCTGCACGCGGCATGGCTGGATCAGGCTTTCGCCC  294

Query  138  ATTGTCCAAAATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAG  197
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Sbjct  293  ATTGTCCAAAATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAG  234

Query  198  TGTGGCTGGTCGTCCTCTCAGACCAGCTACAGATCGAAGGCTTGGTGAGCCTTTACCTCA  257
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  233  TGTGGCTGGTCGTCCTCTCAGACCAGCTACAGATCGAAGGCTTGGTGAGCCTTTACCTCA  174

Query  258  CCAACTACCTAATCTGCCATCGGCCGCTCCATTCG  292
            |||||||||||||||||||||||||||||||||||
Sbjct  173  CCAACTACCTAATCTGCCATCGGCCGCTCCATTCG  139
```

Variovorax sp. GLT-Slr-51 16S ribosomal RNA gene, partial sequence
Sequence ID: **gb|KT343851.1|** Length: 591 Number of Matches: 1
Range 1: 100 to 374

Score	Expect	Identities	Gaps	Strand	Frame
497 bits(550)	6e-137()	275/275(100%)	0/275(0%)	Plus/Minus	

Features:

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Query  18   TCTTACGGTACCGTCATTAGCCCTCTTTATTAGAAAAGGCCGTTTCGTTCCGTACAAAAG  77
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  374  TCTTACGGTACCGTCATTAGCCCTCTTTATTAGAAAAGGCCGTTTCGTTCCGTACAAAAG  315

Query  78   CAGTTTACAACCCGAAGGCCTTCATCCTGCACGCGGCATGGCTGGATCAGGCTTTCGCCC  137
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  314  CAGTTTACAACCCGAAGGCCTTCATCCTGCACGCGGCATGGCTGGATCAGGCTTTCGCCC  255

Query  138  ATTGTCCAAAATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAG  197
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  254  ATTGTCCAAAATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAG  195

Query  198  TGTGGCTGGTCGTCCTCTCAGACCAGCTACAGATCGAAGGCTTGGTGAGCCTTTACCTCA  257
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  194  TGTGGCTGGTCGTCCTCTCAGACCAGCTACAGATCGAAGGCTTGGTGAGCCTTTACCTCA  135

Query  258  CCAACTACCTAATCTGCCATCGGCCGCTCCATTCG  292
            |||||||||||||||||||||||||||||||||||
Sbjct  134  CCAACTACCTAATCTGCCATCGGCCGCTCCATTCG  100
```

Variovorax paradoxus strain PDD-59b-55 16S ribosomal RNA gene, complete sequence
Sequence ID: **gb|KR922177.1|** Length: 1409 Number of Matches: 1
Range 1: 166 to 440

Score	Expect	Identities	Gaps	Strand	Frame
497 bits(550)	6e-137()	275/275(100%)	0/275(0%)	Plus/Minus	

Features:

```
Query  18   TCTTACGGTACCGTCATTAGCCCTCTTTATTAGAAAAGGCCGTTTCGTTCCGTACAAAAG  77
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  440  TCTTACGGTACCGTCATTAGCCCTCTTTATTAGAAAAGGCCGTTTCGTTCCGTACAAAAG  381
```

```
Query  78   CAGTTTACAACCCGAAGGCCTTCATCCTGCACGCGGCATGGCTGGATCAGGCTTTCGCCC  137
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380  CAGTTTACAACCCGAAGGCCTTCATCCTGCACGCGGCATGGCTGGATCAGGCTTTCGCCC  321

Query  138  ATTGTCCAAAATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAG  197
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  320  ATTGTCCAAAATTCCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAG  261

Query  198  TGTGGCTGGTCGTCCTCTCAGACCAGCTACAGATCGAAGGCTTGGTGAGCCTTTACCTCA  257
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  260  TGTGGCTGGTCGTCCTCTCAGACCAGCTACAGATCGAAGGCTTGGTGAGCCTTTACCTCA  201

Query  258  CCAACTACCTAATCTGCCATCGGCCGCTCCATTCG  292
            |||||||||||||||||||||||||||||||||||
Sbjct  200  CCAACTACCTAATCTGCCATCGGCCGCTCCATTCG  166
```

BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BSPENRDK014**
Formatting options
Download
Blast report description

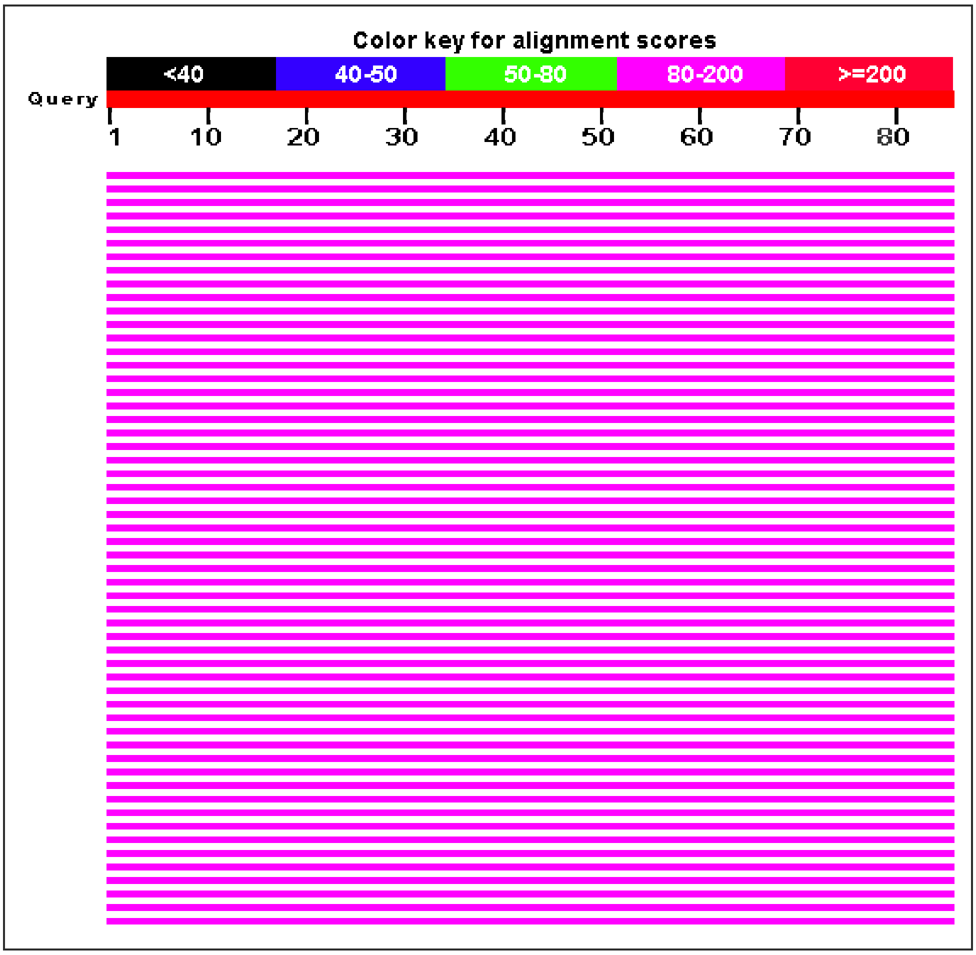
M/C5992.1E-1C_trnL_Clone2,5

RID BSPENRDK014 (Expires on 02-12 16:52 pm)

Query ID	lcl|Query_211747	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	85		

Graphic Summary

Distribution of 102 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Elymus peschkovae voucher 115 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP325400.1
Elymus scandicus voucher 114 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP325399.1
Elymus excelsus voucher 1114 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP325398.1
Elymus pendulinus voucher 113 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP325397.1
Elymus dahuricus var. cylindricus voucher 5509 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP325396.1
Elymus excelsus voucher 5513 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP325395.1
Elymus probatovae voucher 5645 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP325394.1
Elymus ircutensis voucher Alt 10-198 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP325393.1
Elymus vassiljevii voucher 5665 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP325392.1
Elymus peschkovae voucher 5631 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP325391.1
Elymus charkeviczii voucher 5550 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP325390.1
Agropyron cristatum var. pectinatum voucher M.Pinar 4412a trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP723655.1
Agropyron deweyi voucher M.Pinar 4321a trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene, complete	154	154	100%	2e-34	100%	KP723652.1

sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast						
Aegilops geniculata isolate CRF BGE022746 trnL gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	154	154	100%	2e-34	100%	KR559558.1
Aegilops neglecta bio-material USDA:PI170209 trnL gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	154	154	100%	2e-34	100%	KR559557.1
Elymus nevskii voucher Alt 1124 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KJ744043.1
Agropyron cristatum voucher Alt 11-377 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KJ744042.1
Elymus caninus voucher Alt 1031 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KJ744041.1
Campeiostachys dahurica voucher Xa 09-157 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KJ744040.1
Elymus fedtschenkoi voucher Alt 12-133 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KJ755833.1
Agropyron krylovianum voucher Alt 12-264 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KJ755832.1
Elymus subfibrosus tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP257587.1
Elymus lanceolatus subsp. lanceolatus isolate CP3 tRNA-Leu (trnL) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP208327.1
Triticum macha chloroplast DNA, complete genome	154	154	100%	2e-34	100%	LC005978.1
Triticum monococcum subsp. monococcum chloroplast DNA, complete genome	154	154	100%	2e-34	100%	LC005977.1
Triticum turgidum subsp. durum cultivar Langdon chloroplast, complete genome	154	154	100%	2e-34	100%	KM352501.1
Triticum timopheevii chloroplast DNA, complete genome	154	154	100%	2e-34	100%	AB976560.1
Aegilops kotschyi cultivar TA1980 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614420.1
Aegilops sharonensis cultivar TA1995 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614419.1
Aegilops bicornis cultivar Clae57 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614418.1
Aegilops sharonensis cultivar TA1996 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614417.1
Aegilops longissima cultivar TA1924 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614416.1
Aegilops searsii cultivar TA1841 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614415.1
Aegilops searsii cultivar TA1837 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614414.1
Aegilops searsii cultivar TA1926	154	154	100%	2e-34	100%	KJ614413.1

chloroplast, complete genome						
Aegilops tauschii cultivar AL8/78 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614412.1
Triticum urartu cultivar PI428335 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614411.1
Triticum timopheevii cultivar Tim01 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614410.1
Triticum timopheevii cultivar TA944 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614409.1
Triticum timopheevii cultivar TA1485 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614408.1
Triticum timopheevii cultivar TA0941 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614407.1
Aegilops speltoides var. speltoides cultivar PI487232 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614406.1
Aegilops speltoides var. ligustica cultivar TA1796 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614405.1
Aegilops speltoides var. ligustica cultivar AE918 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614404.1
Triticum aestivum cultivar spleta PI384000 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614403.1
Triticum turgidum cultivar TA1133 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614402.1
Triticum turgidum cultivar TA0060 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614401.1
Triticum turgidum cultivar TA0073 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614400.1
Triticum turgidum cultivar TA2801 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614399.1
Triticum turgidum cultivar PI520121 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614398.1
Triticum aestivum cultivar Chinese Spring TA3008 chloroplast, complete genome	154	154	100%	2e-34	100%	KJ614396.1
Elymus repens isolate xt_plant145 tRNA-Leu (trnL) gene, intron; chloroplast	154	154	100%	2e-34	100%	KJ746409.1
Triticum aestivum chromosome 3B, genomic scaffold, cultivar Chinese Spring	154	319	100%	2e-34	100%	HG670306.1
Triticum aestivum chloroplast, complete genome	154	154	100%	2e-34	100%	KJ592713.1
Elymus sibiricus isolate El_201311 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905225.1
Elymus dolichatherus isolate El_201310 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905224.1
Elymus nutans isolate El_201309 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905223.1
Elymus sibiricus isolate El_201307 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905221.1
Elymus tangutorum isolate El_201305 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905219.1
Elymus nutans isolate El_201302 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905216.1

Elymus nutans isolate EI_201301 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905215.1
Elymus dolichatherus isolate EI_201228 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905214.1
Elymus tangutorum isolate EI_201226 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905212.1
Elymus tangutorum isolate EI_201216 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905202.1
Elymus nutans isolate EI_201224 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905210.1
Elymus dahuricus var. cylindricus isolate EI_201222 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905208.1
Elymus tangutorum isolate EI_201221 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905207.1
Elymus sibiricus isolate EI_201220 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905206.1
Elymus antiquus isolate EI_201219 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905205.1
Elymus excelsus isolate EI_201218 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905204.1
Elymus nutans isolate EI_201217 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905203.1
Elymus excelsus isolate EI_201214 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905200.1
Elymus tangutorum isolate EI_201213 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905199.1
Elymus dolichatherus isolate EI_201212 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905198.1
Elymus dolichatherus isolate EI_201211 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene,	154	154	100%	2e-34	100%	KF905197.1

partial sequence; chloroplast						
Elymus tangutorum isolate El_201209 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905195.1
Elymus dahuricus isolate El_201208 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905194.1
Elymus tibeticus isolate El_201206 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905192.1
Elymus tangutorum isolate El_201205 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905191.1
Elymus tangutorum isolate El_201204 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905190.1
Elymus dahuricus var. cylindricus isolate El_201202 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905188.1
Elymus nutans isolate El_201102 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905186.1
Elymus sibiricus isolate El_201101 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905185.1
Triticum urartu plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732946.1
Triticum spelta plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732945.1
Triticum monococcum plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732944.1
Triticum durum plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732942.1
Triticum monococcum subsp. aegilopoides plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732941.1
Triticum aestivum plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732940.1
Elymus tsukushiensis plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732933.1
Elymus racemifer plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732932.1
Elymus humidus plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732931.1
Elymus dahuricus plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732930.1

Elymus caninus plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732929.1
Aegilops geniculata chloroplast, complete genome	154	154	100%	2e-34	100%	KF534490.1
Aegilops cylindrica chloroplast, complete genome	154	154	100%	2e-34	100%	KF534489.1
Elymus tauri isolate Psetau3 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu (trnL) gene, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF600705.1
Elymus tauri isolate Psetau2 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu (trnL) gene, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF600704.1
Elymus stipifolius isolate Psesti3 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu (trnL) gene, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF600702.1
Elymus stipifolius isolate Psesti2 trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF600701.1

Alignments

Elymus peschkovae voucher 115 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast

Sequence ID: **gb|KP325400.1|** Length: 1046 Number of Matches: 1
Range 1: 102 to 186

Score	Expect	Identities	Gaps	Strand	Frame
154 bits(170)	2e-34()	85/85(100%)	0/85(0%)	Plus/Plus	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCGTGTTTTGAGAAAACAAGGGGTTCTCGAACTAGAATACAA  60
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Sbjct  102  GGCAATCCTGAGCCAAATCCGTGTTTTGAGAAAACAAGGGGTTCTCGAACTAGAATACAA  161

Query  61   AGGAAAAGGATAGGTGCAGAGACTC  85
            |||||||||||||||||||||||||
Sbjct  162  AGGAAAAGGATAGGTGCAGAGACTC  186
```

Elymus scandicus voucher 114 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast

Sequence ID: **gb|KP325399.1|** Length: 1039 Number of Matches: 1
Range 1: 102 to 186

Score	Expect	Identities	Gaps	Strand	Frame
154 bits(170)	2e-34()	85/85(100%)	0/85(0%)	Plus/Plus	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCGTGTTTTGAGAAAACAAGGGGTTCTCGAACTAGAATACAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  102  GGCAATCCTGAGCCAAATCCGTGTTTTGAGAAAACAAGGGGTTCTCGAACTAGAATACAA  161

Query  61   AGGAAAAGGATAGGTGCAGAGACTC  85
            |||||||||||||||||||||||||
Sbjct  162  AGGAAAAGGATAGGTGCAGAGACTC  186
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Elymus excelsus voucher 1114 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast

Sequence ID: **gb|KP325398.1|** Length: 1043 Number of Matches: 1
Range 1: 102 to 186

Score	Expect	Identities	Gaps	Strand	Frame
154 bits(170)	2e-34()	85/85(100%)	0/85(0%)	Plus/Plus	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCGTGTTTTGAGAAAACAAGGGGTTCTCGAACTAGAATACAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  102  GGCAATCCTGAGCCAAATCCGTGTTTTGAGAAAACAAGGGGTTCTCGAACTAGAATACAA  161

Query  61   AGGAAAAGGATAGGTGCAGAGACTC  85
            |||||||||||||||||||||||||
Sbjct  162  AGGAAAAGGATAGGTGCAGAGACTC  186
```

Elymus pendulinus voucher 113 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KP325397.1|** Length: 1049 Number of Matches: 1
Range 1: 102 to 186

Score	Expect	Identities	Gaps	Strand	Frame
154 bits(170)	2e-34()	85/85(100%)	0/85(0%)	Plus/Plus	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCGTGTTTTGAGAAAACAAGGGGTTCTCGAACTAGAATACAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  102  GGCAATCCTGAGCCAAATCCGTGTTTTGAGAAAACAAGGGGTTCTCGAACTAGAATACAA  161

Query  61   AGGAAAAGGATAGGTGCAGAGACTC  85
            |||||||||||||||||||||||||
Sbjct  162  AGGAAAAGGATAGGTGCAGAGACTC  186
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Elymus dahuricus var. cylindricus voucher 5509 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KP325396.1|** Length: 1043 Number of Matches: 1
Range 1: 102 to 186

Score	Expect	Identities	Gaps	Strand	Frame
154 bits(170)	2e-34()	85/85(100%)	0/85(0%)	Plus/Plus	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCGTGTTTTGAGAAAACAAGGGGTTCTCGAACTAGAATACAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  102  GGCAATCCTGAGCCAAATCCGTGTTTTGAGAAAACAAGGGGTTCTCGAACTAGAATACAA  161

Query  61   AGGAAAAGGATAGGTGCAGAGACTC  85
            |||||||||||||||||||||||||
Sbjct  162  AGGAAAAGGATAGGTGCAGAGACTC  186
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NCBI/ BLAST/ blastn suite/ **Formatting Results - BT5009U4015**

Formatting options

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Blast report description

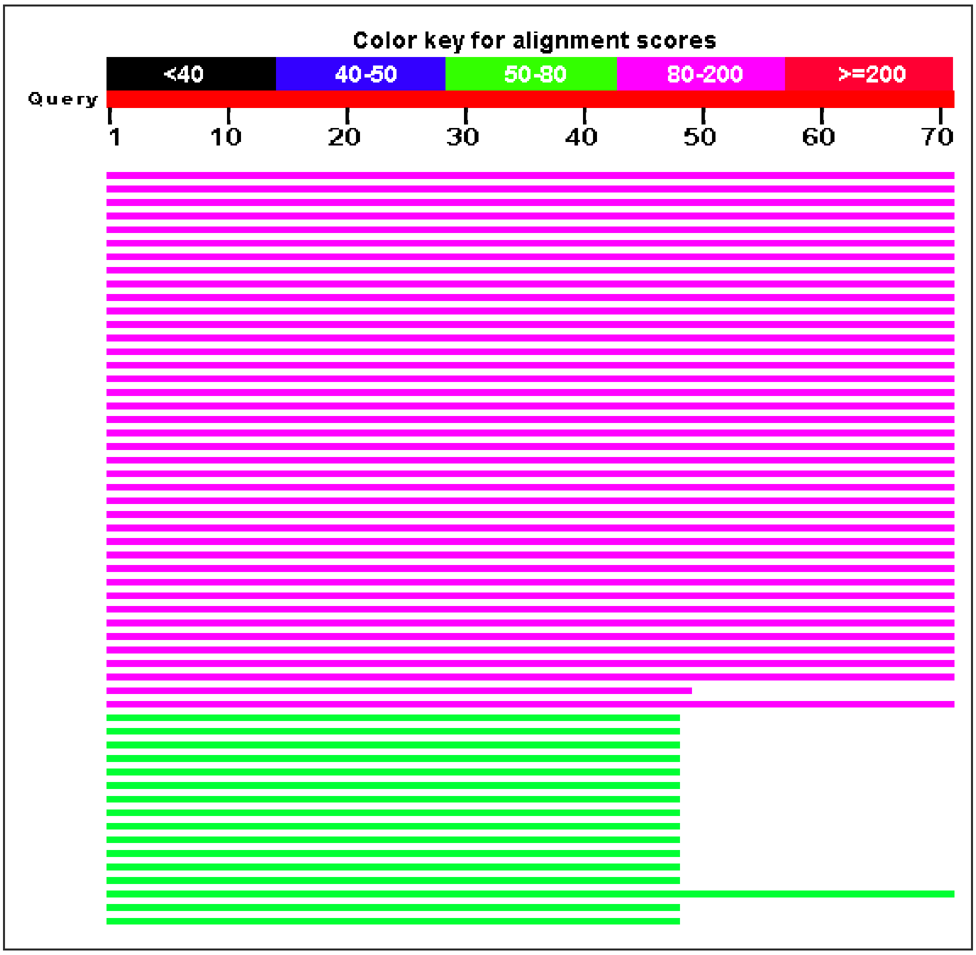
M/C5996.495-1C_trnL_Clone9,10

RID BT5009U4015 (Expires on 02-12 21:00 pm)

Query ID	lcl|Query_78763	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	71		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Vicia faba isolate 7612 tRNA-Leu (trnL) gene, partial sequence; chloroplast	121	121	100%	1e-24	97%	KJ787213.1
Vicia faba plastid, complete genome	121	121	100%	1e-24	97%	KF042344.1
Vicia faba isolate HS879 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	121	121	100%	1e-24	97%	JX505737.1
Vicia faba var. minor tRNA-Leu (trnL) gene, partial sequence; chloroplast	121	121	100%	1e-24	97%	JN617168.1
Vicia faba var. major tRNA-Leu (trnL) gene, partial sequence; chloroplast	121	121	100%	1e-24	97%	JN617167.1
Vicia faba chloroplast transfer RNA-Leu(CAA)	121	121	100%	1e-24	97%	M55084.1
Vicia faba chloroplast tRNA-Leu, tRNA-Phe, tRNA-His, ORFX, NADH-deydrogenase genes & partial sequence ORFx & psbA genes	121	121	100%	1e-24	97%	X51471.1
Broad bean chloroplast genes for tRNA-Leu(CAA) and (UAA) and tRNA-Phe	121	121	100%	1e-24	97%	X02444.1
Melilotus albus isolate xt_plant115 tRNA-Leu (trnL) gene, intron; chloroplast	106	106	100%	4e-20	93%	KJ746436.1
Tracheophyta environmental sample clone N-11 tRNA-Leu (trnL) gene, partial sequence; chloroplast	106	106	100%	4e-20	93%	KF616419.1
Tracheophyta environmental sample clone N-3 tRNA-Leu (trnL) gene, partial sequence; chloroplast	106	106	100%	4e-20	93%	KF616411.1
Tracheophyta environmental sample clone N-6 tRNA-Leu (trnL) gene, partial sequence; chloroplast	106	106	100%	4e-20	93%	KF616414.1
Tracheophyta environmental sample clone N-5 tRNA-Leu (trnL) gene, partial sequence; chloroplast	106	106	100%	4e-20	93%	KF616413.1
Tracheophyta environmental sample clone N-4 tRNA-Leu (trnL) gene, partial sequence; chloroplast	106	106	100%	4e-20	93%	KF616412.1
Melilotus alba tRNA-Leu (trnL) gene, intron; chloroplast	106	106	100%	4e-20	93%	DQ311713.1
Melilotus alba chloroplast tRNA-Leu (trnL) gene, intron sequence	106	106	100%	4e-20	93%	AF124232.1
Tracheophyta environmental sample clone N-2 tRNA-Leu (trnL) gene, partial sequence; chloroplast	100	100	100%	2e-18	92%	KF616410.1
Tracheophyta environmental sample clone N-1 tRNA-Leu (trnL) gene, partial sequence; chloroplast	100	100	100%	2e-18	92%	KF616409.1
Vicia cypria isolate HS866 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	100	100	100%	2e-18	92%	JX505734.1
Ononis hirta tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	95.3	95.3	100%	9e-17	91%	GQ488565.1
Ononis varelae tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	91.6	91.6	100%	1e-15	89%	GQ488605.1
Ononis cristata subsp. cristata tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	91.6	91.6	100%	1e-15	89%	GQ488558.1
Vicia lunata isolate V25 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial	87.9	87.9	100%	2e-14	88%	JX505749.1

sequence; chloroplast						
Ononis dentata tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	87.9	87.9	100%	2e-14	88%	GQ488559.1
Ononis pendula subsp. pendula tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	84.2	84.2	100%	2e-13	88%	GQ488578.1
Trifolium boissieri chloroplast, complete genome	82.4	82.4	100%	7e-13	87%	KJ788284.1
Trifolium grandiflorum plastid, complete genome	82.4	82.4	100%	7e-13	87%	KC894707.1
Ononis paralias tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	82.4	82.4	100%	7e-13	87%	GQ488577.1
Ononis filicaulis tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	82.4	82.4	100%	7e-13	87%	GQ488561.1
Trifolium praetermissum tRNA-Leu (trnL) gene, intron; chloroplast	82.4	82.4	100%	7e-13	87%	DQ311887.1
Trifolium phitosianum tRNA-Leu (trnL) gene, intron; chloroplast	82.4	82.4	100%	7e-13	87%	DQ311871.1
Trifolium philistaeum tRNA-Leu (trnL) gene, intron; chloroplast	82.4	82.4	100%	7e-13	87%	DQ311870.1
Trifolium micranthum tRNA-Leu (trnL) gene, intron; chloroplast	82.4	82.4	100%	7e-13	87%	DQ311836.1
Trifolium grandiflorum tRNA-Leu (trnL) gene, intron; chloroplast	82.4	82.4	100%	7e-13	87%	DQ311800.1
Trifolium erubescens tRNA-Leu (trnL) gene, intron; chloroplast	82.4	82.4	100%	7e-13	87%	DQ311789.1
Trifolium brutium tRNA-Leu (trnL) gene, intron; chloroplast	82.4	82.4	100%	7e-13	87%	DQ311756.1
Trifolium boissieri tRNA-Leu (trnL) gene, intron; chloroplast	82.4	82.4	100%	7e-13	87%	DQ311752.1
Trifolium billardierei tRNA-Leu (trnL) gene, intron; chloroplast	82.4	82.4	100%	7e-13	87%	DQ311750.1
Medicago sativa voucher MS1 tRNA-Leu (trnL) gene, partial sequence; chloroplast	80.5	80.5	69%	3e-12	96%	JQ041881.1
Ononis verae tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	80.5	80.5	100%	3e-12	87%	GQ488607.1
Medicago papillosa chloroplast, complete genome	78.7	78.7	67%	9e-12	96%	KJ850241.1
Medicago hybrida chloroplast, complete genome	78.7	78.7	67%	9e-12	96%	KJ850240.1
Medicago falcata isolate 02MF tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	78.7	78.7	67%	9e-12	96%	KP174819.1
Medicago sativa isolate 01MS tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	78.7	78.7	67%	9e-12	96%	KP174818.1
Medicago falcata isolate xt_plant82 tRNA-Leu (trnL) gene, intron; chloroplast	78.7	78.7	67%	9e-12	96%	KJ746339.1
Medicago lunata isolate EC 583612 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	78.7	78.7	67%	9e-12	96%	JX274180.1
Medicago plicata isolate EC 583608 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	78.7	78.7	67%	9e-12	96%	JX274176.1
Medicago pamphylica isolate EC 583562 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	78.7	78.7	67%	9e-12	96%	JX274143.1
Medicago brachycarpa isolate EC 583556 tRNA-Leu (trnL) gene and trnL-trnF	78.7	78.7	67%	9e-12	96%	JX274140.1

intergenic spacer, partial sequence; chloroplast						
Medicago sativa tRNA-Leu (trnL) gene, intron; chloroplast	78.7	78.7	67%	9e-12	96%	JX874981.1
Medicago sativa tRNA-Leu (trnL) gene, partial sequence; chloroplast	78.7	78.7	67%	9e-12	96%	JN617183.1
Medicago sativa voucher personal collection:I. Hiiesalu 45 tRNA-Leu (trnL) gene, partial sequence; chloroplast	78.7	78.7	67%	9e-12	96%	HM590316.1
Medicago sativa tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	78.7	78.7	67%	9e-12	96%	GQ488614.1
Ononis incisa tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	78.7	78.7	100%	9e-12	87%	GQ488566.1
Medicago sativa tRNA-Leu (trnL) gene, partial sequence; chloroplast	78.7	78.7	67%	9e-12	96%	DQ131554.1
Medicago sativa tRNA-Leu (trnL) gene, intron; chloroplast	78.7	78.7	67%	9e-12	96%	DQ311711.1
Medicago ruthenica tRNA-Leu (trnL) gene, intron; chloroplast	78.7	78.7	67%	9e-12	96%	DQ311710.1
Trifolium aureum plastid, complete genome	76.8	76.8	100%	3e-11	86%	KC894708.1
Trigonella suavissima isolate EC 583624 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	76.8	76.8	100%	3e-11	86%	JX274187.1
Trigonella suavissima isolate EC 583623 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	76.8	76.8	100%	3e-11	86%	JX274186.1
Lathyrus setifolius isolate HS1172 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	76.8	76.8	100%	3e-11	86%	JX505693.1
Lens ervoides chloroplast DNA, tRNA-Leu (trnL) and trnL-trnF intergenic spacer, partial sequence, specimen_voucher: GAZI:2297	76.8	76.8	100%	3e-11	86%	AB546807.1
Trifolium lupinaster isolate 1305o tRNA-Leu (trnL) gene, partial sequence; chloroplast	76.8	76.8	100%	3e-11	86%	GQ245622.1
Trifolium lupinaster isolate 0859g tRNA-Leu (trnL) gene, partial sequence; chloroplast	76.8	76.8	100%	3e-11	86%	GQ245621.1
Lathyrus setifolius tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	76.8	76.8	100%	3e-11	86%	AY839458.1
Trifolium polyphyllum tRNA-Leu (trnL) gene, intron; chloroplast	76.8	76.8	100%	3e-11	86%	DQ311885.1
Trifolium leucanthum tRNA-Leu (trnL) gene, intron; chloroplast	76.8	76.8	100%	3e-11	86%	DQ311819.1
Trifolium gordejevii tRNA-Leu (trnL) gene, intron; chloroplast	76.8	76.8	100%	3e-11	86%	DQ311797.1
Trifolium eximium tRNA-Leu (trnL) gene, intron; chloroplast	76.8	76.8	100%	3e-11	86%	DQ311790.1
Trifolium aureum tRNA-Leu (trnL) gene, intron; chloroplast	76.8	76.8	100%	3e-11	86%	DQ311738.1
Trifolium alpinum tRNA-Leu (trnL) gene, intron; chloroplast	76.8	76.8	100%	3e-11	86%	DQ311725.1
Trifolium bolanderi tRNA-Leu (trnL) gene, intron; chloroplast	75.0	75.0	100%	1e-10	86%	DQ311753.1
Trifolium beckwithii tRNA-Leu (trnL) gene, intron; chloroplast	75.0	75.0	100%	1e-10	86%	DQ311745.1
Lathyrus inconspicuus chloroplast, complete genome	73.1	73.1	67%	4e-10	94%	KJ850236.1
Lathyrus clymenum chloroplast, complete genome	73.1	73.1	67%	4e-10	94%	KJ850235.1
Lathyrus venosus chloroplast, complete	73.1	73.1	67%	4e-10	94%	KJ806202.1

genome						
Lathyrus pubescens chloroplast, complete genome	73.1	73.1	67%	4e-10	94%	KJ806200.1
Lathyrus palustris chloroplast, complete genome	73.1	73.1	67%	4e-10	94%	KJ806199.1
Lathyrus ochroleucus chloroplast, complete genome	73.1	73.1	67%	4e-10	94%	KJ806198.1
Lathyrus ochroleucus chloroplast, complete genome	73.1	73.1	67%	4e-10	94%	KJ806197.1
Lathyrus japonicus chloroplast, complete genome	73.1	73.1	67%	4e-10	94%	KJ806195.1
Lathyrus japonicus chloroplast, complete genome	73.1	73.1	67%	4e-10	94%	KJ806194.1
Lathyrus graminifolius chloroplast, complete genome	73.1	73.1	67%	4e-10	94%	KJ806193.1
Melilotus officinalis isolate CP46 tRNA-Leu (trnL) gene, partial sequence; chloroplast	73.1	73.1	67%	4e-10	94%	KP208370.1
Lathyrus crassipes isolate P025 tRNA-Leu (trnL) gene, partial sequence; chloroplast	73.1	73.1	67%	4e-10	94%	KP057648.1
Vicia crocea isolate 18395 tRNA-Leu (trnL) gene, partial sequence; chloroplast	73.1	73.1	67%	4e-10	94%	KJ787216.1
Melilotus officinalis isolate xt_plant51 tRNA-Leu (trnL) gene, intron; chloroplast	73.1	73.1	67%	4e-10	94%	KJ746435.1
Ononis spinosa isolate xt_plant93 tRNA-Leu (trnL) gene, intron; chloroplast	73.1	73.1	67%	4e-10	94%	KJ746342.1
Medicago lupulina isolate xt_plant73 tRNA-Leu (trnL) gene, intron; chloroplast	73.1	73.1	67%	4e-10	94%	KJ746340.1
Medicago truncatula f. tricycla chloroplast, complete genome	73.1	73.1	67%	4e-10	94%	KF241982.1
Tracheophyta environmental sample clone S4-7 tRNA-Leu (trnL) gene, partial sequence; chloroplast	73.1	73.1	67%	4e-10	94%	KF616483.1
Tracheophyta environmental sample clone S4-6 tRNA-Leu (trnL) gene, partial sequence; chloroplast	73.1	73.1	67%	4e-10	94%	KF616482.1
Tracheophyta environmental sample clone S4-2 tRNA-Leu (trnL) gene, partial sequence; chloroplast	73.1	73.1	67%	4e-10	94%	KF616478.1
Tracheophyta environmental sample clone S4-3 tRNA-Leu (trnL) gene, partial sequence; chloroplast	73.1	73.1	67%	4e-10	94%	KF616479.1
Tracheophyta environmental sample clone S4-1 tRNA-Leu (trnL) gene, partial sequence; chloroplast	73.1	73.1	67%	4e-10	94%	KF616477.1
Vicia monantha isolate HV47 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	73.1	73.1	67%	4e-10	94%	JX505758.1
Lathyrus zionis isolate HV28 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	73.1	73.1	67%	4e-10	94%	JX505707.1
Lathyrus venosus isolate HS1178 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	73.1	73.1	67%	4e-10	94%	JX505704.1
Lathyrus spathulatus isolate Kenicer126 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	73.1	73.1	67%	4e-10	94%	JX505695.1
Lathyrus quinquenervius isolate Kenicer109 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	73.1	73.1	67%	4e-10	94%	JX505686.1

Alignments

Vicia faba isolate 7612 tRNA-Leu (trnL) gene, partial sequence; chloroplast

Sequence ID: **gb|KJ787213.1|** Length: 487 Number of Matches: 1
Range 1: 90 to 160

Score	Expect	Identities	Gaps	Strand	Frame
121 bits(65)	1e-24()	69/71(97%)	0/71(0%)	Plus/Plus	

Features:

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Query  1    CTGAGCCAAATCCTTCTTTCCGAAAACAAATAACTAAAAGCTCAGaaaaaaaGGATAGGT  60
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Sbjct  90   CTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAGGATAGGT  149

Query  61   GCAGAGACTCA  71
            |||||||||||
Sbjct  150  GCAGAGACTCA  160
```

Vicia faba plastid, complete genome
Sequence ID: **gb|KF042344.1|** Length: 123722 Number of Matches: 1
Range 1: 118549 to 118619

Score	Expect	Identities	Gaps	Strand	Frame
121 bits(65)	1e-24()	69/71(97%)	0/71(0%)	Plus/Plus	

Features:

```
Query  1       CTGAGCCAAATCCTTCTTTCCGAAAACAAATAACTAAAAGCTCAGaaaaaaaGGATAGGT  60
               |||||||||||||||||||||||||||||| ||||||||| |||||||||||||||||||
Sbjct  118549  CTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAGGATAGGT  118608

Query  61      GCAGAGACTCA  71
               |||||||||||
Sbjct  118609  GCAGAGACTCA  118619
```

Vicia faba isolate HS879 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|JX505737.1|** Length: 604 Number of Matches: 1
Range 1: 73 to 143

Score	Expect	Identities	Gaps	Strand	Frame
121 bits(65)	1e-24()	69/71(97%)	0/71(0%)	Plus/Plus	

Features:

```
Query  1    CTGAGCCAAATCCTTCTTTCCGAAAACAAATAACTAAAAGCTCAGaaaaaaaGGATAGGT  60
            |||||||||||||||||||||||||||||| ||||||||| |||||||||||||||||||
Sbjct  73   CTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAGGATAGGT  132

Query  61   GCAGAGACTCA  71
            |||||||||||
Sbjct  133  GCAGAGACTCA  143
```

Vicia faba var. minor tRNA-Leu (trnL) gene, partial sequence; chloroplast
Sequence ID: **gb|JN617168.1|** Length: 938 Number of Matches: 1
Range 1: 553 to 623

Score	Expect	Identities	Gaps	Strand	Frame
121 bits(65)	1e-24()	69/71(97%)	0/71(0%)	Plus/Minus	

Features:

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Query  1    CTGAGCCAAATCCTTCTTTCCGAAAACAAATAACTAAAAGCTCAGaaaaaaaGGATAGGT  60
            |||||||||||||||||||||||||||||| ||||||||| |||||||||||||||||||
Sbjct  623  CTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAGGATAGGT  564

Query  61   GCAGAGACTCA  71
            |||||||||||
Sbjct  563  GCAGAGACTCA  553
```

Vicia faba var. major tRNA-Leu (trnL) gene, partial sequence; chloroplast
Sequence ID: **gb|JN617167.1|** Length: 949 Number of Matches: 1
Range 1: 557 to 627

Score	Expect	Identities	Gaps	Strand	Frame
121 bits(65)	1e-24()	69/71(97%)	0/71(0%)	Plus/Minus	

Features:

```
Query  1    CTGAGCCAAATCCTTCTTTCCGAAAACAAATAACTAAAAGCTCAGaaaaaaaGGATAGGT  60
            |||||||||||||||||||||||||||||| ||||||||| |||||||||||||||||||
Sbjct  627  CTGAGCCAAATCCTTCTTTCCGAAAACAAAAAACTAAAAGTTCAGAAAAAAAGGATAGGT  568
```

```
Query  61   GCAGAGACTCA  71
            |||||||||||
Sbjct  567  GCAGAGACTCA  557
```

BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BSPPHFJK014**

Formatting options
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Blast report description

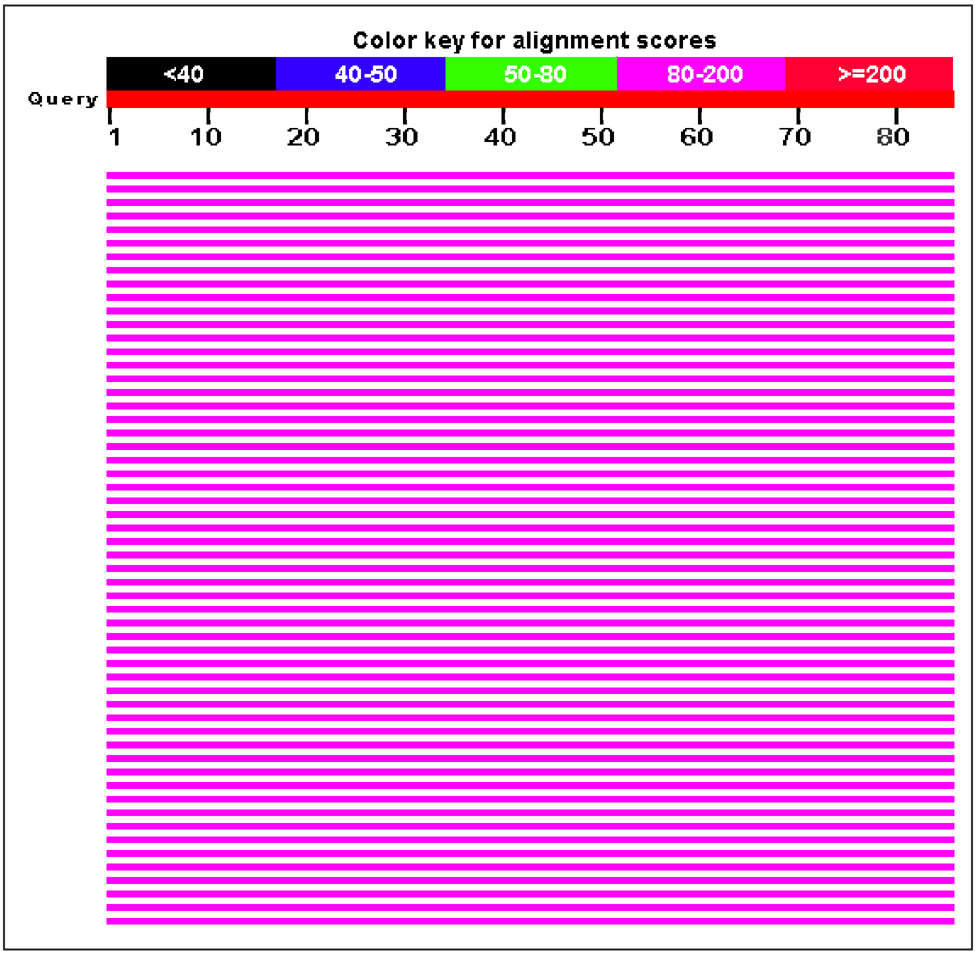
M/C:5992.1E-1C_trnL_Clone10

RID BSPPHFJK014 (Expires on 02-12 16:56 pm)

Query ID	lcl|Query_32495	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	85		

Graphic Summary

Distribution of 102 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Elymus peschkovae voucher 115 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KP325400.1
Elymus scandicus voucher 114 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KP325399.1
Elymus excelsus voucher 1114 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KP325398.1
Elymus pendulinus voucher 113 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KP325397.1
Elymus dahuricus var. cylindricus voucher 5509 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KP325396.1
Elymus excelsus voucher 5513 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KP325395.1
Elymus probatovae voucher 5645 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KP325394.1
Elymus ircutensis voucher Alt 10-198 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KP325393.1
Elymus vassiljevii voucher 5665 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KP325392.1
Elymus peschkovae voucher 5631 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KP325391.1
Elymus charkeviczii voucher 5550 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KP325390.1
Agropyron cristatum var. pectinatum voucher M.Pinar 4412a trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	149	149	100%	7e-33	99%	KP723655.1
Agropyron deweyi voucher M.Pinar 4321a trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene, complete	149	149	100%	7e-33	99%	KP723652.1

sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast						
Aegilops geniculata isolate CRF BGE022746 trnL gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	149	149	100%	7e-33	99%	KR559558.1
Aegilops neglecta bio-material USDA:PI170209 trnL gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	149	149	100%	7e-33	99%	KR559557.1
Elymus nevskii voucher Alt 1124 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KJ744043.1
Agropyron cristatum voucher Alt 11-377 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KJ744042.1
Elymus caninus voucher Alt 1031 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KJ744041.1
Campeiostachys dahurica voucher Xa 09-157 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KJ744040.1
Elymus fedtschenkoi voucher Alt 12-133 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KJ755833.1
Agropyron krylovianum voucher Alt 12-264 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KJ755832.1
Elymus subfibrosus tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KP257587.1
Elymus lanceolatus subsp. lanceolatus isolate CP3 tRNA-Leu (trnL) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KP208327.1
Triticum macha chloroplast DNA, complete genome	149	149	100%	7e-33	99%	LC005978.1
Triticum monococcum subsp. monococcum chloroplast DNA, complete genome	149	149	100%	7e-33	99%	LC005977.1
Triticum turgidum subsp. durum cultivar Langdon chloroplast, complete genome	149	149	100%	7e-33	99%	KM352501.1
Triticum timopheevii chloroplast DNA, complete genome	149	149	100%	7e-33	99%	AB976560.1
Aegilops kotschyi cultivar TA1980 chloroplast, complete genome	149	149	100%	7e-33	99%	KJ614420.1
Aegilops sharonensis cultivar TA1995 chloroplast, complete genome	149	149	100%	7e-33	99%	KJ614419.1
Aegilops bicornis cultivar Clae57 chloroplast, complete genome	149	149	100%	7e-33	99%	KJ614418.1
Aegilops sharonensis cultivar TA1996 chloroplast, complete genome	149	149	100%	7e-33	99%	KJ614417.1
Aegilops longissima cultivar TA1924 chloroplast, complete genome	149	149	100%	7e-33	99%	KJ614416.1
Aegilops searsii cultivar TA1841 chloroplast, complete genome	149	149	100%	7e-33	99%	KJ614415.1
Aegilops searsii cultivar TA1837 chloroplast, complete genome	149	149	100%	7e-33	99%	KJ614414.1
Aegilops searsii cultivar TA1926	149	149	100%	7e-33	99%	KJ614413.1

chloroplast, complete genome						
Aegilops tauschii cultivar AL8/78 chloroplast, complete genome	149	149	100%	7e-33	99%	KJ614412.1
Triticum urartu cultivar PI428335 chloroplast, complete genome	149	149	100%	7e-33	99%	KJ614411.1
Triticum timopheevii cultivar Tim01 chloroplast, complete genome	149	149	100%	7e-33	99%	KJ614410.1
Triticum timopheevii cultivar TA944 chloroplast, complete genome	149	149	100%	7e-33	99%	KJ614409.1
Triticum timopheevii cultivar TA1485 chloroplast, complete genome	149	149	100%	7e-33	99%	KJ614408.1
Triticum timopheevii cultivar TA0941 chloroplast, complete genome	149	149	100%	7e-33	99%	KJ614407.1
Aegilops speltoides var. speltoides cultivar PI487232 chloroplast, complete genome	149	149	100%	7e-33	99%	KJ614406.1
Aegilops speltoides var. ligustica cultivar TA1796 chloroplast, complete genome	149	149	100%	7e-33	99%	KJ614405.1
Aegilops speltoides var. ligustica cultivar AE918 chloroplast, complete genome	149	149	100%	7e-33	99%	KJ614404.1
Triticum aestivum cultivar spleta PI384000 chloroplast, complete genome	149	149	100%	7e-33	99%	KJ614403.1
Triticum turgidum cultivar TA1133 chloroplast, complete genome	149	149	100%	7e-33	99%	KJ614402.1
Triticum turgidum cultivar TA0060 chloroplast, complete genome	149	149	100%	7e-33	99%	KJ614401.1
Triticum turgidum cultivar TA0073 chloroplast, complete genome	149	149	100%	7e-33	99%	KJ614400.1
Triticum turgidum cultivar TA2801 chloroplast, complete genome	149	149	100%	7e-33	99%	KJ614399.1
Triticum turgidum cultivar PI520121 chloroplast, complete genome	149	149	100%	7e-33	99%	KJ614398.1
Triticum aestivum cultivar Chinese Spring TA3008 chloroplast, complete genome	149	149	100%	7e-33	99%	KJ614396.1
Elymus repens isolate xt_plant145 tRNA-Leu (trnL) gene, intron; chloroplast	149	149	100%	7e-33	99%	KJ746409.1
Triticum aestivum chromosome 3B, genomic scaffold, cultivar Chinese Spring	149	308	100%	7e-33	99%	HG670306.1
Triticum aestivum chloroplast, complete genome	149	149	100%	7e-33	99%	KJ592713.1
Elymus sibiricus isolate El_201311 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905225.1
Elymus dolichatherus isolate El_201310 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905224.1
Elymus nutans isolate El_201309 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905223.1
Elymus sibiricus isolate El_201307 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905221.1
Elymus tangutorum isolate El_201305 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905219.1
Elymus nutans isolate El_201302 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905216.1

Elymus nutans isolate EI_201301 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905215.1
Elymus dolichatherus isolate EI_201228 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905214.1
Elymus tangutorum isolate EI_201226 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905212.1
Elymus tangutorum isolate EI_201216 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905202.1
Elymus nutans isolate EI_201224 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905210.1
Elymus dahuricus var. cylindricus isolate EI_201222 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905208.1
Elymus tangutorum isolate EI_201221 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905207.1
Elymus sibiricus isolate EI_201220 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905206.1
Elymus antiquus isolate EI_201219 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905205.1
Elymus excelsus isolate EI_201218 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905204.1
Elymus nutans isolate EI_201217 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905203.1
Elymus excelsus isolate EI_201214 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905200.1
Elymus tangutorum isolate EI_201213 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905199.1
Elymus dolichatherus isolate EI_201212 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905198.1
Elymus dolichatherus isolate EI_201211 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene,	149	149	100%	7e-33	99%	KF905197.1

partial sequence; chloroplast						
Elymus tangutorum isolate EI_201209 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905195.1
Elymus dahuricus isolate EI_201208 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905194.1
Elymus tibeticus isolate EI_201206 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905192.1
Elymus tangutorum isolate EI_201205 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905191.1
Elymus tangutorum isolate EI_201204 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905190.1
Elymus dahuricus var. cylindricus isolate EI_201202 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905188.1
Elymus nutans isolate EI_201102 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905186.1
Elymus sibiricus isolate EI_201101 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905185.1
Triticum urartu plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	149	149	100%	7e-33	99%	AB732946.1
Triticum spelta plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	149	149	100%	7e-33	99%	AB732945.1
Triticum monococcum plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	149	149	100%	7e-33	99%	AB732944.1
Triticum durum plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	149	149	100%	7e-33	99%	AB732942.1
Triticum monococcum subsp. aegilopoides plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	149	149	100%	7e-33	99%	AB732941.1
Triticum aestivum plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	149	149	100%	7e-33	99%	AB732940.1
Elymus tsukushiensis plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	149	149	100%	7e-33	99%	AB732933.1
Elymus racemifer plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	149	149	100%	7e-33	99%	AB732932.1
Elymus humidus plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	149	149	100%	7e-33	99%	AB732931.1
Elymus dahuricus plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	149	149	100%	7e-33	99%	AB732930.1

Elymus caninus plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	149	149	100%	7e-33	99%	AB732929.1
Aegilops geniculata chloroplast, complete genome	149	149	100%	7e-33	99%	KF534490.1
Aegilops cylindrica chloroplast, complete genome	149	149	100%	7e-33	99%	KF534489.1
Elymus tauri isolate Psetau3 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu (trnL) gene, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF600705.1
Elymus tauri isolate Psetau2 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu (trnL) gene, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF600704.1
Elymus stipifolius isolate Psesti3 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu (trnL) gene, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF600702.1
Elymus stipifolius isolate Psesti2 trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF600701.1

Alignments

Elymus peschkovae voucher 115 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast

Sequence ID: **gb|KP325400.1|** Length: 1046 Number of Matches: 1
Range 1: 102 to 186

Score	Expect	Identities	Gaps	Strand	Frame
149 bits(164)	7e-33()	84/85(99%)	0/85(0%)	Plus/Minus	

Features:

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Query  1    GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCCAGTTCGAGAACCCCTTGTTTTCTCAA  60
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Sbjct  186  GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  127

Query  61   AACACGGATTTGGCTCAGGATTGCC  85
            |||||||||||||||||||||||||
Sbjct  126  AACACGGATTTGGCTCAGGATTGCC  102
```

Elymus scandicus voucher 114 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast

Sequence ID: **gb|KP325399.1|** Length: 1039 Number of Matches: 1
Range 1: 102 to 186

Score	Expect	Identities	Gaps	Strand	Frame
149 bits(164)	7e-33()	84/85(99%)	0/85(0%)	Plus/Minus	

Features:

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Query  1    GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCCAGTTCGAGAACCCCTTGTTTTCTCAA  60
            ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  186  GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  127

Query  61   AACACGGATTTGGCTCAGGATTGCC  85
            |||||||||||||||||||||||||
Sbjct  126  AACACGGATTTGGCTCAGGATTGCC  102
```

Elymus excelsus voucher 1114 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast

Sequence ID: **gb|KP325398.1|** Length: 1043 Number of Matches: 1
Range 1: 102 to 186

Score	Expect	Identities	Gaps	Strand	Frame
149 bits(164)	7e-33()	84/85(99%)	0/85(0%)	Plus/Minus	

Features:

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Query  1    GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCCAGTTCGAGAACCCCTTGTTTTCTCAA  60
            ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  186  GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  127

Query  61   AACACGGATTTGGCTCAGGATTGCC  85
            |||||||||||||||||||||||||
Sbjct  126  AACACGGATTTGGCTCAGGATTGCC  102
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Elymus pendulinus voucher 113 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KP325397.1|** Length: 1049 Number of Matches: 1
Range 1: 102 to 186

Score	Expect	Identities	Gaps	Strand	Frame
149 bits(164)	7e-33()	84/85(99%)	0/85(0%)	Plus/Minus	

Features:

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Query  1    GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCCAGTTCGAGAACCCCTTGTTTTCTCAA  60
            ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  186  GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  127

Query  61   AACACGGATTTGGCTCAGGATTGCC  85
            |||||||||||||||||||||||||
Sbjct  126  AACACGGATTTGGCTCAGGATTGCC  102
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Elymus dahuricus var. cylindricus voucher 5509 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KP325396.1|** Length: 1043 Number of Matches: 1
Range 1: 102 to 186

Score	Expect	Identities	Gaps	Strand	Frame
149 bits(164)	7e-33()	84/85(99%)	0/85(0%)	Plus/Minus	

Features:

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Query  1    GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCCAGTTCGAGAACCCCTTGTTTTCTCAA  60
            ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  186  GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  127

Query  61   AACACGGATTTGGCTCAGGATTGCC  85
            |||||||||||||||||||||||||
Sbjct  126  AACACGGATTTGGCTCAGGATTGCC  102
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BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BSR4AP7E014**
 Formatting options
 Download
Blast report description

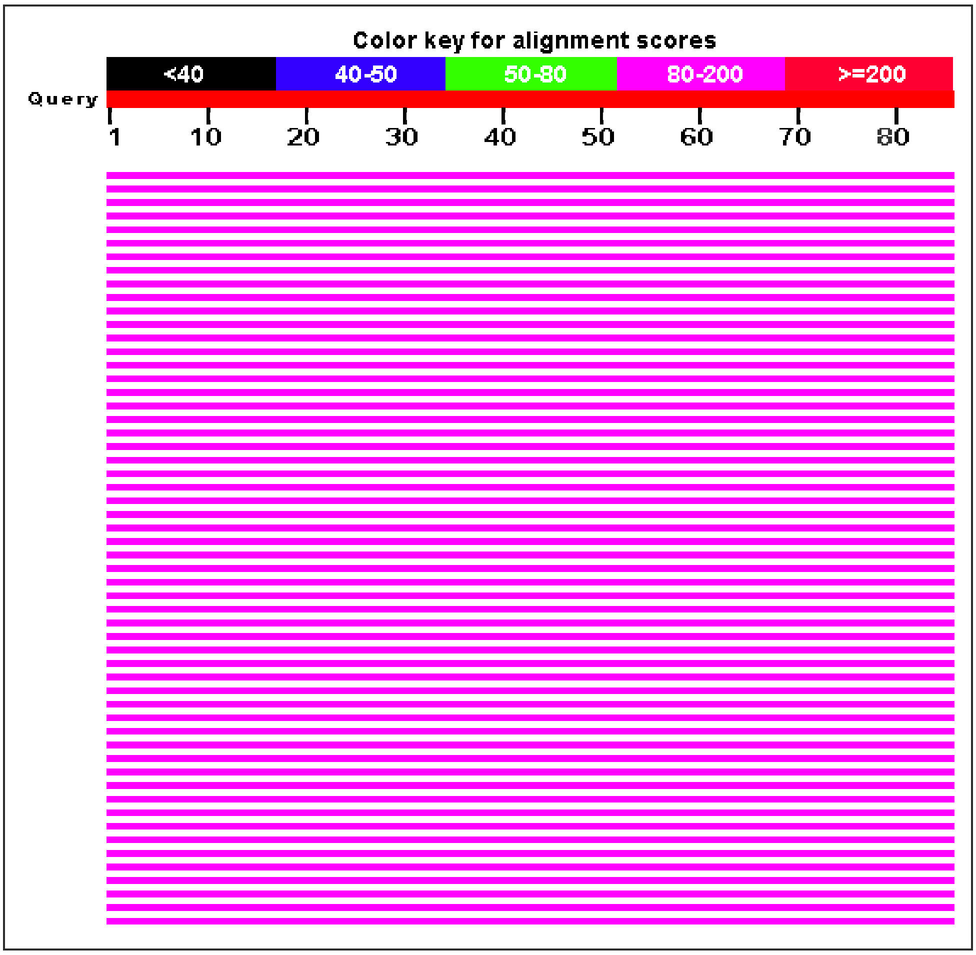
M/C:5992.1E-1C_trnL_Clone9

RID BSR4AP7E014 (Expires on 02-12 17:03 pm)

Query ID	lcl|Query_69361	**Database Name**	nr
Description	Clone9	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	85		

Graphic Summary

Distribution of 102 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Elymus tangutorum isolate El_201207 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	149	149	100%	7e-33	99%	KF905193.1
Elymus peschkovae voucher 115 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KP325400.1
Elymus scandicus voucher 114 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KP325399.1
Elymus excelsus voucher 1114 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KP325398.1
Elymus pendulinus voucher 113 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KP325397.1
Elymus dahuricus var. cylindricus voucher 5509 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KP325396.1
Elymus excelsus voucher 5513 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KP325395.1
Elymus probatovae voucher 5645 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KP325394.1
Elymus ircutensis voucher Alt 10-198 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KP325393.1
Elymus vassiljevii voucher 5665 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KP325392.1
Elymus peschkovae voucher 5631 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KP325391.1
Elymus charkeviczii voucher 5550 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KP325390.1
Agropyron cristatum var. pectinatum voucher M.Pinar 4412a trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF	145	145	100%	9e-32	98%	KP723655.1

intergenic spacer, partial sequence; chloroplast						
Agropyron deweyi voucher M.Pinar 4321a trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	145	145	100%	9e-32	98%	KP723652.1
Aegilops geniculata isolate CRF BGE022746 trnL gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	145	145	100%	9e-32	98%	KR559558.1
Aegilops neglecta bio-material USDA:PI170209 trnL gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	145	145	100%	9e-32	98%	KR559557.1
Elymus nevskii voucher Alt 1124 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KJ744043.1
Agropyron cristatum voucher Alt 11-377 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KJ744042.1
Elymus caninus voucher Alt 1031 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KJ744041.1
Campeiostachys dahurica voucher Xa 09-157 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KJ744040.1
Elymus fedtschenkoi voucher Alt 12-133 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KJ755833.1
Agropyron krylovianum voucher Alt 12-264 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KJ755832.1
Elymus subfibrosus tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KP257587.1
Elymus lanceolatus subsp. lanceolatus isolate CP3 tRNA-Leu (trnL) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KP208327.1
Triticum macha chloroplast DNA, complete genome	145	145	100%	9e-32	98%	LC005978.1
Triticum monococcum subsp. monococcum chloroplast DNA, complete genome	145	145	100%	9e-32	98%	LC005977.1
Triticum turgidum subsp. durum cultivar Langdon chloroplast, complete genome	145	145	100%	9e-32	98%	KM352501.1
Triticum timopheevii chloroplast DNA, complete genome	145	145	100%	9e-32	98%	AB976560.1
Aegilops kotschyi cultivar TA1980 chloroplast, complete genome	145	145	100%	9e-32	98%	KJ614420.1
Aegilops sharonensis cultivar TA1995 chloroplast, complete genome	145	145	100%	9e-32	98%	KJ614419.1
Aegilops bicornis cultivar Clae57 chloroplast, complete genome	145	145	100%	9e-32	98%	KJ614418.1
Aegilops sharonensis cultivar TA1996 chloroplast, complete genome	145	145	100%	9e-32	98%	KJ614417.1
Aegilops longissima cultivar TA1924 chloroplast, complete genome	145	145	100%	9e-32	98%	KJ614416.1
Aegilops searsii cultivar TA1841						

chloroplast, complete genome	145	145	100%	9e-32	98%	KJ614415.1
Aegilops searsii cultivar TA1837 chloroplast, complete genome	145	145	100%	9e-32	98%	KJ614414.1
Aegilops searsii cultivar TA1926 chloroplast, complete genome	145	145	100%	9e-32	98%	KJ614413.1
Aegilops tauschii cultivar AL8/78 chloroplast, complete genome	145	145	100%	9e-32	98%	KJ614412.1
Triticum urartu cultivar PI428335 chloroplast, complete genome	145	145	100%	9e-32	98%	KJ614411.1
Triticum timopheevii cultivar Tim01 chloroplast, complete genome	145	145	100%	9e-32	98%	KJ614410.1
Triticum timopheevii cultivar TA944 chloroplast, complete genome	145	145	100%	9e-32	98%	KJ614409.1
Triticum timopheevii cultivar TA1485 chloroplast, complete genome	145	145	100%	9e-32	98%	KJ614408.1
Triticum timopheevii cultivar TA0941 chloroplast, complete genome	145	145	100%	9e-32	98%	KJ614407.1
Aegilops speltoides var. speltoides cultivar PI487232 chloroplast, complete genome	145	145	100%	9e-32	98%	KJ614406.1
Aegilops speltoides var. ligustica cultivar TA1796 chloroplast, complete genome	145	145	100%	9e-32	98%	KJ614405.1
Aegilops speltoides var. ligustica cultivar AE918 chloroplast, complete genome	145	145	100%	9e-32	98%	KJ614404.1
Triticum aestivum cultivar spleta PI384000 chloroplast, complete genome	145	145	100%	9e-32	98%	KJ614403.1
Triticum turgidum cultivar TA1133 chloroplast, complete genome	145	145	100%	9e-32	98%	KJ614402.1
Triticum turgidum cultivar TA0060 chloroplast, complete genome	145	145	100%	9e-32	98%	KJ614401.1
Triticum turgidum cultivar TA0073 chloroplast, complete genome	145	145	100%	9e-32	98%	KJ614400.1
Triticum turgidum cultivar TA2801 chloroplast, complete genome	145	145	100%	9e-32	98%	KJ614399.1
Triticum turgidum cultivar PI520121 chloroplast, complete genome	145	145	100%	9e-32	98%	KJ614398.1
Triticum aestivum cultivar Chinese Spring TA3008 chloroplast, complete genome	145	145	100%	9e-32	98%	KJ614396.1
Elymus repens isolate xt_plant145 tRNA-Leu (trnL) gene, intron; chloroplast	145	145	100%	9e-32	98%	KJ746409.1
Triticum aestivum chromosome 3B, genomic scaffold, cultivar Chinese Spring	145	301	100%	9e-32	98%	HG670306.1
Triticum aestivum chloroplast, complete genome	145	145	100%	9e-32	98%	KJ592713.1
Elymus sibiricus isolate EI_201311 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905225.1
Elymus dolichatherus isolate EI_201310 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905224.1
Elymus nutans isolate EI_201309 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905223.1
Elymus sibiricus isolate EI_201307 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905221.1
Elymus tangutorum isolate EI_201305 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene,	145	145	100%	9e-32	98%	KF905219.1

partial sequence; chloroplast						
Elymus nutans isolate El_201302 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905216.1
Elymus nutans isolate El_201301 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905215.1
Elymus dolichatherus isolate El_201228 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905214.1
Elymus tangutorum isolate El_201226 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905212.1
Elymus tangutorum isolate El_201216 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905202.1
Elymus nutans isolate El_201224 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905210.1
Elymus dahuricus var. cylindricus isolate El_201222 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905208.1
Elymus tangutorum isolate El_201221 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905207.1
Elymus sibiricus isolate El_201220 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905206.1
Elymus antiquus isolate El_201219 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905205.1
Elymus excelsus isolate El_201218 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905204.1
Elymus nutans isolate El_201217 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905203.1
Elymus excelsus isolate El_201214 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905200.1
Elymus tangutorum isolate El_201213 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905199.1
Elymus dolichatherus isolate El_201212 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete	145	145	100%	9e-32	98%	KF905198.1

sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast						
Elymus dolichatherus isolate El_201211 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905197.1
Elymus tangutorum isolate El_201209 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905195.1
Elymus dahuricus isolate El_201208 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905194.1
Elymus tibeticus isolate El_201206 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905192.1
Elymus tangutorum isolate El_201205 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905191.1
Elymus tangutorum isolate El_201204 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905190.1
Elymus dahuricus var. cylindricus isolate El_201202 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905188.1
Elymus nutans isolate El_201102 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905186.1
Elymus sibiricus isolate El_201101 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF905185.1
Triticum urartu plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	145	145	100%	9e-32	98%	AB732946.1
Triticum spelta plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	145	145	100%	9e-32	98%	AB732945.1
Triticum monococcum plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	145	145	100%	9e-32	98%	AB732944.1
Triticum durum plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	145	145	100%	9e-32	98%	AB732942.1
Triticum monococcum subsp. aegilopoides plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	145	145	100%	9e-32	98%	AB732941.1
Triticum aestivum plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	145	145	100%	9e-32	98%	AB732940.1
Elymus tsukushiensis plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	145	145	100%	9e-32	98%	AB732933.1
Elymus racemifer plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	145	145	100%	9e-32	98%	AB732932.1
Elymus humidus plastid DNA, tRNA-Leu						

(trnL), trnL-trnF intergenic spacer, partial sequence	145	145	100%	9e-32	98%	AB732931.1
Elymus dahuricus plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	145	145	100%	9e-32	98%	AB732930.1
Elymus caninus plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	145	145	100%	9e-32	98%	AB732929.1
Aegilops geniculata chloroplast, complete genome	145	145	100%	9e-32	98%	KF534490.1
Aegilops cylindrica chloroplast, complete genome	145	145	100%	9e-32	98%	KF534489.1
Elymus tauri isolate Psetau3 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu (trnL) gene, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF600705.1
Elymus tauri isolate Psetau2 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu (trnL) gene, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF600704.1
Elymus stipifolius isolate Psesti3 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu (trnL) gene, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	9e-32	98%	KF600702.1

Alignments

Elymus tangutorum isolate EI_201207 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KF905193.1|** Length: 1063 Number of Matches: 1
Range 1: 102 to 186

Score	Expect	Identities	Gaps	Strand	Frame
149 bits(164)	7e-33()	84/85(99%)	0/85(0%)	Plus/Minus	

Features:

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Query  1    GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTAACAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  186  GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCACAA  127

Query  61   AACACGGATTTGGCTCAGGATTGCC  85
            |||||||||||||||||||||||||
Sbjct  126  AACACGGATTTGGCTCAGGATTGCC  102
```

Elymus peschkovae voucher 115 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KP325400.1|** Length: 1046 Number of Matches: 1
Range 1: 102 to 186

Score	Expect	Identities	Gaps	Strand	Frame
145 bits(160)	9e-32()	83/85(98%)	0/85(0%)	Plus/Minus	

Features:

```
Query  1    GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTAACAA  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Sbjct  186  GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  127

Query  61   AACACGGATTTGGCTCAGGATTGCC  85
            |||||||||||||||||||||||||
Sbjct  126  AACACGGATTTGGCTCAGGATTGCC  102
```

Elymus scandicus voucher 114 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KP325399.1|** Length: 1039 Number of Matches: 1

Range 1: 102 to 186

Score	Expect	Identities	Gaps	Strand	Frame
145 bits(160)	9e-32()	83/85(98%)	0/85(0%)	Plus/Minus	

Features:

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Query  1    GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTAACAA  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Sbjct  186  GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  127

Query  61   AACACGGATTTGGCTCAGGATTGCC  85
            |||||||||||||||||||||||||
Sbjct  126  AACACGGATTTGGCTCAGGATTGCC  102
```

Elymus excelsus voucher 1114 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast

Sequence ID: **gb|KP325398.1|** Length: 1043 Number of Matches: 1

Range 1: 102 to 186

Score	Expect	Identities	Gaps	Strand	Frame
145 bits(160)	9e-32()	83/85(98%)	0/85(0%)	Plus/Minus	

Features:

```
Query  1    GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTAACAA  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Sbjct  186  GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  127

Query  61   AACACGGATTTGGCTCAGGATTGCC  85
            |||||||||||||||||||||||||
Sbjct  126  AACACGGATTTGGCTCAGGATTGCC  102
```

Elymus pendulinus voucher 113 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast

Sequence ID: **gb|KP325397.1|** Length: 1049 Number of Matches: 1

Range 1: 102 to 186

Score	Expect	Identities	Gaps	Strand	Frame
145 bits(160)	9e-32()	83/85(98%)	0/85(0%)	Plus/Minus	

Features:

```
Query  1    GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTAACAA  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Sbjct  186  GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  127

Query  61   AACACGGATTTGGCTCAGGATTGCC  85
            |||||||||||||||||||||||||
Sbjct  126  AACACGGATTTGGCTCAGGATTGCC  102
```

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Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BSMWGB6M014**
Formatting options
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Blast report description

PB1A_RbcL_Direct_sequence

RID BSMWGB6M014 (Expires on 02-12 16:25 pm)

Query ID	lcl|Query_212991	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	90		

Graphic Summary

Distribution of 101 Blast Hits on the Query Sequence

Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Melica altissima voucher Chase 22006 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	143	143	96%	3e-31	98%	KC123375.1
Phaenosperma globosum voucher BH:J.I. Davis 779 plastid, complete genome	143	143	96%	3e-31	98%	KM974745.1
Melica subulata voucher CAN:Saarela 836 plastid, complete genome	143	143	96%	3e-31	98%	KM974743.1
Melica mutica voucher US:W.J. Kress & M. Butts 04-7461 plastid, complete genome	143	143	96%	3e-31	98%	KM974742.1
Diarrhena obovata voucher BH:J.I. Davis 756 plastid, complete genome	143	143	96%	3e-31	98%	KM974739.1
Melica uniflora ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid	143	143	96%	3e-31	98%	KM360877.1
Schizachne purpurascens voucher WAB_0132469024 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	143	143	96%	3e-31	98%	KJ593680.1
Schizachne purpurascens voucher WAB_0132469015 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	143	143	96%	3e-31	98%	KJ593679.1
Melica uniflora voucher G00199178 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	143	143	96%	3e-31	98%	KJ204376.1
Schizachne purpurascens voucher TJD-203 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	143	143	96%	3e-31	98%	KJ841556.1
Anisopogon avenaceus voucher iAD54_aven861 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	143	143	96%	3e-31	98%	KC129544.1
Anisopogon avenaceus chloroplast partial rbcL gene for RuBisCO large subunit, specimen voucher TCD:S.J. & T.R. Hodkinson 9370	143	143	96%	3e-31	98%	HE573296.1
Melica onoei ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	143	143	96%	3e-31	98%	HQ600456.1
Melica nutans ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	143	143	96%	3e-31	98%	HQ600444.1
Melica scabrosa ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	143	143	96%	3e-31	98%	HQ600442.1
Neomolinia japonica ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	143	143	96%	3e-31	98%	HQ600431.1
Neomolinia fauriei ribulose-1,5-						

bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	143	143	96%	3e-31	98%	HQ600429.1
Melica nutans isolate NMW3307 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	143	143	96%	3e-31	98%	JN893063.1
Melica nutans isolate NMW537 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	143	143	96%	3e-31	98%	JN892940.1
Melica uniflora isolate NMW538 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	143	143	96%	3e-31	98%	JN892933.1
Schizachne purpurascens voucher AP105 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	143	143	96%	3e-31	98%	HQ590262.1
Phaenosperma globosa chloroplast partial rbcL gene for ribulose bisphosphate carboxylase large chain	143	143	96%	3e-31	98%	AJ784824.1
Melica uniflora chloroplast partial rbcL gene for ribulose bisphosphate carboxylase large chain	143	143	96%	3e-31	98%	AJ746294.1
Melica uniflora chloroplast partial rbcL gene for ribulose bisphosphate carboxylase large chain	143	143	96%	3e-31	98%	AJ746263.1
Diarrhena obovata ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gene, partial cds; chloroplast	143	143	96%	3e-31	98%	AY622890.1
Anisopogon avenaceus ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gene, partial cds; chloroplast	143	143	96%	3e-31	98%	AY622886.1
Brachypodium distachyon ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	141	141	95%	1e-30	98%	HM849819.1
Melica uniflora isolate NMW3310 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	140	140	96%	4e-30	97%	JN893344.1
Oryza sativa Japonica Group Os06g0598500 (Os06g0598500) mRNA, complete cds	140	140	100%	4e-30	96%	NM_001064530.2
Hordeum vulgare subsp. vulgare chloroplast, complete genome	138	138	96%	1e-29	97%	KT962228.1
Fargesia rufa ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KU054399.1
Festuca bromoides chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV1607	138	138	96%	1e-29	97%	LN908031.1
Valiha diffusa chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV1487	138	138	96%	1e-29	97%	LN908028.1
Sirochloa parvifolia chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher NOP224	138	138	96%	1e-29	97%	LN908013.1
Nastus aristatus chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase	138	138	96%	1e-29	97%	LN907971.1

large subunit, specimen voucher MSV1464						
Humbertochloa bambusiuscula chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV956	138	138	96%	1e-29	97%	LN907952.1
Hickelia madagascariensis chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV724	138	138	96%	1e-29	97%	LN907951.1
Festuca camusiana chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV617	138	138	96%	1e-29	97%	LN907946.1
Bromus leptoclados chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV1617	138	138	96%	1e-29	97%	LN907903.1
Brachypodium madagascariense chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV735	138	138	96%	1e-29	97%	LN907902.1
Arundinaria sp. 1 GB-2015 chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV723	138	138	96%	1e-29	97%	LN907889.1
Poaceae sp. SERC-1076419263 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KP402760.1
Elymus sp. SERC-1076419241 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KP402751.1
Elymus virginicus voucher SERC-1076419296 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KP402747.1
Elymus sp. SERC-1076419302 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KP402713.1
Poaceae sp. SERC-1076419267 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KP402694.1
Panicum virgatum voucher SERC-1076419297 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KP402686.1
Elymus sp. SERC-1076419260 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KP402592.1
Oryza sativa cultivar 7502 ATP beta subunit (atpB) gene, promoter region; and ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KM979465.1
Oryza sativa cultivar IRRI-6 ATP beta subunit (atpB) gene, promoter region; and ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KM979464.1
Oryza sativa cultivar 7860 ATP beta						

subunit (atpB) gene, promoter region; and ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KM979463.1
Oryza sativa cultivar 7190 ATP beta subunit (atpB) gene, promoter region; and ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KM979460.1
Bromus diandrus ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KP149548.1
Lolium sp. KK-0011 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KP149535.1
Connorochloa tenuis voucher CHR:605880 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KT007201.1
Protea scolopendriifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KP110421.1
Festuca scabra ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KP110319.1
Oryza sativa cultivar DR-82 ATP beta subunit (atpB) gene, partial sequence; and ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KM525659.1
Pseudosasa japonica isolate Pjc_a-1 cultivar akebonosuji chloroplast, complete genome	138	138	96%	1e-29	97%	KT428378.1
Pseudosasa japonica isolate Pjc-1 cultivar akebonosuji chloroplast, complete genome	138	138	96%	1e-29	97%	KT428377.1
Oryza sativa Japonica Group DNA, chromosome 12, cultivar: Nipponbare, complete sequence	138	138	96%	1e-29	97%	AP014968.1
Oryza sativa Japonica Group DNA, chromosome 10, cultivar: Nipponbare, complete sequence	138	138	96%	1e-29	97%	AP014966.1
Oryza sativa Japonica Group DNA, chromosome 6, cultivar: Nipponbare, complete sequence	138	138	96%	1e-29	97%	AP014962.1
Oryza sativa Japonica Group DNA, chromosome 1, cultivar: Nipponbare, complete sequence	138	138	96%	1e-29	97%	AP014957.1
Oryza sativa Indica Group cultivar RP Bio-226 chromosome 5 sequence	138	271	96%	1e-29	97%	CP012613.1
Bromus kalmii voucher BIOUG24048-E05 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KT695565.1
Bromus inermis voucher BIOUG24048-G05 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KT695423.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KR092108.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KR092107.1

Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KR092106.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KR092105.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KR092104.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KR092103.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KR092102.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KR092101.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KR092100.1
Triticum turgidum subsp. durum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KR092099.1
Triticum turgidum subsp. durum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KR092098.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KR092097.1
Triticum turgidum subsp. durum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KR092096.1
Oryza sativa Tropical Japonica Group chloroplast, complete genome	138	138	96%	1e-29	97%	KT289404.1
Oryza sativa Aromatic Japonica Group cultivar basmati chloroplast, complete genome	138	138	96%	1e-29	97%	KT289403.1
Medicago truncatula ribulose bisphosphate carboxylase large chain domain protein partial mRNA	138	138	96%	1e-29	97%	XM_013588237.1
Oryza sativa cultivar NARC 17958 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KP827660.1
Hordeum vulgare cultivar NARC 4064 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KP827658.1
Triticum aestivum cultivar NARC 10727 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KP827657.1
Oryza longistaminata chloroplast, complete genome	138	138	96%	1e-29	97%	KM088024.1
Oryza barthii chloroplast, complete genome	138	138	96%	1e-29	97%	KM088023.1
Oryza nivara chloroplast, complete genome	138	138	96%	1e-29	97%	KM088022.1

Lolium temulentum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KM538824.1
Festuca parvigluma ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KM538821.1
Pseudosasa japonica ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KM538818.1
Phyllostachys nigra ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KM538816.1
Chikusichloa aquatica chloroplast, complete genome	138	138	96%	1e-29	97%	KR078265.1
Vulpia octoflora ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KJ773986.1
Luziola fluitans ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KJ773657.1
Oryza sativa isolate GBVN15800 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	138	138	96%	1e-29	97%	KR073275.1
Elymus caninus ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid	138	138	96%	1e-29	97%	KM360764.1
Bromus sterilis ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid	138	138	96%	1e-29	97%	KM360634.1
Guadua weberbaueri voucher TULV:XL & MK 582 plastid, complete genome	138	138	96%	1e-29	97%	KP793062.1

Alignments

Melica altissima voucher Chase 22006 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast

Sequence ID: **gb|KC123375.1|** Length: 1313 Number of Matches: 1

Range 1: 69 to 155

Score	Expect	Identities	Gaps	Strand	Frame
143 bits(158)	3e-31()	86/88(98%)	2/88(2%)	Plus/Minus	

Features:

```
Query  4    CATGTAC-AGTAGCAAGATTCGGCAGCTACTGCAGCCCCTGCTTCTTCGGGCGGAACCCC  62
            ||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  155  CATGTACCAGTAG-AAGATTCGGCAGCTACTGCAGCCCCTGCTTCTTCGGGCGGAACCCC  97

Query  63   AGGCTGAGGAGTTACTCGGAATGCTGCC  90
            ||||||||||||||||||||||||||||
Sbjct  96   AGGCTGAGGAGTTACTCGGAATGCTGCC  69
```

Phaenosperma globosum voucher BH:J.I. Davis 779 plastid, complete genome

Sequence ID: **gb|KM974745.1|** Length: 137897 Number of Matches: 1

Range 1: 55814 to 55900

Score	Expect	Identities	Gaps	Strand	Frame
143 bits(158)	3e-31()	86/88(98%)	2/88(2%)	Plus/Minus	

Features:

```
Query  4    CATGTAC-AGTAGCAAGATTCGGCAGCTACTGCAGCCCCTGCTTCTTCGGGCGGAACCCC  62
```

```
              ||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  55900  CATGTACCAGTAG-AAGATTCGGCAGCTACTGCAGCCCCTGCTTCTTCGGGCGGAACCCC  55842

Query  63     AGGCTGAGGAGTTACTCGGAATGCTGCC  90
              ||||||||||||||||||||||||||||
Sbjct  55841  AGGCTGAGGAGTTACTCGGAATGCTGCC  55814
```

Melica subulata voucher CAN:Saarela 836 plastid, complete genome
Sequence ID: **gb|KM974743.1|** Length: 134765 Number of Matches: 1
Range 1: 55088 to 55174

Score	Expect	Identities	Gaps	Strand	Frame
143 bits(158)	3e-31()	86/88(98%)	2/88(2%)	Plus/Minus	

Features:

```
Query  4      CATGTAC-AGTAGCAAGATTCGGCAGCTACTGCAGCCCCTGCTTCTTCGGGCGGAACCCC  62
              ||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  55174  CATGTACCAGTAG-AAGATTCGGCAGCTACTGCAGCCCCTGCTTCTTCGGGCGGAACCCC  55116

Query  63     AGGCTGAGGAGTTACTCGGAATGCTGCC  90
              ||||||||||||||||||||||||||||
Sbjct  55115  AGGCTGAGGAGTTACTCGGAATGCTGCC  55088
```

Melica mutica voucher US:W.J. Kress & M. Butts 04-7461 plastid, complete genome
Sequence ID: **gb|KM974742.1|** Length: 134710 Number of Matches: 1
Range 1: 55183 to 55269

Score	Expect	Identities	Gaps	Strand	Frame
143 bits(158)	3e-31()	86/88(98%)	2/88(2%)	Plus/Minus	

Features:

```
Query  4      CATGTAC-AGTAGCAAGATTCGGCAGCTACTGCAGCCCCTGCTTCTTCGGGCGGAACCCC  62
              ||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  55269  CATGTACCAGTAG-AAGATTCGGCAGCTACTGCAGCCCCTGCTTCTTCGGGCGGAACCCC  55211

Query  63     AGGCTGAGGAGTTACTCGGAATGCTGCC  90
              ||||||||||||||||||||||||||||
Sbjct  55210  AGGCTGAGGAGTTACTCGGAATGCTGCC  55183
```

Diarrhena obovata voucher BH:J.I. Davis 756 plastid, complete genome
Sequence ID: **gb|KM974739.1|** Length: 137421 Number of Matches: 1
Range 1: 55036 to 55122

Score	Expect	Identities	Gaps	Strand	Frame
143 bits(158)	3e-31()	86/88(98%)	2/88(2%)	Plus/Minus	

Features:

```
Query  4      CATGTAC-AGTAGCAAGATTCGGCAGCTACTGCAGCCCCTGCTTCTTCGGGCGGAACCCC  62
              ||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  55122  CATGTACCAGTAG-AAGATTCGGCAGCTACTGCAGCCCCTGCTTCTTCGGGCGGAACCCC  55064

Query  63     AGGCTGAGGAGTTACTCGGAATGCTGCC  90
              ||||||||||||||||||||||||||||
Sbjct  55063  AGGCTGAGGAGTTACTCGGAATGCTGCC  55036
```

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Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BSMST7Z7014**
Formatting options
Download
Blast report description

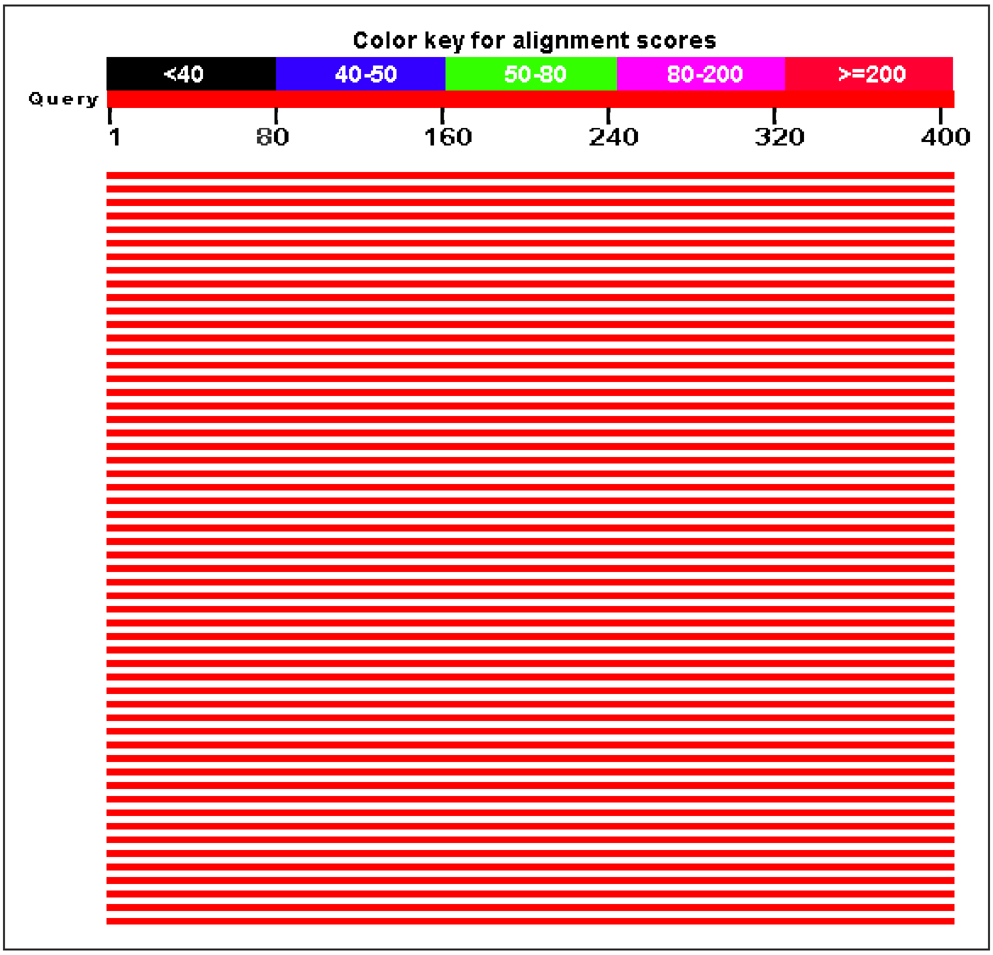
PB1A_S2S_Fwd_ssequence

RID BSMST7Z7014 (Expires on 02-12 16:23 pm)

Query ID	lcl|Query_120369	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	408		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Saccharomyces paradoxus strain DBAM49 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207250.1
Saccharomyces paradoxus strain DBAC37 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207247.1
Saccharomyces paradoxus strain DBAC33 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207246.1
Saccharomyces paradoxus strain DBAC24 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207245.1
Saccharomyces paradoxus strain DBV10 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207242.1
Saccharomyces paradoxus strain DBAC27 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207241.1
Saccharomyces paradoxus strain DBAM46 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207240.1
Saccharomyces paradoxus strain DBAA44 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207239.1
Saccharomyces paradoxus strain DBAB08 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207237.1
Saccharomyces paradoxus strain DBAB09 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207236.1
Saccharomyces paradoxus strain DBW26 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207235.1
Saccharomyces paradoxus strain DBAG40 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207234.1
Saccharomyces paradoxus strain DBW24 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal	731	731	100%	0.0	99%	KT207233.1

transcribed spacer 2, partial sequence						
Saccharomyces paradoxus strain DBW25 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207232.1
Saccharomyces paradoxus strain DBW23 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207231.1
Saccharomyces paradoxus strain DBAM44 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207228.1
Saccharomyces paradoxus strain DBW58 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207226.1
Saccharomyces paradoxus strain DBW60 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207225.1
Saccharomyces paradoxus strain DBW61 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207224.1
Saccharomyces paradoxus strain DBAC22 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207223.1
Saccharomyces paradoxus strain DBW16 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207220.1
Saccharomyces paradoxus strain DBAB24 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207194.1
Saccharomyces paradoxus strain DBAB21 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207193.1
Saccharomyces paradoxus strain DBAG39 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207153.1
Saccharomyces paradoxus strain DBAI30 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207139.1
Saccharomyces paradoxus strain DBAL15 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207136.1
Saccharomyces paradoxus strain DBZ34 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207134.1
Saccharomyces paradoxus strain DBZ25 internal transcribed spacer 1, partial						

sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207129.1
Saccharomyces paradoxus strain DBZ42 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207127.1
Saccharomyces paradoxus strain DBZ40 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207126.1
Saccharomyces paradoxus strain DBT67 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207122.1
Saccharomyces paradoxus strain DBT64 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207121.1
Saccharomyces paradoxus strain DBAC72 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207120.1
Saccharomyces paradoxus strain DBAC70 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207119.1
Saccharomyces paradoxus strain DBT62 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207118.1
Saccharomyces paradoxus strain DBT59 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207117.1
Saccharomyces paradoxus strain DBT57 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207116.1
Saccharomyces paradoxus strain DBAC81 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207115.1
Saccharomyces paradoxus strain DBT55 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207114.1
Saccharomyces paradoxus strain DBAI72 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207113.1
Saccharomyces paradoxus strain DBT56 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207112.1
Saccharomyces paradoxus strain DBT75 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial	731	731	100%	0.0	99%	KT207110.1

sequence						
Saccharomyces paradoxus strain DBT71 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207109.1
Saccharomyces paradoxus strain DBT69 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207108.1
Saccharomyces paradoxus strain DBAF25 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207084.1
Saccharomyces paradoxus strain DBAH12 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207083.1
Saccharomyces paradoxus strain DBAH11 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207082.1
Saccharomyces paradoxus strain DBAH09 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207081.1
Saccharomyces paradoxus strain DBAH08 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207080.1
Saccharomyces paradoxus strain DBAH56 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207079.1
Saccharomyces paradoxus strain DBAH51 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207078.1
Saccharomyces paradoxus strain DBAJ32 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT207076.1
Saccharomyces sp. DBP57 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KT206983.1
Saccharomyces paradoxus strain yHRM73 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384524.1
Saccharomyces paradoxus strain yHRM71 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384523.1
Saccharomyces paradoxus strain yHRM69 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384522.1
Saccharomyces paradoxus strain yHRM48 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene,	731	731	100%	0.0	99%	KM384521.1

complete sequence; and internal transcribed spacer 2, partial sequence						
Saccharomyces paradoxus strain yHKS414 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384519.1
Saccharomyces paradoxus strain yHKS402 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384518.1
Saccharomyces paradoxus strain yHKS343 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384516.1
Saccharomyces paradoxus strain yHKS341 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384515.1
Saccharomyces paradoxus strain yHKS339 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384514.1
Saccharomyces paradoxus strain yHKS331 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384513.1
Saccharomyces paradoxus strain yHKS320 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384512.1
Saccharomyces paradoxus strain yHKS306 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384511.1
Saccharomyces paradoxus strain yHKS267 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384510.1
Saccharomyces paradoxus strain yHKS254 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384509.1
Saccharomyces paradoxus strain yHKS253 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384508.1
Saccharomyces paradoxus strain yHKS248 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384507.1
Saccharomyces paradoxus strain yHKS246 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384506.1
Saccharomyces paradoxus strain yHKS226 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal	731	731	100%	0.0	99%	KM384505.1

transcribed spacer 2, partial sequence						
Saccharomyces paradoxus strain yHKS225 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384504.1
Saccharomyces paradoxus strain yHKS224 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384503.1
Saccharomyces paradoxus strain yHKS223 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384502.1
Saccharomyces paradoxus strain yHKS183 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384501.1
Saccharomyces paradoxus strain yHKS182 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384500.1
Saccharomyces paradoxus strain yHKS175 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384499.1
Saccharomyces paradoxus strain yHKS172 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384498.1
Saccharomyces paradoxus strain yHKS157 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384497.1
Saccharomyces paradoxus strain yHKS145 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384495.1
Saccharomyces paradoxus strain yHKS71 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384494.1
Saccharomyces paradoxus strain yHKS58 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384492.1
Saccharomyces paradoxus strain yHKS5 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384489.1
Saccharomyces paradoxus strain yHBJ24 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384488.1
Saccharomyces paradoxus strain yHBJ23 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384487.1
Saccharomyces paradoxus strain yHBJ17						

internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384486.1
Saccharomyces paradoxus strain yHBJ12 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384484.1
Saccharomyces paradoxus strain yHBJ11 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384483.1
Saccharomyces paradoxus strain yHBJ9 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384482.1
Saccharomyces paradoxus strain yHBJ5 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384480.1
Saccharomyces paradoxus strain yHBJ1 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384479.1
Saccharomyces paradoxus strain yHAB204 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KM384478.1
Saccharomyces paradoxus strain LL12_021 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KF153074.1
Saccharomyces paradoxus strain LL12_020 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KF153073.1
Saccharomyces paradoxus strain LL12_018 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KF153071.1
Saccharomyces paradoxus strain LL12_016 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KF153069.1
Saccharomyces paradoxus strain LL12_003 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KF153068.1
Saccharomyces paradoxus strain LL12_015 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KF153066.1
Saccharomyces paradoxus strain LL12_014 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	731	731	100%	0.0	99%	KF153065.1
Saccharomyces paradoxus strain DBAA8 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	728	728	100%	0.0	99%	KT207151.1

Alignments

Saccharomyces paradoxus strain DBAM49 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence

Sequence ID: **gb|KT207250.1|** Length: 786 Number of Matches: 1

Range 1: 276 to 683

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Sbjct  623  GCCAGCAATTTCAAGTTAACTCCAAAGAGTATCACTCACTACCAAACAGAATGTTTGAGA  564

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Sbjct  563  AGGAAATGACGCTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTCA  504

Query  181  AAGATTCGATGATTCACGGAATTCTGCAATTCACATTACGTATCGCATTTCGCTGCGTTC  240
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Query  301  CAGTTACGAAAATTCTTGTTTTTGACAAAAATTTAATGAATAAATAAAATTGTTTGTGTT  360
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Sbjct  383  CAGTTACGAAAATTCTTGTTTTTGACAAAAATTTAATGAATAAATAAAATTGTTTGTGTT  324

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Sbjct  323  TGTTACCTCTGGGCCTCGATTGCTCGAATGCCCAAAGAAAAAGTTGCA  276
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Saccharomyces paradoxus strain DBAC37 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence

Sequence ID: **gb|KT207247.1|** Length: 742 Number of Matches: 1

Range 1: 241 to 648

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731 bits(810)	0.0()	407/408(99%)	0/408(0%)	Plus/Minus	

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Sbjct  588  GCCAGCAATTTCAAGTTAACTCCAAAGAGTATCACTCACTACCAAACAGAATGTTTGAGA  529

Query  121  AGGAAATGACGCTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTCA  180
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Sbjct  528  AGGAAATGACGCTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTCA  469

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Sbjct  468  AAGATTCGATGATTCACGGAATTCTGCAATTCACATTACGTATCGCATTTCGCTGCGTTC  409

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Query  301  CAGTTACGAAAATTCTTGTTTTTGACAAAAATTTAATGAATAAATAAAATTGTTTGTGTT  360
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Sbjct  348  CAGTTACGAAAATTCTTGTTTTTGACAAAAATTTAATGAATAAATAAAATTGTTTGTGTT  289

Query  361  TGTTACCTCTGGGCCTCGATTGCTCGAATGCCCAAAGAAAAAGTTGCA  408
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Sbjct  288  TGTTACCTCTGGGCCTCGATTGCTCGAATGCCCAAAGAAAAAGTTGCA  241
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Saccharomyces paradoxus strain DBAC33 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence

Sequence ID: **gb|KT207246.1|** Length: 687 Number of Matches: 1

Range 1: 211 to 618

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731 bits(810)	0.0()	407/408(99%)	0/408(0%)	Plus/Minus	

Features:

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Sbjct  558  GCCAGCAATTTCAAGTTAACTCCAAAGAGTATCACTCACTACCAAACAGAATGTTTGAGA  499

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Sbjct  498  AGGAAATGACGCTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTCA  439

Query  181  AAGATTCGATGATTCACGGAATTCTGCAATTCACATTACGTATCGCATTTCGCTGCGTTC  240
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Sbjct  438  AAGATTCGATGATTCACGGAATTCTGCAATTCACATTACGTATCGCATTTCGCTGCGTTC  379

Query  241  TTCATCGATGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTTTAATATTTTTAAAATTTC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  378  TTCATCGATGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTTTAATATTTTTAAAATTTC  319

Query  301  CAGTTACGAAAATTCTTGTTTTTGACAAAAATTTAATGAATAAATAAAATTGTTTGTGTT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  318  CAGTTACGAAAATTCTTGTTTTTGACAAAAATTTAATGAATAAATAAAATTGTTTGTGTT  259

Query  361  TGTTACCTCTGGGCCTCGATTGCTCGAATGCCCAAAGAAAAAGTTGCA  408
            ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  258  TGTTACCTCTGGGCCTCGATTGCTCGAATGCCCAAAGAAAAAGTTGCA  211
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Saccharomyces paradoxus strain DBAC24 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence

Sequence ID: **gb|KT207245.1|** Length: 823 Number of Matches: 1
Range 1: 279 to 686

Score	Expect	Identities	Gaps	Strand	Frame
731 bits(810)	0.0()	407/408(99%)	0/408(0%)	Plus/Minus	

Features:

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Query  1    GCATTATACCTCAAGCACGCATAGAAACCTCTCTTTGGaaaaaaaaCATCCAATGAAAAG  60
            ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  686  GCATTATACCTCAAGCACGCAGAGAAACCTCTCTTTGGAAAAAAAACATCCAATGAAAAG  627

Query  61   GCCAGCAATTTCAAGTTAACTCCAAAGAGTATCACTCACTACCAAACAGAATGTTTGAGA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  626  GCCAGCAATTTCAAGTTAACTCCAAAGAGTATCACTCACTACCAAACAGAATGTTTGAGA  567

Query  121  AGGAAATGACGCTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTCA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  566  AGGAAATGACGCTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTCA  507

Query  181  AAGATTCGATGATTCACGGAATTCTGCAATTCACATTACGTATCGCATTTCGCTGCGTTC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  506  AAGATTCGATGATTCACGGAATTCTGCAATTCACATTACGTATCGCATTTCGCTGCGTTC  447

Query  241  TTCATCGATGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTTTAATATTTTTAAAATTTC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  446  TTCATCGATGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTTTAATATTTTTAAAATTTC  387

Query  301  CAGTTACGAAAATTCTTGTTTTTGACAAAAATTTAATGAATAAATAAAATTGTTTGTGTT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  386  CAGTTACGAAAATTCTTGTTTTTGACAAAAATTTAATGAATAAATAAAATTGTTTGTGTT  327

Query  361  TGTTACCTCTGGGCCTCGATTGCTCGAATGCCCAAAGAAAAAGTTGCA  408
            ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  326  TGTTACCTCTGGGCCTCGATTGCTCGAATGCCCAAAGAAAAAGTTGCA  279
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Saccharomyces paradoxus strain DBV10 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence

Sequence ID: **gb|KT207242.1|** Length: 750 Number of Matches: 1
Range 1: 238 to 645

Score	Expect	Identities	Gaps	Strand	Frame
731 bits(810)	0.0()	407/408(99%)	0/408(0%)	Plus/Minus	

Features:

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Query  1    GCATTATACCTCAAGCACGCATAGAAACCTCTCTTTGGaaaaaaaaCATCCAATGAAAAG  60
            ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  645  GCATTATACCTCAAGCACGCAGAGAAACCTCTCTTTGGAAAAAAAACATCCAATGAAAAG  586

Query  61   GCCAGCAATTTCAAGTTAACTCCAAAGAGTATCACTCACTACCAAACAGAATGTTTGAGA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  585  GCCAGCAATTTCAAGTTAACTCCAAAGAGTATCACTCACTACCAAACAGAATGTTTGAGA  526

Query  121  AGGAAATGACGCTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTCA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  525  AGGAAATGACGCTCAAACAGGCATGCCCCCTGGAATACCAAGGGGCGCAATGTGCGTTCA  466

Query  181  AAGATTCGATGATTCACGGAATTCTGCAATTCACATTACGTATCGCATTTCGCTGCGTTC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  465  AAGATTCGATGATTCACGGAATTCTGCAATTCACATTACGTATCGCATTTCGCTGCGTTC  406

Query  241  TTCATCGATGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTTTAATATTTTTAAAATTTC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  405  TTCATCGATGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTTTAATATTTTTAAAATTTC  346

Query  301  CAGTTACGAAAATTCTTGTTTTTGACAAAAATTTAATGAATAAATAAAATTGTTTGTGTT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  345  CAGTTACGAAAATTCTTGTTTTTGACAAAAATTTAATGAATAAATAAAATTGTTTGTGTT  286

Query  361  TGTTACCTCTGGGCCTCGATTGCTCGAATGCCCAAAGAAAAAGTTGCA  408
            ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  285  TGTTACCTCTGGGCCTCGATTGCTCGAATGCCCAAAGAAAAAGTTGCA  238
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BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BSMUW4YT014**
Formatting options
Download
Blast report description

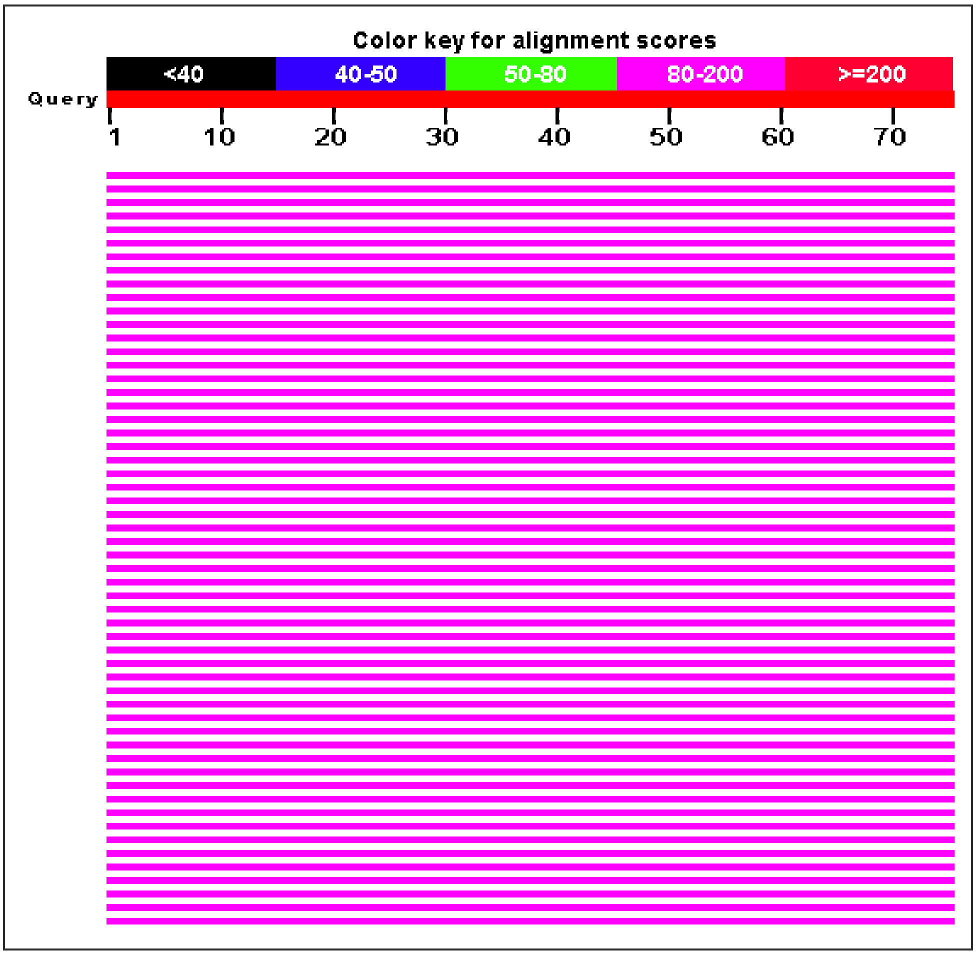
PB1A_S2S_Rev_sequence

RID BSMUW4YT014 (Expires on 02-12 16:24 pm)

Query ID	lcl|Query_174123	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	75		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Saccharomyces paradoxus strain DBAM49 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207250.1
Saccharomyces paradoxus strain DBAC37 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207247.1
Saccharomyces paradoxus strain DBAC24 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207245.1
Saccharomyces paradoxus strain DBAG55 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207244.1
Saccharomyces paradoxus strain DBV9 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207243.1
Saccharomyces paradoxus strain DBV10 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207242.1
Saccharomyces paradoxus strain DBAC27 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207241.1
Saccharomyces paradoxus strain DBAM46 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207240.1
Saccharomyces paradoxus strain DBAA44 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207239.1
Saccharomyces paradoxus strain DBAB08 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207237.1
Saccharomyces paradoxus strain DBAB09 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207236.1
Saccharomyces paradoxus strain DBW26 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207235.1
Saccharomyces paradoxus strain DBAG40 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal	127	127	100%	2e-26	97%	KT207234.1

transcribed spacer 2, partial sequence						
Saccharomyces paradoxus strain DBW24 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207233.1
Saccharomyces paradoxus strain DBW25 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207232.1
Saccharomyces paradoxus strain DBW23 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207231.1
Saccharomyces paradoxus strain DBAM44 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207228.1
Saccharomyces paradoxus strain DBW58 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207226.1
Saccharomyces paradoxus strain DBW60 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207225.1
Saccharomyces paradoxus strain DBW61 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207224.1
Saccharomyces paradoxus strain DBAC22 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207223.1
Saccharomyces paradoxus strain DBW16 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207220.1
Saccharomyces paradoxus strain DBAE70 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	127	127	100%	2e-26	97%	KT207214.1
Saccharomyces paradoxus strain DBAE67 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207211.1
Saccharomyces paradoxus strain DBAE69 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207210.1
Saccharomyces paradoxus strain DBU35 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207209.1
Saccharomyces paradoxus strain DBAE63 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207205.1

Saccharomyces paradoxus strain DBAB24 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207194.1
Saccharomyces paradoxus strain DBAB21 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207193.1
Saccharomyces paradoxus strain DBAH02 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207154.1
Saccharomyces paradoxus strain DBAG39 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207153.1
Saccharomyces paradoxus strain DBAA8 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207151.1
Saccharomyces paradoxus strain DBAI30 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207139.1
Saccharomyces paradoxus strain DBAL15 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207136.1
Saccharomyces paradoxus strain DBZ34 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207134.1
Saccharomyces paradoxus strain DBZ25 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207129.1
Saccharomyces paradoxus strain DBZ42 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207127.1
Saccharomyces paradoxus strain DBZ40 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207126.1
Saccharomyces paradoxus strain DBT67 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207122.1
Saccharomyces paradoxus strain DBT64 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207121.1
Saccharomyces paradoxus strain DBAC72 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207120.1
Saccharomyces paradoxus strain DBAC70 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal	127	127	100%	2e-26	97%	KT207119.1

transcribed spacer 2, partial sequence						
Saccharomyces paradoxus strain DBT62 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207118.1
Saccharomyces paradoxus strain DBT59 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207117.1
Saccharomyces paradoxus strain DBT57 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207116.1
Saccharomyces paradoxus strain DBAC81 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207115.1
Saccharomyces paradoxus strain DBT55 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207114.1
Saccharomyces paradoxus strain DBAI72 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207113.1
Saccharomyces paradoxus strain DBT56 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207112.1
Saccharomyces paradoxus strain DBT75 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207110.1
Saccharomyces paradoxus strain DBT71 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207109.1
Saccharomyces paradoxus strain DBT69 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207108.1
Saccharomyces paradoxus strain DBAH14 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207086.1
Saccharomyces paradoxus strain DBAF25 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207084.1
Saccharomyces paradoxus strain DBAH12 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207083.1
Saccharomyces paradoxus strain DBAH11 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207082.1
Saccharomyces paradoxus strain DBAH09						

internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207081.1
Saccharomyces paradoxus strain DBAH08 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207080.1
Saccharomyces paradoxus strain DBAH56 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207079.1
Saccharomyces paradoxus strain DBAH51 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207078.1
Saccharomyces paradoxus strain DBAJ32 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207076.1
Saccharomyces paradoxus strain yHRM73 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KM384524.1
Saccharomyces paradoxus strain yHRM71 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KM384523.1
Saccharomyces paradoxus strain yHKS421 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KM384520.1
Saccharomyces paradoxus strain yHKS414 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KM384519.1
Saccharomyces paradoxus strain yHKS402 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KM384518.1
Saccharomyces paradoxus strain yHKS341 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KM384515.1
Saccharomyces paradoxus strain yHKS320 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KM384512.1
Saccharomyces paradoxus strain yHKS254 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KM384509.1
Saccharomyces paradoxus strain yHKS225 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KM384504.1
Saccharomyces paradoxus strain yHKS172 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal	127	127	100%	2e-26	97%	KM384498.1

transcribed spacer 2, partial sequence						
Saccharomyces paradoxus strain LL12_020 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KF153073.1
Saccharomyces paradoxus strain LL12_016 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KF153069.1
Saccharomyces paradoxus strain LL12_001 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KF153060.1
Saccharomyces paradoxus strain LL12_007 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KF153058.1
Saccharomyces paradoxus strain LL12_005 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KF153057.1
Saccharomyces paradoxus strain LL12_004 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KF153056.1
Saccharomyces paradoxus strain LL11_011 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	127	127	100%	2e-26	97%	KF057740.1
Saccharomyces paradoxus strain LL11_009 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	127	127	100%	2e-26	97%	KF057736.1
Saccharomyces paradoxus strain LL12_036 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	127	127	100%	2e-26	97%	KF057713.1
Saccharomyces paradoxus strain LL12_026 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	127	127	100%	2e-26	97%	KF057712.1
Saccharomyces paradoxus strain LL11_001 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KF057635.1
Saccharomyces paradoxus strain LL11_008 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	127	127	100%	2e-26	97%	KF057609.1
Saccharomyces paradoxus strain LL11_007 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	127	127	100%	2e-26	97%	KF057607.1
Saccharomyces paradoxus strain LL11-006 internal transcribed spacer 1, partial						

sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	127	127	100%	2e-26	97%	KF057583.1
Saccharomyces paradoxus strain LL11_006 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KF057551.1
Saccharomyces paradoxus strain LL11_005 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	127	127	100%	2e-26	97%	KF057527.1
Saccharomyces paradoxus strain LL11_004 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KF057514.1
Saccharomyces paradoxus strain LL11_012 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	127	127	100%	2e-26	97%	KF057505.1
Saccharomyces paradoxus strain ATCC 76856 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	JQ070083.1
Saccharomycetes sp. HZ178 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	127	127	100%	2e-26	97%	GU213443.1
Saccharomyces paradoxus isolate T7B internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	FJ713072.1
TPA: Saccharomyces paradoxus NRRL Y-17217 genes for 25S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA, complete sequence	127	127	100%	2e-26	97%	BR000309.1
Saccharomyces paradoxus internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	AY046148.1
Saccharomyces paradoxus 5.8S gene and ITS1 and ITS2 (strain CBS 432)	127	127	100%	2e-26	97%	AJ229059.1
Saccharomyces cerevisiae 5.8S rRNA gene and ITS1 and ITS2 DNA (strain CBS 432)	127	127	100%	2e-26	97%	Z95933.1
S.paradoxus DNA for internal transcribed spacer 1	127	127	100%	2e-26	97%	Z75729.1
Saccharomyces paradoxus genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2, 28S rRNA, partial and complete sequence	127	127	100%	2e-26	97%	D89890.1
Saccharomyces paradoxus genes for ITS1, 5.8S rRNA, ITS2, partial and complete sequence, strain: AK 43	123	123	97%	2e-25	97%	AB533545.1
Saccharomyces paradoxus genes for ITS1, 5.8S rRNA, ITS2, partial and complete sequence, strain: NBRC 1804	123	123	97%	2e-25	97%	AB533544.1

Alignments

Saccharomyces paradoxus strain DBAM49 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete

sequence; and internal transcribed spacer 2, partial sequence
Sequence ID: **gb|KT207250.1|** Length: 786 Number of Matches: 1
Range 1: 148 to 222

Score	Expect	Identities	Gaps	Strand	Frame
127 bits(140)	2e-26()	73/75(97%)	0/75(0%)	Plus/Plus	

Features:

```
Query  1    AAGTGCGCGGTCTTGCTTGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGATAAAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| | ||
Sbjct  148  AAGTGCGCGGTCTTGCTTGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGAT  207

Query  61   TTCTGTGCTATTGTT  75
            |||||||||||||||
Sbjct  208  TTCTGTGCTATTGTT  222
```

Saccharomyces paradoxus strain DBAC37 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence
Sequence ID: **gb|KT207247.1|** Length: 742 Number of Matches: 1
Range 1: 113 to 187

Score	Expect	Identities	Gaps	Strand	Frame
127 bits(140)	2e-26()	73/75(97%)	0/75(0%)	Plus/Plus	

Features:

```
Query  1    AAGTGCGCGGTCTTGCTTGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGATAAAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| | ||
Sbjct  113  AAGTGCGCGGTCTTGCTTGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGAT  172

Query  61   TTCTGTGCTATTGTT  75
            |||||||||||||||
Sbjct  173  TTCTGTGCTATTGTT  187
```

Saccharomyces paradoxus strain DBAC24 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence
Sequence ID: **gb|KT207245.1|** Length: 823 Number of Matches: 1
Range 1: 151 to 225

Score	Expect	Identities	Gaps	Strand	Frame
127 bits(140)	2e-26()	73/75(97%)	0/75(0%)	Plus/Plus	

Features:

```
Query  1    AAGTGCGCGGTCTTGCTTGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGATAAAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| | ||
Sbjct  151  AAGTGCGCGGTCTTGCTTGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGAT  210

Query  61   TTCTGTGCTATTGTT  75
            |||||||||||||||
Sbjct  211  TTCTGTGCTATTGTT  225
```

Saccharomyces paradoxus strain DBAG55 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence
Sequence ID: **gb|KT207244.1|** Length: 717 Number of Matches: 1
Range 1: 109 to 183

Score	Expect	Identities	Gaps	Strand	Frame
127 bits(140)	2e-26()	73/75(97%)	0/75(0%)	Plus/Plus	

Features:

```
Query  1    AAGTGCGCGGTCTTGCTTGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGATAAAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| | ||
Sbjct  109  AAGTGCGCGGTCTTGCTTGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGAT  168

Query  61   TTCTGTGCTATTGTT  75
            |||||||||||||||
Sbjct  169  TTCTGTGCTATTGTT  183
```

Saccharomyces paradoxus strain DBV9 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence
Sequence ID: **gb|KT207243.1|** Length: 799 Number of Matches: 1
Range 1: 142 to 216

Score	Expect	Identities	Gaps	Strand	Frame

```
127 bits(140)        2e-26()      73/75(97%)        0/75(0%)        Plus/Plus
```

Features:

```
Query  1    AAGTGCGCGGTCTTGCTTGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGATAAAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| | ||
Sbjct  142  AAGTGCGCGGTCTTGCTTGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGAT  201

Query  61   TTCTGTGCTATTGTT  75
            |||||||||||||||
Sbjct  202  TTCTGTGCTATTGTT  216
```

BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BSMTZZT6014**
Formatting options
Download
Blast report description

PB1A_S2S_Rev_ssequence

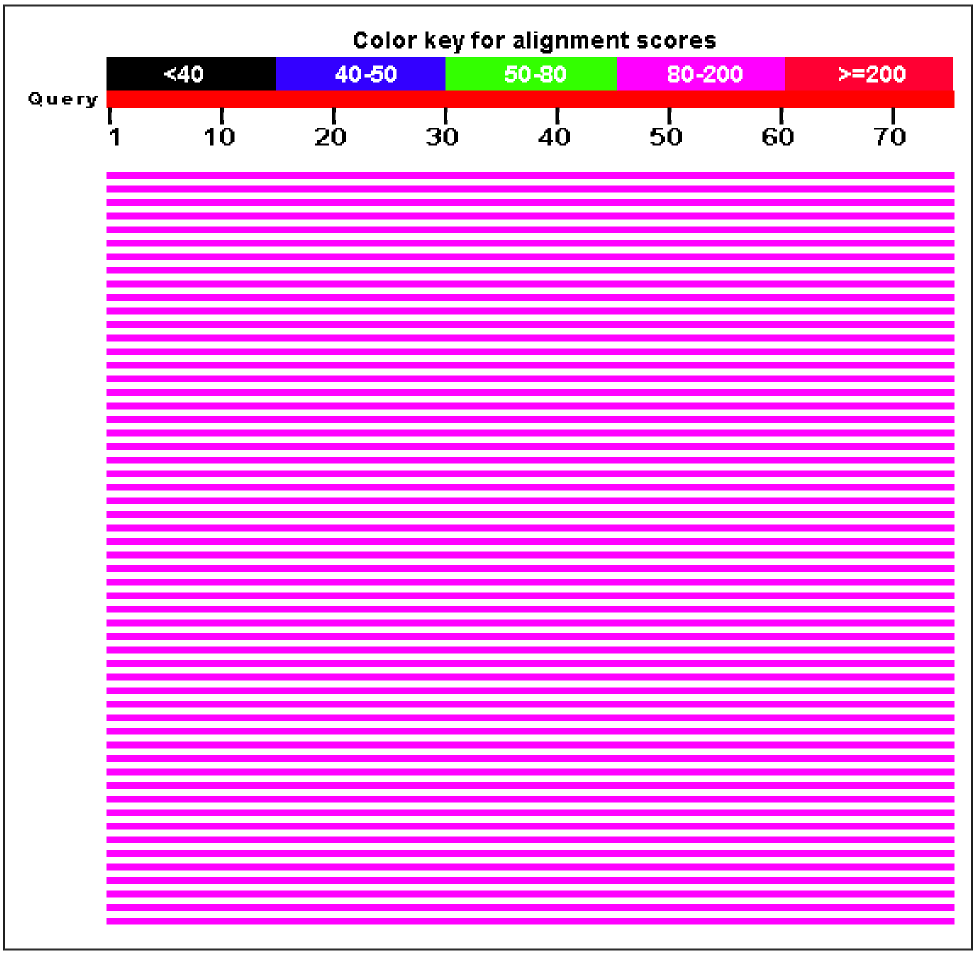
RID BSMTZZT6014 (Expires on 02-12 16:24 pm)

Query ID lcl|Query_161811
Description None
Molecule type nucleic acid
Query Length 75

Database Name nr
Description Nucleotide collection (nt)
Program BLASTN 2.3.1+

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Saccharomyces paradoxus strain DBAM49 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207250.1
Saccharomyces paradoxus strain DBAC37 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207247.1
Saccharomyces paradoxus strain DBAC24 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207245.1
Saccharomyces paradoxus strain DBAG55 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207244.1
Saccharomyces paradoxus strain DBV9 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207243.1
Saccharomyces paradoxus strain DBV10 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207242.1
Saccharomyces paradoxus strain DBAC27 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207241.1
Saccharomyces paradoxus strain DBAM46 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207240.1
Saccharomyces paradoxus strain DBAA44 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207239.1
Saccharomyces paradoxus strain DBAB08 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207237.1
Saccharomyces paradoxus strain DBAB09 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207236.1
Saccharomyces paradoxus strain DBW26 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207235.1
Saccharomyces paradoxus strain DBAG40 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal	127	127	100%	2e-26	97%	KT207234.1

transcribed spacer 2, partial sequence						
Saccharomyces paradoxus strain DBW24 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207233.1
Saccharomyces paradoxus strain DBW25 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207232.1
Saccharomyces paradoxus strain DBW23 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207231.1
Saccharomyces paradoxus strain DBAM44 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207228.1
Saccharomyces paradoxus strain DBW58 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207226.1
Saccharomyces paradoxus strain DBW60 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207225.1
Saccharomyces paradoxus strain DBW61 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207224.1
Saccharomyces paradoxus strain DBAC22 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207223.1
Saccharomyces paradoxus strain DBW16 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207220.1
Saccharomyces paradoxus strain DBAE70 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	127	127	100%	2e-26	97%	KT207214.1
Saccharomyces paradoxus strain DBAE67 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207211.1
Saccharomyces paradoxus strain DBAE69 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207210.1
Saccharomyces paradoxus strain DBU35 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207209.1
Saccharomyces paradoxus strain DBAE63 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207205.1

Saccharomyces paradoxus strain DBAB24 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207194.1
Saccharomyces paradoxus strain DBAB21 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207193.1
Saccharomyces paradoxus strain DBAH02 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207154.1
Saccharomyces paradoxus strain DBAG39 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207153.1
Saccharomyces paradoxus strain DBAA8 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207151.1
Saccharomyces paradoxus strain DBAI30 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207139.1
Saccharomyces paradoxus strain DBAL15 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207136.1
Saccharomyces paradoxus strain DBZ34 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207134.1
Saccharomyces paradoxus strain DBZ25 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207129.1
Saccharomyces paradoxus strain DBZ42 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207127.1
Saccharomyces paradoxus strain DBZ40 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207126.1
Saccharomyces paradoxus strain DBT67 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207122.1
Saccharomyces paradoxus strain DBT64 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207121.1
Saccharomyces paradoxus strain DBAC72 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207120.1
Saccharomyces paradoxus strain DBAC70 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal	127	127	100%	2e-26	97%	KT207119.1

transcribed spacer 2, partial sequence						
Saccharomyces paradoxus strain DBT62 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207118.1
Saccharomyces paradoxus strain DBT59 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207117.1
Saccharomyces paradoxus strain DBT57 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207116.1
Saccharomyces paradoxus strain DBAC81 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207115.1
Saccharomyces paradoxus strain DBT55 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207114.1
Saccharomyces paradoxus strain DBAI72 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207113.1
Saccharomyces paradoxus strain DBT56 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207112.1
Saccharomyces paradoxus strain DBT75 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207110.1
Saccharomyces paradoxus strain DBT71 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207109.1
Saccharomyces paradoxus strain DBT69 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207108.1
Saccharomyces paradoxus strain DBAH14 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207086.1
Saccharomyces paradoxus strain DBAF25 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207084.1
Saccharomyces paradoxus strain DBAH12 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207083.1
Saccharomyces paradoxus strain DBAH11 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207082.1
Saccharomyces paradoxus strain DBAH09						

internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207081.1
Saccharomyces paradoxus strain DBAH08 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207080.1
Saccharomyces paradoxus strain DBAH56 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207079.1
Saccharomyces paradoxus strain DBAH51 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207078.1
Saccharomyces paradoxus strain DBAJ32 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KT207076.1
Saccharomyces paradoxus strain yHRM73 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KM384524.1
Saccharomyces paradoxus strain yHRM71 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KM384523.1
Saccharomyces paradoxus strain yHKS421 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KM384520.1
Saccharomyces paradoxus strain yHKS414 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KM384519.1
Saccharomyces paradoxus strain yHKS402 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KM384518.1
Saccharomyces paradoxus strain yHKS341 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KM384515.1
Saccharomyces paradoxus strain yHKS320 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KM384512.1
Saccharomyces paradoxus strain yHKS254 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KM384509.1
Saccharomyces paradoxus strain yHKS225 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KM384504.1
Saccharomyces paradoxus strain yHKS172 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal	127	127	100%	2e-26	97%	KM384498.1

transcribed spacer 2, partial sequence						
Saccharomyces paradoxus strain LL12_020 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KF153073.1
Saccharomyces paradoxus strain LL12_016 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KF153069.1
Saccharomyces paradoxus strain LL12_001 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KF153060.1
Saccharomyces paradoxus strain LL12_007 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KF153058.1
Saccharomyces paradoxus strain LL12_005 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KF153057.1
Saccharomyces paradoxus strain LL12_004 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KF153056.1
Saccharomyces paradoxus strain LL11_011 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	127	127	100%	2e-26	97%	KF057740.1
Saccharomyces paradoxus strain LL11_009 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	127	127	100%	2e-26	97%	KF057736.1
Saccharomyces paradoxus strain LL12_036 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	127	127	100%	2e-26	97%	KF057713.1
Saccharomyces paradoxus strain LL12_026 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	127	127	100%	2e-26	97%	KF057712.1
Saccharomyces paradoxus strain LL11_001 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KF057635.1
Saccharomyces paradoxus strain LL11_008 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	127	127	100%	2e-26	97%	KF057609.1
Saccharomyces paradoxus strain LL11_007 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	127	127	100%	2e-26	97%	KF057607.1
Saccharomyces paradoxus strain LL11-006 internal transcribed spacer 1, partial						

sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	127	127	100%	2e-26	97%	KF057583.1
Saccharomyces paradoxus strain LL11_006 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KF057551.1
Saccharomyces paradoxus strain LL11_005 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	127	127	100%	2e-26	97%	KF057527.1
Saccharomyces paradoxus strain LL11_004 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	KF057514.1
Saccharomyces paradoxus strain LL11_012 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	127	127	100%	2e-26	97%	KF057505.1
Saccharomyces paradoxus strain ATCC 76856 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	JQ070083.1
Saccharomycetes sp. HZ178 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	127	127	100%	2e-26	97%	GU213443.1
Saccharomyces paradoxus isolate T7B internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	FJ713072.1
TPA: Saccharomyces paradoxus NRRL Y-17217 genes for 25S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA, complete sequence	127	127	100%	2e-26	97%	BR000309.1
Saccharomyces paradoxus internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	127	127	100%	2e-26	97%	AY046148.1
Saccharomyces paradoxus 5.8S gene and ITS1 and ITS2 (strain CBS 432)	127	127	100%	2e-26	97%	AJ229059.1
Saccharomyces cerevisiae 5.8S rRNA gene and ITS1 and ITS2 DNA (strain CBS 432)	127	127	100%	2e-26	97%	Z95933.1
S.paradoxus DNA for internal transcribed spacer 1	127	127	100%	2e-26	97%	Z75729.1
Saccharomyces paradoxus genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2, 28S rRNA, partial and complete sequence	127	127	100%	2e-26	97%	D89890.1
Saccharomyces paradoxus genes for ITS1, 5.8S rRNA, ITS2, partial and complete sequence, strain: AK 43	123	123	97%	2e-25	97%	AB533545.1
Saccharomyces paradoxus genes for ITS1, 5.8S rRNA, ITS2, partial and complete sequence, strain: NBRC 1804	123	123	97%	2e-25	97%	AB533544.1

Alignments

Saccharomyces paradoxus strain DBAM49 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete

sequence; and internal transcribed spacer 2, partial sequence
Sequence ID: **gb|KT207250.1|** Length: 786 Number of Matches: 1
Range 1: 148 to 222

Score	Expect	Identities	Gaps	Strand	Frame
127 bits(140)	2e-26()	73/75(97%)	0/75(0%)	Plus/Plus	

Features:

```
Query  1    AAGTGCGCGGTCTTGCTTGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGATAAAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| | ||
Sbjct  148  AAGTGCGCGGTCTTGCTTGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGAT  207

Query  61   TTCTGTGCTATTGTT  75
            |||||||||||||||
Sbjct  208  TTCTGTGCTATTGTT  222
```

Saccharomyces paradoxus strain DBAC37 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence
Sequence ID: **gb|KT207247.1|** Length: 742 Number of Matches: 1
Range 1: 113 to 187

Score	Expect	Identities	Gaps	Strand	Frame
127 bits(140)	2e-26()	73/75(97%)	0/75(0%)	Plus/Plus	

Features:

```
Query  1    AAGTGCGCGGTCTTGCTTGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGATAAAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| | ||
Sbjct  113  AAGTGCGCGGTCTTGCTTGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGAT  172

Query  61   TTCTGTGCTATTGTT  75
            |||||||||||||||
Sbjct  173  TTCTGTGCTATTGTT  187
```

Saccharomyces paradoxus strain DBAC24 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence
Sequence ID: **gb|KT207245.1|** Length: 823 Number of Matches: 1
Range 1: 151 to 225

Score	Expect	Identities	Gaps	Strand	Frame
127 bits(140)	2e-26()	73/75(97%)	0/75(0%)	Plus/Plus	

Features:

```
Query  1    AAGTGCGCGGTCTTGCTTGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGATAAAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| | ||
Sbjct  151  AAGTGCGCGGTCTTGCTTGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGAT  210

Query  61   TTCTGTGCTATTGTT  75
            |||||||||||||||
Sbjct  211  TTCTGTGCTATTGTT  225
```

Saccharomyces paradoxus strain DBAG55 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence
Sequence ID: **gb|KT207244.1|** Length: 717 Number of Matches: 1
Range 1: 109 to 183

Score	Expect	Identities	Gaps	Strand	Frame
127 bits(140)	2e-26()	73/75(97%)	0/75(0%)	Plus/Plus	

Features:

```
Query  1    AAGTGCGCGGTCTTGCTTGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGATAAAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| | ||
Sbjct  109  AAGTGCGCGGTCTTGCTTGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGAT  168

Query  61   TTCTGTGCTATTGTT  75
            |||||||||||||||
Sbjct  169  TTCTGTGCTATTGTT  183
```

Saccharomyces paradoxus strain DBV9 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence
Sequence ID: **gb|KT207243.1|** Length: 799 Number of Matches: 1
Range 1: 142 to 216

Score	Expect	Identities	Gaps	Strand	Frame

127 bits(140) 2e-26() 73/75(97%) 0/75(0%) Plus/Plus

Features:

```
Query  1    AAGTGCGCGGTCTTGCTTGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGATAAAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| | ||
Sbjct  142  AAGTGCGCGGTCTTGCTTGGCTTGTAAGTTTCTTTCTTGCTATTCCAAACGGTGAGAGAT  201

Query  61   TTCTGTGCTATTGTT  75
            |||||||||||||||
Sbjct  202  TTCTGTGCTATTGTT  216
```

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NCBI/ BLAST/ blastn suite/ **Formatting Results - BSMY8XNR015**

Formatting options
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Blast report description

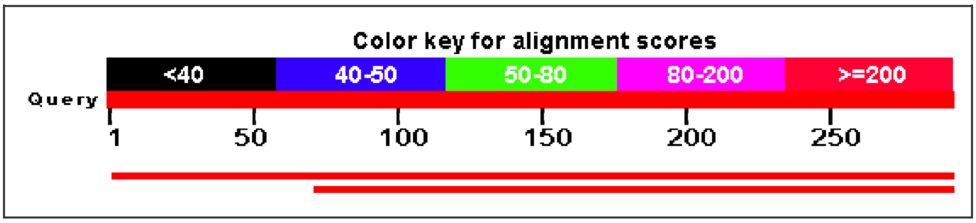
PB1B_S2S_Direct_sequence

RID BSMY8XNR015 (Expires on 02-12 16:26 pm)

Query ID	lcl|Query_233787	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	291		

Graphic Summary

Distribution of 2 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Fungal sp. 498 MCS-2014 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	331	331	99%	5e-87	81%	KM374243.1
Fungal sp. 508 MCS-2014 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	248	248	75%	5e-62	80%	KM374081.1

Alignments

Fungal sp. 498 MCS-2014 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence

Sequence ID: **gb|KM374243.1|** Length: 884 Number of Matches: 1
Range 1: 214 to 502

Score	Expect	Identities	Gaps	Strand	Frame
331 bits(366)	5e-87()	236/290(81%)	2/290(0%)	Plus/Minus	

Features:

```
Query  3    ttttttGAACTT-GCTTTGGGAGGTGAGCCCCNGCTTACTGCCCAAAGGTCTAAACACAt  61
            || |||||| |  | | |||| ||||| ||   | |    |||||||| ||||||||| |
Sbjct  502  TTYTTTGAAYTYCGSTYTGGGTGGTGARCCG-GGTTKGMWGCCCAAAGKTCTAAACACMT  444

Query  62   tttttttAATGTTAAAACCTTTATCCAATAGTCATGAAAATTTTTAACAANAATTAAAAT  121
            |||||  |||||||||||||||| |||||||||||||||||||  ||||| |||||||||
Sbjct  443  TTTTTKWAATGTTAAAACCTTTAWCCAATAGTCATGAAAATTTWWAACAAAAATTAAAAT  384

Query  122  NTTCNNAANTTTCAACAACGGATCTCNTGGTTCTCGCANCGNTGNANNACGCAGCGAAAT  181
             |||  || ||||||||||||||||| ||||||||||| || || |  ||||||||||||
Sbjct  383  CTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCAACGATGAAGAACGCAGCGAAAT  324

Query  182  GCGATNCGTNTTGTGAATTGCAGANTTNCGTGNNTCATNNNATNTTTGNACGCNCNTTGC  241
            ||||| ||| |||||||||||||| || ||||  ||||   || |||| || | | ||||
Sbjct  323  GCGATACGTATTGTGAATTGCAGATTTTCGTGAATCATMGAATCTTTGAACSCACATTGC  264

Query  242  NCCCNNTGGTATTCCNGANGGTATGCCTGTTTGANCGTCATTTCTCTCTC  291
             |||  ||||||||| || ||||||||||||||| |||||||||||||||
Sbjct  263  ACCCTYTGGTATTCCAGAGGGTATGCCTGTTTGAGCGTCATTTCTCTCTC  214
```

Fungal sp. 508 MCS-2014 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence

Sequence ID: **gb|KM374081.1|** Length: 361 Number of Matches: 1
Range 1: 142 to 361

Score	Expect	Identities	Gaps	Strand	Frame
248 bits(274)	5e-62()	176/220(80%)	0/220(0%)	Plus/Minus	

Features:

```
Query  72   GTTAAAACCTTTATCCAATAGTCATGAAAATTTTTAACAANAATTAAAATNTTCNNAANT  131
            |||||||||| || |||||||||||||||||||||||||| ||||||||| |||  || |
Sbjct  361  GTTAAAACCTWTAWCCAATAGTCATGAAAATTTTTAACAAAAATTAAAATRTTCAAAACT  302

Query  132  TTCAACAACGGATCTCNTGGTTCTCGCANCGNTGNANNACGCAGCGAAATGCGATNCGTN  191
            |||||||| ||||||  ||||||| |||  |  | |  |||||||||||| || |  || 
Sbjct  301  TTCAACAAMGGATCTMTTGGTTCTMGCAAMGAWGAAGAACGCAGCGAAATSCGTTASGTA  242

Query  192  TTGTGAATTGCAGANTTNCGTGNNTCATNNNATNTTTGNACGCNCNTTGCNCCCNNTGGT  251
            ||| |||||||||| || ||||  ||||   || |||| |||| |  ||| |||  ||||
Sbjct  241  TTGCGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACAYTGCACCCTCTGGT  182

Query  252  ATTCCNGANGGTATGCCTGTTTGANCGTCATTTCTCTCTC  291
            ||||| || |||| |||||||||| |||||||| ||||||
Sbjct  181  ATTCCAGAGGGTAWGCCTGTTTGAGCGTCATTTYTCTCTC  142
```

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NCBI/ BLAST/ blastn suite/ **Formatting Results - BSN4W5FE015**

Formatting options
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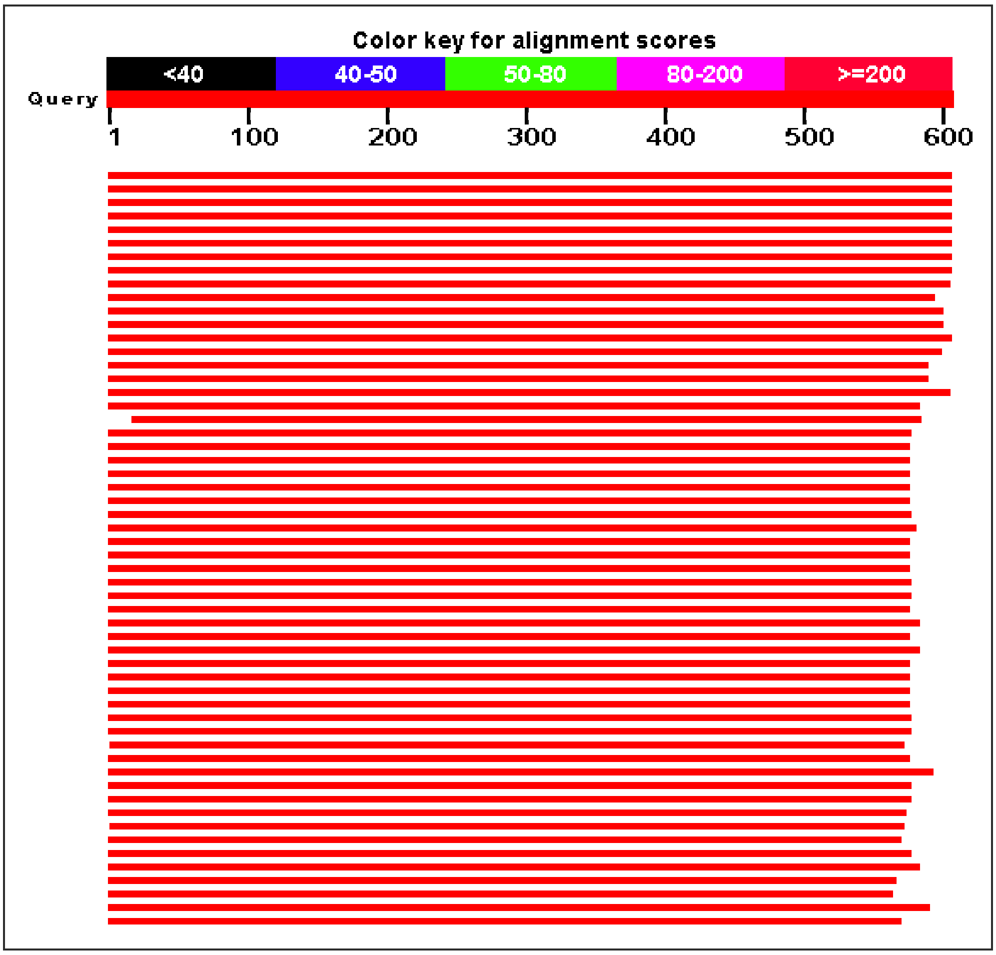
Blast report description

PB3A_S2S_Direct_sequence

RID	BSN4W5FE015 (Expires on 02-12 16:30 pm)		
Query ID	lcl|Query_146789	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	604		

Graphic Summary

Distribution of 101 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Wickerhamomyces anomalus isolate LMICRO189 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	1063	1063	99%	0.0	99%	KJ451713.1
Wickerhamomyces anomalus isolate LMICRO187 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	1063	1063	99%	0.0	99%	KJ451711.1
Wickerhamomyces anomalus 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	1063	1063	99%	0.0	99%	KJ659884.1
Uncultured eukaryote clone FS2_2_12 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	1063	1063	99%	0.0	99%	FJ176542.1
Wickerhamomyces anomalus isolate LMICRO150 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	1056	1056	99%	0.0	99%	KJ451674.1
Wickerhamomyces anomalus strain PMM10-516L isolate ISHAM-ITS_ID MITS492 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	1056	1056	99%	0.0	99%	KP132887.1
Wickerhamomyces anomalus strain PMM08-1902L isolate ISHAM-ITS_ID MITS489 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	1056	1056	99%	0.0	99%	KP132884.1
Pichia sp. 1 TMS-2011 voucher SC9d50p12-4 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	1056	1056	99%	0.0	99%	HQ631071.1
Wickerhamomyces anomalus strain EG2 18S ribosomal RNA gene, partial sequence	1052	1052	99%	0.0	99%	GQ280811.1
Wickerhamomyces anomalus strain IHEM 4425 isolate ISHAM-ITS_ID MITS488 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal	1047	1047	97%	0.0	99%	KP132883.1

transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence						
Wickerhamomyces anomalus strain UOA/HCPF 2651 isolate ISHAM-ITS_ID MITS498 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	1045	1045	98%	0.0	99%	GQ376075.1
Wickerhamomyces anomalus genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2, 28S rRNA, partial and complete sequence, strain: FL08-0094	1045	1045	98%	0.0	99%	AB469881.1
Wickerhamomyces anomalus strain PMM10-1024113L isolate ISHAM-ITS_ID MITS491 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	1043	1043	99%	0.0	99%	KP132886.1
Wickerhamomyces anomalus isolate AM20 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	1041	1041	98%	0.0	99%	KM246175.1
Wickerhamomyces anomalus strain IHEM 10271 isolate ISHAM-ITS_ID MITS487 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	1038	1038	96%	0.0	99%	KP132882.1
Wickerhamomyces anomalus strain IHEM 10262 isolate ISHAM-ITS_ID MITS485 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	1038	1038	96%	0.0	99%	KP132880.1
Wickerhamomyces anomalus strain PMM08-751L isolate ISHAM-ITS_ID MITS490 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	1034	1034	99%	0.0	99%	KP132885.1
Candida membranifaciens strain MUCL 30392 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	1018	1018	95%	0.0	99%	EU343844.1
Wickerhamomyces anomalus strain DBAJ78 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	1016	1016	93%	0.0	100%	KT207050.1
Pichia anomala strain MTCC 3815 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	1016	1016	94%	0.0	99%	AY231612.1
Wickerhamomyces anomalus strain WM						

05.34 isolate ISHAM-ITS_ID MITS518 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	1014	1014	94%	0.0	99%	KP069017.1
Wickerhamomyces anomalus strain SX1 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	1014	1014	94%	0.0	99%	JN839959.1
Pichia anomala internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	1014	1014	94%	0.0	99%	EU330185.1
Pichia anomala isolate P7 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	1014	1014	94%	0.0	99%	AY349443.1
Pichia anomala strain ST3-1d 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	1014	1014	94%	0.0	99%	AY168783.1
Wickerhamomyces anomalus strain 73 CF01 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	1009	1009	94%	0.0	99%	KR909092.1
Wickerhamomyces anomalus strain DBAK1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	1009	1009	95%	0.0	99%	KT207052.1
Wickerhamomyces anomalus strain DBM73 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	1009	1009	94%	0.0	99%	KT207036.1
Wickerhamomyces anomalus isolate YN7 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	1009	1009	94%	0.0	99%	KJ502666.1
Uncultured Wickerhamomyces clone LZQZ-19 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	1009	1009	94%	0.0	99%	KF984346.1
Wickerhamomyces anomalus isolate CAT 1 L1 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	1007	1007	94%	0.0	99%	KP638728.1
Wickerhamomyces anomalus strain UFLA CWFY49 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal	1007	1007	94%	0.0	99%	KM402087.1

transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence						
Wickerhamomyces anomalus strain YE06 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	1005	1005	94%	0.0	99%	KR024781.1
Wickerhamomyces anomalus strain DBH77 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	1005	1005	95%	0.0	98%	KT207256.1
Wickerhamomyces anomalus strain WM 02.425 isolate ISHAM-ITS_ID MITS501 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	1005	1005	94%	0.0	99%	KP132889.1
Candida membranifaciens strain DBMY181 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	1005	1005	95%	0.0	99%	KJ706399.1
Wickerhamomyces anomalus isolate YN1 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	1005	1005	94%	0.0	99%	KJ502660.1
Wickerhamomyces anomalus strain 40 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	1005	1005	94%	0.0	99%	KC568565.1
Wickerhamomyces anomalus 18S rRNA gene (partial), ITS1, 5.8S rRNA gene, ITS2 and 26S rRNA gene (partial), strain MUCL 51259	1005	1005	94%	0.0	99%	FN394001.1
Pichia anomala isolate 0732-1 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 gene, partial sequence	1005	1005	94%	0.0	99%	EU380207.1
Wickerhamomyces anomalus isolate KDLYL8-1 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	1003	1003	94%	0.0	99%	JX174410.1
Wickerhamomyces anomalus isolate 14 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	1002	1002	94%	0.0	99%	KT175180.1
Wickerhamomyces anomalus strain DBAK41 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer	1002	1002	93%	0.0	99%	KT207044.1

2, partial sequence						
Wickerhamomyces anomalus isolate YN4 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	1002	1002	94%	0.0	99%	KJ502663.1
Wickerhamomyces anomalus strain P42B001 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	1002	1002	97%	0.0	98%	JX188245.1
Wickerhamomyces anomalus isolate WA92-CN4 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	1000	1326	94%	0.0	99%	KT580797.1
Wickerhamomyces anomalus isolate WA40-CN4 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	1000	1000	94%	0.0	99%	KT580793.1
Wickerhamomyces anomalus strain DBAK3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	998	998	94%	0.0	99%	KT207053.1
Wickerhamomyces anomalus strain DBAK42 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	998	998	93%	0.0	99%	KT207045.1
Pichia anomala strain YF07b 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	998	998	93%	0.0	99%	DQ534406.1
Wickerhamomyces anomalus isolate 54 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	996	996	94%	0.0	99%	KT175201.1
Candida membranifaciens strain DBMY659 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	996	996	95%	0.0	98%	KJ706876.1
Pichia anomala strain MTCC 3303 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	996	996	93%	0.0	99%	AY231608.1
Wickerhamomyces anomalus genomic DNA containing ITS1 (partial), 5.8S rRNA gene, ITS2, and 28S rRNA gene (partial), strain F17.12	993	993	92%	0.0	99%	FN556013.1
Wickerhamomyces anomalus 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence;	993	993	97%	0.0	98%	HM044864.1

and 26S ribosomal RNA gene, partial sequence						
Pichia anomala strain SM19 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	993	993	93%	0.0	99%	**FJ515180.1**
Wickerhamomyces anomalus isolate Tcy27 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	991	991	94%	0.0	99%	**JN210893.1**
Wickerhamomyces anomalus strain DBAI17 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	989	989	93%	0.0	99%	**KT207144.1**
Pichia anomala genomic DNA containing ITS1, 5.8S rRNA gene and ITS2, isolated from olive brine	987	987	93%	0.0	99%	**LK392318.1**
Pichia anomala strain MTCC 237 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	987	987	93%	0.0	99%	**AY231606.1**
Wickerhamomyces anomalus isolate 16 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	985	985	92%	0.0	99%	**KT175181.1**
Wickerhamomyces anomalus strain DBM78 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	985	985	93%	0.0	98%	**KT207024.1**
Wickerhamomyces anomalus strain OUCMBI110149 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	985	985	92%	0.0	99%	**KP269059.1**
Wickerhamomyces anomalus strain UFLA CWFY47 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	985	985	92%	0.0	99%	**KM402085.1**
Pichia anomala 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	985	985	92%	0.0	99%	**AF270936.1**
Wickerhamomyces anomalus isolate WA45-CN4 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	984	984	94%	0.0	99%	**KT580795.1**
Wickerhamomyces anomalus strain M297B internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	984	984	92%	0.0	99%	**KP675493.1**
Wickerhamomyces anomalus strain H318A internal transcribed spacer 1, partial						

sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	982	982	92%	0.0	99%	KP675054.1
Wickerhamomyces anomalus strain DBAK46 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	980	980	94%	0.0	98%	KT207047.1
Wickerhamomyces anomalus strain DBMY247 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	980	980	93%	0.0	99%	KJ706464.1
Pichia anomala strain ZY4 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	980	980	95%	0.0	98%	EF449518.1
Wickerhamomyces anomalus strain yHKS399 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	978	978	91%	0.0	99%	KM384617.1
Wickerhamomyces anomalus genomic DNA containing ITS1 (partial), 5.8S rRNA gene, ITS2, and 28S rRNA gene (partial), strain M9.11	978	978	91%	0.0	99%	FN556015.1
Pichia anomala 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	978	978	94%	0.0	98%	AF321543.1
Wickerhamomyces anomalus strain H318B internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	976	976	92%	0.0	99%	KP675055.1
Wickerhamomyces anomalus strain RChB001 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	976	976	95%	0.0	98%	JX188246.1
Wickerhamomyces anomalus genomic DNA containing ITS1 (partial), 5.8S rRNA gene, ITS2, and 28S rRNA gene (partial), strain F21.8	976	976	91%	0.0	99%	FN556014.1
Pichia anomala isolate P5 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	976	976	94%	0.0	98%	AY349435.1
Wickerhamomyces anomalus strain IHEM 10268 isolate ISHAM-ITS_ID MITS486 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	975	975	91%	0.0	99%	KP132881.1
Wickerhamomyces anomalus strain UFLA CWFY48 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	975	975	91%	0.0	99%	KM402086.1
Wickerhamomyces anomalus strain DBAK44 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA	973	973	94%	0.0	98%	KT207046.1

gene, complete sequence; and internal transcribed spacer 2, partial sequence						
Wickerhamomyces anomalus strain yHKS398 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	973	973	90%	0.0	99%	KM384616.1
Wickerhamomyces anomalus strain DBMY724 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	971	971	93%	0.0	98%	KJ706941.1
Wickerhamomyces anomalus strain WM 04.499 isolate ISHAM-ITS_ID MITS517 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	969	969	94%	0.0	98%	KP132905.1
Wickerhamomyces anomalus strain LL11_091 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	969	969	89%	0.0	99%	KF057582.1
Pichia anomala strain CTSP F5 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	969	969	94%	0.0	98%	EU862187.1
Wickerhamomyces anomalus strain yHKS235 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	967	967	88%	0.0	100%	KM384614.1
Wickerhamomyces anomalus strain CNRMA10.1139 isolate ISHAM-ITS_ID MITS521 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	967	967	94%	0.0	98%	KP132877.1
Wickerhamomyces anomalus strain DAOM 216362 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	967	967	91%	0.0	99%	JN942844.1
Wickerhamomyces anomalus genomic DNA sequence contains ITS1, isolate Wa_L4.8	966	966	90%	0.0	99%	LN871206.1
Wickerhamomyces anomalus genomic DNA sequence contains ITS1, isolate Wa_1f1	966	966	90%	0.0	99%	LN871205.1
Wickerhamomyces anomalus strain yHRM29 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	966	966	88%	0.0	100%	KM384621.1
Wickerhamomyces anomalus strain Tsy1 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	964	964	94%	0.0	98%	JF728870.1
Wickerhamomyces anomalus strain DBF02 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	960	960	96%	0.0	97%	KT207267.1

sequence						
Wickerhamomyces anomalus strain DBAH16 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	958	958	90%	0.0	99%	KT207087.1
Uncultured compost fungus partial 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 partial 28S rRNA gene, clone AP17	958	958	91%	0.0	99%	AM711382.1
Wickerhamomyces anomalus strain WM 825 isolate ISHAM-ITS_ID MITS496 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	958	958	90%	0.0	99%	DQ249195.2
Wickerhamomyces anomalus voucher UFLA FFT5.1 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	957	957	88%	0.0	99%	KM368826.1
Pichia anomala isolate M10 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	957	957	93%	0.0	98%	FJ865436.1
Fungal sp. 124 MCS-2014 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence	953	953	89%	0.0	99%	KM374072.1

Alignments

Wickerhamomyces anomalus isolate LMICRO189 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
Sequence ID: **gb|KJ451713.1|** Length: 942 Number of Matches: 1
Range 1: 116 to 717

Score	Expect	Identities	Gaps	Strand	Frame
1063 bits(1178)	0.0()	597/602(99%)	0/602(0%)	Plus/Minus	

Features:

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Query  2    ATTTGAGGTCAAACTTTAAGAACATTGTTGTTAAGCCGAGCCTAAAATACTTCTAAACCT  61
            ||||||||||||||||| ||   |||||||||||||||||||||||||||||||||||||
Sbjct  717  ATTTGAGGTCAAACTTTTAGTTTATTGTTGTTAAGCCGAGCCTAAAATACTTCTAAACCT  658

Query  62   GCCTAGCTGATATAACGAGTTGGAAGAACCTAATACATTATTTCAGAAAGACTGCTTATT  121
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  657  GCCTAGCTGATATAACGAGTTGGAAGAACCTAATACATTATTTCAGAAAGACTGCTTATT  598

Query  122  AGTACACTCTTGCTAAGTCAATATTTCAAGTTAACCCTTGACAGAGTATCACTCAATACC  181
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  597  AGTACACTCTTGCTAAGTCAATATTTCAAGTTAACCCTTGACAGAGTATCACTCAATACC  538

Query  182  AAACCCGAAGGTTTGAGAGAGAAATGACGCTCAAACAGGCATACCCTCTGGAATACCAGA  241
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  537  AAACCCGAAGGTTTGAGAGAGAAATGACGCTCAAACAGGCATACCCTCTGGAATACCAGA  478

Query  242  GGGTGCAATGTGCGTTCAAAGATTCGATGATTCACGAAAATCTGCAATTCACAATACGTA  301
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  477  GGGTGCAATGTGCGTTCAAAGATTCGATGATTCACGAAAATCTGCAATTCACAATACGTA  418

Query  302  TCGCATTTCGCTGCGTTCTTCATCGTTGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTT  361
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  417  TCGCATTTCGCTGCGTTCTTCATCGTTGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTT  358

Query  362  GAAGATTTTAATTTTTGTTAAAAATTTTCATGACTATTGGTTAAAGGTTTTAACATTaaa  421
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  357  GAAGATTTTAATTTTTGTTAAAAATTTTCATGACTATTGGTTAAAGGTTTTAACATTAAA  298

Query  422  aaaaaTGTGTTTAGACCTTTGGGCAGTAAGCCAGGCTCACCACCCAAAGCAAAGTTCaaa  481
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  297  AAAAATGTGTTTAGACCTTTGGGCAGTAAGCCAGGCTCACCACCCAAAGCAAAGTTCAAA  238

Query  482  aaaaCTAGACAATGTGTGTAAGGTTTATCGCCGCGCAATTAAGCGCTGGCAATAGAATAC  541
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  237  AAAACTAGACAATGTGTGTAAGGTTTATCGCCGCGCAATTAAGCGCTGGCAATAGAATAC  178

Query  542  TATAATGATCCTTCCGCAGGTTCACCTACGGAAACCTTGTTACGACTTTTAGTTCCTCTA  601
            ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
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Sbjct  177  TATAATGATCCTTCCGCAGGTTCACCTACGGAAACCTTGTTACGACTTTTACTTCCTCTA  118

Query  602  AA  603
            ||
Sbjct  117  AA  116
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Wickerhamomyces anomalus isolate LMICRO187 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
Sequence ID: **gb|KJ451711.1|** Length: 942 Number of Matches: 1
Range 1: 116 to 717

Score	Expect	Identities	Gaps	Strand	Frame
1063 bits(1178)	0.0()	597/602(99%)	0/602(0%)	Plus/Minus	

Features:

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Query  2    ATTTGAGGTCAAACTTTAAGAACATTGTTGTTAAGCCGAGCCTAAAATACTTCTAAACCT  61
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Sbjct  717  ATTTGAGGTCAAACTTTTAGTTTATTGTTGTTAAGCCGAGCCTAAAATACTTCTAAACCT  658

Query  62   GCCTAGCTGATATAACGAGTTGGAAGAACCTAATACATTATTTCAGAAAGACTGCTTATT  121
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  657  GCCTAGCTGATATAACGAGTTGGAAGAACCTAATACATTATTTCAGAAAGACTGCTTATT  598

Query  122  AGTACACTCTTGCTAAGTCAATATTTCAAGTTAACCCTTGACAGAGTATCACTCAATACC  181
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  597  AGTACACTCTTGCTAAGTCAATATTTCAAGTTAACCCTTGACAGAGTATCACTCAATACC  538

Query  182  AAACCCGAAGGTTTGAGAGAGAAATGACGCTCAAACAGGCATACCCTCTGGAATACCAGA  241
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  537  AAACCCGAAGGTTTGAGAGAGAAATGACGCTCAAACAGGCATACCCTCTGGAATACCAGA  478

Query  242  GGGTGCAATGTGCGTTCAAAGATTCGATGATTCACGAAAATCTGCAATTCACAATACGTA  301
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  477  GGGTGCAATGTGCGTTCAAAGATTCGATGATTCACGAAAATCTGCAATTCACAATACGTA  418

Query  302  TCGCATTTCGCTGCGTTCTTCATCGTTGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTT  361
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  417  TCGCATTTCGCTGCGTTCTTCATCGTTGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTT  358

Query  362  GAAGATTTTAATTTTTGTTAAAAATTTTCATGACTATTGGTTAAAGGTTTTAACATTaaa  421
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  357  GAAGATTTTAATTTTTGTTAAAAATTTTCATGACTATTGGTTAAAGGTTTTAACATTAAA  298

Query  422  aaaaaTGTGTTTAGACCTTTGGGCAGTAAGCCAGGCTCACCACCCAAAGCAAAGTTCaaa  481
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  297  AAAAATGTGTTTAGACCTTTGGGCAGTAAGCCAGGCTCACCACCCAAAGCAAAGTTCAAA  238

Query  482  aaaaCTAGACAATGTGTGTAAGGTTTATCGCCGCGCAATTAAGCGCTGGCAATAGAATAC  541
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  237  AAAACTAGACAATGTGTGTAAGGTTTATCGCCGCGCAATTAAGCGCTGGCAATAGAATAC  178

Query  542  TATAATGATCCTTCCGCAGGTTCACCTACGGAAACCTTGTTACGACTTTTAGTTCCTCTA  601
            ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  177  TATAATGATCCTTCCGCAGGTTCACCTACGGAAACCTTGTTACGACTTTTACTTCCTCTA  118

Query  602  AA  603
            ||
Sbjct  117  AA  116
```

Wickerhamomyces anomalus 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
Sequence ID: **gb|KJ659884.1|** Length: 2365 Number of Matches: 1
Range 1: 1718 to 2319

Score	Expect	Identities	Gaps	Strand	Frame
1063 bits(1178)	0.0()	597/602(99%)	0/602(0%)	Plus/Minus	

Features:

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Query  2     ATTTGAGGTCAAACTTTAAGAACATTGTTGTTAAGCCGAGCCTAAAATACTTCTAAACCT  61
             ||||||||||||||||| ||   |||||||||||||||||||||||||||||||||||||
Sbjct  2319  ATTTGAGGTCAAACTTTTAGTTTATTGTTGTTAAGCCGAGCCTAAAATACTTCTAAACCT  2260

Query  62    GCCTAGCTGATATAACGAGTTGGAAGAACCTAATACATTATTTCAGAAAGACTGCTTATT  121
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2259  GCCTAGCTGATATAACGAGTTGGAAGAACCTAATACATTATTTCAGAAAGACTGCTTATT  2200

Query  122   AGTACACTCTTGCTAAGTCAATATTTCAAGTTAACCCTTGACAGAGTATCACTCAATACC  181
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2199  AGTACACTCTTGCTAAGTCAATATTTCAAGTTAACCCTTGACAGAGTATCACTCAATACC  2140

Query  182   AAACCCGAAGGTTTGAGAGAGAAATGACGCTCAAACAGGCATACCCTCTGGAATACCAGA  241
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2139  AAACCCGAAGGTTTGAGAGAGAAATGACGCTCAAACAGGCATACCCTCTGGAATACCAGA  2080

Query  242   GGGTGCAATGTGCGTTCAAAGATTCGATGATTCACGAAAATCTGCAATTCACAATACGTA  301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2079  GGGTGCAATGTGCGTTCAAAGATTCGATGATTCACGAAAATCTGCAATTCACAATACGTA  2020

Query  302   TCGCATTTCGCTGCGTTCTTCATCGTTGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTT  361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2019  TCGCATTTCGCTGCGTTCTTCATCGTTGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTT  1960

Query  362   GAAGATTTTAATTTTTGTTAAAAATTTTCATGACTATTGGTTAAAGGTTTTAACATTaaa  421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  1959   GAAGATTTTAATTTTTGTTAAAAATTTTCATGACTATTGGTTAAAGGTTTTAACATTAAA  1900

Query  422    aaaaaTGTGTTTAGACCTTTGGGCAGTAAGCCAGGCTCACCACCCAAAGCAAAGTTCaaa  481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1899   AAAAATGTGTTTAGACCTTTGGGCAGTAAGCCAGGCTCACCACCCAAAGCAAAGTTCAAA  1840

Query  482    aaaaCTAGACAATGTGTGTAAGGTTTATCGCCGCGCAATTAAGCGCTGGCAATAGAATAC  541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1839   AAAACTAGACAATGTGTGTAAGGTTTATCGCCGCGCAATTAAGCGCTGGCAATAGAATAC  1780

Query  542    TATAATGATCCTTCCGCAGGTTCACCTACGGAAACCTTGTTACGACTTTTAGTTCCTCTA  601
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  1779   TATAATGATCCTTCCGCAGGTTCACCTACGGAAACCTTGTTACGACTTTTACTTCCTCTA  1720

Query  602    AA  603
              ||
Sbjct  1719   AA  1718
```

Uncultured eukaryote clone FS2_2_12 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

Sequence ID: **gb|FJ176542.1|** Length: 857 Number of Matches: 1
Range 1: 16 to 617

Score	Expect	Identities	Gaps	Strand	Frame
1063 bits(1178)	0.0()	597/602(99%)	0/602(0%)	Plus/Minus	

Features:

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Query  2      ATTTGAGGTCAAACTTTAAGAACATTGTTGTTAAGCCGAGCCTAAAATACTTCTAAACCT  61
              ||||||||||||||||| ||   |||||||||||||||||||||||||||||||||||||
Sbjct  617    ATTTGAGGTCAAACTTTTAGTTTATTGTTGTTAAGCCGAGCCTAAAATACTTCTAAACCT  558

Query  62     GCCTAGCTGATATAACGAGTTGGAAGAACCTAATACATTATTTCAGAAAGACTGCTTATT  121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  557    GCCTAGCTGATATAACGAGTTGGAAGAACCTAATACATTATTTCAGAAAGACTGCTTATT  498

Query  122    AGTACACTCTTGCTAAGTCAATATTTCAAGTTAACCCTTGACAGAGTATCACTCAATACC  181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  497    AGTACACTCTTGCTAAGTCAATATTTCAAGTTAACCCTTGACAGAGTATCACTCAATACC  438

Query  182    AAACCCGAAGGTTTGAGAGAGAAATGACGCTCAAACAGGCATACCCTCTGGAATACCAGA  241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  437    AAACCCGAAGGTTTGAGAGAGAAATGACGCTCAAACAGGCATACCCTCTGGAATACCAGA  378

Query  242    GGGTGCAATGTGCGTTCAAAGATTCGATGATTCACGAAAATCTGCAATTCACAATACGTA  301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  377    GGGTGCAATGTGCGTTCAAAGATTCGATGATTCACGAAAATCTGCAATTCACAATACGTA  318

Query  302    TCGCATTTCGCTGCGTTCTTCATCGTTGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTT  361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  317    TCGCATTTCGCTGCGTTCTTCATCGTTGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTT  258

Query  362    GAAGATTTTAATTTTTGTTAAAAATTTTCATGACTATTGGTTAAAGGTTTTAACATTaaa  421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  257    GAAGATTTTAATTTTTGTTAAAAATTTTCATGACTATTGGTTAAAGGTTTTAACATTAAA  198

Query  422    aaaaaTGTGTTTAGACCTTTGGGCAGTAAGCCAGGCTCACCACCCAAAGCAAAGTTCaaa  481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  197    AAAAATGTGTTTAGACCTTTGGGCAGTAAGCCAGGCTCACCACCCAAAGCAAAGTTCAAA  138

Query  482    aaaaCTAGACAATGTGTGTAAGGTTTATCGCCGCGCAATTAAGCGCTGGCAATAGAATAC  541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  137    AAAACTAGACAATGTGTGTAAGGTTTATCGCCGCGCAATTAAGCGCTGGCAATAGAATAC  78

Query  542    TATAATGATCCTTCCGCAGGTTCACCTACGGAAACCTTGTTACGACTTTTAGTTCCTCTA  601
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  77     TATAATGATCCTTCCGCAGGTTCACCTACGGAAACCTTGTTACGACTTTTACTTCCTCTA  18

Query  602    AA  603
              ||
Sbjct  17     AA  16
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Wickerhamomyces anomalus isolate LMICRO150 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

Sequence ID: **gb|KJ451674.1|** Length: 871 Number of Matches: 1
Range 1: 116 to 716

Score	Expect	Identities	Gaps	Strand	Frame
1056 bits(1170)	0.0()	596/602(99%)	1/602(0%)	Plus/Minus	

Features:

```
Query  2      ATTTGAGGTCAAACTTTAAGAACATTGTTGTTAAGCCGAGCCTAAAATACTTCTAAACCT  61
              ||||||||||||||||| ||   |||||||||||||||||||||||||||||||||||||
Sbjct  716    ATTTGAGGTCAAACTTTTAGTTTATTGTTGTTAAGCCGAGCCTAAAATACTTCTAAACCT  657

Query  62     GCCTAGCTGATATAACGAGTTGGAAGAACCTAATACATTATTTCAGAAAGACTGCTTATT  121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  656    GCCTAGCTGATATAACGAGTTGGAAGAACCTAATACATTATTTCAGAAAGACTGCTTATT  597

Query  122    AGTACACTCTTGCTAAGTCAATATTTCAAGTTAACCCTTGACAGAGTATCACTCAATACC  181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  596    AGTACACTCTTGCTAAGTCAATATTTCAAGTTAACCCTTGACAGAGTATCACTCAATACC  537

Query  182    AAACCCGAAGGTTTGAGAGAGAAATGACGCTCAAACAGGCATACCCTCTGGAATACCAGA  241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  536  AAACCCGAAGGTTTGAGAGAGAAATGACGCTCAAACAGGCATACCCTCTGGAATACCAGA  477

Query  242  GGGTGCAATGTGCGTTCAAAGATTCGATGATTCACGAAAATCTGCAATTCACAATACGTA  301
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  476  GGGTGCAATGTGCGTTCAAAGATTCGATGATTCACGAAAATCTGCAATTCACAATACGTA  417

Query  302  TCGCATTTCGCTGCGTTCTTCATCGTTGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTT  361
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  416  TCGCATTTCGCTGCGTTCTTCATCGTTGCGAGAACCAAGAGATCCGTTGTTGAAAGTTTT  357

Query  362  GAAGATTTTAATTTTTGTTAAAAATTTTCATGACTATTGGTTAAAGGTTTTAACATTaaa  421
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  356  GAAGATTTTAATTTTTGTTAAAAATTTTCATGACTATTGGTTAAAGGTTTTAACATT-AA  298

Query  422  aaaaaTGTGTTTAGACCTTTGGGCAGTAAGCCAGGCTCACCACCCAAAGCAAAGTTCaaa  481
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  297  AAAAATGTGTTTAGACCTTTGGGCAGTAAGCCAGGCTCACCACCCAAAGCAAAGTTCAAA  238

Query  482  aaaaCTAGACAATGTGTGTAAGGTTTATCGCCGCGCAATTAAGCGCTGGCAATAGAATAC  541
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  237  AAAACTAGACAATGTGTGTAAGGTTTATCGCCGCGCAATTAAGCGCTGGCAATAGAATAC  178

Query  542  TATAATGATCCTTCCGCAGGTTCACCTACGGAAACCTTGTTACGACTTTTAGTTCCTCTA  601
            ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  177  TATAATGATCCTTCCGCAGGTTCACCTACGGAAACCTTGTTACGACTTTTACTTCCTCTA  118

Query  602  AA  603
            ||
Sbjct  117  AA  116
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Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BU1FHAEP014**
Formatting options
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Blast report description

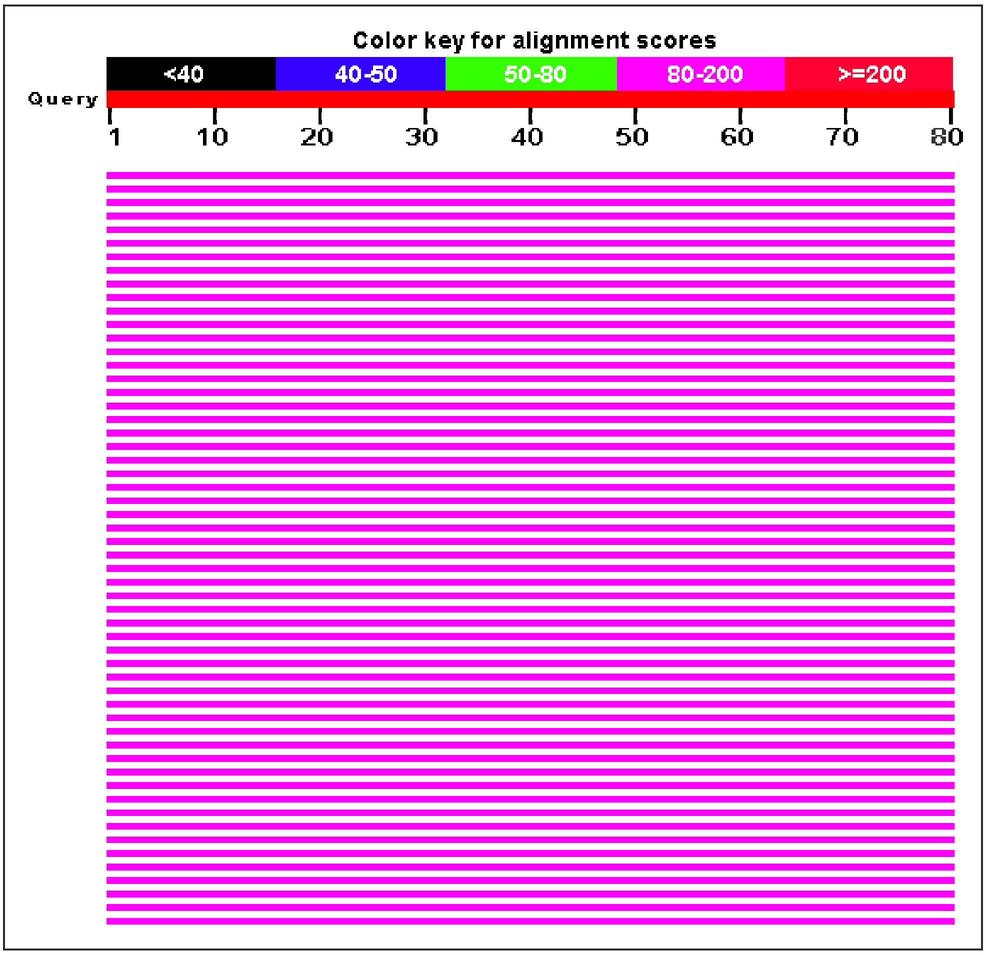
YK07-2-B5.1A2_trnL_Clone5

RID BU1FHAEP014 (Expires on 02-13 05:06 am)

Query ID	lcl|Query_64979	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	80		

Graphic Summary

Distribution of 101 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Musa yunnanensis isolate SS&JS 473 Montharop Khun Nan tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257604.1
Musella lasiocarpa isolate SS&JS 231 Dararassami tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257602.1
Musa yunnanensis isolate SS&JS 444 Yunnan Namtok Pa Way tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257599.1
Musa yunnanensis isolate SS&JS 349 Yunnan Inthanon tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257598.1
Musa yunnanensis isolate SS&JS 235 Yunnan QSBG tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257597.1
Musa yunnanensis isolate SS&JS 125 Yunnan Huai Nam Dang tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257596.1
Musa laterita isolate SS&JS 412 Bua Si Som Pli Lueang tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257595.1
Musa serpentina isolate SS&JS 353 Nakkharat Huay Hang Pon tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257594.1
Musa serpentina isolate SS&JS 246 Nakkharat Dan Chedi Sam Ong tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257593.1
Musa ornata isolate SS&JS 449 Bua Si Chomphu Luk Khieo tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257592.1
Musa ornata isolate SS&JS 433 Bua Luang tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257591.1
Musa ornata isolate SS&JS 169 Bua Si Muang tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257590.1
Musa laterita isolate SS&JS 308 Bua Si Som Dan Mae Lamao tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic	140	140	100%	3e-30	99%	KT257589.1

spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast						
Musa itinerans isolate SS&JS 175 Hok Khao Soi Dao tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257588.1
Musa balbisiana isolate SS&JS 12 Tani Pa Tat Luang tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257585.1
Musa acuminata var. zebrina isolate SS&JS 155 Thahan Phran tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257584.1
Musa acuminata subsp. truncata isolate SS&JS 368 Pa Cameron tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257583.1
Musa acuminata subsp. siamea isolate SS&JS 450 Pa Kanchanaburi Campus tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257582.1
Musa acuminata subsp. siamea isolate SS&JS 173 Pa Pli Lueang Ban Pa Kluai tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257581.1
Musa acuminata subsp. siamea isolate SS&JS 136 Pa Namtok Kha-On tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257580.1
Musa acuminata subsp. siamea isolate SS&JS 131 Pa La-U tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257579.1
Musa acuminata subsp. siamea isolate SS&JS 1 Khae Phetchabun tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257578.1
Musa acuminata subsp. malaccensis isolate SS&JS 374 Pa Kao Talu tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257577.1
Musa acuminata subsp. malaccensis isolate SS&JS 108 Pa Hat Prapat tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257576.1
Musa acuminata subsp. malaccensis isolate SS&JS 107 Pa Pato tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257575.1
Musa acuminata subsp. malaccensis isolate SS&JS 104 Pa Chumphon tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257574.1
Musa acuminata subsp. malaccensis isolate SS&JS 445 Pa Namtok Pa Way tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and	140	140	100%	3e-30	99%	KT257573.1

tRNA-Phe (trnF) gene, partial sequence; chloroplast						
Musa acuminata subsp. malaccensis isolate SS&JS 202 Pa Tanopute tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257572.1
Musa balbisiana chloroplast, complete genome	140	140	100%	3e-30	99%	KT595228.1
Musa textilis plastid, complete genome	140	140	100%	3e-30	99%	KF601567.1
Musa acuminata subsp. malaccensis chloroplast complete genome, biomaterial CIRAD:930	140	140	100%	3e-30	99%	HF677508.1
Musa environmental sample tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	140	140	100%	3e-30	99%	JX113269.1
Musa sp. Ogasawara06 chloroplast trnL gene, intron, partial sequence, isolate: OGA0508	140	140	100%	3e-30	99%	AB817687.1
Musa basjoo tRNA-Leu (trnL(UAA)) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF(GAA)) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ428188.2
Musella lasiocarpa isolate Kress-GH01-210 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621287.1
Musa mannii tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621285.1
Musa nagensium tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621284.1
Musa rubra tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621277.1
Musa splendida tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621282.1
Musa balbisiana isolate Bangladesh tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621280.1
Musa balbisiana isolate Yunnan tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621279.1
Musa ornata tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621278.1
Musa itinerans tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621276.1
Musa formosana tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621275.1
Musa sanguinea tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621274.1
Musa campestris tRNA-Leu (trnL) gene,						

partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621273.1
Musa beccarii tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621272.1
Musa basjoo tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621270.1
Musa maclayi tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621269.1
Musa laterita tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621268.1
Musa salaccensis tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621266.1
Musa velutina tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621264.1
Musa rosea tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621263.1
Angiosperm environmental sample chloroplast partial tRNA-Leu gene, intron region, isolated from Cryptorhynchinae sp.34 BMNH:796424	140	140	100%	3e-30	99%	FN398125.1
Musa beccarii tRNA-Leu gene, partial sequence; tRNA-Leu(UAA)-tRNA-Phe(GAA) intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	AF431635.1
Musa gracilis isolate SS&JS 128 Sri Nara QSBG tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257587.1
Musa borneensis tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	FJ621265.1
Musa violascens tRNA-Leu (trnL(UAA)) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF(GAA)) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	FJ428195.1
Musa rosea plastid partial tRNA-Leu gene and trnL-trnF IGS, specimen voucher Asmussen 101 (CP)	136	136	100%	4e-29	98%	AM113703.1
Musella lasiocarpa isolate Yunnan tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	134	134	100%	1e-28	98%	FJ621286.1
Musa textilis tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	134	224	100%	1e-28	99%	FJ621281.1
Thaumatococcus daniellii plastid, partial genome	131	131	100%	2e-27	96%	KF601575.1
Heliconia collinsiana plastid, complete genome	131	131	100%	2e-27	96%	JX088660.1
Hypselodelphys hirsuta voucher A.Ley 269 (WAG) tRNA-Leu (trnL) gene, partial	131	131	100%	2e-27	96%	JN413110.1

sequence; chloroplast						
Heliconia stricta tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	FJ621299.1
Megaphrynium trichogynum voucher Ley 114 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	131	131	100%	2e-27	96%	EU647828.1
Thaumatococcus sp. Ley 179 voucher Ley 179 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	131	131	100%	2e-27	96%	EU647827.1
Thaumatococcus daniellii voucher Ley 96 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	131	131	100%	2e-27	96%	EU647826.1
Hypselodelphys sp. Ley 125 voucher Ley 125 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	131	131	100%	2e-27	96%	EU647825.1
Hypselodelphys scandens voucher Ley 160 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	131	131	100%	2e-27	96%	EU647824.1
Trachyphrynium braunianum voucher Ley 171 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	131	131	100%	2e-27	96%	EU647823.1
Hypselodelphys violacea voucher Ley 28 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	131	131	100%	2e-27	96%	EU647821.1
Hypselodelphys hirsuta voucher Ley 156 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	131	131	100%	2e-27	96%	EU647820.1
Hypselodelphys poggeana voucher Ley 168 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	131	131	100%	2e-27	96%	EU647819.1
Heliconia solomonensis tRNA-Leu gene, partial sequence; tRNA-Leu(UAA)-tRNA-Phe(GAA) intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	AF431634.1
Heliconia rostrata tRNA-Leu gene, partial sequence; tRNA-Leu(UAA)-tRNA-Phe(GAA) intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	AF431633.1
Hypselodelphys velutina voucher Jongkind 4839 (WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	129	129	100%	6e-27	95%	EU647818.1
Syagrus coronata chloroplast, complete genome	127	127	100%	2e-26	95%	KT896548.1
Ensete superbum isolate SS&JS 242 Pha Pli Lueang Vachiralongkorn Dam tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	127	127	100%	2e-26	93%	KT257601.1

Ensete glaucum isolate SS&JS 229 Nuan Sae-Lae tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	127	127	100%	2e-26	93%	KT257600.1
Musa coccinea isolate SS&JS 223 Rattakatthali tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	127	127	100%	2e-26	93%	KT257586.1
Costus zingiberoides voucher BTM86-00-01 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011345.1
Costus talbotii voucher 2003-0109009 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011343.1
Costus aff. tappenbeckianus SMS-2014 voucher 2005-0100002 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011342.1
Costus aff. tappenbeckianus SMS-2014 voucher 2005-0100001 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011341.1
Costus scaber voucher R2253 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011339.1
Costus ricus voucher R2970 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011338.1
Costus quasi-appendiculatus voucher CSpecht 99-233 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011337.1
Costus aff. phyllocephalus SMS-2014 voucher BB870057 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011334.1
Costus osae voucher M9501 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011333.1
Costus maboumiensis voucher M10227 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011330.1
Costus lucanusianus voucher Breteler5297 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011329.1
Costus aff. ligularis SMS-2014 voucher 2005-0100003 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011324.1
Costus aff. ligularis SMS-2014 voucher 1998-0923003 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011323.1
Costus leucanthus voucher 1996-1105001						

tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011322.1
Costus lateriflorus voucher M10331 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011321.1
Costus dubius voucher M10206 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011314.1
Costus barbatus voucher CSpecht 01-256 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011308.1
Costus vinosus voucher M9568 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	123	123	100%	3e-25	94%	KJ011344.1
Costus erythrophyllus voucher R2847 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	122	122	100%	9e-25	93%	KJ011315.1

Alignments

Musa yunnanensis isolate SS&JS 473 Montharop Khun Nan tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast

Sequence ID: **gb|KT257604.1|** Length: 1002 Number of Matches: 1
Range 1: 102 to 181

Score	Expect	Identities	Gaps	Strand	Frame
140 bits(154)	3e-30()	79/80(99%)	0/80(0%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTATTTTGAGATAACAAAGGTTTATAAAACTAGAATTTAA  60
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  102  GGCAATCCTGAGCCAAATCCTTATTTTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  161

Query  61   AAGGATAGGTGCAGAGACTC  80
            ||||||||||||||||||||
Sbjct  162  AAGGATAGGTGCAGAGACTC  181
```

Musella lasiocarpa isolate SS&JS 231 Dararassami tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast

Sequence ID: **gb|KT257602.1|** Length: 902 Number of Matches: 1
Range 1: 82 to 161

Score	Expect	Identities	Gaps	Strand	Frame
140 bits(154)	3e-30()	79/80(99%)	0/80(0%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTATTTTGAGATAACAAAGGTTTATAAAACTAGAATTTAA  60
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  82   GGCAATCCTGAGCCAAATCCTTATTTTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  141

Query  61   AAGGATAGGTGCAGAGACTC  80
            ||||||||||||||||||||
Sbjct  142  AAGGATAGGTGCAGAGACTC  161
```

Musa yunnanensis isolate SS&JS 444 Yunnan Namtok Pa Way tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast

Sequence ID: **gb|KT257599.1|** Length: 971 Number of Matches: 1
Range 1: 102 to 181

Score	Expect	Identities	Gaps	Strand	Frame

140 bits(154)	3e-30()	79/80(99%)	0/80(0%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTATTTTGAGATAACAAAGGTTTATAAAACTAGAATTTAA  60
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  102  GGCAATCCTGAGCCAAATCCTTATTTTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  161

Query  61   AAGGATAGGTGCAGAGACTC  80
            ||||||||||||||||||||
Sbjct  162  AAGGATAGGTGCAGAGACTC  181
```

Musa yunnanensis isolate SS&JS 349 Yunnan Inthanon tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast

Sequence ID: **gb|KT257598.1|** Length: 971 Number of Matches: 1
Range 1: 102 to 181

Score	Expect	Identities	Gaps	Strand	Frame
140 bits(154)	3e-30()	79/80(99%)	0/80(0%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTATTTTGAGATAACAAAGGTTTATAAAACTAGAATTTAA  60
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  102  GGCAATCCTGAGCCAAATCCTTATTTTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  161

Query  61   AAGGATAGGTGCAGAGACTC  80
            ||||||||||||||||||||
Sbjct  162  AAGGATAGGTGCAGAGACTC  181
```

Musa yunnanensis isolate SS&JS 235 Yunnan QSBG tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast

Sequence ID: **gb|KT257597.1|** Length: 971 Number of Matches: 1
Range 1: 102 to 181

Score	Expect	Identities	Gaps	Strand	Frame
140 bits(154)	3e-30()	79/80(99%)	0/80(0%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTATTTTGAGATAACAAAGGTTTATAAAACTAGAATTTAA  60
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  102  GGCAATCCTGAGCCAAATCCTTATTTTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  161

Query  61   AAGGATAGGTGCAGAGACTC  80
            ||||||||||||||||||||
Sbjct  162  AAGGATAGGTGCAGAGACTC  181
```

BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BU1D6XG2015**

Formatting options
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Blast report description

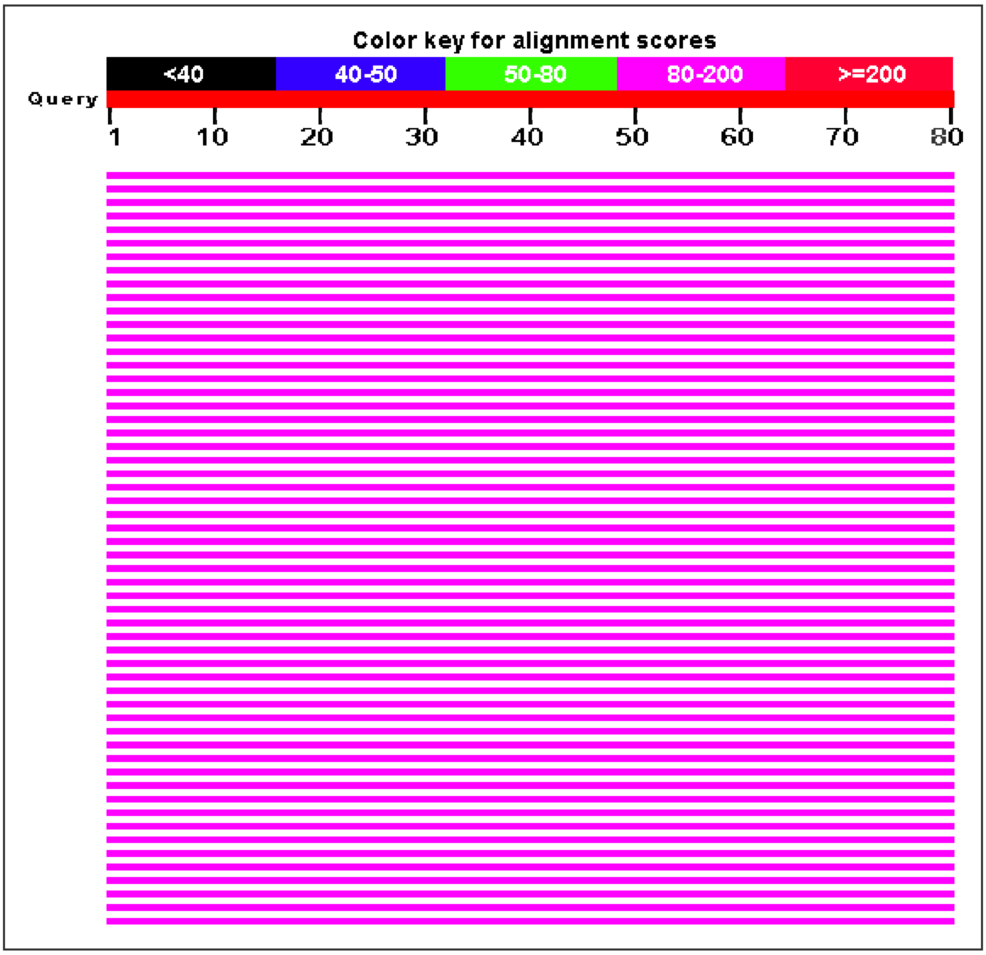
YK07-2-B5.1A2_trnL_Clone6

RID BU1D6XG2015 (Expires on 02-13 05:05 am)

Query ID	lcl|Query_120141	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	80		

Graphic Summary

Distribution of 101 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Musa yunnanensis isolate SS&JS 473 Montharop Khun Nan tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257604.1
Musella lasiocarpa isolate SS&JS 231 Dararassami tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257602.1
Musa yunnanensis isolate SS&JS 444 Yunnan Namtok Pa Way tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257599.1
Musa yunnanensis isolate SS&JS 349 Yunnan Inthanon tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257598.1
Musa yunnanensis isolate SS&JS 235 Yunnan QSBG tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257597.1
Musa yunnanensis isolate SS&JS 125 Yunnan Huai Nam Dang tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257596.1
Musa laterita isolate SS&JS 412 Bua Si Som Pli Lueang tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257595.1
Musa serpentina isolate SS&JS 353 Nakkharat Huay Hang Pon tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257594.1
Musa serpentina isolate SS&JS 246 Nakkharat Dan Chedi Sam Ong tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257593.1
Musa ornata isolate SS&JS 449 Bua Si Chomphu Luk Khieo tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257592.1
Musa ornata isolate SS&JS 433 Bua Luang tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257591.1
Musa ornata isolate SS&JS 169 Bua Si Muang tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257590.1
Musa laterita isolate SS&JS 308 Bua Si Som Dan Mae Lamao tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic	140	140	100%	3e-30	99%	KT257589.1

spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast						
Musa itinerans isolate SS&JS 175 Hok Khao Soi Dao tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257588.1
Musa balbisiana isolate SS&JS 12 Tani Pa Tat Luang tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257585.1
Musa acuminata var. zebrina isolate SS&JS 155 Thahan Phran tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257584.1
Musa acuminata subsp. truncata isolate SS&JS 368 Pa Cameron tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257583.1
Musa acuminata subsp. siamea isolate SS&JS 450 Pa Kanchanaburi Campus tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257582.1
Musa acuminata subsp. siamea isolate SS&JS 173 Pa Pli Lueang Ban Pa Kluai tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257581.1
Musa acuminata subsp. siamea isolate SS&JS 136 Pa Namtok Kha-On tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257580.1
Musa acuminata subsp. siamea isolate SS&JS 131 Pa La-U tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257579.1
Musa acuminata subsp. siamea isolate SS&JS 1 Khae Phetchabun tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257578.1
Musa acuminata subsp. malaccensis isolate SS&JS 374 Pa Kao Talu tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257577.1
Musa acuminata subsp. malaccensis isolate SS&JS 108 Pa Hat Prapat tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257576.1
Musa acuminata subsp. malaccensis isolate SS&JS 107 Pa Pato tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257575.1
Musa acuminata subsp. malaccensis isolate SS&JS 104 Pa Chumphon tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257574.1
Musa acuminata subsp. malaccensis isolate SS&JS 445 Pa Namtok Pa Way tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and	140	140	100%	3e-30	99%	KT257573.1

tRNA-Phe (trnF) gene, partial sequence; chloroplast						
Musa acuminata subsp. malaccensis isolate SS&JS 202 Pa Tanopute tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257572.1
Musa balbisiana chloroplast, complete genome	140	140	100%	3e-30	99%	KT595228.1
Musa textilis plastid, complete genome	140	140	100%	3e-30	99%	KF601567.1
Musa acuminata subsp. malaccensis chloroplast complete genome, biomaterial CIRAD:930	140	140	100%	3e-30	99%	HF677508.1
Musa environmental sample tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	140	140	100%	3e-30	99%	JX113269.1
Musa sp. Ogasawara06 chloroplast trnL gene, intron, partial sequence, isolate: OGA0508	140	140	100%	3e-30	99%	AB817687.1
Musa basjoo tRNA-Leu (trnL(UAA)) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF(GAA)) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ428188.2
Musella lasiocarpa isolate Kress-GH01-210 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621287.1
Musa mannii tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621285.1
Musa nagensium tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621284.1
Musa rubra tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621277.1
Musa splendida tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621282.1
Musa balbisiana isolate Bangladesh tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621280.1
Musa balbisiana isolate Yunnan tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621279.1
Musa ornata tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621278.1
Musa itinerans tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621276.1
Musa formosana tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621275.1
Musa sanguinea tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621274.1
Musa campestris tRNA-Leu (trnL) gene,						

partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621273.1
Musa beccarii tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621272.1
Musa basjoo tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621270.1
Musa maclayi tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621269.1
Musa laterita tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621268.1
Musa salaccensis tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621266.1
Musa velutina tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621264.1
Musa rosea tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621263.1
Angiosperm environmental sample chloroplast partial tRNA-Leu gene, intron region, isolated from Cryptorhynchinae sp.34 BMNH:796424	140	140	100%	3e-30	99%	FN398125.1
Musa beccarii tRNA-Leu gene, partial sequence; tRNA-Leu(UAA)-tRNA-Phe(GAA) intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	AF431635.1
Musa gracilis isolate SS&JS 128 Sri Nara QSBG tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257587.1
Musa borneensis tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	FJ621265.1
Musa violascens tRNA-Leu (trnL(UAA)) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF(GAA)) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	FJ428195.1
Musa rosea plastid partial tRNA-Leu gene and trnL-trnF IGS, specimen voucher Asmussen 101 (CP)	136	136	100%	4e-29	98%	AM113703.1
Musella lasiocarpa isolate Yunnan tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	134	134	100%	1e-28	98%	FJ621286.1
Musa textilis tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	134	224	100%	1e-28	99%	FJ621281.1
Thaumatococcus daniellii plastid, partial genome	131	131	100%	2e-27	96%	KF601575.1
Heliconia collinsiana plastid, complete genome	131	131	100%	2e-27	96%	JX088660.1
Calathea villosa voucher R.Dressler 2912 (COL) tRNA-Leu (trnL) gene, partial	131	131	100%	2e-27	96%	JN413158.1

sequence; chloroplast						
Hypselodelphys hirsuta voucher A.Ley 269 (WAG) tRNA-Leu (trnL) gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	JN413110.1
Heliconia stricta tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	FJ621299.1
Megaphrynium trichogynum voucher Ley 114 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	131	131	100%	2e-27	96%	EU647828.1
Thaumatococcus sp. Ley 179 voucher Ley 179 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	131	131	100%	2e-27	96%	EU647827.1
Thaumatococcus daniellii voucher Ley 96 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	131	131	100%	2e-27	96%	EU647826.1
Hypselodelphys sp. Ley 125 voucher Ley 125 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	131	131	100%	2e-27	96%	EU647825.1
Hypselodelphys scandens voucher Ley 160 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	131	131	100%	2e-27	96%	EU647824.1
Trachyphrynium braunianum voucher Ley 171 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	131	131	100%	2e-27	96%	EU647823.1
Hypselodelphys violacea voucher Ley 28 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	131	131	100%	2e-27	96%	EU647821.1
Hypselodelphys hirsuta voucher Ley 156 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	131	131	100%	2e-27	96%	EU647820.1
Hypselodelphys poggeana voucher Ley 168 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	131	131	100%	2e-27	96%	EU647819.1
Heliconia solomonensis tRNA-Leu gene, partial sequence; tRNA-Leu(UAA)-tRNA-Phe(GAA) intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	AF431634.1
Heliconia rostrata tRNA-Leu gene, partial sequence; tRNA-Leu(UAA)-tRNA-Phe(GAA) intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	AF431633.1
Hypselodelphys velutina voucher Jongkind 4839 (WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	129	129	100%	6e-27	95%	EU647818.1
Syagrus coronata chloroplast, complete genome	127	127	100%	2e-26	95%	KT896548.1
Ensete superbum isolate SS&JS 242 Pha Pli Lueang Vachiralongkorn Dam tRNA-Lue (trnL) gene, partial sequence; trnL-trnF	127	127	100%	2e-26	93%	KT257601.1

intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast						
Ensete glaucum isolate SS&JS 229 Nuan Sae-Lae tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	127	127	100%	2e-26	93%	KT257600.1
Musa coccinea isolate SS&JS 223 Rattakatthali tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	127	127	100%	2e-26	93%	KT257586.1
Costus zingiberoides voucher BTM86-00-01 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011345.1
Costus talbotii voucher 2003-0109009 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011343.1
Costus aff. tappenbeckianus SMS-2014 voucher 2005-0100002 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011342.1
Costus aff. tappenbeckianus SMS-2014 voucher 2005-0100001 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011341.1
Costus scaber voucher R2253 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011339.1
Costus ricus voucher R2970 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011338.1
Costus quasi-appendiculatus voucher CSpecht 99-233 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011337.1
Costus aff. phyllocephalus SMS-2014 voucher BB870057 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011334.1
Costus osae voucher M9501 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011333.1
Costus maboumiensis voucher M10227 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011330.1
Costus lucanusianus voucher Breteler5297 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011329.1
Costus aff. ligularis SMS-2014 voucher 2005-0100003 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011324.1
Costus aff. ligularis SMS-2014 voucher 1998-0923003 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer,	127	127	100%	2e-26	95%	KJ011323.1

complete sequence; and tRNA-Phe gene, partial sequence; chloroplast						
Costus leucanthus voucher 1996-1105001 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011322.1
Costus lateriflorus voucher M10331 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011321.1
Costus dubius voucher M10206 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011314.1
Costus vinosus voucher M9568 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	123	123	100%	3e-25	94%	KJ011344.1
Costus erythrophyllus voucher R2847 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	122	122	100%	9e-25	93%	KJ011315.1

Alignments

Musa yunnanensis isolate SS&JS 473 Montharop Khun Nan tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KT257604.1|** Length: 1002 Number of Matches: 1
Range 1: 102 to 181

Score	Expect	Identities	Gaps	Strand	Frame
140 bits(154)	3e-30()	79/80(99%)	0/80(0%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCtttttttGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  60
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  102  GGCAATCCTGAGCCAAATCCTTATTTTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  161

Query  61   AAGGATAGGTGCAGAGACTC  80
            ||||||||||||||||||||
Sbjct  162  AAGGATAGGTGCAGAGACTC  181
```

Musella lasiocarpa isolate SS&JS 231 Dararassami tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KT257602.1|** Length: 902 Number of Matches: 1
Range 1: 82 to 161

Score	Expect	Identities	Gaps	Strand	Frame
140 bits(154)	3e-30()	79/80(99%)	0/80(0%)	Plus/Plus	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCtttttttGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  60
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  82   GGCAATCCTGAGCCAAATCCTTATTTTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  141
Query  61   AAGGATAGGTGCAGAGACTC  80
            ||||||||||||||||||||
Sbjct  142  AAGGATAGGTGCAGAGACTC  161
```

Musa yunnanensis isolate SS&JS 444 Yunnan Namtok Pa Way tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KT257599.1|** Length: 971 Number of Matches: 1
Range 1: 102 to 181

Score	Expect	Identities	Gaps	Strand	Frame
140 bits(154)	3e-30()	79/80(99%)	0/80(0%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCtttttttGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  60
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  102  GGCAATCCTGAGCCAAATCCTTATTTTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  161

Query  61   AAGGATAGGTGCAGAGACTC  80
            ||||||||||||||||||||
Sbjct  162  AAGGATAGGTGCAGAGACTC  181
```

Musa yunnanensis isolate SS&JS 349 Yunnan Inthanon tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast

Sequence ID: **gb|KT257598.1|** Length: 971 Number of Matches: 1
Range 1: 102 to 181

Score	Expect	Identities	Gaps	Strand	Frame
140 bits(154)	3e-30()	79/80(99%)	0/80(0%)	Plus/Plus	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCtttttttGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  60
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  102  GGCAATCCTGAGCCAAATCCTTATTTTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  161

Query  61   AAGGATAGGTGCAGAGACTC  80
            ||||||||||||||||||||
Sbjct  162  AAGGATAGGTGCAGAGACTC  181
```

Musa yunnanensis isolate SS&JS 235 Yunnan QSBG tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast

Sequence ID: **gb|KT257597.1|** Length: 971 Number of Matches: 1
Range 1: 102 to 181

Score	Expect	Identities	Gaps	Strand	Frame
140 bits(154)	3e-30()	79/80(99%)	0/80(0%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCtttttttGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  60
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  102  GGCAATCCTGAGCCAAATCCTTATTTTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  161

Query  61   AAGGATAGGTGCAGAGACTC  80
            ||||||||||||||||||||
Sbjct  162  AAGGATAGGTGCAGAGACTC  181
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BLAST ®

Basic Local Alignment Search Tool

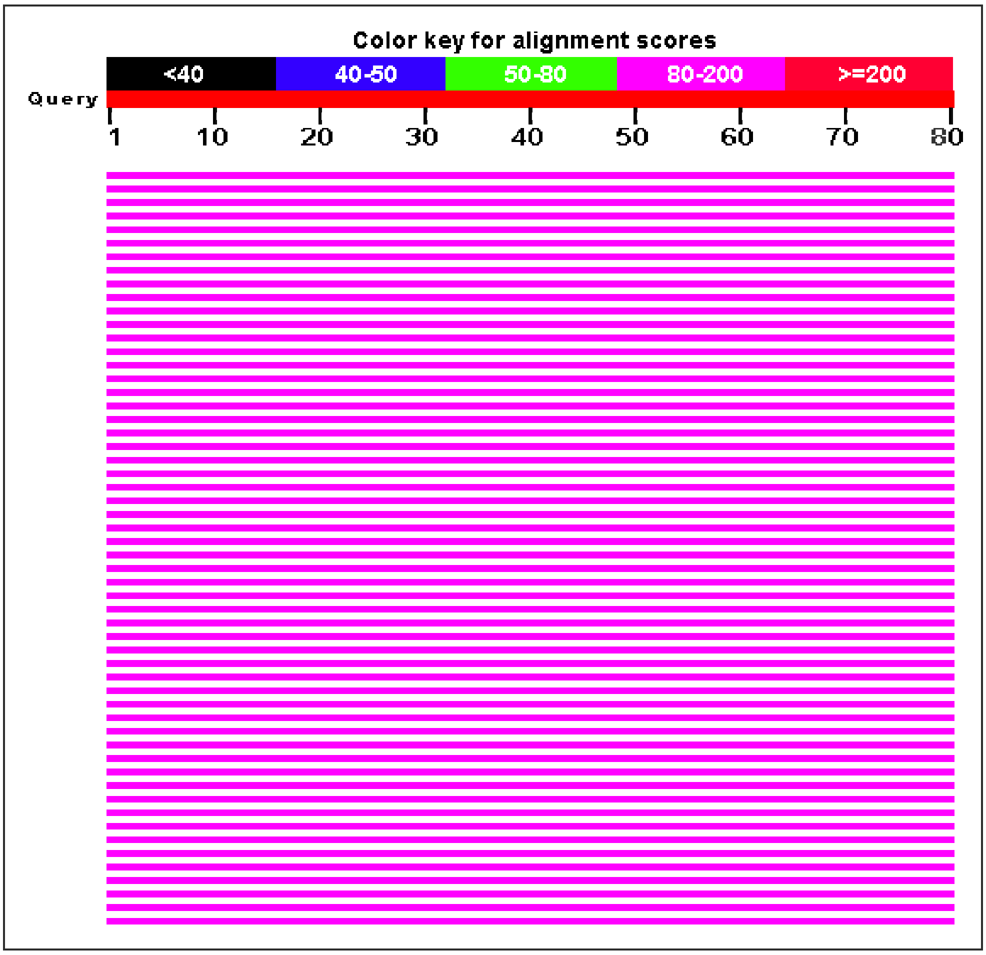
NCBI/ BLAST/ blastn suite/ **Formatting Results - BU18DVMM014**
  Formatting options
  Download
Blast report description

YK07-2-B5.1A2_trnL_Clones1,3,4

RID	BU18DVMM014 (Expires on 02-13 05:02 am)		
Query ID	lcl|Query_231443	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	80		

Graphic Summary

Distribution of 101 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Musa yunnanensis isolate SS&JS 473 Montharop Khun Nan tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257604.1
Musella lasiocarpa isolate SS&JS 231 Dararassami tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257602.1
Musa yunnanensis isolate SS&JS 444 Yunnan Namtok Pa Way tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257599.1
Musa yunnanensis isolate SS&JS 349 Yunnan Inthanon tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257598.1
Musa yunnanensis isolate SS&JS 235 Yunnan QSBG tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257597.1
Musa yunnanensis isolate SS&JS 125 Yunnan Huai Nam Dang tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257596.1
Musa laterita isolate SS&JS 412 Bua Si Som Pli Lueang tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257595.1
Musa serpentina isolate SS&JS 353 Nakkharat Huay Hang Pon tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257594.1
Musa serpentina isolate SS&JS 246 Nakkharat Dan Chedi Sam Ong tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257593.1
Musa ornata isolate SS&JS 449 Bua Si Chomphu Luk Khieo tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257592.1
Musa ornata isolate SS&JS 433 Bua Luang tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257591.1
Musa ornata isolate SS&JS 169 Bua Si Muang tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257590.1
Musa laterita isolate SS&JS 308 Bua Si Som Dan Mae Lamao tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic	145	145	100%	8e-32	100%	KT257589.1

spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast						
Musa itinerans isolate SS&JS 175 Hok Khao Soi Dao tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257588.1
Musa balbisiana isolate SS&JS 12 Tani Pa Tat Luang tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257585.1
Musa acuminata var. zebrina isolate SS&JS 155 Thahan Phran tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257584.1
Musa acuminata subsp. truncata isolate SS&JS 368 Pa Cameron tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257583.1
Musa acuminata subsp. siamea isolate SS&JS 450 Pa Kanchanaburi Campus tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257582.1
Musa acuminata subsp. siamea isolate SS&JS 173 Pa Pli Lueang Ban Pa Kluai tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257581.1
Musa acuminata subsp. siamea isolate SS&JS 136 Pa Namtok Kha-On tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257580.1
Musa acuminata subsp. siamea isolate SS&JS 131 Pa La-U tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257579.1
Musa acuminata subsp. siamea isolate SS&JS 1 Khae Phetchabun tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257578.1
Musa acuminata subsp. malaccensis isolate SS&JS 374 Pa Kao Talu tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257577.1
Musa acuminata subsp. malaccensis isolate SS&JS 108 Pa Hat Prapat tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257576.1
Musa acuminata subsp. malaccensis isolate SS&JS 107 Pa Pato tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257575.1
Musa acuminata subsp. malaccensis isolate SS&JS 104 Pa Chumphon tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257574.1
Musa acuminata subsp. malaccensis isolate SS&JS 445 Pa Namtok Pa Way tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and	145	145	100%	8e-32	100%	KT257573.1

tRNA-Phe (trnF) gene, partial sequence; chloroplast						
Musa acuminata subsp. malaccensis isolate SS&JS 202 Pa Tanopute tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	KT257572.1
Musa balbisiana chloroplast, complete genome	145	145	100%	8e-32	100%	KT595228.1
Musa textilis plastid, complete genome	145	145	100%	8e-32	100%	KF601567.1
Musa acuminata subsp. malaccensis chloroplast complete genome, biomaterial CIRAD:930	145	145	100%	8e-32	100%	HF677508.1
Musa environmental sample tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	145	145	100%	8e-32	100%	JX113269.1
Musa sp. Ogasawara06 chloroplast trnL gene, intron, partial sequence, isolate: OGA0508	145	145	100%	8e-32	100%	AB817687.1
Musa basjoo tRNA-Leu (trnL(UAA)) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF(GAA)) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	FJ428188.2
Musella lasiocarpa isolate Kress-GH01-210 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	FJ621287.1
Musa mannii tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	FJ621285.1
Musa nagensium tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	FJ621284.1
Musa rubra tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	FJ621277.1
Musa splendida tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	FJ621282.1
Musa balbisiana isolate Bangladesh tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	FJ621280.1
Musa balbisiana isolate Yunnan tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	FJ621279.1
Musa ornata tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	FJ621278.1
Musa itinerans tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	FJ621276.1
Musa formosana tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	FJ621275.1
Musa sanguinea tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	FJ621274.1
Musa campestris tRNA-Leu (trnL) gene,						

partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	FJ621273.1
Musa beccarii tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	FJ621272.1
Musa basjoo tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	FJ621270.1
Musa maclayi tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	FJ621269.1
Musa laterita tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	FJ621268.1
Musa salaccensis tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	FJ621266.1
Musa velutina tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	FJ621264.1
Musa rosea tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	FJ621263.1
Angiosperm environmental sample chloroplast partial tRNA-Leu gene, intron region, isolated from Cryptorhynchinae sp.34 BMNH:796424	145	145	100%	8e-32	100%	FN398125.1
Musa beccarii tRNA-Leu gene, partial sequence; tRNA-Leu(UAA)-tRNA-Phe(GAA) intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	145	145	100%	8e-32	100%	AF431635.1
Musa gracilis isolate SS&JS 128 Sri Nara QSBG tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	KT257587.1
Musa textilis tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	235	100%	3e-30	100%	FJ621281.1
Musa borneensis tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ621265.1
Musa violascens tRNA-Leu (trnL(UAA)) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF(GAA)) gene, partial sequence; chloroplast	140	140	100%	3e-30	99%	FJ428195.1
Musa rosea plastid partial tRNA-Leu gene and trnL-trnF IGS, specimen voucher Asmussen 101 (CP)	140	140	100%	3e-30	99%	AM113703.1
Musella lasiocarpa isolate Yunnan tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	138	138	100%	1e-29	99%	FJ621286.1
Thaumatococcus daniellii plastid, partial genome	136	136	100%	4e-29	98%	KF601575.1
Heliconia collinsiana plastid, complete genome	136	136	100%	4e-29	98%	JX088660.1
Hypselodelphys hirsuta voucher A.Ley 269 (WAG) tRNA-Leu (trnL) gene, partial	136	136	100%	4e-29	98%	JN413110.1

sequence; chloroplast						
Heliconia stricta tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	FJ621299.1
Megaphrynium trichogynum voucher Ley 114 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	136	136	100%	4e-29	98%	EU647828.1
Thaumatococcus sp. Ley 179 voucher Ley 179 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	136	136	100%	4e-29	98%	EU647827.1
Thaumatococcus daniellii voucher Ley 96 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	136	136	100%	4e-29	98%	EU647826.1
Hypselodelphys sp. Ley 125 voucher Ley 125 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	136	136	100%	4e-29	98%	EU647825.1
Hypselodelphys scandens voucher Ley 160 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	136	136	100%	4e-29	98%	EU647824.1
Trachyphrynium braunianum voucher Ley 171 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	136	136	100%	4e-29	98%	EU647823.1
Hypselodelphys violacea voucher Ley 28 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	136	136	100%	4e-29	98%	EU647821.1
Hypselodelphys hirsuta voucher Ley 156 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	136	136	100%	4e-29	98%	EU647820.1
Hypselodelphys poggeana voucher Ley 168 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	136	136	100%	4e-29	98%	EU647819.1
Heliconia solomonensis tRNA-Leu gene, partial sequence; tRNA-Leu(UAA)-tRNA-Phe(GAA) intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	AF431634.1
Heliconia rostrata tRNA-Leu gene, partial sequence; tRNA-Leu(UAA)-tRNA-Phe(GAA) intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	AF431633.1
Hypselodelphys velutina voucher Jongkind 4839 (WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	132	132	100%	5e-28	96%	EU647818.1
Syagrus coronata chloroplast, complete genome	131	131	100%	2e-27	96%	KT896548.1
Ensete superbum isolate SS&JS 242 Pha Pli Lueang Vachiralongkorn Dam tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	131	131	100%	2e-27	94%	KT257601.1

Ensete glaucum isolate SS&JS 229 Nuan Sae-Lae tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	131	131	100%	2e-27	94%	KT257600.1
Musa coccinea isolate SS&JS 223 Rattakatthali tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	131	131	100%	2e-27	94%	KT257586.1
Costus zingiberoides voucher BTM86-00-01 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	KJ011345.1
Costus talbotii voucher 2003-0109009 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	KJ011343.1
Costus aff. tappenbeckianus SMS-2014 voucher 2005-0100002 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	KJ011342.1
Costus aff. tappenbeckianus SMS-2014 voucher 2005-0100001 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	KJ011341.1
Costus scaber voucher R2253 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	KJ011339.1
Costus ricus voucher R2970 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	KJ011338.1
Costus quasi-appendiculatus voucher CSpecht 99-233 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	KJ011337.1
Costus aff. phyllocephalus SMS-2014 voucher BB870057 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	KJ011334.1
Costus osae voucher M9501 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	KJ011333.1
Costus maboumiensis voucher M10227 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	KJ011330.1
Costus lucanusianus voucher Breteler5297 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	KJ011329.1
Costus aff. ligularis SMS-2014 voucher 2005-0100003 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	KJ011324.1
Costus aff. ligularis SMS-2014 voucher 1998-0923003 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	KJ011323.1
Costus leucanthus voucher 1996-1105001						

tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	KJ011322.1
Costus lateriflorus voucher M10331 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	KJ011321.1
Costus dubius voucher M10206 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	KJ011314.1
Costus barbatus voucher CSpecht 01-256 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	KJ011308.1
Costus vinosus voucher M9568 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	KJ011344.1
Costus erythrophyllus voucher R2847 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	125	125	100%	7e-26	94%	KJ011315.1

Alignments

Musa yunnanensis isolate SS&JS 473 Montharop Khun Nan tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KT257604.1|** Length: 1002 Number of Matches: 1
Range 1: 102 to 181

Score	Expect	Identities	Gaps	Strand	Frame
145 bits(160)	8e-32()	80/80(100%)	0/80(0%)	Plus/Plus	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCTTATTTTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  102  GGCAATCCTGAGCCAAATCCTTATTTTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  161

Query  61   AAGGATAGGTGCAGAGACTC  80
            ||||||||||||||||||||
Sbjct  162  AAGGATAGGTGCAGAGACTC  181
```

Musella lasiocarpa isolate SS&JS 231 Dararassami tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KT257602.1|** Length: 902 Number of Matches: 1
Range 1: 82 to 161

Score	Expect	Identities	Gaps	Strand	Frame
145 bits(160)	8e-32()	80/80(100%)	0/80(0%)	Plus/Plus	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCTTATTTTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  82   GGCAATCCTGAGCCAAATCCTTATTTTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  141

Query  61   AAGGATAGGTGCAGAGACTC  80
            ||||||||||||||||||||
Sbjct  142  AAGGATAGGTGCAGAGACTC  161
```

Musa yunnanensis isolate SS&JS 444 Yunnan Namtok Pa Way tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KT257599.1|** Length: 971 Number of Matches: 1
Range 1: 102 to 181

Score	Expect	Identities	Gaps	Strand	Frame

145 bits(160)	8e-32()	80/80(100%)	0/80(0%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTATTTTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  102  GGCAATCCTGAGCCAAATCCTTATTTTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  161

Query  61   AAGGATAGGTGCAGAGACTC  80
            ||||||||||||||||||||
Sbjct  162  AAGGATAGGTGCAGAGACTC  181
```

Musa yunnanensis isolate SS&JS 349 Yunnan Inthanon tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KT257598.1|** Length: 971 Number of Matches: 1
Range 1: 102 to 181

Score	Expect	Identities	Gaps	Strand	Frame
145 bits(160)	8e-32()	80/80(100%)	0/80(0%)	Plus/Plus	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCTTATTTTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  102  GGCAATCCTGAGCCAAATCCTTATTTTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  161

Query  61   AAGGATAGGTGCAGAGACTC  80
            ||||||||||||||||||||
Sbjct  162  AAGGATAGGTGCAGAGACTC  181
```

Musa yunnanensis isolate SS&JS 235 Yunnan QSBG tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KT257597.1|** Length: 971 Number of Matches: 1
Range 1: 102 to 181

Score	Expect	Identities	Gaps	Strand	Frame
145 bits(160)	8e-32()	80/80(100%)	0/80(0%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTATTTTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  102  GGCAATCCTGAGCCAAATCCTTATTTTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  161

Query  61   AAGGATAGGTGCAGAGACTC  80
            ||||||||||||||||||||
Sbjct  162  AAGGATAGGTGCAGAGACTC  181
```

BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BU9R5U7F015**

Formatting options

Download

Blast report description

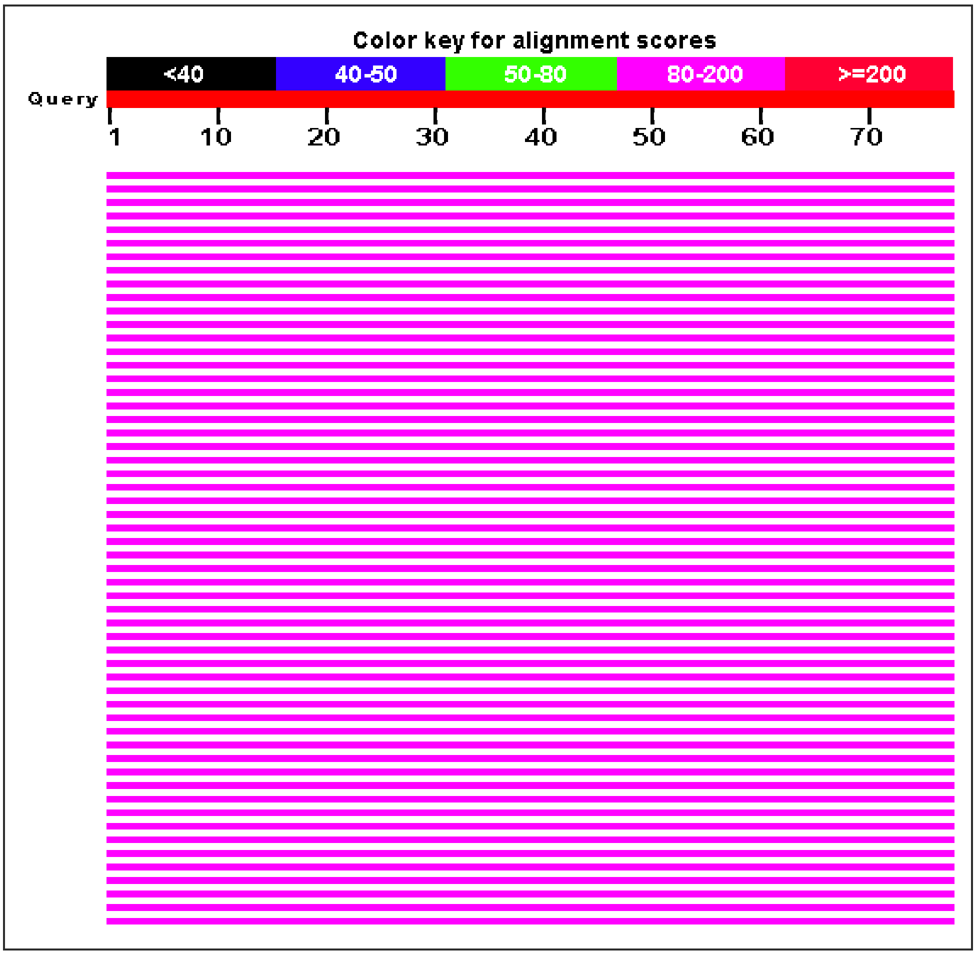
YK072A41C1_TRNL1_C1,5-6,8

RID BU9R5U7F015 (Expires on 02-13 07:27 am)

Query ID	lcl|Query_216967	**Database Name**	nr
Description	c1	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	78		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Pinus sibirica chloroplast, complete genome	132	132	100%	5e-28	97%	KT723438.2
Pinus tabuliformis voucher PTAB20150818V5 chloroplast, complete genome	132	132	100%	5e-28	97%	KT740995.1
Pinus bungeana voucher Pbungeana2015 chloroplast, complete genome	132	132	100%	5e-28	97%	KR873010.1
Pinus taiwanensis voucher Ptaiwanensis14 chloroplast, complete genome	132	132	100%	5e-28	97%	KP771703.1
Pinus strobus plastid, complete genome	132	132	100%	5e-28	97%	KP099650.1
Tracheophyta environmental sample clone C6 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KJ015985.1
Tracheophyta environmental sample clone C5 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KJ015984.1
Tracheophyta environmental sample clone C4 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KJ015983.1
Tracheophyta environmental sample clone C3 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KJ015982.1
Tracheophyta environmental sample clone C2 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KJ015981.1
Tracheophyta environmental sample clone C1 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KJ015980.1
Tracheophyta environmental sample clone S5-3 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616492.1
Tracheophyta environmental sample clone S5-2 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616491.1
Tracheophyta environmental sample clone S5-1 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616490.1
Tracheophyta environmental sample clone S4-11 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616487.1
Tracheophyta environmental sample clone S4-10 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616486.1
Tracheophyta environmental sample clone S2-7 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616474.1
Tracheophyta environmental sample clone S2-6 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616473.1
Tracheophyta environmental sample clone S2-2 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616469.1
Tracheophyta environmental sample clone S2-1 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616468.1
Pinus luchuensis chloroplast trnL gene, intron, partial sequence, isolate: OGA0449	132	132	100%	5e-28	97%	AB817641.1
Pinus luchuensis chloroplast trnL gene, intron, partial sequence, isolate:	132	132	100%	5e-28	97%	AB817461.1

OGA0239						
Pinus taeda chloroplast, complete genome	132	132	100%	5e-28	97%	KC427273.1
Pinus massoniana chloroplast, complete genome	132	132	100%	5e-28	97%	KC427272.1
Pinus thunbergii trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504692.1
Pinus bungeana trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504691.1
Pinus koraiensis trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504690.1
Pinus densiflora trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504689.1
Pinus x rigitaeda trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504688.1
Pinus sylvestris trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504686.1
Pinus rigida trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504685.1
Pinus densiflora cultivar Multicaulis trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504684.1
Pinus sylvestris voucher Psy01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739418.1
Pinus peuce voucher Ppe01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739417.1
Pinus halepensis voucher Pha01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739416.1
Pinus brutia voucher Pb01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739415.1
Pinus brutia var. eldarica voucher Pe01.120311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739414.1
Pinus nigra voucher Pn01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739413.1
Pinus pinea voucher Ppi01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739412.1
Pinus heldreichii voucher Phe01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739411.1
Pinus arizonica var. cooperi isolate COOP01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854216.1
Pinus coulteri isolate COUL03 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854215.1
Pinus cubensis isolate CUBE01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854214.1
Pinus culminicola isolate CULM01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854213.1
Pinus fenzeliana var. dabeshanensis isolate DABE01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854212.1
Pinus dalatensis isolate DALA03 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854211.1
Pinus densiflora isolate DENS02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854210.1
Pinus densata isolate DENT01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854209.1
Pinus devoniana isolate DEVO02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854208.1
Pinus discolor isolate DISC02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854207.1

Pinus hartwegii isolate DONN02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854206.1
Pinus douglasiana isolate DOUG01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854205.1
Pinus echinata isolate ECHI01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854204.1
Pinus edulis isolate EDUL08 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854203.1
Pinus elliottii isolate ELLI01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854202.1
Pinus engelmannii isolate ENGE02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854201.1
Pinus fragilissima isolate FRAG01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854200.1
Pinus glabra isolate GLAB01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854199.1
Pinus greggii isolate GREG02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854198.1
Pinus halepensis isolate HALE03 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854197.1
Pinus hartwegii isolate HART07 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854196.1
Pinus heldreichii isolate HELD07 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854195.1
Pinus hwangshanensis isolate HWAN01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854194.1
Pinus jeffreyi isolate JEFF04 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854193.1
Pinus johannis chloroplast, partial genome	132	132	100%	5e-28	97%	JN854192.1
Pinus kesiya isolate KESI11 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854191.1
Pinus latteri isolate LATT02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854190.1
Pinus pringlei isolate PRIN02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854189.1
Pinus lawsonii isolate LAWS02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854188.1
Pinus leiophylla isolate LEIO03 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854187.1
Pinus lumholtzii isolate LUMH07 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854186.1
Pinus massoniana isolate MASS02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854185.1
Pinus maximartinezii isolate MAXZ01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854184.1
Pinus montezumae isolate MONZ01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854183.1
Pinus morrisonicola isolate MORR01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854182.1
Pinus mugo isolate MUGO01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854181.1
Pinus muricata isolate MURI01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854180.1
Pinus nigra isolate NIGR20 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854179.1
Pinus pseudostrobus var. apulcensis isolate OAXA02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854178.1
Pinus occidentalis isolate OCCI02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854177.1
Pinus palustris isolate PALU02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854176.1
Pinus patula isolate PATU01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854175.1
Pinus pinceana isolate PINC13 chloroplast,						

partial genome	132	132	100%	5e-28	97%	JN854174.1
Pinus pinea isolate PINE03 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854173.1
Pinus ponderosa var. benthamiana isolate POND21 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854172.1
Pinus ponderosa var. scopulorum isolate POND59 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854171.1
Pinus pseudostrobus isolate PSEU03 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854169.1
Pinus pumila isolate PUMI07 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854168.1
Pinus pungens isolate PUNG01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854167.1
Pinus quadrifolia isolate QUAD02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854166.1
Pinus radiata isolate RADI01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854165.1
Pinus remota isolate REMO05 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854164.1
Pinus rigida isolate RIGI01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854163.1
Pinus roxburghii isolate ROXB04 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854162.1
Pinus sabiniana isolate SABI04 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854161.1
Pinus serotina isolate SERO01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854160.1
Pinus strobiformis isolate STRF17 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854159.1
Pinus sylvestris isolate SYLV02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854158.1
Pinus taiwanensis isolate TAIW04 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854157.1
Pinus tropicalis isolate TROP02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854156.1

Alignments

Pinus sibirica chloroplast, complete genome

Sequence ID: **gb|KT723438.2|** Length: 116635 Number of Matches: 1

Range 1: 66690 to 66767

Score	Expect	Identities	Gaps	Strand	Frame
132 bits(146)	5e-28()	76/78(97%)	0/78(0%)	Plus/Minus	

Features:

```
Query  1      GGCAATCCTGAGCCAAATCCGGTTCATGAAGACAATGTTTCTTCTCCTAAGATAGGAAGA  60
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  66767  GGTAATCCTGAGCCAAATCCGGTTCATGAAGACAATGTTTCTTCTCCTAAGATAGGAAGG  66708

Query  61     GGATAGGTGCAGAGACTC  78
              ||||||||||||||||||
Sbjct  66707  GGATAGGTGCAGAGACTC  66690
```

Pinus tabuliformis voucher PTAB20150818V5 chloroplast, complete genome

Sequence ID: **gb|KT740995.1|** Length: 119646 Number of Matches: 1

Range 1: 68565 to 68642

Score	Expect	Identities	Gaps	Strand	Frame
132 bits(146)	5e-28()	76/78(97%)	0/78(0%)	Plus/Minus	

Features:

```
Query  1      GGCAATCCTGAGCCAAATCCGGTTCATGAAGACAATGTTTCTTCTCCTAAGATAGGAAGA  60
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  68642  GGTAATCCTGAGCCAAATCCGGTTCATGAAGACAATGTTTCTTCTCCTAAGATAGGAAGG  68583

Query  61     GGATAGGTGCAGAGACTC  78
```

```
              ||||||||||||||||||
Sbjct  68582  GGATAGGTGCAGAGACTC  68565
```

Pinus bungeana voucher Pbungeana2015 chloroplast, complete genome
Sequence ID: **gb|KR873010.1|** Length: 117861 Number of Matches: 1
Range 1: 68182 to 68259

Score	Expect	Identities	Gaps	Strand	Frame
132 bits(146)	5e-28()	76/78(97%)	0/78(0%)	Plus/Minus	

Features:

```
Query  1      GGCAATCCTGAGCCAAATCCGGTTCATGAAGACAATGTTTCTTCTCCTAAGATAGGAAGA  60
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  68259  GGTAATCCTGAGCCAAATCCGGTTCATGAAGACAATGTTTCTTCTCCTAAGATAGGAAGG  68200

Query  61     GGATAGGTGCAGAGACTC  78
              ||||||||||||||||||
Sbjct  68199  GGATAGGTGCAGAGACTC  68182
```

Pinus taiwanensis voucher Ptaiwanensis14 chloroplast, complete genome
Sequence ID: **gb|KP771703.1|** Length: 119741 Number of Matches: 1
Range 1: 68622 to 68699

Score	Expect	Identities	Gaps	Strand	Frame
132 bits(146)	5e-28()	76/78(97%)	0/78(0%)	Plus/Minus	

Features:

```
Query  1      GGCAATCCTGAGCCAAATCCGGTTCATGAAGACAATGTTTCTTCTCCTAAGATAGGAAGA  60
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  68699  GGTAATCCTGAGCCAAATCCGGTTCATGAAGACAATGTTTCTTCTCCTAAGATAGGAAGG  68640

Query  61     GGATAGGTGCAGAGACTC  78
              ||||||||||||||||||
Sbjct  68639  GGATAGGTGCAGAGACTC  68622
```

Pinus strobus plastid, complete genome
Sequence ID: **gb|KP099650.1|** Length: 115576 Number of Matches: 1
Range 1: 65526 to 65603

Score	Expect	Identities	Gaps	Strand	Frame
132 bits(146)	5e-28()	76/78(97%)	0/78(0%)	Plus/Minus	

Features:

```
Query  1      GGCAATCCTGAGCCAAATCCGGTTCATGAAGACAATGTTTCTTCTCCTAAGATAGGAAGA  60
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  65603  GGTAATCCTGAGCCAAATCCGGTTCATGAAGACAATGTTTCTTCTCCTAAGATAGGAAGG  65544

Query  61     GGATAGGTGCAGAGACTC  78
              ||||||||||||||||||
Sbjct  65543  GGATAGGTGCAGAGACTC  65526
```

BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BTRGAZ5J015**

Formatting options

Download

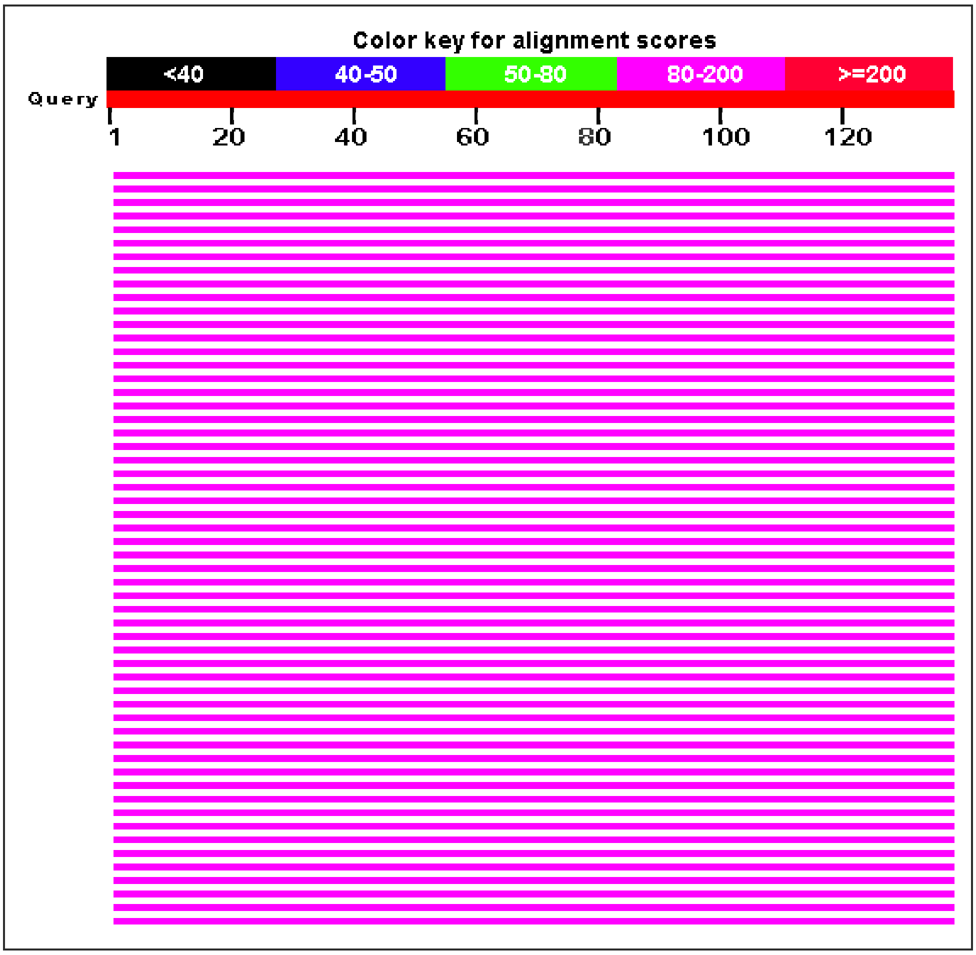
Blast report description

YK072A41C1_TRNL1_C2

RID	BTRGAZ5J015 (Expires on 02-13 02:16 am)		
Query ID	lcl|Query_233831	**Database Name**	nr
Description	YK072A41C1_TRNL1_C2	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	137		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Phaenosperma globosum voucher BH:J.I. Davis 779 plastid, complete genome	154	154	99%	3e-34	85%	KM974745.1
Diarrhena obovata voucher BH:J.I. Davis 756 plastid, complete genome	154	154	99%	3e-34	85%	KM974739.1
Sesleria autumnalis partial rbcL gene for RuBisCo, specimen voucher MIB:ZPL:03100	154	154	99%	3e-34	85%	HE963664.1
Neomolinia japonica ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	154	154	99%	3e-34	85%	HQ600431.1
Neomolinia fauriei ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	154	154	99%	3e-34	85%	HQ600429.1
Sesleria caerulea isolate NMW836 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	154	154	99%	3e-34	85%	JN891400.1
Sesleria caerulea plastid partial rbcL gene for RuBisCO large subunit, specimen voucher MIB Zpl:02017	154	154	99%	3e-34	85%	FR865131.1
Sesleria caerulea voucher Hodkinson45 TCD ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	154	154	99%	3e-34	85%	EF125156.1
Phaenosperma globosa chloroplast partial rbcL gene for ribulose bisphosphate carboxylase large chain	154	154	99%	3e-34	85%	AJ784824.1
Diarrhena obovata ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gene, partial cds; chloroplast	154	154	99%	3e-34	85%	AY622890.1
Festuca bromoides chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV1607	149	149	99%	1e-32	85%	LN908031.1
Festuca camusiana chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV617	149	149	99%	1e-32	85%	LN907946.1
Poaceae sp. SERC-1076419263 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KP402760.1
Poaceae sp. SERC-1076419267 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KP402694.1
Panicum virgatum voucher SERC-1076419297 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KP402686.1
Melica altissima voucher Chase 22006 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KC123375.1
Festuca hyperborea voucher ZA-PL34 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KT960726.1
Festuca rubra voucher ZA-PL33 ribulose-1,5-bisphosphate carboxylase/oxygenase	149	149	99%	1e-32	85%	KT960718.1

large subunit (rbcL) gene, partial cds; chloroplast						
Festuca rubra voucher ZA-PL07 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KT960690.1
Festuca rubra voucher ZA-PL06 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KT960652.1
Festuca rubra voucher ZA-PL31 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KT960647.1
Festuca baffinensis voucher ZA-PL37 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KT960606.1
Festuca brachyphylla voucher ZA2012-4969 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KT960595.1
Festuca rubra voucher ZA-PL08 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KT960585.1
Pleuropogon sabinei voucher ZA2012-5062 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KT960577.1
Festuca brachyphylla voucher ZA2012-3932 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KT960576.1
Festuca brachyphylla voucher ZA2012-4970 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KT960548.1
Festuca baffinensis voucher ZA-PL36 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KT960504.1
Festuca hyperborea voucher ZA-PL35 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KT960498.1
Festuca rubra voucher ZA-PL32 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KT960444.1
Festuca vivipara voucher ZA2012-5144 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KT960433.1
Pleuropogon sabinei voucher ZA2012-5064 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KT960420.1
Festuca vivipara voucher ZA2012-5145 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KT960411.1
Pleuropogon sabinei voucher ZA2012-5063 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KT960388.1
Festuca vivipara voucher ZA2012-5146 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KT960383.1
Festuca baffinensis voucher ZA-PL38						

ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KT960381.1
Poaceae sp. SNP_13_0362 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KP644019.1
Lolium sp. KK-0011 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KP149535.1
Protea scolopendriifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KP110421.1
Festuca scabra ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KP110319.1
Festuca arundinacea voucher CAN:Saarela 331 plastid, complete genome	149	149	99%	1e-32	85%	KM974751.1
Melica subulata voucher CAN:Saarela 836 plastid, complete genome	149	149	99%	1e-32	85%	KM974743.1
Melica mutica voucher US:W.J. Kress & M. Butts 04-7461 plastid, complete genome	149	149	99%	1e-32	85%	KM974742.1
Helictochloa hookeri voucher CAN:Saarela 18359 plastid, complete genome	149	149	99%	1e-32	85%	KM974734.1
Lolium temulentum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KM538824.1
Vulpia octoflora ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ773986.1
Melica uniflora ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid	149	149	99%	1e-32	85%	KM360877.1
Schizachne purpurascens voucher WAB_0132469024 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ593680.1
Schizachne purpurascens voucher WAB_0132469015 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ593679.1
Festuca subverticillata voucher WAB_0132469186 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ593413.1
Melica uniflora voucher G00199178 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ204376.1
Lolium perenne voucher G00199055 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ204368.1
Lolium multiflorum voucher G00199131 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ204367.1
Festuca arundinacea voucher G00199163 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ204343.1
Festuca armoricana isolate BF303 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KF997423.1

Festuca longifolia isolate BF301 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KF997420.1
Vulpia unilateralis isolate BF336 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KF997332.1
Schizachne purpurascens voucher TJD-203 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ841556.1
Festuca arundinacea voucher TJD-592 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ841555.1
Festuca subverticillata voucher TJD-316 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ841326.1
Festuca subverticillata voucher TJD-204 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ841325.1
Festuca rubra subsp. rubra voucher TJD-159 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ841324.1
Lolium perenne voucher Batianoff 2010513 (MEL 2132634A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ599220.1
Lolium multiflorum voucher Jackson s.n. (MEL 2035113A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ599219.1
Lolium loliaceum voucher Whinray 829 (MEL 0534323A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ599218.1
Festuca rubra voucher Reid 2361 (MEL 2323513A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ599217.1
Festuca pratensis voucher Lepschi 3922 (MEL 2274993A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ599216.1
Festuca plebeia voucher Morris 86664 (MEL 2131516A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ599215.1
Festuca muelleri voucher Walsh 6797 (MEL 2314310A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ599214.1
Festuca asperula voucher Walsh 6242 (MEL 2275915A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ599213.1
Festuca arundinacea voucher McKenzie 07/11 (MEL 2331054A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ599212.1
Festuca arundinacea voucher Leeman s.n. (MEL 2105597A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ599211.1
Dryopoa dives voucher Cochrane 716 (MEL 2062412A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ599210.1

Lolium temulentum f. arvense voucher Gray 1614 (HO 537164) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ599185.1
Dryopoa dives voucher Birch 476 (MEL 2355932A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ599175.1
Hainardia cylindrica voucher Reid 2754 (MEL 2330507A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ599172.1
Parapholis strigosa voucher Stajsic 975 (MEL 2024132A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ599171.1
Psilurus incurvus voucher Adair 2157 (MEL 1592359A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ599169.1
Lamarckia aurea voucher Stajsic 5306 (MEL 2339294A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ599168.1
Lolium canariense bio-material JBCVCDNABanK3883.1 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ595696.1
Festuca agustinii bio-material JBCVCDNABanK1346 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ595658.1
Festuca agustinii bio-material JBCVCDNABanK1321 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ595657.1
Festuca agustinii bio-material JBCVCDNABanK5217.2 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ595656.1
Festuca agustinii bio-material JBCVCDNABanK3882.1 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KJ595653.1
Festuca idahoensis isolate DNAS-62-57853 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds	149	149	99%	1e-32	85%	KJ756344.1
Helictotrichon versicolor ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KF602198.1
Festuca violacea ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KF602187.1
Festuca quadriflora ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KF602176.1
Agrostis stolonifera ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KF602123.1
Anisopogon avenaceus voucher iAD54_aven861 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KC129544.1
Pleuropogon sabinei voucher Gillespie_10231_CAN ribulose-1,5-bisphosphate carboxylase/oxygenase large	149	149	99%	1e-32	85%	KC483465.1

subunit (rbcL) gene, partial cds; chloroplast						
Pleuropogon sabinei voucher Elven_2854-99_CAN ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KC483463.1
Festuca viviparoidea subsp. viviparoidea voucher Consaul_4045_CAN ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KC482922.1
Festuca rubra subsp. arctica voucher Gillespie_9913_CAN ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KC482916.1
Festuca hyperborea voucher Gillespie_6987a ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KC482894.1
Festuca brachyphylla subsp. brachyphylla voucher Aiken_99-190_CAN ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KC482879.1
Festuca brachyphylla subsp. brachyphylla voucher Saarela_1468_CAN ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KC482877.1
Festuca brachyphylla subsp. brachyphylla voucher Boles_RB00-32 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KC482876.1
Festuca brachyphylla subsp. brachyphylla voucher Gillespie_9062 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KC482875.1
Festuca baffinensis voucher Gillespie_6920 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	149	149	99%	1e-32	85%	KC482867.1

Alignments

Phaenosperma globosum voucher BH:J.I. Davis 779 plastid, complete genome
Sequence ID: **gb|KM974745.1|** Length: 137897 Number of Matches: 1
Range 1: 55814 to 55950

Score	Expect	Identities	Gaps	Strand	Frame
154 bits(170)	3e-34()	117/137(85%)	1/137(0%)	Plus/Minus	

Features:

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Query  2      GTCTTTTGAAGCGATCCCGACTGGTC-GTCGGTCAGTCCGAAAAGTTGTCCTTGTTACAG  60
              ||| |||| | |||||  |||||||  |||  ||||||| || |||||||| |||  |||
Sbjct  55950  GTCCTTTGTAACGATCAAGACTGGTAAGTCCATCAGTCCAAACAGTTGTCCATGTACCAG  55891

Query  61     TAGAAGATTCGGCAGCTGCTGTGGCCCCTGCTTCTTCGTACGGAACACCAGGCTGAGGAG  120
              ||||||||||||||||| |||  |||||||||||||||  |||||| |||||||||||||
Sbjct  55890  TAGAAGATTCGGCAGCTACTGCAGCCCCTGCTTCTTCGGGCGGAACCCCAGGCTGAGGAG  55831

Query  121    TTACTCGGAATGCTGCC  137
              |||||||||||||||||
Sbjct  55830  TTACTCGGAATGCTGCC  55814
```

Diarrhena obovata voucher BH:J.I. Davis 756 plastid, complete genome
Sequence ID: **gb|KM974739.1|** Length: 137421 Number of Matches: 1
Range 1: 55036 to 55172

Score	Expect	Identities	Gaps	Strand	Frame

154 bits(170)	3e-34()	117/137(85%)	1/137(0%)	Plus/Minus	

Features:

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Query  2      GTCTTTTGAAGCGATCCCGACTGGTC-GTCGGTCAGTCCGAAAAGTTGTCCTTGTTACAG  60
              ||| |||| | |||||  |||||||  |||  ||||||| || |||||||| |||  |||
Sbjct  55172  GTCCTTTGTAACGATCAAGACTGGTAAGTCCATCAGTCCAAACAGTTGTCCATGTACCAG  55113

Query  61     TAGAAGATTCGGCAGCTGCTGTGGCCCCTGCTTCTTCGTACGGAACACCAGGCTGAGGAG  120
              ||||||||||||||||| |||  |||||||||||||||  |||||| |||||||||||||
Sbjct  55112  TAGAAGATTCGGCAGCTACTGCAGCCCCTGCTTCTTCGGGCGGAACCCCAGGCTGAGGAG  55053

Query  121    TTACTCGGAATGCTGCC  137
              |||||||||||||||||
Sbjct  55052  TTACTCGGAATGCTGCC  55036
```

Sesleria autumnalis partial rbcL gene for RuBisCo, specimen voucher MIB:ZPL:03100
Sequence ID: **emb|HE963664.1|** Length: 583 Number of Matches: 1
Range 1: 41 to 177

Score	**Expect**	**Identities**	**Gaps**	**Strand**	**Frame**
154 bits(170)	3e-34()	117/137(85%)	1/137(0%)	Plus/Minus	

Features:

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Query  2    GTCTTTTGAAGCGATCCCGACTGGTC-GTCGGTCAGTCCGAAAAGTTGTCCTTGTTACAG  60
            ||| |||| | |||||| |||||||  |||  ||||||| || |||||||| |||  |||
Sbjct  177  GTCCTTTGTAACGATCCAGACTGGTAAGTCCATCAGTCCAAACAGTTGTCCATGTACCAG  118

Query  61   TAGAAGATTCGGCAGCTGCTGTGGCCCCTGCTTCTTCGTACGGAACACCAGGCTGAGGAG  120
            ||||||||||||||||| |||  ||||||||||||||   |||||| |||||||||||||
Sbjct  117  TAGAAGATTCGGCAGCTACTGCAGCCCCTGCTTCTTCCGGCGGAACCCCAGGCTGAGGAG  58

Query  121  TTACTCGGAATGCTGCC  137
            |||||||||||||||||
Sbjct  57   TTACTCGGAATGCTGCC  41
```

Neomolinia japonica ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast
Sequence ID: **gb|HQ600431.1|** Length: 751 Number of Matches: 1

See 1 more title(s)
Range 1: 113 to 249

Score	**Expect**	**Identities**	**Gaps**	**Strand**	**Frame**
154 bits(170)	3e-34()	117/137(85%)	1/137(0%)	Plus/Minus	

Features:

```
Query  2    GTCTTTTGAAGCGATCCCGACTGGTC-GTCGGTCAGTCCGAAAAGTTGTCCTTGTTACAG  60
            ||| |||| | |||||  |||||||  |||  ||||||| || |||||||| |||  |||
Sbjct  249  GTCCTTTGTAACGATCAAGACTGGTAAGTCCATCAGTCCAAACAGTTGTCCATGTACCAG  190

Query  61   TAGAAGATTCGGCAGCTGCTGTGGCCCCTGCTTCTTCGTACGGAACACCAGGCTGAGGAG  120
            ||||||||||||||||| |||  |||||||||||||||  |||||| |||||||||||||
Sbjct  189  TAGAAGATTCGGCAGCTACTGCAGCCCCTGCTTCTTCGGGCGGAACCCCAGGCTGAGGAG  130

Query  121  TTACTCGGAATGCTGCC  137
            |||||||||||||||||
Sbjct  129  TTACTCGGAATGCTGCC  113
```

Neomolinia fauriei ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast
Sequence ID: **gb|HQ600429.1|** Length: 751 Number of Matches: 1
Range 1: 113 to 249

Score	**Expect**	**Identities**	**Gaps**	**Strand**	**Frame**
154 bits(170)	3e-34()	117/137(85%)	1/137(0%)	Plus/Minus	

Features:

```
Query  2    GTCTTTTGAAGCGATCCCGACTGGTC-GTCGGTCAGTCCGAAAAGTTGTCCTTGTTACAG  60
            ||| |||| | |||||  |||||||  |||  ||||||| || |||||||| |||  |||
Sbjct  249  GTCCTTTGTAACGATCAAGACTGGTAAGTCCATCAGTCCAAACAGTTGTCCATGTACCAG  190

Query  61   TAGAAGATTCGGCAGCTGCTGTGGCCCCTGCTTCTTCGTACGGAACACCAGGCTGAGGAG  120
            ||||||||||||||||| |||  |||||||||||||||  |||||| |||||||||||||
Sbjct  189  TAGAAGATTCGGCAGCTACTGCAGCCCCTGCTTCTTCGGGCGGAACCCCAGGCTGAGGAG  130

Query  121  TTACTCGGAATGCTGCC  137
            |||||||||||||||||
Sbjct  129  TTACTCGGAATGCTGCC  113
```

BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BTRXW2Y5015**
Formatting options
Download
Blast report description

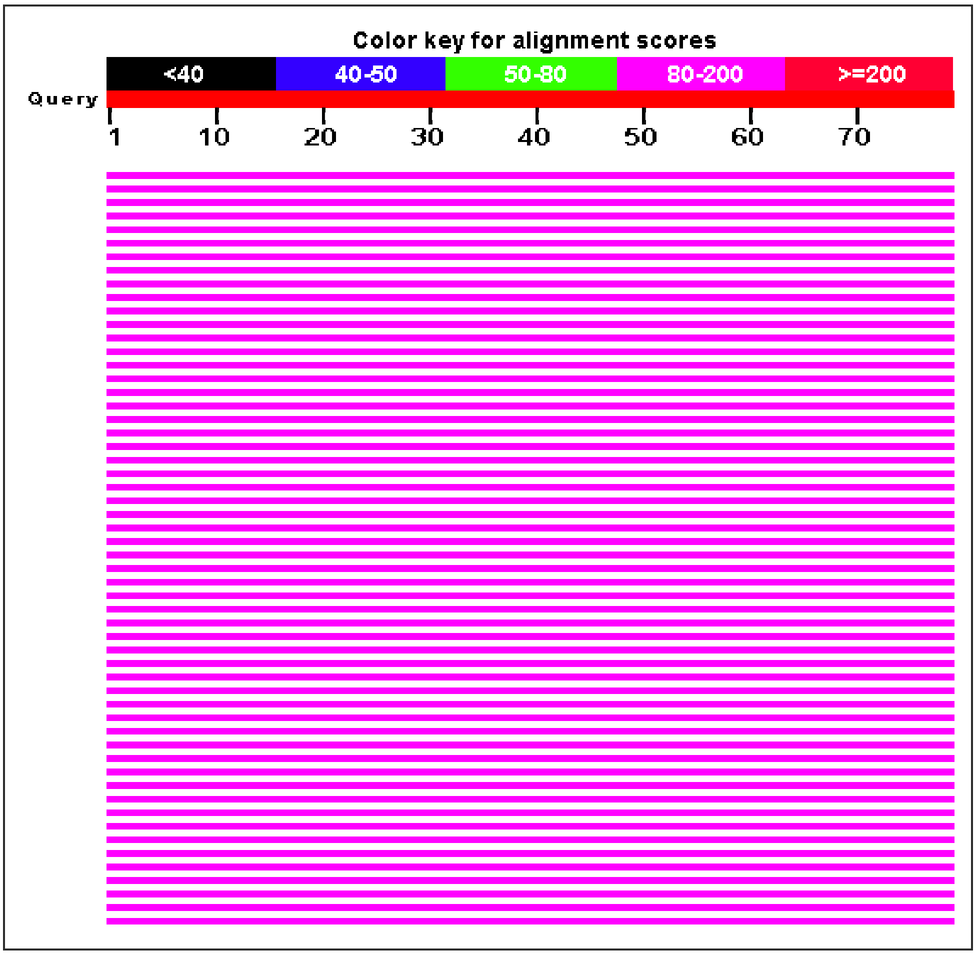
YK072A41C1_TRNL1_C4

RID BTRXW2Y5015 (Expires on 02-13 02:23 am)

Query ID	lcl|Query_108997	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	79		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Pinus sibirica chloroplast, complete genome	125	125	100%	7e-26	96%	KT723438.2
Pinus tabuliformis voucher PTAB20150818V5 chloroplast, complete genome	125	125	100%	7e-26	96%	KT740995.1
Pinus bungeana voucher Pbungeana2015 chloroplast, complete genome	125	125	100%	7e-26	96%	KR873010.1
Pinus taiwanensis voucher Ptaiwanensis14 chloroplast, complete genome	125	125	100%	7e-26	96%	KP771703.1
Pinus strobus plastid, complete genome	125	125	100%	7e-26	96%	KP099650.1
Tracheophyta environmental sample clone C6 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	125	125	100%	7e-26	96%	KJ015985.1
Tracheophyta environmental sample clone C5 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	125	125	100%	7e-26	96%	KJ015984.1
Tracheophyta environmental sample clone C4 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	125	125	100%	7e-26	96%	KJ015983.1
Tracheophyta environmental sample clone C3 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	125	125	100%	7e-26	96%	KJ015982.1
Tracheophyta environmental sample clone C2 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	125	125	100%	7e-26	96%	KJ015981.1
Tracheophyta environmental sample clone C1 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	125	125	100%	7e-26	96%	KJ015980.1
Tracheophyta environmental sample clone S5-3 tRNA-Leu (trnL) gene, partial sequence; chloroplast	125	125	100%	7e-26	96%	KF616492.1
Tracheophyta environmental sample clone S5-2 tRNA-Leu (trnL) gene, partial sequence; chloroplast	125	125	100%	7e-26	96%	KF616491.1
Tracheophyta environmental sample clone S5-1 tRNA-Leu (trnL) gene, partial sequence; chloroplast	125	125	100%	7e-26	96%	KF616490.1
Tracheophyta environmental sample clone S4-11 tRNA-Leu (trnL) gene, partial sequence; chloroplast	125	125	100%	7e-26	96%	KF616487.1
Tracheophyta environmental sample clone S4-10 tRNA-Leu (trnL) gene, partial sequence; chloroplast	125	125	100%	7e-26	96%	KF616486.1
Tracheophyta environmental sample clone S2-7 tRNA-Leu (trnL) gene, partial sequence; chloroplast	125	125	100%	7e-26	96%	KF616474.1
Tracheophyta environmental sample clone S2-6 tRNA-Leu (trnL) gene, partial sequence; chloroplast	125	125	100%	7e-26	96%	KF616473.1
Tracheophyta environmental sample clone S2-2 tRNA-Leu (trnL) gene, partial sequence; chloroplast	125	125	100%	7e-26	96%	KF616469.1
Tracheophyta environmental sample clone S2-1 tRNA-Leu (trnL) gene, partial sequence; chloroplast	125	125	100%	7e-26	96%	KF616468.1
Pinus luchuensis chloroplast trnL gene, intron, partial sequence, isolate: OGA0449	125	125	100%	7e-26	96%	AB817641.1
Pinus luchuensis chloroplast trnL gene, intron, partial sequence, isolate:	125	125	100%	7e-26	96%	AB817461.1

OGA0239						
Pinus taeda chloroplast, complete genome	125	125	100%	7e-26	96%	**KC427273.1**
Pinus massoniana chloroplast, complete genome	125	125	100%	7e-26	96%	**KC427272.1**
Pinus thunbergii trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	125	125	100%	7e-26	96%	**JX504692.1**
Pinus bungeana trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	125	125	100%	7e-26	96%	**JX504691.1**
Pinus koraiensis trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	125	125	100%	7e-26	96%	**JX504690.1**
Pinus densiflora trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	125	125	100%	7e-26	96%	**JX504689.1**
Pinus x rigitaeda trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	125	125	100%	7e-26	96%	**JX504688.1**
Pinus sylvestris trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	125	125	100%	7e-26	96%	**JX504686.1**
Pinus rigida trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	125	125	100%	7e-26	96%	**JX504685.1**
Pinus densiflora cultivar Multicaulis trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	125	125	100%	7e-26	96%	**JX504684.1**
Pinus sylvestris voucher Psy01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	125	125	100%	7e-26	96%	**JQ739418.1**
Pinus peuce voucher Ppe01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	125	125	100%	7e-26	96%	**JQ739417.1**
Pinus halepensis voucher Pha01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	125	125	100%	7e-26	96%	**JQ739416.1**
Pinus brutia voucher Pb01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	125	125	100%	7e-26	96%	**JQ739415.1**
Pinus brutia var. eldarica voucher Pe01.120311 tRNA-Leu (trnL) gene, intron; chloroplast	125	125	100%	7e-26	96%	**JQ739414.1**
Pinus nigra voucher Pn01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	125	125	100%	7e-26	96%	**JQ739413.1**
Pinus pinea voucher Ppi01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	125	125	100%	7e-26	96%	**JQ739412.1**
Pinus heldreichii voucher Phe01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	125	125	100%	7e-26	96%	**JQ739411.1**
Pinus arizonica var. cooperi isolate COOP01 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854216.1**
Pinus coulteri isolate COUL03 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854215.1**
Pinus cubensis isolate CUBE01 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854214.1**
Pinus culminicola isolate CULM01 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854213.1**
Pinus fenzeliana var. dabeshanensis isolate DABE01 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854212.1**
Pinus dalatensis isolate DALA03 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854211.1**
Pinus densiflora isolate DENS02 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854210.1**
Pinus densata isolate DENT01 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854209.1**
Pinus devoniana isolate DEVO02 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854208.1**
Pinus discolor isolate DISC02 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854207.1**

Pinus hartwegii isolate DONN02 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854206.1**
Pinus douglasiana isolate DOUG01 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854205.1**
Pinus echinata isolate ECHI01 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854204.1**
Pinus edulis isolate EDUL08 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854203.1**
Pinus elliottii isolate ELLI01 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854202.1**
Pinus engelmannii isolate ENGE02 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854201.1**
Pinus fragilissima isolate FRAG01 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854200.1**
Pinus glabra isolate GLAB01 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854199.1**
Pinus greggii isolate GREG02 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854198.1**
Pinus halepensis isolate HALE03 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854197.1**
Pinus hartwegii isolate HART07 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854196.1**
Pinus heldreichii isolate HELD07 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854195.1**
Pinus hwangshanensis isolate HWAN01 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854194.1**
Pinus jeffreyi isolate JEFF04 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854193.1**
Pinus johannis chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854192.1**
Pinus kesiya isolate KESI11 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854191.1**
Pinus latteri isolate LATT02 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854190.1**
Pinus pringlei isolate PRIN02 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854189.1**
Pinus lawsonii isolate LAWS02 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854188.1**
Pinus leiophylla isolate LEIO03 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854187.1**
Pinus lumholtzii isolate LUMH07 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854186.1**
Pinus massoniana isolate MASS02 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854185.1**
Pinus maximartinezii isolate MAXZ01 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854184.1**
Pinus montezumae isolate MONZ01 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854183.1**
Pinus morrisonicola isolate MORR01 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854182.1**
Pinus mugo isolate MUGO01 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854181.1**
Pinus muricata isolate MURI01 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854180.1**
Pinus nigra isolate NIGR20 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854179.1**
Pinus pseudostrobus var. apulcensis isolate OAXA02 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854178.1**
Pinus occidentalis isolate OCCI02 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854177.1**
Pinus palustris isolate PALU02 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854176.1**
Pinus patula isolate PATU01 chloroplast, partial genome	125	125	100%	7e-26	96%	**JN854175.1**
Pinus pinceana isolate PINC13 chloroplast,						

partial genome	125	125	100%	7e-26	96%	JN854174.1
Pinus pinea isolate PINE03 chloroplast, partial genome	125	125	100%	7e-26	96%	JN854173.1
Pinus ponderosa var. benthamiana isolate POND21 chloroplast, partial genome	125	125	100%	7e-26	96%	JN854172.1
Pinus ponderosa var. scopulorum isolate POND59 chloroplast, partial genome	125	125	100%	7e-26	96%	JN854171.1
Pinus pseudostrobus isolate PSEU03 chloroplast, partial genome	125	125	100%	7e-26	96%	JN854169.1
Pinus pumila isolate PUMI07 chloroplast, partial genome	125	125	100%	7e-26	96%	JN854168.1
Pinus pungens isolate PUNG01 chloroplast, partial genome	125	125	100%	7e-26	96%	JN854167.1
Pinus quadrifolia isolate QUAD02 chloroplast, partial genome	125	125	100%	7e-26	96%	JN854166.1
Pinus radiata isolate RADI01 chloroplast, partial genome	125	125	100%	7e-26	96%	JN854165.1
Pinus remota isolate REMO05 chloroplast, partial genome	125	125	100%	7e-26	96%	JN854164.1
Pinus rigida isolate RIGI01 chloroplast, partial genome	125	125	100%	7e-26	96%	JN854163.1
Pinus roxburghii isolate ROXB04 chloroplast, partial genome	125	125	100%	7e-26	96%	JN854162.1
Pinus sabiniana isolate SABI04 chloroplast, partial genome	125	125	100%	7e-26	96%	JN854161.1
Pinus serotina isolate SERO01 chloroplast, partial genome	125	125	100%	7e-26	96%	JN854160.1
Pinus strobiformis isolate STRF17 chloroplast, partial genome	125	125	100%	7e-26	96%	JN854159.1
Pinus sylvestris isolate SYLV02 chloroplast, partial genome	125	125	100%	7e-26	96%	JN854158.1
Pinus taiwanensis isolate TAIW04 chloroplast, partial genome	125	125	100%	7e-26	96%	JN854157.1
Pinus tropicalis isolate TROP02 chloroplast, partial genome	125	125	100%	7e-26	96%	JN854156.1

Alignments

Pinus sibirica chloroplast, complete genome
Sequence ID: **gb|KT723438.2|** Length: 116635 Number of Matches: 1
Range 1: 66690 to 66767

Score	Expect	Identities	Gaps	Strand	Frame
125 bits(138)	7e-26()	76/79(96%)	1/79(1%)	Plus/Minus	

Features:

```
Query  1      GGCAATCCTGAGCCAAATCCGGTTCATAGAAGACAATGTTTCTTCTCCTAAGATAGGAAG  60
              || |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  66767  GGTAATCCTGAGCCAAATCCGGTTCAT-GAAGACAATGTTTCTTCTCCTAAGATAGGAAG  66709

Query  61     AGGATAGGTGCAGAGACTC  79
               ||||||||||||||||||
Sbjct  66708  GGGATAGGTGCAGAGACTC  66690
```

Pinus tabuliformis voucher PTAB20150818V5 chloroplast, complete genome
Sequence ID: **gb|KT740995.1|** Length: 119646 Number of Matches: 1
Range 1: 68565 to 68642

Score	Expect	Identities	Gaps	Strand	Frame
125 bits(138)	7e-26()	76/79(96%)	1/79(1%)	Plus/Minus	

Features:

```
Query  1      GGCAATCCTGAGCCAAATCCGGTTCATAGAAGACAATGTTTCTTCTCCTAAGATAGGAAG  60
              || |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  68642  GGTAATCCTGAGCCAAATCCGGTTCAT-GAAGACAATGTTTCTTCTCCTAAGATAGGAAG  68584

Query  61     AGGATAGGTGCAGAGACTC  79
               ..................
```

```
               ||||||||||||||||||
Sbjct  68583  GGGATAGGTGCAGAGACTC  68565
```

Pinus bungeana voucher Pbungeana2015 chloroplast, complete genome
Sequence ID: **gb|KR873010.1|** Length: 117861 Number of Matches: 1
Range 1: 68182 to 68259

Score	Expect	Identities	Gaps	Strand	Frame
125 bits(138)	7e-26()	76/79(96%)	1/79(1%)	Plus/Minus	

Features:

```
Query  1      GGCAATCCTGAGCCAAATCCGGTTCATAGAAGACAATGTTTCTTCTCCTAAGATAGGAAG  60
              || |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  68259  GGTAATCCTGAGCCAAATCCGGTTCAT-GAAGACAATGTTTCTTCTCCTAAGATAGGAAG  68201

Query  61     AGGATAGGTGCAGAGACTC  79
               ||||||||||||||||||
Sbjct  68200  GGGATAGGTGCAGAGACTC  68182
```

Pinus taiwanensis voucher Ptaiwanensis14 chloroplast, complete genome
Sequence ID: **gb|KP771703.1|** Length: 119741 Number of Matches: 1
Range 1: 68622 to 68699

Score	Expect	Identities	Gaps	Strand	Frame
125 bits(138)	7e-26()	76/79(96%)	1/79(1%)	Plus/Minus	

Features:

```
Query  1      GGCAATCCTGAGCCAAATCCGGTTCATAGAAGACAATGTTTCTTCTCCTAAGATAGGAAG  60
              || |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  68699  GGTAATCCTGAGCCAAATCCGGTTCAT-GAAGACAATGTTTCTTCTCCTAAGATAGGAAG  68641

Query  61     AGGATAGGTGCAGAGACTC  79
               ||||||||||||||||||
Sbjct  68640  GGGATAGGTGCAGAGACTC  68622
```

Pinus strobus plastid, complete genome
Sequence ID: **gb|KP099650.1|** Length: 115576 Number of Matches: 1
Range 1: 65526 to 65603

Score	Expect	Identities	Gaps	Strand	Frame
125 bits(138)	7e-26()	76/79(96%)	1/79(1%)	Plus/Minus	

Features:

```
Query  1      GGCAATCCTGAGCCAAATCCGGTTCATAGAAGACAATGTTTCTTCTCCTAAGATAGGAAG  60
              || |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  65603  GGTAATCCTGAGCCAAATCCGGTTCAT-GAAGACAATGTTTCTTCTCCTAAGATAGGAAG  65545

Query  61     AGGATAGGTGCAGAGACTC  79
               ||||||||||||||||||
Sbjct  65544  GGGATAGGTGCAGAGACTC  65526
```

BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BTWEMHN8015**
Formatting options
Download
Blast report description

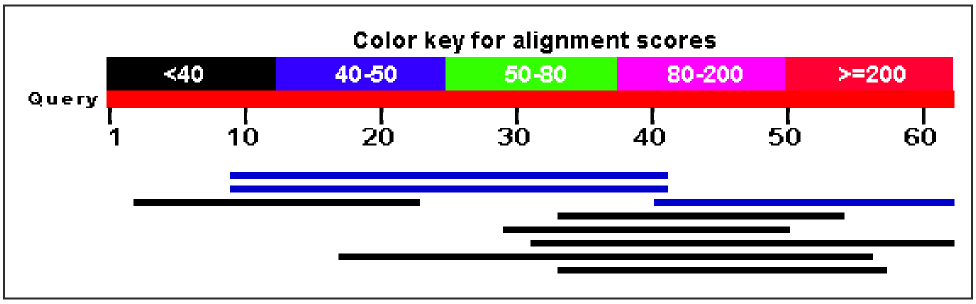
YK08-AB9-L7B_trnL_Clone1

RID BTWEMHN8015 (Expires on 02-13 03:40 am)

Query ID	lcl|Query_63429	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	62		

Graphic Summary

Distribution of 9 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: Ochotona princeps lysine (K)-specific demethylase 2A (KDM2A), transcript variant X2, mRNA	41.0	41.0	51%	1.5	88%	XM_004598199.1
PREDICTED: Ochotona princeps lysine (K)-specific demethylase 2A (KDM2A), transcript variant X1, mRNA	41.0	41.0	51%	1.5	88%	XM_004598198.1
Saccharophagus degradans 2-40, complete genome	41.0	41.0	35%	1.5	100%	CP000282.1
Apteryx australis mantelli genome assembly AptMant0, scaffold scaffold3924	39.2	39.2	33%	5.2	100%	LK068494.1
PREDICTED: Bactrocera dorsalis protein screw (LOC105226937), mRNA	39.2	39.2	33%	5.2	100%	XM_011206074.1
PREDICTED: Phalacrocorax carbo thyroid peroxidase-like (LOC104047200), partial mRNA	39.2	39.2	33%	5.2	100%	XM_009507480.1
Fusarium fujikuroi IMI 58289 draft genome, chromosome FFUJ_chr07	39.2	39.2	50%	5.2	87%	HF679029.1
Marinobacter sp. BSs20148, complete genome	39.2	39.2	62%	5.2	85%	CP003735.1
Mus musculus BAC clone RP23-166C2 from 18, complete sequence	39.2	39.2	38%	5.2	96%	AC124578.4

Alignments

PREDICTED: Ochotona princeps lysine (K)-specific demethylase 2A (KDM2A), transcript variant X2, mRNA
Sequence ID: **ref|XM_004598199.1|** Length: 3653 Number of Matches: 1
Range 1: 1773 to 1804

Score	Expect	Identities	Gaps	Strand	Frame
41.0 bits(44)	1.5()	28/32(88%)	0/32(0%)	Plus/Plus	

Features:

```
Query  10    CACCAATCCTTACATCATGGAAGCAGCTCCGC  41
             |||||| ||| ||| |||| ||||||||||||
Sbjct  1773  CACCAAGCCTCACACCATGAAAGCAGCTCCGC  1804
```

PREDICTED: Ochotona princeps lysine (K)-specific demethylase 2A (KDM2A), transcript variant X1, mRNA
Sequence ID: **ref|XM_004598198.1|** Length: 3531 Number of Matches: 1
Range 1: 1651 to 1682

Score	Expect	Identities	Gaps	Strand	Frame
41.0 bits(44)	1.5()	28/32(88%)	0/32(0%)	Plus/Plus	

Features:

```
Query  10    CACCAATCCTTACATCATGGAAGCAGCTCCGC  41
             |||||| ||| ||| |||| ||||||||||||
Sbjct  1651  CACCAAGCCTCACACCATGAAAGCAGCTCCGC  1682
```

Saccharophagus degradans 2-40, complete genome
Sequence ID: **gb|CP000282.1|** Length: 5057531 Number of Matches: 1
Range 1: 2896978 to 2896999

Score	Expect	Identities	Gaps	Strand	Frame

41.0 bits(44)	1.5()	22/22(100%)	0/22(0%)	Plus/Plus	

Features:

```
Query  41       CTTGCATTTGGCTTGGATTGCC  62
                ||||||||||||||||||||||
Sbjct  2896978  CTTGCATTTGGCTTGGATTGCC  2896999
```

Apteryx australis mantelli genome assembly AptMant0, scaffold scaffold3924
Sequence ID: **emb|LK068494.1|** Length: 224514 Number of Matches: 1
Range 1: 196700 to 196720

Score	Expect	Identities	Gaps	Strand	Frame
39.2 bits(42)	5.2()	21/21(100%)	0/21(0%)	Plus/Minus	

Features:

```
Query  34      AGCTCCGCTTGCATTTGGCTT  54
               |||||||||||||||||||||
Sbjct  196720  AGCTCCGCTTGCATTTGGCTT  196700
```

PREDICTED: Bactrocera dorsalis protein screw (LOC105226937), mRNA
Sequence ID: **ref|XM_011206074.1|** Length: 1619 Number of Matches: 1
Range 1: 944 to 964

Score	Expect	Identities	Gaps	Strand	Frame
39.2 bits(42)	5.2()	21/21(100%)	0/21(0%)	Plus/Minus	

Features:

```
Query  30   AAGCAGCTCCGCTTGCATTTG  50
            |||||||||||||||||||||
Sbjct  964  AAGCAGCTCCGCTTGCATTTG  944
```

BLAST ®

Basic Local Alignment Search Tool

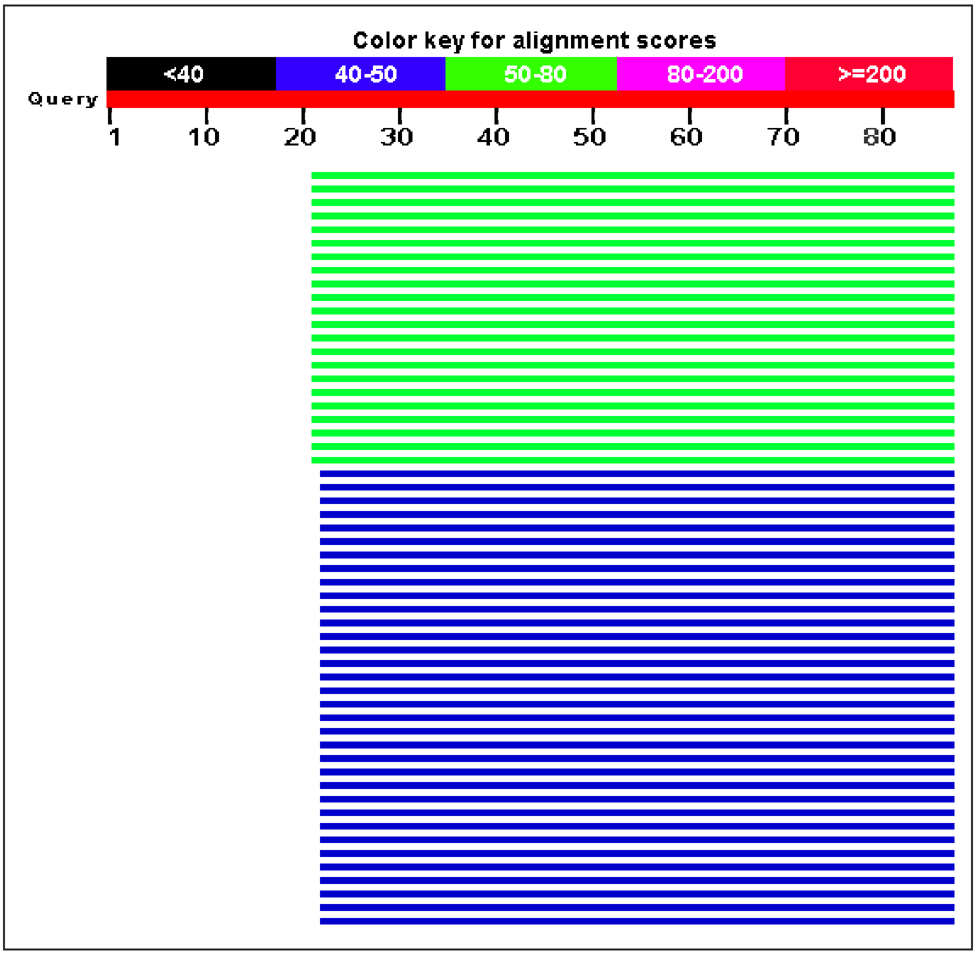
NCBI/ BLAST/ blastn suite/ **Formatting Results - BTWBYAJB014**
Formatting options
Download
Blast report description

YK08-AB9-L7B_trnL_Clone10

RID	BTWBYAJB014 (Expires on 02-13 03:39 am)		
Query ID	lcl|Query_15021	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	87		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Osmunda vachellii tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	55.4	55.4	75%	1e-04	81%	FJ262720.1
Osmunda mildei tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	55.4	55.4	75%	1e-04	81%	FJ262718.1
Osmunda japonica tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	55.4	55.4	75%	1e-04	81%	FJ262717.1
Osmunda vachellii voucher Mickel & Beitel s.n. (UC) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	55.4	55.4	75%	1e-04	81%	EF588818.1
Osmunda regalis voucher Schwertfeger 2 (GOET) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	55.4	55.4	75%	1e-04	81%	EF588817.1
Osmunda regalis voucher Schwertfeger 1 (GOET) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	55.4	55.4	75%	1e-04	81%	EF588816.1
Osmunda regalis voucher M.J.M. Christenhusz 4271 (DUKE, TUR) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	55.4	55.4	75%	1e-04	81%	EF588815.1
Osmunda lancea voucher K. Hirai 99-0305 (KYO) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	55.4	55.4	75%	1e-04	81%	EF588813.1
Osmunda javanica voucher Cubey 49 (E) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	55.4	55.4	75%	1e-04	81%	EF588812.1
Osmunda japonica voucher Y. Yatabe 99-0303 (KYO) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	55.4	55.4	75%	1e-04	81%	EF588811.1
Osmunda claytoniana voucher S. Nemoto 99-307 (KYO) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	55.4	55.4	75%	1e-04	81%	EF588810.1
Osmunda claytoniana voucher T. Bradley 7411 (GMUF) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	55.4	55.4	75%	1e-04	81%	EF588809.1
Osmunda banksiifolia voucher Cubey 55 (E) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	55.4	55.4	75%	1e-04	81%	EF588808.1
Osmunda regalis isolate CR009 tRNA-Leu gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	55.4	55.4	75%	1e-04	81%	AY651837.1
Paepalanthus tuberosus isolate FS1641 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	53.6	53.6	75%	4e-04	79%	EU924486.1
Vicia kotschyana isolate 64063 tRNA-Leu (trnL) gene, partial sequence; chloroplast	51.8	51.8	75%	0.002	78%	KJ787258.1
Osmundastrum cinnamomeum chloroplast, complete genome	51.8	51.8	75%	0.002	79%	KF225592.1

Hordeum comosum chloroplast tRNA-Leu gene (partial), trnL-trnF intergenic spacer and tRNA-Phe gene (partial), haplotype HT121	51.8	51.8	75%	0.002	77%	FM163524.1
Osmundastrum cinnamomeum voucher Hasebe 27624 (TI, KYO) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	51.8	51.8	75%	0.002	79%	EF588821.1
Osmundastrum cinnamomeum voucher M.J.M. Christenhusz 3380 (IJ, TUR) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	51.8	51.8	75%	0.002	79%	EF588819.1
Osmunda regalis voucher M.J.M. Christenhusz 4245 (DUKE, TUR) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	51.8	51.8	75%	0.002	79%	EF588814.1
Georgeantha hexandra tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	51.8	51.8	75%	0.002	79%	AF148733.1
Ephedra foeminea voucher K. Bolinder 542 chloroplast, complete genome	50.0	50.0	74%	0.005	78%	KT934791.1
Ephedra sinica haplotype H8 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KT033395.1
Ephedra sinica haplotype H7 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KT033394.1
Ephedra sinica haplotype H6 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KT033393.1
Ephedra foeminea haplotype H24 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	74%	0.005	78%	KT033390.1
Ephedra viridis voucher Elias & Morefield 10376 (MEXU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KP788807.1
Ephedra tweediana voucher Ickert-Bond 1225 (ASU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KP788806.1
Ephedra triandra voucher Ickert-Bond 1227 (ASU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KP788805.1
Ephedra torreyana voucher Gentry & Engard 23198 (MEXU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KP788804.1
Ephedra sinica voucher 986 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KP788803.1
Ephedra rupestris voucher Ickert-Bond 1220 (ASU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL)	50.0	50.0	74%	0.005	76%	KP788802.1

gene, partial sequence; chloroplast						
Ephedra rupestris voucher Ickert-Bond 1110 (ASU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KP788801.1
Ephedra pseudodistachya voucher Freitag 33002 (KAS) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KP788800.1
Ephedra ochreata voucher Muhlen s.n. tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KP788799.1
Ephedra multiflora voucher Ickert-Bond 1211 (ASU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KP788798.1
Ephedra minuta voucher JBM1106 00 tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KP788796.1
Ephedra intermedia voucher XJ 08070801 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KP788794.1
Ephedra gracilis voucher Ickert-Bond 1201 (ASU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KP788793.1
Ephedra intermedia voucher YYNH08070502 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KP788792.1
Ephedra funerea voucher Ickert-Bond 473 (ASU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KP788791.1
Ephedra funerea voucher Ickert-Bond 964 (ASU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KP788790.1
Ephedra frustillata voucher Ickert-Bond 1247 (ASU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KP788789.1
Ephedra breana voucher Ickert-Bond 1234 (ASU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KP788788.1
Ephedra boelckei voucher Ickert-Bond 1252 (ASU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KP788787.1
Ephedra boelckei voucher Ickert-Bond 1251 (ASU) trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KP788786.1
Ephedra aphylla voucher Freitag 30181 (KAS) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	78%	KP788785.1

Ephedra americana voucher Ickert-Bond 1105 (ASU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KP788784.1
Ephedra major isolate H26 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	74%	0.005	78%	KC407803.1
Ephedra equisetina isolate H23 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KC407800.1
Ephedra przewalskii isolate H21 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KC407798.1
Ephedra przewalskii isolate H20 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KC407797.1
Ephedra intermedia isolate H19 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KC407796.1
Ephedra intermedia isolate H16 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KC407793.1
Ephedra saxatilis var. mairei isolate H13 tRNA-Thr (trnT) gene, partial sequence; and trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; chloroplast	50.0	50.0	74%	0.005	76%	KC407790.1
Ephedra saxatilis var. mairei isolate H12 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KC407789.1
Ephedra saxatilis var. mairei isolate H11 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KC407788.1
Ephedra saxatilis var. mairei isolate H9 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KC407786.1
Ephedra rituensis isolate H7 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KC407784.1
Ephedra saxatilis isolate H4 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KC407781.1
Ephedra gerardiana isolate H1 tRNA-Thr						

(trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	KC407778.1
Ephedra trifurca voucher Reina-G. & Van Devender 96-208 (MEXU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	JX217737.1
Ephedra nevadensis voucher Felger & Dimmitt 85-724 (MEXU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	JX217734.1
Ephedra nevadensis voucher Phillips & Phillips 93141 (MEXU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	JX217733.1
Ephedra aspera voucher Spellenberg & Bacon s.n. (MEXU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	JX217721.1
Ephedra antisyphilitica voucher Loera 22 (XAL) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	JX217719.1
Ephedra foeminea voucher H. Freitag 19.807 (KAS) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	78%	GU111523.1
Ephedra distachya voucher H. Freitag 28.834 (KAS) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	GU111514.1
Ephedra dahurica voucher H. Freitag 33.130 (KAS) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	GU111507.1
Ephedra distachya voucher H. Freitag 33.259 (KAS) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	GU111506.1
Ephedra gerardiana tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	74%	0.005	76%	EU326056.1
Ephedra torreyana tRNA-Thr (trnT) gene, partial sequence; and trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; chloroplast	50.0	50.0	74%	0.005	76%	AY513736.1
Ephedra viridis tRNA-Thr (trnT) gene, partial sequence; and tRNA-Leu (trnL) gene, complete sequence; chloroplast	50.0	50.0	74%	0.005	76%	AY513735.1
Ephedra trifurca tRNA-Thr (trnT) gene, partial sequence; and trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; chloroplast	50.0	50.0	74%	0.005	76%	AY513734.1
Ephedra przewalskii voucher Kamp03071340 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	AY730598.1
Ephedra viridis tRNA-Leu (trnL) gene, intron sequence; chloroplast gene for chloroplast product	50.0	50.0	74%	0.005	76%	AF479869.1
Ephedra minuta voucher 1017 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF						

intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	AY423439.1
Ephedra minuta tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	AY423438.1
Ephedra sinica tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	AY423431.1
Ephedra intermedia tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	50.0	50.0	74%	0.005	76%	AY423430.1
Lygodium japonicum chloroplast, complete genome	48.2	48.2	74%	0.018	78%	KF225593.1
Avena barbata isolate AG06 tRNA-Leu (trnL-UAA) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	75%	0.018	74%	KF996088.1
Lygodium japonicum chloroplast, complete genome	48.2	48.2	74%	0.018	78%	KC536645.1
Eupomatia laurina voucher UQ WellsJ 83-Elr tRNA-Leu (trnL) gene and trnL-F intergenic spacer, partial sequence; chloroplast	48.2	48.2	75%	0.018	76%	KC428512.1
Avena fatua voucher PI 447299 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	75%	0.018	74%	GU367222.1
Avena damascena voucher CN 19457 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	75%	0.018	74%	GU367219.1
Juniperus hybrid sp. LO-2009 voucher J.Q. Liu 1216_14 trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	75%	0.018	76%	GQ285837.1
Avena damascena voucher CN 19459 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence	48.2	48.2	75%	0.018	74%	EU833870.1
Avena damascena isolate 7261 tRNA-Leu (trnL) gene, intron; chloroplast	48.2	48.2	75%	0.018	74%	EU276595.1
Lygodium flexuosum voucher L82C tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	74%	0.018	77%	DQ845239.1
Lygodium flexuosum voucher L82AS tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	74%	0.018	77%	DQ845238.1
Lygodium flexuosum voucher L180A tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	74%	0.018	77%	DQ845235.1
Lygodium japonicum voucher L51B tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	74%	0.018	78%	DQ845232.1
Lygodium japonicum voucher L57B tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	74%	0.018	78%	DQ845231.1
Roscoea sp. JLZ-2014 haplotype 31 tRNA-Leu (trnL-UAA) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF-GAA) gene, partial sequence; chloroplast	46.4	46.4	75%	0.064	76%	KF907054.1
Roscoea sp. JLZ-2014 haplotype 26 tRNA-Leu (trnL-UAA) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF-GAA) gene, partial sequence; chloroplast	46.4	46.4	75%	0.064	76%	KF907049.1
Eupomatia bennettii tRNA-Leu (trnL) gene, intron; chloroplast	46.4	46.4	74%	0.064	75%	KF586705.1

Dioscorea esculenta voucher Lu 20826 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	46.4	46.4	75%	0.064	76%	JQ733878.1
Dioscorea esculenta var. spinosa voucher Chen 20 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	46.4	46.4	75%	0.064	76%	JQ733833.1

Alignments

Osmunda vachellii tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|FJ262720.1|** Length: 849 Number of Matches: 1
Range 1: 18 to 82

Score	Expect	Identities	Gaps	Strand	Frame
55.4 bits(60)	1e-04()	55/68(81%)	5/68(7%)	Plus/Minus	

Features:

```
Query  22  TGAGTCTCTGCACCTATCCTTCATCAATGGATGCTAGCTCC--GACTTGGATTTGGCTCA  79
           ||||||||||||||||||  ||||   ||||| || |||||  ||    |||||||||||
Sbjct  82  TGAGTCTCTGCACCTATC--TCATTTTTGGATCCT-GCTCCTGGAACAAGATTTGGCTCA  26

Query  80  GGATTGCC  87
           ||||||||
Sbjct  25  GGATTGCC  18
```

Osmunda mildei tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|FJ262718.1|** Length: 885 Number of Matches: 1
Range 1: 45 to 109

Score	Expect	Identities	Gaps	Strand	Frame
55.4 bits(60)	1e-04()	55/68(81%)	5/68(7%)	Plus/Minus	

Features:

```
Query  22   TGAGTCTCTGCACCTATCCTTCATCAATGGATGCTAGCTCC--GACTTGGATTTGGCTCA  79
            ||||||||||||||||||  ||||   ||||| || |||||  ||    |||||||||||
Sbjct  109  TGAGTCTCTGCACCTATC--TCATTTTTGGATCCT-GCTCCTGGAACAAGATTTGGCTCA  53

Query  80   GGATTGCC  87
            ||||||||
Sbjct  52   GGATTGCC  45
```

Osmunda japonica tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|FJ262717.1|** Length: 934 Number of Matches: 1
Range 1: 15 to 79

Score	Expect	Identities	Gaps	Strand	Frame
55.4 bits(60)	1e-04()	55/68(81%)	5/68(7%)	Plus/Minus	

Features:

```
Query  22  TGAGTCTCTGCACCTATCCTTCATCAATGGATGCTAGCTCC--GACTTGGATTTGGCTCA  79
           ||||||||||||||||||  ||||   ||||| || |||||  ||    |||||||||||
Sbjct  79  TGAGTCTCTGCACCTATC--TCATTTTTGGATCCT-GCTCCTGGAACAAGATTTGGCTCA  23

Query  80  GGATTGCC  87
           ||||||||
Sbjct  22  GGATTGCC  15
```

Osmunda vachellii voucher Mickel & Beitel s.n. (UC) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|EF588818.1|** Length: 981 Number of Matches: 1
Range 1: 82 to 146

Score	Expect	Identities	Gaps	Strand	Frame
55.4 bits(60)	1e-04()	55/68(81%)	5/68(7%)	Plus/Minus	

Features:

```
Query  22   TGAGTCTCTGCACCTATCCTTCATCAATGGATGCTAGCTCC--GACTTGGATTTGGCTCA  79
            ||||||||||||||||||  ||||   ||||| || |||||  ||    |||||||||||
Sbjct  146  TGAGTCTCTGCACCTATC--TCATTTTTGGATCCT-GCTCCTGGAACAAGATTTGGCTCA  90

Query  80   GGATTGCC  87
            ||||||||
```

```
Sbjct  89    GGATTGCC  82
```

Osmunda regalis voucher Schwertfeger 2 (GOET) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|EF588817.1|** Length: 919 Number of Matches: 1
Range 1: 49 to 113

Score	Expect	Identities	Gaps	Strand	Frame
55.4 bits(60)	1e-04()	55/68(81%)	5/68(7%)	Plus/Minus	

Features:

```
Query  22    TGAGTCTCTGCACCTATCCTTCATCAATGGATGCTAGCTCC--GACTTGGATTTGGCTCA  79
             ||||||||||||||||||  ||||   ||||| || |||||  ||    |||||||||||
Sbjct  113   TGAGTCTCTGCACCTATC--TCATTTTTGGATCCT-GCTCCTGGAACAAGATTTGGCTCA  57

Query  80    GGATTGCC  87
             ||||||||
Sbjct  56    GGATTGCC  49
```

BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BTVEP4G1014**
Formatting options
Download
Blast report description

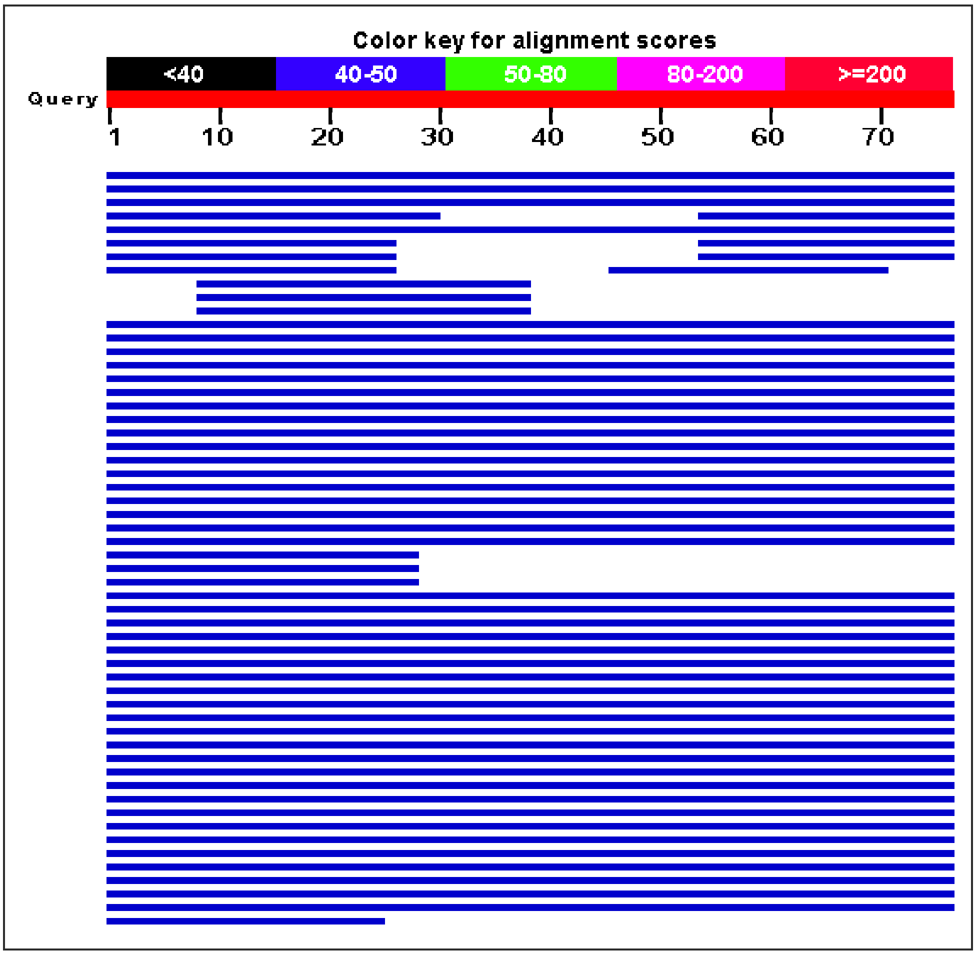
YK08-AB9-L7B_trnL_Clone5

RID BTVEP4G1014 (Expires on 02-13 03:23 am)

Query ID	lcl|Query_170279	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	76		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Syngonanthus trichophyllus voucher INPA:Carvalho1580b tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; plastid	46.4	46.4	100%	0.051	74%	KT724343.1
Syngonanthus flavidulus voucher JR Massey 3284 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; plastid	46.4	46.4	100%	0.051	74%	KF840875.1
Stackhousia muricata voucher AD:98952198 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	46.4	46.4	100%	0.051	75%	GU169158.1
Staurastrum punctulatum chloroplast, complete genome	46.4	46.4	39%	0.051	93%	AY958085.1
Syngonanthus flavidulus tRNA-Leu (trnL) gene, partial sequence; chloroplast	44.6	44.6	100%	0.18	72%	DQ189019.1
Angelica dahurica voucher 13T-05 chloroplast, complete genome	42.8	42.8	34%	0.62	96%	KT963037.1
Apiaceae sp. 13R31re1 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	34%	0.62	96%	KP665036.1
Apiaceae sp. 13R29re3 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	34%	0.62	96%	KP665035.1
PREDICTED: Austrofundulus limnaeus sarcalumenin (srl), transcript variant X3, mRNA	42.8	42.8	39%	0.62	93%	XM_014010092.1
PREDICTED: Austrofundulus limnaeus sarcalumenin (srl), transcript variant X2, mRNA	42.8	42.8	39%	0.62	93%	XM_014010091.1
PREDICTED: Austrofundulus limnaeus sarcalumenin (srl), transcript variant X1, mRNA	42.8	42.8	39%	0.62	93%	XM_014010090.1
Wollemia nobilis voucher AF20030492AC chloroplast, complete genome	42.8	42.8	100%	0.62	75%	KP259800.1
Juniperus microsperma isolate JM-1-1 trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	42.8	42.8	100%	0.62	74%	KP208827.1
Juniperus microsperma isolate JM-7-87 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	100%	0.62	74%	KP208826.1
Juniperus microsperma isolate JM-1-10 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	100%	0.62	74%	KP208825.1
Juniperus microsperma isolate JM-1-1 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	100%	0.62	74%	KP208824.1
Araucaria columnaris chloroplast, partial genome	42.8	42.8	100%	0.62	75%	KM678417.1
Araucaria heterophylla plastid, complete genome	42.8	42.8	100%	0.62	75%	KM067155.1

Agathis dammara chloroplast DNA, complete genome	42.8	42.8	100%	0.62	75%	AB830884.1
Wollemia nobilis voucher J.Q.Liu-WolNob tRNA-Leu (trnL) gene, partial sequence; chloroplast	42.8	42.8	100%	0.62	75%	JF725907.1
Thujopsis dolabrata voucher J.Q.Liu-TBG-TOD tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	100%	0.62	75%	HM024613.1
Juniperus phoenicea voucher WO-2118 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	100%	0.62	75%	HM024582.1
Juniperus microsperma voucher J.Q.Liu-1216 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	100%	0.62	74%	HM024576.1
Juniperus microsperma voucher LO_04_68_043 trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	100%	0.62	74%	GQ268212.1
Juniperus microsperma voucher LO_04_68_037 trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	100%	0.62	74%	GQ268211.1
Juniperus hybrid sp. LO-2009 voucher LO_04_12_008 trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	100%	0.62	75%	GQ268201.1
Juniperus microsperma voucher LO_04_10_014 trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	100%	0.62	74%	GQ268199.1
Thujopsis dolabrata trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence	42.8	42.8	100%	0.62	75%	EU183473.1
Chlorokybus atmophyticus chloroplast, complete genome	42.8	42.8	36%	0.62	93%	DQ422812.2
Bracteacoccus minor tRNA-Leu (trnL) gene, intron; chloroplast	42.8	42.8	36%	0.62	93%	AY344781.1
Chlorokybus atmophyticus tRNA-Leu (trnL) gene, intron; chloroplast	42.8	42.8	36%	0.62	93%	AY344772.1
Araucaria araucana trnT-trnL intergenic spacer, trnL gene and trnL-trnF intergenic spacer sequence	42.8	42.8	100%	0.62	75%	AY145321.1
Podocarpus latifolius tRNA-Leu (trnL), gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	100%	0.62	75%	AY678112.1
Araucaria angustifolia tRNA-Leu (trnL) gene, intron sequence; chloroplast gene for chloroplast product	42.8	42.8	100%	0.62	75%	AF479866.1
Agathis dammara tRNA-Leu (trnL) gene, partial intron and 3' exon, and trnL-trnF intergenic spacer region; chloroplast gene for chloroplast	42.8	42.8	100%	0.62	75%	AY013738.1

product						
Agathis australis chloroplast trnL gene, intron sequence	42.8	42.8	100%	0.62	75%	AY083115.1
Araucaria biramulata chloroplast trnL gene, intron sequence	42.8	42.8	100%	0.62	75%	AY083114.1
Thujopsis dolabrata chloroplast trnL gene for tRNA-Leu, partial sequence	42.8	42.8	100%	0.62	75%	AB030062.1
Lycopodiella pendulina chloroplast trnL gene intron	42.8	42.8	30%	0.62	100%	AJ224607.1
Lycopodiella glaucescens chloroplast trnL gene intron	42.8	42.8	30%	0.62	100%	AJ224606.1
Lycopodiella cernua chloroplast trnL gene intron	42.8	42.8	30%	0.62	100%	AJ224608.1
Torreya fargesii chloroplast, complete genome	41.0	41.0	100%	2.2	73%	KT027377.1
Torreya jackii isolate 7-6 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	41.0	41.0	100%	2.2	73%	KJ589075.1
Torreya jackii isolate 7-5 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	41.0	41.0	100%	2.2	73%	KJ589074.1
Torreya jackii isolate 7-4 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	41.0	41.0	100%	2.2	73%	KJ589073.1
Torreya jackii isolate 7-3 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	41.0	41.0	100%	2.2	73%	KJ589072.1
Torreya jackii isolate 7-2 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	41.0	41.0	100%	2.2	73%	KJ589071.1
Torreya jackii isolate 7-1 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	41.0	41.0	100%	2.2	73%	KJ589070.1
Torreya californica isolate 6-2 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	41.0	41.0	100%	2.2	73%	KJ589069.1
Torreya californica isolate 6-1 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	41.0	41.0	100%	2.2	73%	KJ589068.1
Torreya taxifolia isolate 5-3 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	41.0	41.0	100%	2.2	73%	KJ589067.1
Torreya taxifolia isolate 5-2 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	41.0	41.0	100%	2.2	73%	KJ589066.1
Torreya taxifolia isolate 5-1 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	41.0	41.0	100%	2.2	73%	KJ589065.1
Torreya fargesii isolate 4-3 tRNA-Leu						

(trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	41.0	41.0	100%	2.2	73%	KJ589064.1
Torreya fargesii isolate 4-2 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	41.0	41.0	100%	2.2	73%	KJ589063.1
Torreya fargesii isolate 4-1 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	41.0	41.0	100%	2.2	73%	KJ589062.1
Torreya fargesii var. yunnanensis isolate 3-2 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	41.0	41.0	100%	2.2	73%	KJ589061.1
Torreya fargesii var. yunnanensis isolate 3-1 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	41.0	41.0	100%	2.2	73%	KJ589060.1
Opisthorchis viverrini hypothetical protein partial mRNA	41.0	41.0	32%	2.2	96%	XM_009168548.1
Lomatogonium rotatum voucher Groff 08.UT.212.A1 tRNA-Leu (trnL) gene, partial sequence; trnL-F intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	41.0	41.0	32%	2.2	96%	KF317124.1
Goodenia nuda voucher NSW 411219 Mitchell PRP 547 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	41.0	41.0	28%	2.2	100%	JQ682710.1
Pimelea stricta tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	41.0	41.0	32%	2.2	96%	FJ649638.1
Podocarpus beecherae tRNA-Leu (trnL) gene, intron; plastid	41.0	41.0	100%	2.2	73%	JN001428.1
Gymnadenia conopsea tRNA-Leu (trnL) gene, intron; chloroplast	41.0	41.0	32%	2.2	96%	HQ323922.1
Coeloglossum viride tRNA-Leu (trnL) gene, intron; chloroplast	41.0	41.0	32%	2.2	96%	HQ323868.1
Disa patula tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	41.0	41.0	32%	2.2	96%	GU117882.1
Pseudorchis albida tRNA-Leu (trnL) gene, partial sequence; chloroplast	41.0	41.0	32%	2.2	96%	GQ245349.1
Platanthera obtusata tRNA-Leu (trnL) gene, partial sequence; chloroplast	41.0	41.0	32%	2.2	96%	GQ245265.1
Platanthera hyperborea tRNA-Leu (trnL) gene, partial sequence; chloroplast	41.0	41.0	32%	2.2	96%	GQ245264.1
Lomatogonium rotatum isolate 1316o tRNA-Leu (trnL) gene, partial sequence; chloroplast	41.0	41.0	32%	2.2	96%	GQ245087.1
Lomatogonium rotatum isolate 0537g tRNA-Leu (trnL) gene, partial sequence; chloroplast	41.0	41.0	32%	2.2	96%	GQ245086.1
Coeloglossum viride isolate 1732o tRNA-Leu (trnL) gene, partial sequence; chloroplast	41.0	41.0	32%	2.2	96%	GQ244815.1
Coeloglossum viride isolate 1357o tRNA-Leu (trnL) gene, partial sequence; chloroplast	41.0	41.0	32%	2.2	96%	GQ244814.1

Amerorchis rotundifolia tRNA-Leu (trnL) gene, partial sequence; chloroplast	41.0	41.0	32%	2.2	96%	GQ244552.1
Prescottia petiolaris plastid partial tRNA-Leu gene, trnL-trnF intergenic spacer and partial tRNA-Phe gene	41.0	41.0	32%	2.2	96%	AM412728.1
Dactylorhiza saccifera trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; plastid	41.0	41.0	32%	2.2	96%	EU884281.1
Dactylorhiza incarnata trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; plastid	41.0	41.0	32%	2.2	96%	EU884280.1
Torreya nucifera voucher 876809 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and trnF gene, partial sequence; chloroplast	41.0	41.0	100%	2.2	73%	EF660644.1
Torreya fargesii voucher WH20070101 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and trnF gene, partial sequence; chloroplast	41.0	41.0	100%	2.2	73%	EF660640.1
Torreya fargesii var. yunnanensis voucher AF20070401 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and trnF gene, partial sequence; chloroplast	41.0	41.0	100%	2.2	73%	EF660625.1
Torreya jackii voucher HZ20070101 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and trnF gene, partial sequence; chloroplast	41.0	41.0	100%	2.2	73%	EF660624.1
Orchis anthropophora tRNA-Leu (trnL) gene, intron; chloroplast	41.0	41.0	32%	2.2	96%	EU294186.1
Torreya jackii tRNA-Leu (trnL) gene, partial intron and 3' exon, and trnL-trnF intergenic spacer region; chloroplast gene for chloroplast product	41.0	41.0	100%	2.2	73%	AY013732.1
Gymnadenia odoratissima isolate Davos 2 tRNA-Leu (trnL) gene, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast genes for chloroplast products	41.0	41.0	32%	2.2	96%	AF105327.1
Gymnadenia odoratissima isolate Davos 1 tRNA-Leu (trnL) gene, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast genes for chloroplast products	41.0	41.0	32%	2.2	96%	AF105326.1
Gymnadenia conopsea subsp. densiflora isolate St.Moritz 2 tRNA-Leu (trnL) gene, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast genes for chloroplast products	41.0	41.0	32%	2.2	96%	AF105325.1
Gymnadenia conopsea subsp. densiflora isolate St.Moritz 1 tRNA-Leu (trnL) gene, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast genes for chloroplast products	41.0	41.0	32%	2.2	96%	AF105324.1
Gymnadenia conopsea subsp. conopsea isolate Hessenberg 2 tRNA-Leu (trnL) gene, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast genes for chloroplast products	41.0	41.0	32%	2.2	96%	AF105323.1
Gymnadenia conopsea subsp. conopsea isolate Hessenberg 1 tRNA-Leu (trnL) gene, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast genes for	41.0	41.0	32%	2.2	96%	AF105322.1

chloroplast products						
Torreya yunnanensis chloroplast DNA, trnL-trnF intergenic spacer region	41.0	41.0	100%	2.2	73%	AB083243.1
Swertia abyssinica chloroplast tRNA-Leu gene, intron	41.0	41.0	32%	2.2	96%	AJ408012.1
Lomatogonium rotatum chloroplast tRNA-Leu gene, intron	41.0	41.0	32%	2.2	96%	AJ408011.1
Gentianella moorcroftiana chloroplast tRNA-Leu gene, intron	41.0	41.0	100%	2.2	74%	AJ408007.1
Gentianella angustiflora chloroplast tRNA-Leu gene, intron	41.0	41.0	32%	2.2	96%	AJ408004.1
Peristylus ngoyensis chloroplast tRNA-Leu gene for transfer RNA-Leu and trnL-F intergenic spacer	41.0	41.0	32%	2.2	96%	AJ409437.1
Monadenia bracteata chloroplast tRNA-Leu gene for transfer RNA-Leu and trnL-F intergenic spacer	41.0	41.0	32%	2.2	96%	AJ409430.1
Disa glandulosa chloroplast tRNA-Leu gene for transfer RNA-Leu and trnL-F intergenic spacer	41.0	41.0	32%	2.2	96%	AJ409401.1
Lomatogonium perenne chloroplast tRNA-Leu gene intron	41.0	41.0	32%	2.2	96%	AJ315199.1
Jaeschkea microsperma chloroplast tRNA-Leu gene intron	41.0	41.0	100%	2.2	74%	AJ315195.1
Phlebocarya ciliata chloroplast tRNA-Leu intron and trnL-F intergenic spacer	41.0	41.0	42%	2.2	88%	AJ387736.1

Alignments

Syngonanthus trichophyllus voucher INPA:Carvalho1580b tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; plastid

Sequence ID: **gb|KT724343.1|** Length: 779 Number of Matches: 1
Range 1: 84 to 160

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.051()	57/77(74%)	1/77(1%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCGTAAAACCTTTGTAT-AGCAATACAGCTCGTCTTCCAGCAG  59
            || |||||||||||||||| |||  |||  |||| | ||| |  | |   ||   |  ||
Sbjct  84   GGTAATCCTGAGCCAAATCCTAAGTCCTAAGTATAATCAAAAAGGGTTTACTCGAAAAAG  143

Query  60   GATAGGTGCAGAGACTC  76
            |||||||||||||||||
Sbjct  144  GATAGGTGCAGAGACTC  160
```

Syngonanthus flavidulus voucher JR Massey 3284 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; plastid

Sequence ID: **gb|KF840875.1|** Length: 780 Number of Matches: 1
Range 1: 82 to 158

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.051()	57/77(74%)	1/77(1%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCGTAAAACCTTTGTAT-AGCAATACAGCTCGTCTTCCAGCAG  59
            || |||||||||||||||| |||  |||  |||| | ||| |  | |   ||   |  ||
Sbjct  82   GGTAATCCTGAGCCAAATCCTAAGTCCTAAGTATAATCAAAAAGGGTTTACTCGAAAAAG  141

Query  60   GATAGGTGCAGAGACTC  76
            |||||||||||||||||
Sbjct  142  GATAGGTGCAGAGACTC  158
```

Stackhousia muricata voucher AD:98952198 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast

Sequence ID: **gb|GU169158.1|** Length: 961 Number of Matches: 1
Range 1: 77 to 152

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.051()	58/77(75%)	2/77(2%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCGT-AAAACCTTTGTATAGCAATACAGCTCGTCTTCCAGCAG  59
            ||||||||||||||||||| | ||||  ||   | ||||| | |   | |  ||||   |
Sbjct  77   GGCAATCCTGAGCCAAATCCTAAAAAGATTCAGAAAGCAAGA-ATAACATAATCCAAGGG  135

Query  60   GATAGGTGCAGAGACTC  76
            |||||||||||||||||
Sbjct  136  GATAGGTGCAGAGACTC  152
```

Staurastrum punctulatum chloroplast, complete genome

Sequence ID: **gb|AY958085.1|** Length: 157089 Number of Matches: 1
Range 1: 68338 to 68367

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.051()	28/30(93%)	0/30(0%)	Plus/Plus	

Features:

```
Query  1      GGCAATCCTGAGCCAAATCGTAAAACCTTT  30
              ||||||||||||||||||| |||||| |||
Sbjct  68338  GGCAATCCTGAGCCAAATCCTAAAACTTTT  68367
```

Syngonanthus flavidulus tRNA-Leu (trnL) gene, partial sequence; chloroplast

Sequence ID: **gb|DQ189019.1|** Length: 464 Number of Matches: 1
Range 1: 102 to 184

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	0.18()	60/83(72%)	7/83(8%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCGTAAAACCTTTGTATAGCAATACA---GCTCGT----CTTC  53
            || |||||||||||||||| |||  |||  |||||  || |||   | |  |    |||
Sbjct  102  GGTAATCCTGAGCCAAATCCTAAGTCCTAAGTATAATAAAACAAGGGTTTATCAAACTTG  161

Query  54   CAGCAGGATAGGTGCAGAGACTC  76
             |  ||||||||||||||||||
Sbjct  162  AAAAAGGATAGGTGCAGAGACTC  184
```

BLAST ®

Basic Local Alignment Search Tool

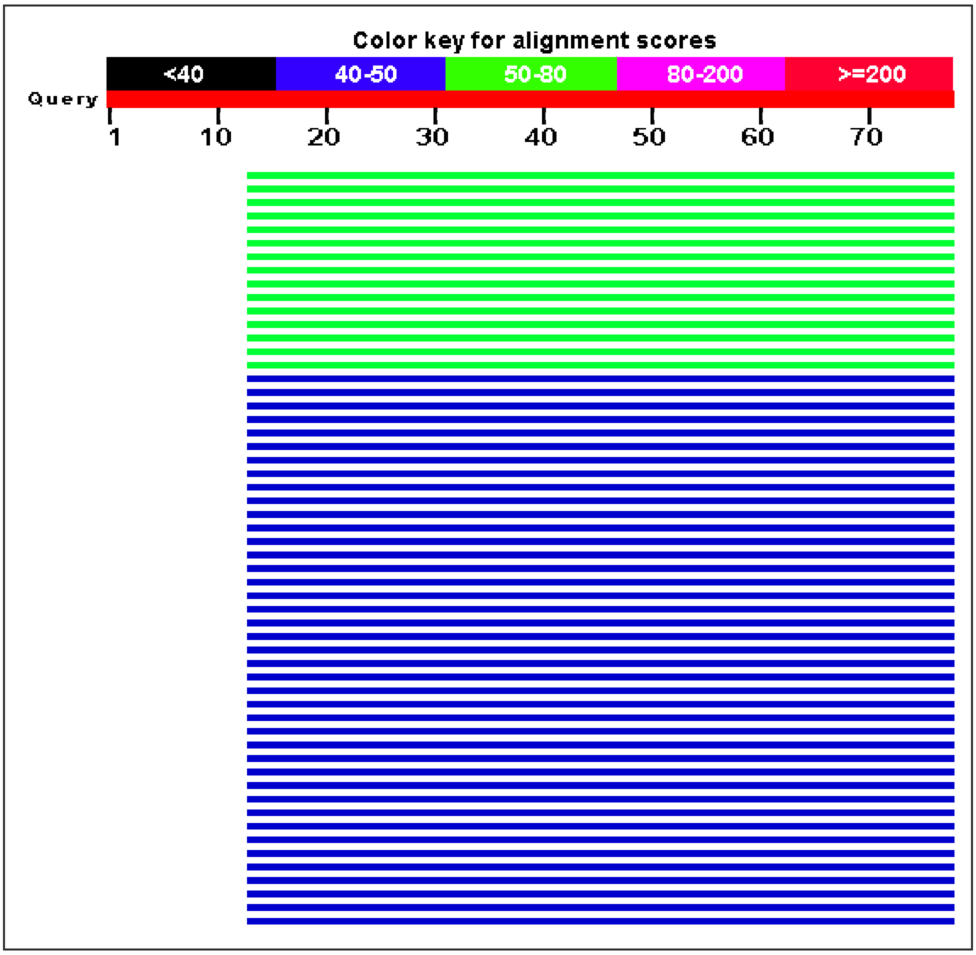
NCBI/ BLAST/ blastn suite/ **Formatting Results - BTVASJFT014**
Formatting options
Download
Blast report description

YK08-AB9-L7B_trnL_Clone8

RID	BTVASJFT014 (Expires on 02-13 03:21 am)		
Query ID	lcl|Query_112745	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	78		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Osmunda vachellii tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	53.6	53.6	83%	4e-04	81%	FJ262720.1
Osmunda mildei tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	53.6	53.6	83%	4e-04	81%	FJ262718.1
Osmunda japonica tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	53.6	53.6	83%	4e-04	81%	FJ262717.1
Osmunda vachellii voucher Mickel & Beitel s.n. (UC) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	53.6	53.6	83%	4e-04	81%	EF588818.1
Osmunda regalis voucher Schwertfeger 2 (GOET) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	53.6	53.6	83%	4e-04	81%	EF588817.1
Osmunda regalis voucher Schwertfeger 1 (GOET) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	53.6	53.6	83%	4e-04	81%	EF588816.1
Osmunda regalis voucher M.J.M. Christenhusz 4271 (DUKE, TUR) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	53.6	53.6	83%	4e-04	81%	EF588815.1
Osmunda lancea voucher K. Hirai 99-0305 (KYO) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	53.6	53.6	83%	4e-04	81%	EF588813.1
Osmunda javanica voucher Cubey 49 (E) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	53.6	53.6	83%	4e-04	81%	EF588812.1
Osmunda japonica voucher Y. Yatabe 99-0303 (KYO) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	53.6	53.6	83%	4e-04	81%	EF588811.1
Osmunda claytoniana voucher S. Nemoto 99-307 (KYO) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	53.6	53.6	83%	4e-04	81%	EF588810.1
Osmunda claytoniana voucher T. Bradley 7411 (GMUF) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	53.6	53.6	83%	4e-04	81%	EF588809.1
Osmunda banksiifolia voucher Cubey 55 (E) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	53.6	53.6	83%	4e-04	81%	EF588808.1
Osmunda regalis isolate CR009 tRNA-Leu gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	53.6	53.6	83%	4e-04	81%	AY651837.1
Paepalanthus tuberosus isolate FS1641 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	51.8	51.8	83%	0.001	79%	EU924486.1
Ephedra foeminea voucher K. Bolinder 542 chloroplast, complete genome	50.0	50.0	83%	0.004	78%	KT934791.1
Ephedra sinica haplotype H8 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL)						

gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KT033395.1
Ephedra sinica haplotype H7 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KT033394.1
Ephedra sinica haplotype H6 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KT033393.1
Ephedra foeminea haplotype H24 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	83%	0.004	78%	KT033390.1
Ephedra viridis voucher Elias & Morefield 10376 (MEXU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KP788807.1
Ephedra tweediana voucher Ickert-Bond 1225 (ASU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KP788806.1
Ephedra triandra voucher Ickert-Bond 1227 (ASU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KP788805.1
Ephedra torreyana voucher Gentry & Engard 23198 (MEXU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KP788804.1
Ephedra sinica voucher 986 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KP788803.1
Ephedra rupestris voucher Ickert-Bond 1220 (ASU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KP788802.1
Ephedra rupestris voucher Ickert-Bond 1110 (ASU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KP788801.1
Ephedra pseudodistachya voucher Freitag 33002 (KAS) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KP788800.1
Ephedra ochreata voucher Muhlen s.n. tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KP788799.1
Ephedra multiflora voucher Ickert-Bond 1211 (ASU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KP788798.1
Ephedra minuta voucher JBM1106 00 tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KP788796.1

Ephedra intermedia voucher XJ 08070801 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KP788794.1
Ephedra gracilis voucher Ickert-Bond 1201 (ASU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KP788793.1
Ephedra intermedia voucher YYNH08070502 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KP788792.1
Ephedra funerea voucher Ickert-Bond 473 (ASU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KP788791.1
Ephedra funerea voucher Ickert-Bond 964 (ASU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KP788790.1
Ephedra frustillata voucher Ickert-Bond 1247 (ASU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KP788789.1
Ephedra breana voucher Ickert-Bond 1234 (ASU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KP788788.1
Ephedra boelckei voucher Ickert-Bond 1252 (ASU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KP788787.1
Ephedra boelckei voucher Ickert-Bond 1251 (ASU) trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KP788786.1
Ephedra aphylla voucher Freitag 30181 (KAS) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	78%	KP788785.1
Ephedra americana voucher Ickert-Bond 1105 (ASU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KP788784.1
Vicia kotschyana isolate 64063 tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	78%	KJ787258.1
Osmundastrum cinnamomeum chloroplast, complete genome	50.0	50.0	83%	0.004	79%	KF225592.1
Ephedra major isolate H26 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	83%	0.004	78%	KC407803.1
Ephedra equisetina isolate H23 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KC407800.1
Ephedra przewalskii isolate H21 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF	50.0	50.0	83%	0.004	76%	KC407798.1

intergenic spacer, partial sequence; chloroplast						
Ephedra przewalskii isolate H20 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KC407797.1
Ephedra intermedia isolate H19 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KC407796.1
Ephedra intermedia isolate H16 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KC407793.1
Ephedra saxatilis var. mairei isolate H13 tRNA-Thr (trnT) gene, partial sequence; and trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; chloroplast	50.0	50.0	83%	0.004	76%	KC407790.1
Ephedra saxatilis var. mairei isolate H12 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KC407789.1
Ephedra saxatilis var. mairei isolate H11 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KC407788.1
Ephedra saxatilis var. mairei isolate H9 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KC407786.1
Ephedra rituensis isolate H7 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KC407784.1
Ephedra saxatilis isolate H4 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KC407781.1
Ephedra gerardiana isolate H1 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	KC407778.1
Ephedra trifurca voucher Reina-G. & Van Devender 96-208 (MEXU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	JX217737.1
Ephedra nevadensis voucher Felger & Dimmitt 85-724 (MEXU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	JX217734.1
Ephedra nevadensis voucher Phillips & Phillips 93141 (MEXU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu	50.0	50.0	83%	0.004	76%	JX217733.1

(trnL) gene, partial sequence; chloroplast						
Ephedra aspera voucher Spellenberg & Bacon s.n. (MEXU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	JX217721.1
Ephedra antisyphilitica voucher Loera 22 (XAL) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	JX217719.1
Ephedra foeminea voucher H. Freitag 19.807 (KAS) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	78%	GU111523.1
Ephedra distachya voucher H. Freitag 28.834 (KAS) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	GU111514.1
Ephedra dahurica voucher H. Freitag 33.130 (KAS) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	GU111507.1
Ephedra distachya voucher H. Freitag 33.259 (KAS) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	GU111506.1
Hordeum comosum chloroplast tRNA-Leu gene (partial), trnL-trnF intergenic spacer and tRNA-Phe gene (partial), haplotype HT121	50.0	50.0	83%	0.004	77%	FM163524.1
Osmundastrum cinnamomeum voucher Hasebe 27624 (TI, KYO) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	83%	0.004	79%	EF588821.1
Osmundastrum cinnamomeum voucher M.J.M. Christenhusz 3380 (IJ, TUR) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	83%	0.004	79%	EF588819.1
Osmunda regalis voucher M.J.M. Christenhusz 4245 (DUKE, TUR) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	83%	0.004	79%	EF588814.1
Ephedra gerardiana tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	83%	0.004	76%	EU326056.1
Ephedra torreyana tRNA-Thr (trnT) gene, partial sequence; and trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; chloroplast	50.0	50.0	83%	0.004	76%	AY513736.1
Ephedra viridis tRNA-Thr (trnT) gene, partial sequence; and tRNA-Leu (trnL) gene, complete sequence; chloroplast	50.0	50.0	83%	0.004	76%	AY513735.1
Ephedra trifurca tRNA-Thr (trnT) gene, partial sequence; and trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; chloroplast	50.0	50.0	83%	0.004	76%	AY513734.1
Ephedra przewalskii voucher Kamp03071340 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	AY730598.1
Georgeantha hexandra tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	79%	AF148733.1
Ephedra viridis tRNA-Leu (trnL) gene, intron sequence; chloroplast gene for chloroplast product	50.0	50.0	83%	0.004	76%	AF479869.1
Ephedra minuta voucher 1017 tRNA-Leu						

(trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	AY423439.1
Ephedra minuta tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	AY423438.1
Ephedra sinica tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	AY423431.1
Ephedra intermedia tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	50.0	50.0	83%	0.004	76%	AY423430.1
Lygodium japonicum chloroplast, complete genome	48.2	48.2	83%	0.015	78%	KF225593.1
Lygodium japonicum chloroplast, complete genome	48.2	48.2	83%	0.015	78%	KC536645.1
Lygodium flexuosum voucher L82C tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	83%	0.015	77%	DQ845239.1
Lygodium flexuosum voucher L82AS tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	83%	0.015	77%	DQ845238.1
Lygodium flexuosum voucher L180A tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	83%	0.015	77%	DQ845235.1
Lygodium japonicum voucher L51B tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	83%	0.015	78%	DQ845232.1
Lygodium japonicum voucher L57B tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	83%	0.015	78%	DQ845231.1
Avena barbata isolate AG06 tRNA-Leu (trnL-UAA) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	46.4	46.4	83%	0.053	75%	KF996088.1
Eupomatia bennettii tRNA-Leu (trnL) gene, intron; chloroplast	46.4	46.4	83%	0.053	75%	KF586705.1
Eupomatia laurina voucher UQ WellsJ 83-Elr tRNA-Leu (trnL) gene and trnL-F intergenic spacer, partial sequence; chloroplast	46.4	46.4	83%	0.053	75%	KC428512.1
Eupomatia barbata voucher QRS 129447 tRNA-Leu (trnL) gene and trnL-F intergenic spacer, partial sequence; chloroplast	46.4	46.4	83%	0.053	75%	KC428511.1
Avena fatua voucher PI 447299 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	46.4	46.4	83%	0.053	75%	GU367222.1
Avena damascena voucher CN 19457 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	46.4	46.4	83%	0.053	75%	GU367219.1
Juniperus hybrid sp. LO-2009 voucher J.Q. Liu 1216_14 trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	46.4	46.4	83%	0.053	76%	GQ285837.1
Avena damascena voucher CN 19459 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence	46.4	46.4	83%	0.053	75%	EU833870.1
Avena damascena isolate 7261 tRNA-Leu (trnL) gene, intron; chloroplast	46.4	46.4	83%	0.053	75%	EU276595.1
Eupomatia bennettii isolate 1411 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	46.4	46.4	83%	0.053	75%	DQ861842.1
Welwitschia mirabilis plastid, complete genome	44.6	44.6	30%	0.19	100%	KT347148.1

Ephedra equisetina haplotype H15 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	44.6	44.6	83%	0.19	75%	KT033392.1

Alignments

Osmunda vachellii tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|FJ262720.1|** Length: 849 Number of Matches: 1
Range 1: 18 to 81

Score	Expect	Identities	Gaps	Strand	Frame
53.6 bits(58)	4e-04()	54/67(81%)	5/67(7%)	Plus/Plus	

Features:

```
Query  14  GGCAATCCTGAGCCAAATCCAAGTC--GGAGCTAGCATCCATTGATGAAGGATAGGTGCA  71
           |||||||||||||||||||    ||  ||||| || |||||   ||||  ||||||||||
Sbjct  18  GGCAATCCTGAGCCAAATCTTGTTCCAGGAGC-AGGATCCAAAAATGA--GATAGGTGCA  74

Query  72  GAGACTC  78
           |||||||
Sbjct  75  GAGACTC  81
```

Osmunda mildei tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|FJ262718.1|** Length: 885 Number of Matches: 1
Range 1: 45 to 108

Score	Expect	Identities	Gaps	Strand	Frame
53.6 bits(58)	4e-04()	54/67(81%)	5/67(7%)	Plus/Plus	

Features:

```
Query  14   GGCAATCCTGAGCCAAATCCAAGTC--GGAGCTAGCATCCATTGATGAAGGATAGGTGCA  71
            |||||||||||||||||||    ||  ||||| || |||||   ||||  ||||||||||
Sbjct  45   GGCAATCCTGAGCCAAATCTTGTTCCAGGAGC-AGGATCCAAAAATGA--GATAGGTGCA  101

Query  72   GAGACTC  78
            |||||||
Sbjct  102  GAGACTC  108
```

Osmunda japonica tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|FJ262717.1|** Length: 934 Number of Matches: 1
Range 1: 15 to 78

Score	Expect	Identities	Gaps	Strand	Frame
53.6 bits(58)	4e-04()	54/67(81%)	5/67(7%)	Plus/Plus	

Features:

```
Query  14  GGCAATCCTGAGCCAAATCCAAGTC--GGAGCTAGCATCCATTGATGAAGGATAGGTGCA  71
           |||||||||||||||||||    ||  ||||| || |||||   ||||  ||||||||||
Sbjct  15  GGCAATCCTGAGCCAAATCTTGTTCCAGGAGC-AGGATCCAAAAATGA--GATAGGTGCA  71

Query  72  GAGACTC  78
           |||||||
Sbjct  72  GAGACTC  78
```

Osmunda vachellii voucher Mickel & Beitel s.n. (UC) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|EF588818.1|** Length: 981 Number of Matches: 1
Range 1: 82 to 145

Score	Expect	Identities	Gaps	Strand	Frame
53.6 bits(58)	4e-04()	54/67(81%)	5/67(7%)	Plus/Plus	

Features:

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Query  14   GGCAATCCTGAGCCAAATCCAAGTC--GGAGCTAGCATCCATTGATGAAGGATAGGTGCA  71
            |||||||||||||||||||    ||  ||||| || |||||   ||||  ||||||||||
Sbjct  82   GGCAATCCTGAGCCAAATCTTGTTCCAGGAGC-AGGATCCAAAAATGA--GATAGGTGCA  138

Query  72   GAGACTC  78
            |||||||
Sbjct  139  GAGACTC  145
```

Osmunda regalis voucher Schwertfeger 2 (GOET) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|EF588817.1|** Length: 919 Number of Matches: 1
Range 1: 49 to 112

Score	Expect	Identities	Gaps	Strand	Frame
53.6 bits(58)	4e-04()	54/67(81%)	5/67(7%)	Plus/Plus	

Features:

```
Query  14    GGCAATCCTGAGCCAAATCCAAGTC--GGAGCTAGCATCCATTGATGAAGGATAGGTGCA  71
             |||||||||||||||||||    ||  ||||| || |||||   ||||  ||||||||||
Sbjct  49    GGCAATCCTGAGCCAAATCTTGTTCCAGGAGC-AGGATCCAAAAATGA--GATAGGTGCA  105

Query  72    GAGACTC  78
             |||||||
Sbjct  106   GAGACTC  112
```

BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BTV7NDWC014**

Formatting options
Download

Blast report description

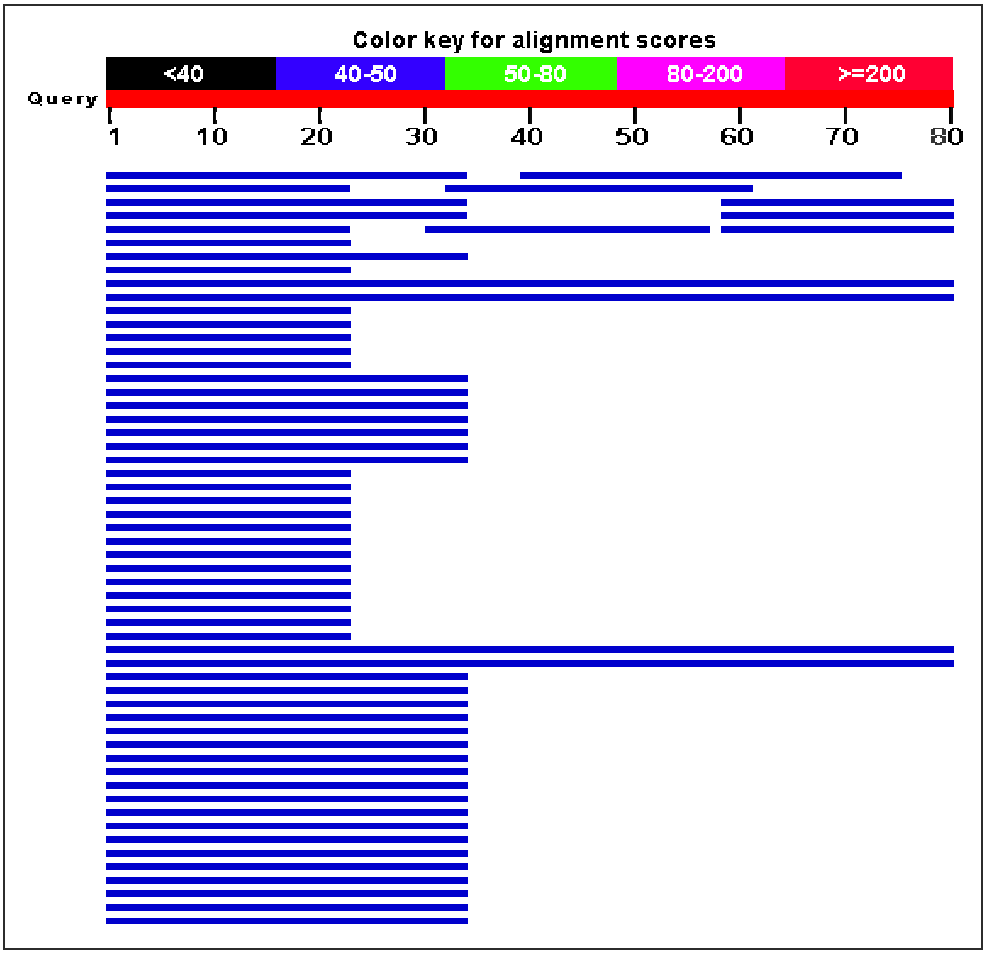
YK08-AB9-L7B_trnL_Clone9

RID BTV7NDWC014 (Expires on 02-13 03:20 am)

Query ID	lcl|Query_230983	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	80		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Geoalkalibacter subterraneus strain Red1, complete genome	44.6	44.6	45%	0.19	89%	CP010311.1
Emiliania huxleyi CCMP1516 hypothetical protein partial mRNA	44.6	44.6	36%	0.19	93%	XM_005789341.1
Stipa purpurea voucher SPUR20151101 chloroplast, complete genome	42.8	42.8	42%	0.68	89%	KT983629.1
Piptochaetium avenaceum voucher CAN:R.J. Soreng & K. Romaschenko 430 plastid, complete genome	42.8	42.8	42%	0.68	89%	KM974748.1
Ampelodesmos mauritanicus voucher B:Royl & Schiers s.n. plastid, complete genome	42.8	42.8	42%	0.68	89%	KM974731.1
Hydrilla verticillata isolate A2 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	28%	0.68	100%	KM982396.1
Hydrilla verticillata isolate A1 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	28%	0.68	100%	KM982395.1
Andreadoxa flava voucher Groppo 1562 (SPFR) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	28%	0.68	100%	KP866586.1
Piptochaetium montevidense isolate P003 tRNA-Leu (trnL) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	KP057669.1
Primulina bullata isolate GXJX06 tRNA-Leu (tRNA-Leu) gene, partial sequence; trnL-F intergenic spacer, complete sequence; and tRNA-Phe (tRNA-Phe) gene, partial sequence; chloroplast	42.8	42.8	28%	0.68	100%	KF498184.1
Hydrocotyle novae-zealandiae voucher Allan Herbarium CHR 630405 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	100%	0.68	73%	KF591269.1
Hydrocotyle novae-zealandiae voucher Allan Herbarium CHR 630394 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	100%	0.68	73%	KF591253.1
Myosotis alpestris tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	28%	0.68	100%	JX976916.1
Myosotis olympica chloroplast gene for tRNA-Leu (trnL) and trnL-trnF intergenic spacer, partial and complete sequence, specimen_voucher: TARI:65961	42.8	42.8	28%	0.68	100%	AB758343.1
Myosotis lithospermifolia chloroplast gene for tRNA-Leu (trnL) and trnL-trnF intergenic spacer, partial and complete sequence, specimen_voucher: TARI:18179	42.8	42.8	28%	0.68	100%	AB758342.1
Collomia debilis subsp. trifida voucher						

BRY:04-171 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	28%	0.68	100%	HQ117060.1
Myosotis alpestris tRNA-Leu (trnL) gene, intron; chloroplast	42.8	42.8	28%	0.68	100%	HQ323971.1
Anatherostipa orurensis voucher Peterson at al. 12987 (MO) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	GU192019.1
Ortachne erectifolia voucher Wood 5263 (MO) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	GU192016.1
Ptilagrostis porteri voucher Barkworth 99117 (COAH) tRNA-Leu (trnL) gene, trnL-trnF intergenic spacer, and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	GU192014.1
Amelichloa brevipes voucher Humano 3 (SI) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	GU192013.1
Ortachne erectifolia voucher Morrone 4724 (SI) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	GU192010.1
Aciachne flagellifera voucher Laegaard 54503 (MO) tRNA-Leu (trnL) gene, trnL-trnF intergenic spacer, and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	GU192002.1
Aciachne pulvinata voucher Laegaard 55350 (MO) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	GU192001.1
Primula chionantha isolate P.chioH156 tRNA-Leu (trnL) gene and trnL(UAA)-trnF(GAA) intergenic spacer, partial sequence; chloroplast	42.8	42.8	28%	0.68	100%	FJ794199.1
Caryocar glabrum voucher NH200116 tRNA-Leu(UAA) (trnL) gene, intron; chloroplast	42.8	42.8	28%	0.68	100%	FJ039259.1
Caryocar glabrum voucher NL110014 tRNA-Leu(UAA) (trnL) gene, intron; chloroplast	42.8	42.8	28%	0.68	100%	FJ039114.1
Myosotis alpestris isolate 1682o tRNA-Leu (trnL) gene, partial sequence; chloroplast	42.8	42.8	28%	0.68	100%	GQ245141.1
Myosotis alpestris isolate 1115o tRNA-Leu (trnL) gene, partial sequence; chloroplast	42.8	42.8	28%	0.68	100%	GQ245140.1
Caryocar brasiliense isolate BTOF1 tRNA-Leu (trnL) gene, intron; chloroplast	42.8	42.8	28%	0.68	100%	EU339920.1
Caryocar microcarpum isolate MPF02L tRNA-Leu (trnL) gene, intron; chloroplast	42.8	42.8	28%	0.68	100%	EU339918.1
Caryocar microcarpum isolate MRA22R tRNA-Leu (trnL) gene, intron; chloroplast	42.8	42.8	28%	0.68	100%	EU339916.1
Caryocar microcarpum isolate						

MSB28R tRNA-Leu (trnL) gene, intron; chloroplast	42.8	42.8	28%	0.68	100%	EU339889.1
Caryocar microcarpum isolate MMR40R tRNA-Leu (trnL) gene, intron; chloroplast	42.8	42.8	28%	0.68	100%	EU339882.1
Caryocar microcarpum isolate MMR38R tRNA-Leu (trnL) gene, intron; chloroplast	42.8	42.8	28%	0.68	100%	EU339880.1
Caryocar microcarpum isolate MJA17L tRNA-Leu (trnL) gene, intron; chloroplast	42.8	42.8	28%	0.68	100%	EU339876.1
Caryocar villosum isolate VRD13L tRNA-Leu (trnL) gene, intron; chloroplast	42.8	42.8	28%	0.68	100%	EU339829.1
Ruta montana voucher Lewalle J. 9612 (Z) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	100%	0.68	75%	EF489211.1
Ruta montana voucher Renaux 349 (Z) tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	100%	0.68	75%	EF489210.1
Jarava neaei voucher BA 81433 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	EU200924.1
Ptilagrostis porteri voucher UTC 227957 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	EU200923.1
Ptilagrostis kingii voucher UTC 173686 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	EU200921.1
Piptochaetium bicolor voucher BA 80508 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	EU200917.1
Piptochaetium stipoides voucher BA 80510 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	EU200919.1
Piptochaetium fimbriatum voucher BA 76525 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	EU200918.1
Piptochaetium bicolor voucher BA 91108 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	EU200916.1
Piptatherum racemosum voucher UTC 225634 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	EU200914.1
Piptatherum micranthum voucher UTC 191276 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	EU200909.1
Piptatherum canadense voucher UTC 238734 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	EU200906.1
Jarava vaginata voucher BA 91002 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	EU200901.1
Jarava chubutensis voucher BA 81509 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	EU200883.1
Nassella trichotoma voucher BA 91103 tRNA-Leu (trnL) gene and trnL-trnF						

intergenic spacer, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	EU200880.1
Nassella hyalina voucher BA 91107 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	EU200869.1
Anatherostipa obtusa voucher UTC 136726 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	EU200841.1
Anatherostipa bomanii voucher UTC 210632 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	EU200839.1
Ampelodesmos mauritanicus voucher UTC 246449 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	EU200838.1
Aciachne pulvinata voucher UTC 203408 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	EU200822.1
Aciachne pulvinata voucher UTC 210601 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	EU200821.1
Achnatherum stillmanii voucher UTC 235202 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	EU200807.1
Hydrilla verticillata isolate Tank 37 (TG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	28%	0.68	100%	EF458060.1
Hydrilla verticillata isolate HSA 1-4 (SA) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	28%	0.68	100%	EF458055.1
Piptochaetium virescens tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	DQ887480.1
Piptochaetium uruguense tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	DQ887479.1
Piptochaetium tovarii tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	DQ887478.1
Piptochaetium stipoides var. stipoides tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	DQ887477.1
Piptochaetium stipoides var. echinulatum tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	DQ887476.1
Piptochaetium setosum tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial	42.8	42.8	42%	0.68	89%	DQ887475.1

sequence; chloroplast						
Piptochaetium seleri tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	DQ887474.1
Piptochaetium sagasteguii tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	DQ887473.1
Piptochaetium ruprechtianum tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	DQ887472.1
Piptochaetium pilosum tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	DQ887471.1
Piptochaetium panicoides tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	DQ887470.1
Piptochaetium napostaense tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	DQ887469.1
Piptochaetium montevidense tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	DQ887468.1
Piptochaetium medium tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	DQ887467.1
Piptochaetium leiopodum tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	DQ887466.1
Piptochaetium lasianthum tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	DQ887465.1
Piptochaetium indutum tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	DQ887464.1
Piptochaetium hackelii tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	DQ887463.1
Piptochaetium fimbriatum tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	DQ887462.1
Piptochaetium calvescens tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	DQ887461.1
Piptochaetium bicolor tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence;	42.8	42.8	42%	0.68	89%	DQ887460.1

and tRNA-Phe (trnF) gene, partial sequence; chloroplast						
Piptochaetium avenaceum tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	DQ887459.1
Anatherostipa brevis tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	DQ887427.1
Aciachne acicularis tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	42%	0.68	89%	DQ887426.1
Cuscuta corymbosa var. stylosa voucher Medrano et al 7965 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	28%	0.68	100%	EF194347.1
Cuscuta prismatica voucher Mille 112 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	28%	0.68	100%	EF194346.1
Cuscuta corymbosa var. grandiflora voucher Tellez 9976 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	28%	0.68	100%	EF194345.1
Cuscuta corymbosa var. grandiflora voucher Iltis & Guzman 29077 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	42.8	42.8	28%	0.68	100%	EF194343.1
Primula nivalis tRNA-Leu (trnL) gene, intron; chloroplast	42.8	42.8	28%	0.68	100%	DQ378580.1
Primula nivalis tRNA-Leu (trnL) gene, intron; chloroplast	42.8	42.8	28%	0.68	100%	DQ378579.1
Primula orbicularis tRNA-Leu (trnL) gene, intron; chloroplast	42.8	42.8	28%	0.68	100%	DQ378578.1
Primula chionantha subsp. chionantha tRNA-Leu (trnL) gene, intron; chloroplast	42.8	42.8	28%	0.68	100%	DQ378577.1
Primula chionantha subsp. sinopurpurea tRNA-Leu (trnL) gene, intron; chloroplast	42.8	42.8	28%	0.68	100%	DQ378576.1
Hydrocotyle bowlesioides tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	42.8	42.8	100%	0.68	73%	AY393699.1
Nylandtia spinosa tRNA-Leu gene intron	42.8	42.8	100%	0.68	73%	AJ829617.1
Welwitschia mirabilis plastid, complete genome	41.0	41.0	27%	2.4	100%	KT347148.1
Rugoloa pilosa voucher C. Silva & N.M. Correa 335 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	41.0	41.0	27%	2.4	100%	KP879152.1
Myxococcus sp. mixupus, complete genome	41.0	41.0	33%	2.4	93%	CP012109.1
Barleria spinisepala trnL-trnF intergenic spacer, partial sequence; chloroplast	41.0	41.0	27%	2.4	100%	KR738690.1

Alignments

Geoalkalibacter subterraneus strain Red1, complete genome

Sequence ID: **gb|CP010311.1|** Length: 3475523 Number of Matches: 1
Range 1: 3247998 to 3248032

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	0.19()	32/36(89%)	1/36(2%)	Plus/Minus	

Features:
278 bp at 5' side: hypothetical protein116 bp at 3' side: hypothetical protein

```
Query  40       CAGGAGGTTGCGCACCAGGTTGGATTTGGCTCAGGA  75
                |||| || ||| ||||| ||||||||||||||||||
Sbjct  3248032  CAGG-GGATGCCCACCAAGTTGGATTTGGCTCAGGA  3247998
```

Emiliania huxleyi CCMP1516 hypothetical protein partial mRNA

Sequence ID: **ref|XM_005789341.1|** Length: 900 Number of Matches: 1
Range 1: 723 to 751

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	0.19()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

```
Query  33   GCACCTCCAGGAGGTTGCGCACCAGGTTG  61
            || |||||||||||||||||||||| |||
Sbjct  751  GCGCCTCCAGGAGGTTGCGCACCAGCTTG  723
```

Stipa purpurea voucher SPUR20151101 chloroplast, complete genome

Sequence ID: **gb|KT983629.1|** Length: 137370 Number of Matches: 1
Range 1: 47235 to 47269

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	0.68()	31/35(89%)	1/35(2%)	Plus/Minus	

Features:

```
Query  1      GAGTCTCTGCACCTATCCTC-CTTGCGAGAACCGC  34
              ||||||||||||||||||||   | ||||||||||
Sbjct  47269  GAGTCTCTGCACCTATCCTCTAGTTCGAGAACCGC  47235
```

Piptochaetium avenaceum voucher CAN:R.J. Soreng & K. Romaschenko 430 plastid, complete genome

Sequence ID: **gb|KM974748.1|** Length: 137701 Number of Matches: 1
Range 1: 47552 to 47586

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	0.68()	31/35(89%)	1/35(2%)	Plus/Minus	

Features:

```
Query  1      GAGTCTCTGCACCTATCCTC-CTTGCGAGAACCGC  34
              ||||||||||||||||||||   | ||||||||||
Sbjct  47586  GAGTCTCTGCACCTATCCTCTAGTTCGAGAACCGC  47552
```

Ampelodesmos mauritanicus voucher B:Royl & Schiers s.n. plastid, complete genome

Sequence ID: **gb|KM974731.1|** Length: 136937 Number of Matches: 1
Range 1: 46550 to 46584

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	0.68()	31/35(89%)	1/35(2%)	Plus/Minus	

Features:

```
Query  1      GAGTCTCTGCACCTATCCTC-CTTGCGAGAACCGC  34
              ||||||||||||||||||||   | ||||||||||
Sbjct  46584  GAGTCTCTGCACCTATCCTCTAGTTCGAGAACCGC  46550
```

BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BTWK40YY014**
Formatting options
Download
Blast report description

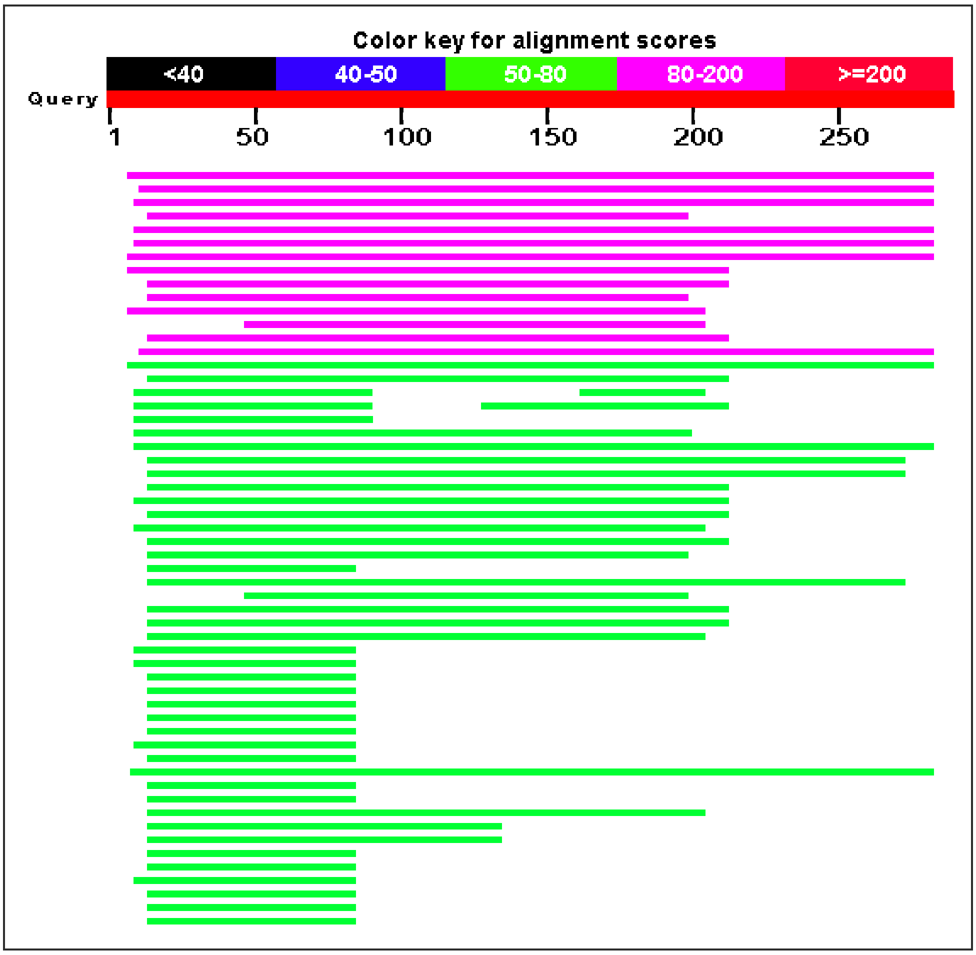
YK08AB9L7B_TRNL1_C4

RID BTWK40YY014 (Expires on 02-13 03:43 am)

Query ID	lcl|Query_49083	**Database Name**	nr
Description	YK08AB9L7B_TRNL1_C4	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	290		

Graphic Summary

Distribution of 107 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Acidovorax sp. KKS102, complete genome	100	100	95%	2e-17	69%	CP003872.1
Uncultured bacterium clone contig10067 genomic sequence	91.5	91.5	93%	8e-15	68%	KP424940.1
Methylibium petroleiphilum PM1, complete genome	87.8	87.8	94%	1e-13	68%	CP000555.1
Ralstonia eutropha H16 chromosome 1	87.8	87.8	63%	1e-13	71%	AM260479.1
Alicycliphilus denitrificans K601, complete genome	86.0	86.0	94%	4e-13	68%	CP002657.1
Alicycliphilus denitrificans BC, complete genome	86.0	86.0	94%	4e-13	68%	CP002449.1
Acidovorax ebreus TPSY, complete genome	86.0	86.0	95%	4e-13	67%	CP001392.1
Verminephrobacter eiseniae EF01-2, complete genome	86.0	86.0	71%	4e-13	70%	CP000542.1
Ralstonia pickettii DTP0602 chromosome 1, complete sequence	84.2	84.2	68%	1e-12	71%	CP006667.1
Cupriavidus necator N-1 chromosome 1, complete sequence	84.2	84.2	63%	1e-12	71%	CP002877.1
Acidovorax sp. JS42, complete genome	84.2	84.2	68%	1e-12	70%	CP000539.1
Comamonas testosteroni TK102, complete genome	82.4	82.4	54%	4e-12	72%	CP006704.1
Cupriavidus taiwanensis str. LMG19424 chromosome 1, complete genome	82.4	82.4	68%	4e-12	69%	CU633749.1
Comamonadaceae bacterium A1 DNA, complete genome	80.6	80.6	93%	1e-11	67%	AP014568.1
PREDICTED: Pantholops hodgsonii probable replicative DNA helicase-like (LOC102340214), mRNA	77.0	77.0	95%	2e-10	67%	XM_005965581.1
Ralstonia solanacearum CMR15 chromosome, complete genome	77.0	77.0	68%	2e-10	70%	FP885895.1
Achromobacter xylosoxidans genome assembly NCTC10807, chromosome : 1	71.6	71.6	28%	8e-09	79%	LN831029.1
Achromobacter xylosoxidans C54, complete genome	71.6	71.6	28%	8e-09	79%	CP009448.1
Achromobacter xylosoxidans NH44784-1996 complete genome	71.6	71.6	28%	8e-09	79%	HE798385.1
Paucibacter sp. KCTC 42545, complete genome	69.8	69.8	65%	3e-08	69%	CP013692.1
Ramlibacter tataouinensis TTB310, complete genome	69.8	69.8	94%	3e-08	66%	CP000245.1
Ralstonia solanacearum Po82, complete genome	69.8	69.8	89%	3e-08	68%	CP002819.1
Ralstonia solanacearum CFBP2957 chromosome complete genome	69.8	69.8	89%	3e-08	68%	FP885897.1
Ralstonia solanacearum genome assembly 9 genomes, chromosome : I	68.0	68.0	68%	9e-08	69%	LN899819.1
Limnohabitans sp. 63ED37-2, complete genome	68.0	68.0	70%	9e-08	68%	CP011774.1
Cupriavidus gilardii CR3 chromosome 1, complete sequence	68.0	68.0	68%	9e-08	68%	CP010516.1
Herbaspirillum hiltneri N3, complete	68.0	68.0	67%	9e-08	68%	CP011409.1

genome						
blood disease bacterium R229, genomic contig 00003-1626	68.0	68.0	68%	9e-08	69%	FR854076.1
Cupriavidus metallidurans CH34, complete genome	68.0	68.0	63%	9e-08	69%	CP000352.1
Pseudomonas stutzeri RCH2, complete genome	66.2	66.2	24%	3e-07	80%	CP003071.1
Ralstonia solanacearum strain UY031, complete genome	64.4	64.4	89%	1e-06	68%	CP012687.1
Comamonas testosteroni P19 genome assembly Comamonas testosteroni P19, chromosome : I	62.6	62.6	52%	4e-06	69%	LN879547.1
Ralstonia syzygii R24, genomic contig 00001-1628	62.6	62.6	68%	4e-06	68%	FR854086.1
Ralstonia solanacearum str. PSI07 chromosome, complete genome	62.6	62.6	68%	4e-06	68%	FP885906.2
Ralstonia pickettii 12J chromosome 1, complete sequence	62.6	62.6	65%	4e-06	69%	CP001068.1
Achromobacter denitrificans strain USDA-ARS-USMARC-56712, complete genome	60.8	60.8	26%	1e-05	78%	CP013923.1
Massilia sp. WG5, complete genome	60.8	60.8	14%	1e-05	91%	CP012640.1
Achromobacter xylosoxidans strain MN001, complete genome	60.8	60.8	26%	1e-05	78%	CP012046.1
Pseudomonas stutzeri strain SLG510A3-8, complete genome	60.8	60.8	24%	1e-05	79%	CP011854.1
Pseudomonas fluorescens SBW25 plasmid pQBR55, complete sequence	60.8	112	24%	1e-05	83%	LN713927.1
Pseudomonas cremoricolorata strain ND07, complete genome	60.8	60.8	24%	1e-05	79%	CP009455.1
Pseudomonas stutzeri ATCC 17588 = LMG 11199, complete genome	60.8	60.8	24%	1e-05	79%	CP002881.1
Pseudomonas stutzeri DSM 4166, complete genome	60.8	60.8	24%	1e-05	79%	CP002622.1
Achromobacter xylosoxidans A8, complete genome	60.8	60.8	26%	1e-05	78%	CP002287.1
Pseudomonas stutzeri A1501, complete genome	60.8	60.8	24%	1e-05	79%	CP000304.1
Rhodoferax ferrireducens T118, complete genome	60.8	60.8	94%	1e-05	65%	CP000267.1
Pseudomonas sp. SLT2001 plasmid pQBR55	60.8	112	24%	1e-05	83%	AJ421512.3
Pseudomonas syringae pv. tomato str. DC3000, complete genome	60.8	60.8	24%	1e-05	79%	AE016853.1
Cupriavidus basilensis strain 4G11 chromosome main, complete sequence	59.0	59.0	65%	5e-05	67%	CP010536.1
Burkholderia sp. RPE67 DNA, complete genome, chromosome: 1	59.0	59.0	41%	5e-05	73%	AP014576.1
Burkholderia sp. YI23 chromosome 1, complete sequence	59.0	59.0	41%	5e-05	73%	CP003087.1
Pseudomonas oryzihabitans strain USDA-ARS-USMARC-56511, complete genome	57.2	57.2	24%	2e-04	77%	CP013987.1
Pseudomonas sp. URMO17WK12:I11 genome assembly Shine, chromosome : 1	57.2	57.2	24%	2e-04	77%	LN854573.1
Bordetella sp. N genome	57.2	57.2	26%	2e-04	76%	CP013111.1
Pseudomonas syringae pv. actinidiae ICMP 18884, complete genome	57.2	57.2	24%	2e-04	77%	CP011972.1
Pseudomonas trivialis strain IHBB745, complete genome	57.2	57.2	24%	2e-04	77%	CP011507.1
Pseudomonas fluorescens PICF7, complete genome	57.2	57.2	24%	2e-04	77%	CP005975.1

Pseudomonas fluorescens strain PCL1751, complete genome	57.2	57.2	24%	2e-04	77%	CP010896.1
Pseudomonas simiae strain WCS417 genome	57.2	57.2	24%	2e-04	77%	CP007637.1
Pseudomonas mandelii JR-1 plasmid, complete sequence	57.2	57.2	24%	2e-04	77%	CP005961.1
Pseudomonas cichorii JBC1, complete genome	57.2	57.2	24%	2e-04	77%	CP007039.1
Candidatus Symbiobacter mobilis CR, complete genome	57.2	57.2	71%	2e-04	66%	CP004885.1
Ralstonia eutropha JMP134 chromosome 1, complete sequence	57.2	57.2	63%	2e-04	68%	CP000090.1
Vibrio vulnificus strain FORC_009 chromosome 1, complete sequence	55.4	55.4	25%	6e-04	77%	CP009984.1
Vibrio anguillarum chromosome 1, strain NB10, complete sequence	55.4	55.4	25%	6e-04	77%	LK021130.1
Brugia timori genome assembly B_timori_Indonesia_v1_0_4, scaffold BTMF_contig0009673	55.4	55.4	29%	6e-04	74%	LK921785.1
Vibrio vulnificus strain 93U204 chromosome I, complete sequence	55.4	55.4	25%	6e-04	77%	CP009261.1
Listonella anguillarum M3 chromosome 1, complete sequence	55.4	55.4	25%	6e-04	77%	CP006699.1
Vibrio anguillarum 775 chromosome I, complete sequence	55.4	55.4	25%	6e-04	77%	CP002284.1
Vibrio vulnificus CMCP6 chromosome I, complete sequence	55.4	55.4	25%	6e-04	77%	AE016795.3
Vibrio vulnificus MO6-24/O chromosome I, complete sequence	55.4	55.4	25%	6e-04	77%	CP002469.1
Thiomonas sp. str. 3As chromosome, complete genome	55.4	55.4	63%	6e-04	67%	FP475956.1
Vibrio vulnificus YJ016 DNA, chromosome I, complete sequence	55.4	55.4	25%	6e-04	77%	BA000037.2
Pseudomonas aeruginosa strain T63266, complete genome	53.6	105	26%	0.002	76%	CP008868.1
Pandoraea apista strain DSM 16535, complete genome	53.6	53.6	24%	0.002	76%	CP013481.1
Ralstonia solanacearum genome assembly 9 genomes, chromosome : IV	53.6	53.6	68%	0.002	67%	LN899822.1
Ralstonia solanacearum genome assembly 9 genomes, chromosome : II	53.6	53.6	68%	0.002	67%	LN899820.1
Ralstonia solanacearum genome assembly 9 genomes, chromosome : IX	53.6	53.6	68%	0.002	67%	LN899827.1
Ralstonia solanacearum genome assembly 9 genomes, chromosome : VIII	53.6	53.6	68%	0.002	67%	LN899826.1
Ralstonia solanacearum genome assembly 9 genomes, chromosome : VII	53.6	53.6	68%	0.002	67%	LN899825.1
Ralstonia solanacearum genome assembly 9 genomes, chromosome : VI	53.6	53.6	68%	0.002	67%	LN899824.1
Ralstonia solanacearum genome assembly 9 genomes, chromosome : V	53.6	53.6	68%	0.002	67%	LN899823.1
Ralstonia solanacearum genome assembly 9 genomes, chromosome : III	53.6	53.6	68%	0.002	67%	LN899821.1
Pseudoalteromonas phenolica strain KCTC 12086 chromosome I, complete sequence	53.6	53.6	23%	0.002	78%	CP013187.1
Ralstonia solanacearum strain YC45, complete genome	53.6	53.6	68%	0.002	67%	CP011997.1
Bordetella hinzii strain H568, complete						

genome	53.6	53.6	26%	0.002	75%	CP012077.1
Bordetella hinzii strain F582, complete genome	53.6	53.6	26%	0.002	75%	CP012076.1
Pandoraea apista strain AU2161, complete genome	53.6	53.6	24%	0.002	76%	CP011501.1
Pandoraea apista strain TF80G25, complete genome	53.6	53.6	24%	0.002	76%	CP011279.1
Pandoraea apista strain TF81F4, complete genome	53.6	53.6	24%	0.002	76%	CP010518.3
Ralstonia mannitolilytica strain SN82F48 chromosome 1, complete sequence	53.6	53.6	68%	0.002	67%	CP010799.2
Pseudomonas mosselii SJ10, complete genome	53.6	96.3	24%	0.002	77%	CP009365.1
Ralstonia solanacearum FQY_4, complete genome	53.6	53.6	68%	0.002	67%	CP004012.1
Ralstonia solanacearum GMI1000 chromosome complete sequence	53.6	53.6	68%	0.002	67%	AL646052.1
Pseudomonas fragi strain P121, complete genome	51.8	51.8	24%	0.007	76%	CP013861.1
Pseudomonas aeruginosa strain F9670, complete genome	51.8	98.2	26%	0.007	76%	CP008873.1
Pseudomonas aeruginosa strain X78812, complete genome	51.8	51.8	24%	0.007	76%	CP008872.1
Pseudomonas aeruginosa DHS01, complete genome	51.8	98.2	26%	0.007	76%	CP013993.1
Pseudomonas aeruginosa strain USDA-ARS-USMARC-41639, complete genome	51.8	51.8	24%	0.007	76%	CP013989.1
Pseudomonas aeruginosa strain W45909, complete genome	51.8	94.5	26%	0.007	76%	CP008871.1

Alignments

Acidovorax sp. KKS102, complete genome

Sequence ID: **gb|CP003872.1|** Length: 5196935 Number of Matches: 1

Range 1: 1639536 to 1639811

Score	Expect	Identities	Gaps	Strand	Frame
100 bits(110)	2e-17()	194/282(69%)	12/282(4%)	Plus/Plus	

Features:

```
Query  8        GTTGCGCGTTCCTCCTCACTCTATCGAAGCTGAGCAAAGTGTGCCTGGTGGTTTGCTGCT  67
                |||||| || || || ||||| ||||| || |||   || ||||  || ||  |||||||
Sbjct  1639536  GTTGCGTGTGCCACCGCACTCCATCGAGGCGGAGTCCAGCGTGCTGGGGGGGCTGCTGCT  1639595

Query  68       GGACAACCAAGCCTGGGATATTGCGGG---CTTTCATGTCAGCAAGTCCCATTTCTATCG  124
                ||||||| | ||||||||    | |||   ||| |  ||     ||  ||||||||| ||
Sbjct  1639596  GGACAACAACGCCTGGGACCGCGTGGGTGACTTGCTGGTGG---AGAGCCATTTCTACCG  1639652

Query  125      ATGGGAGCATCAGGAGATCTTCGATGCGATCGGGGCCTTGATCATTGCCTGCAAGCCTGC  184
                    || || |||  ||||| |   || ||||| ||  ||||| |||| ||||||| ||
Sbjct  1639653  CCATGAACACCAGATGATCTACACCGCCATCGGCGCGCTGATCAATGCCAGCAAGCCAGC  1639712

Query  185      CGACGTGATCACTGTGCACGATCTGTTGCGCGACAAGGGCCTTGC---GGACCGTTGTGG  241
                ||| |||||||| |||  ||| |   |||   || |||||   ||   |||  | || ||
Sbjct  1639713  CGATGTGATCACGGTGTTCGAGCACCTGCAGAACCAGGGCAAGGCACAGGA--GATGGGG  1639770

Query  242      TGGCTTAACCTACCTCAACAATCTCGCCCAGAGCGTGCCCAG  283
                 ||||   ||||||||||||| || || ||   |||||||||
Sbjct  1639771  GGGCTCG-CCTACCTCAACAACCTGGCGCAATACGTGCCCAG  1639811
```

Uncultured bacterium clone contig10067 genomic sequence

Sequence ID: **gb|KP424940.1|** Length: 936 Number of Matches: 1

Range 1: 348 to 617

Score	Expect	Identities	Gaps	Strand	Frame
91.5 bits(100)	8e-15()	185/272(68%)	2/272(0%)	Plus/Minus	

Features:

```
Query  12   CGCGTTCCTCCTCACTCTATCGAAGCTGAGCAAAGTGTGCCTGGTGGTTTGCTGCTGGAC  71
```

```
            ||| | || || |||||  |||| || ||||| || ||||  || ||  ||||||| |||
Sbjct  617  CGCATCCCGCCGCACTCGGTCGAGGCCGAGCAGAGCGTGCTCGGCGGCCTGCTGCTCGAC  558
Query  72   AACCAAGCCTGGGATATTGCGGGCTTTCATGTCAGCAAGTCCCATTTCTATCGATGGGAG  131
            |||   |||||||||   || |||   |   | | | |   | | ||||| || |  |||
Sbjct  557  AACAGCGCCTGGGATCGCGCCGGCGACCTGCTGACCGACAGCGACTTCTACCGCTTCGAG  498
Query  132  CATCAGGAGATCTTCGATGCGATCGGGGCCTTGATCATTGCCTGCAAGCCTGCCGACGTG  191
            || |    ||||| ||  ||||||||| | | ||||||  ||   |||||| |||||||||
Sbjct  497  CACCGCCTGATCTACGCGGCGATCGGCGGCCTGATCAGCGCGACCAAGCCGGCCGACGTG  438
Query  192  ATCACTGTGCACGATCTGTTGCGCGACAAGGGCCTTGCGGACCGTTGTGGTGGCTTAACC  251
            ||||| |||  ||| | |||||  | |   |||   || ||  | || || ||| |   |
Sbjct  437  ATCACCGTGTTCGAGCAGTTGCAGGGCCTCGGCAAGGCCGAGAG-TGCGGCGGCCT-GTC  380
Query  252  TACCTCAACAATCTCGCCCAGAGCGTGCCCAG  283
            |||||||||   ||||| ||||||||||| ||
Sbjct  379  TACCTCAACGCGCTCGCGCAGAGCGTGCCGAG  348
```

Methylibium petroleiphilum PM1, complete genome
Sequence ID: **gb|CP000555.1|** Length: 4044195 Number of Matches: 1
Range 1: 1648095 to 1648368

Score	Expect	Identities	Gaps	Strand	Frame
87.8 bits(96)	1e-13()	189/280(68%)	12/280(4%)	Plus/Plus	

Features:

```
Query  10       TGCGCGTTCCTCCTCACTCTATCGAAGCTGAGCAAAGTGTGCCTGGTGGTTTGCTGCTGG  69
                ||||| | || || || || ||||| || |||| || ||||  || || ||  ||||| | |
Sbjct  1648095  TGCGCATCCCGCCGCAATCCATCGAGGCCGAGCAGAGCGTGCTGGGGGGGCTGCTGATCG  1648154
Query  70       ACAACCAAGCCTGGGATATTGCGGGCTTTCATGTCAGCAAGTCCCATTTCTATCGATGGG  129
                |||||   ||||||||    || |||   |   | | | |   | ||||||| ||    |
Sbjct  1648155  ACAACGGCGCCTGGGACCGGGCCGGCGACCTGCTGAACGACGGCGATTTCTACCGCCACG  1648214
Query  130      AGCATCAGGAGATCTTCGATGCGATCGGGGCCTTGATCATTGCCTGCAAGCCTGCCGACG  189
                |||| |||  ||||| || ||| |||||     ||||||  ||| ||||||| |||||||
Sbjct  1648215  AGCACCAGTTGATCTACGGTGCCATCGGCAAGCTGATCAACGCCAGCAAGCCGGCCGACG  1648274
Query  190      TGATCACTGTGCACGA------TCTGTTGCGCGACAAGGGCCTTGCGGACCGTTGTGGTG  243
                ||||||| ||  ||||       | || || || ||||| |   | |||  | || || |
Sbjct  1648275  TGATCACCGTCTACGAGCAGCTGCAGTCGCTCGGCAAGGCC---GAGGA--GGTG-GGCG  1648328
Query  244      GCTTAACCTACCTCAACAATCTCGCCCAGAGCGTGCCCAG  283
                |  |  ||||||| ||| | ||||| ||||||||||| ||
Sbjct  1648329  GGCTGGCCTACCTGAACCAGCTCGCGCAGAGCGTGCCGAG  1648368
```

Ralstonia eutropha H16 chromosome 1
Sequence ID: **emb|AM260479.1|** Length: 4052032 Number of Matches: 1
Range 1: 2470528 to 2470712

Score	Expect	Identities	Gaps	Strand	Frame
87.8 bits(96)	1e-13()	134/188(71%)	6/188(3%)	Plus/Minus	

Features:
Replicative DNA helicase

```
Query  15       GTTCCTCCTCACTCTATCGAAGCTGAGCAAAGTGTGCCTGGTGGTTTGCTGCTGGACAAC  74
                || || || || || |||||||| ||||||   ||||  |||||  ||||||||||||||
Sbjct  2470712  GTCCCGCCGCATTCCATCGAAGCCGAGCAATCGGTGCTGGGTGGCCTGCTGCTGGACAAC  2470653
Query  75       CAAGCCTGGGAT---ATTGCGGGCTTTCATGTCAGCAAGTCCCATTTCTATCGATGGGAG  131
                   ||||||||    ||||||| ||| ||| || |  || |  |||||||||| |  ||
Sbjct  2470652  GCCGCCTGGGACCGCATTGCGGACTT-CATTTCCG--AGGCGGATTTCTATCGTTTTGAC  2470596
Query  132      CATCAGGAGATCTTCGATGCGATCGGGGCCTTGATCATTGCCTGCAAGCCTGCCGACGTG  191
                || | |  |||||||| |     ||||     ||||||   |||  |||||| |||||||||
Sbjct  2470595  CACCGGATGATCTTCCAGAGCATCGCCCGGTTGATCTCGGCCACCAAGCCGGCCGACGTG  2470536
Query  192      ATCACTGT  199
                ||||| ||
Sbjct  2470535  ATCACGGT  2470528
```

Alicycliphilus denitrificans K601, complete genome
Sequence ID: **gb|CP002657.1|** Length: 4995263 Number of Matches: 1
Range 1: 1388517 to 1388790

Score	Expect	Identities	Gaps	Strand	Frame
86.0 bits(94)	4e-13()	189/278(68%)	8/278(2%)	Plus/Plus	

Features:

```
Query  10       TGCGCGTTCCTCCTCACTCTATCGAAGCTGAGCAAAGTGTGCCTGGTGGTTTGCTGCTGG  69
                ||||||| || || || || ||||| || |||   || |||| ||| || |||||| |||
Sbjct  1388517  TGCGCGTGCCGCCGCATTCCATCGAGGCCGAGTCTAGCGTGCTTGGCGGCTTGCTGTTGG  1388576
Query  70       ACAACCAAGCCTGGGATATTGCGGGCTTTCATGTCAGCAAGTC--CCATTTCTATCGATG  127
                |||||   ||||||||    | ||||   | || | |   | |  | | ||||| ||
Sbjct  1388577  ACAACATGGCCTGGGACCGCGTGGGCGACC-TG-CTGGTGGACGGCGACTTCTACCGCCA  1388634
```

```
Query  128      GGAGCATCAGGAGATCT--TCGATGCGATCGGGGCCTTGATCATTGCCTGCAAGCCTGCC  185
                 ||||| ||| ||||||  |||  || || || ||  ||||||  ||| ||||||| |||
Sbjct  1388635  CGAGCACCAGCAGATCTATTCG--GCCATTGGCGCGCTGATCAACGCCAGCAAGCCCGCC  1388692

Query  186      GACGTGATCACTGTGCACGATCTGTTGCGCGACAAGGGCCTTGCGGACCGTTGTGGTGGC  245
                ||||||||||| ||| |||| |   |||  | |  ||||   || ||       || |||
Sbjct  1388693  GACGTGATCACGGTGTACGAGCACCTGCAGGGCCTGGGCAAGGCCGAGGAAACCGGCGGC  1388752

Query  246      TTAACCTACCTCAACAATCTCGCCCAGAGCGTGCCCAG  283
                 |  ||||||||||||  || || |||  |||||||||
Sbjct  1388753  CTGGCCTACCTCAACAGCCTGGCGCAGTACGTGCCCAG  1388790
```

BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BT70YPBD015**
Formatting options
Download
Blast report description

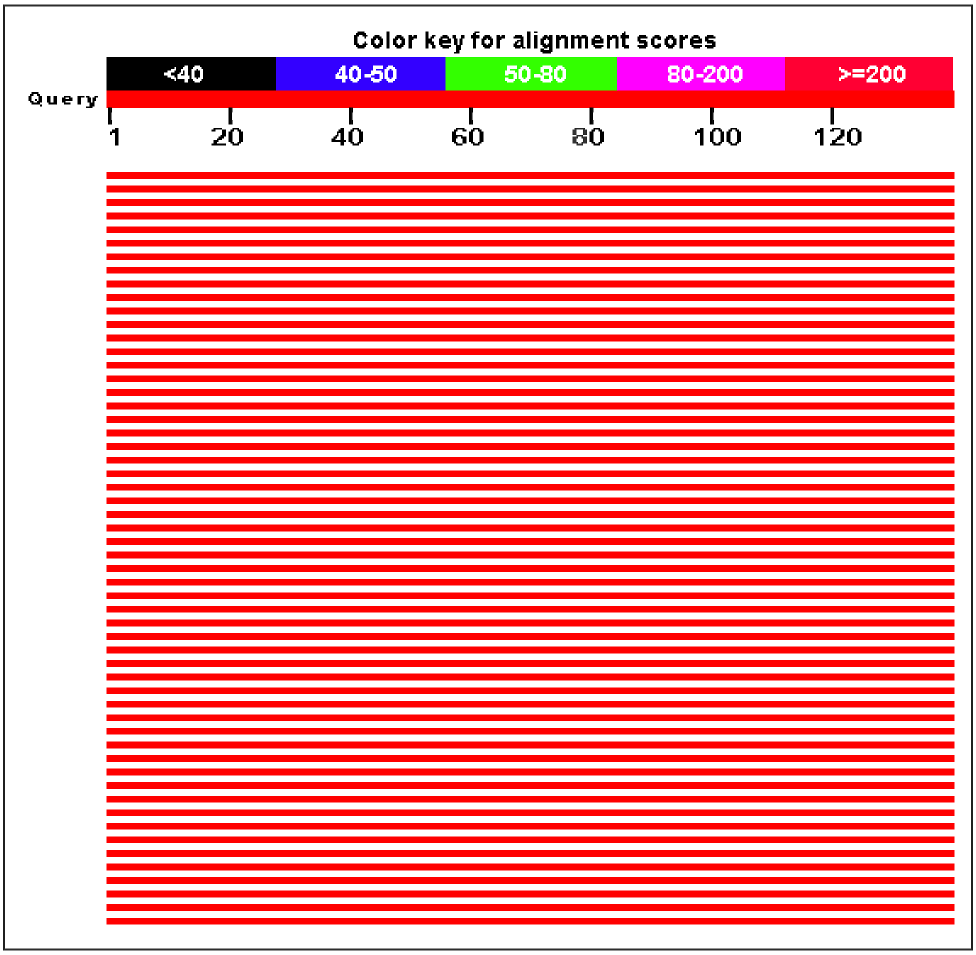
YK10D11.3I_RbcL_CLONE3

RID BT70YPBD015 (Expires on 02-12 21:35 pm)

Query ID	lcl|Query_1269	**Database Name**	nr
Description	YK10D11.3I_RbcL_CLONE3	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	139		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Phaenosperma globosum voucher BH:J.I. Davis 779 plastid, complete genome	239	239	100%	1e-59	99%	KM974745.1
Diarrhena obovata voucher BH:J.I. Davis 756 plastid, complete genome	239	239	100%	1e-59	99%	KM974739.1
Neomolinia japonica ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	239	239	100%	1e-59	99%	HQ600431.1
Neomolinia fauriei ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	239	239	100%	1e-59	99%	HQ600429.1
Phaenosperma globosa chloroplast partial rbcL gene for ribulose bisphosphate carboxylase large chain	239	239	100%	1e-59	99%	AJ784824.1
Diarrhena obovata ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gene, partial cds; chloroplast	239	239	100%	1e-59	99%	AY622890.1
Hordeum vulgare subsp. vulgare chloroplast, complete genome	233	233	100%	4e-58	98%	KT962228.1
Festuca bromoides chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV1607	233	233	100%	4e-58	98%	LN908031.1
Valiha diffusa chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV1487	233	233	100%	4e-58	98%	LN908028.1
Sirochloa parvifolia chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher NOP224	233	233	100%	4e-58	98%	LN908013.1
Nastus aristatus chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV1464	233	233	100%	4e-58	98%	LN907971.1
Humbertochloa bambusiuscula chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV956	233	233	100%	4e-58	98%	LN907952.1
Hickelia madagascariensis chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV724	233	233	100%	4e-58	98%	LN907951.1
Festuca camusiana chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV617	233	233	100%	4e-58	98%	LN907946.1
Bromus leptoclados chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV1617	233	233	100%	4e-58	98%	LN907903.1

Poaceae sp. SERC-1076419263 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KP402760.1
Poaceae sp. SERC-1076419267 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KP402694.1
Panicum virgatum voucher SERC-1076419297 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KP402686.1
Bromus diandrus ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KP149548.1
Lolium sp. KK-0011 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KP149535.1
Protea scolopendriifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KP110421.1
Festuca scabra ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KP110319.1
Oryza sativa Japonica Group DNA, chromosome 6, cultivar: Nipponbare, complete sequence	233	233	100%	4e-58	98%	AP014962.1
Bromus kalmii voucher BIOUG24048-E05 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KT695565.1
Bromus inermis voucher BIOUG24048-G05 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KT695423.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KR092108.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KR092107.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KR092106.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KR092105.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KR092104.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KR092103.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KR092102.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KR092101.1

Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KR092100.1
Triticum turgidum subsp. durum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KR092099.1
Triticum turgidum subsp. durum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KR092098.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KR092097.1
Triticum turgidum subsp. durum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KR092096.1
Medicago truncatula ribulose bisphosphate carboxylase large chain domain protein partial mRNA	233	233	100%	4e-58	98%	XM_013588237.1
Hordeum vulgare cultivar NARC 4064 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KP827658.1
Triticum aestivum cultivar NARC 10727 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KP827657.1
Pseudostachyum polymorphum isolate J725 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KR529912.1
Festuca arundinacea voucher CAN:Saarela 331 plastid, complete genome	233	233	100%	4e-58	98%	KM974751.1
Melica subulata voucher CAN:Saarela 836 plastid, complete genome	233	233	100%	4e-58	98%	KM974743.1
Melica mutica voucher US:W.J. Kress & M. Butts 04-7461 plastid, complete genome	233	233	100%	4e-58	98%	KM974742.1
Hordeum jubatum voucher CAN:Saarela 18478 plastid, complete genome	233	233	100%	4e-58	98%	KM974741.1
Bromus vulgaris voucher CAN:Saarela 822 plastid, complete genome	233	233	100%	4e-58	98%	KM974737.1
Brachyelytrum aristosum voucher BH:J.I. Davis 777 plastid, complete genome	233	233	100%	4e-58	98%	KM974735.1
Helictochloa hookeri voucher CAN:Saarela 18359 plastid, complete genome	233	233	100%	4e-58	98%	KM974734.1
Thinopyrum ponticum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KR824042.1
Lolium temulentum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KM538824.1
Chikusichloa aquatica chloroplast, complete genome	233	233	100%	4e-58	98%	KR078265.1
Vulpia octoflora ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ773986.1
Luziola fluitans ribulose-1,5-bisphosphate carboxylase/oxygenase	233	233	100%	4e-58	98%	KJ773657.1

large subunit (rbcL) gene, partial cds; chloroplast						
Melica uniflora ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid	233	233	100%	4e-58	98%	KM360877.1
Elymus caninus ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid	233	233	100%	4e-58	98%	KM360764.1
Bromus sterilis ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid	233	233	100%	4e-58	98%	KM360634.1
Guadua weberbaueri voucher TULV:XL & MK 582 plastid, complete genome	233	233	100%	4e-58	98%	KP793062.1
Triticum macha chloroplast DNA, complete genome	233	233	100%	4e-58	98%	LC005978.1
Triticum monococcum subsp. monococcum chloroplast DNA, complete genome	233	233	100%	4e-58	98%	LC005977.1
Triticum aestivum chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco, cultivar Cadenza	233	233	100%	4e-58	98%	LN626616.2
Hordeum vulgare chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco	233	233	100%	4e-58	98%	LN626641.1
Secale cereale chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco	233	233	100%	4e-58	98%	LN626639.1
Aegilops tauschii chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco	233	233	100%	4e-58	98%	LN626630.1
Aegilops juvenalis chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco	233	233	100%	4e-58	98%	LN626628.1
Aegilops cylindrica chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco	233	233	100%	4e-58	98%	LN626627.1
Triticum dicoccon chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco, cultivar CI12214 INTRID:CWI47369 ENT:2129	233	233	100%	4e-58	98%	LN626623.1
Triticum monococcum chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco	233	233	100%	4e-58	98%	LN626620.1
Triticum aestivum chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco, cultivar SATYN_II_9428	233	233	100%	4e-58	98%	LN626619.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KM212132.1
Schizachne purpurascens voucher TJD-203 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ841556.1
Festuca arundinacea voucher TJD-592 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ841555.1
Leersia oryzoides voucher TJD-294						

ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ841375.1
Hordeum jubatum voucher TJD-322 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ841357.1
Festuca subverticillata voucher TJD-316 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ841326.1
Festuca subverticillata voucher TJD-204 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ841325.1
Festuca rubra subsp. rubra voucher TJD-159 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ841324.1
Elymus trachycaulus subsp. trachycaulus voucher TJD-625 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ841297.1
Elymus repens voucher TJD-224 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ841296.1
Bromus inermis voucher TJD-578 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ841141.1
Brachyelytrum erectum voucher TJD-343 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ841140.1
Triticum turgidum subsp. durum cultivar Langdon chloroplast, complete genome	233	233	100%	4e-58	98%	KM352501.1
Triticum timopheevii chloroplast DNA, complete genome	233	233	100%	4e-58	98%	AB976560.1
Elymus strictus voucher Y2137 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KM017751.1
Lolium perenne voucher Batianoff 2010513 (MEL 2132634A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ599220.1
Lolium multiflorum voucher Jackson s.n. (MEL 2035113A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ599219.1
Lolium loliaceum voucher Whinray 829 (MEL 0534323A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ599218.1
Festuca rubra voucher Reid 2361 (MEL 2323513A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ599217.1
Festuca pratensis voucher Lepschi 3922 (MEL 2274993A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ599216.1
Festuca plebeia voucher Morris 86664 (MEL 2131516A) ribulose-1,5-						

bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ599215.1
Festuca muelleri voucher Walsh 6797 (MEL 2314310A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ599214.1
Festuca asperula voucher Walsh 6242 (MEL 2275915A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ599213.1
Festuca arundinacea voucher McKenzie 07/11 (MEL 2331054A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ599212.1
Festuca arundinacea voucher Leeman s.n. (MEL 2105597A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ599211.1
Dryopoa dives voucher Cochrane 716 (MEL 2062412A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ599210.1
Lolium temulentum f. arvense voucher Gray 1614 (HO 537164) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ599185.1
Dryopoa dives voucher Birch 476 (MEL 2355932A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ599175.1
Hainardia cylindrica voucher Reid 2754 (MEL 2330507A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ599172.1
Parapholis strigosa voucher Stajsic 975 (MEL 2024132A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ599171.1
Psilurus incurvus voucher Adair 2157 (MEL 1592359A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	233	233	100%	4e-58	98%	KJ599169.1

Alignments

Phaenosperma globosum voucher BH:J.I. Davis 779 plastid, complete genome
Sequence ID: **gb|KM974745.1|** Length: 137897 Number of Matches: 1
Range 1: 55814 to 55951

Score	Expect	Identities	Gaps	Strand	Frame
239 bits(264)	1e-59()	137/139(99%)	1/139(0%)	Plus/Plus	

Features:

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Query  1      GGCAGCATTCCGAGTAACTCCTCAGCCTGGGGTTCCGCCCGAAGAAGCAGGGGCTGCAGT  60
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Sbjct  55814  GGCAGCATTCCGAGTAACTCCTCAGCCTGGGGTTCCGCCCGAAGAAGCAGGGGCTGCAGT  55873

Query  61     AGCTGCCGAATCTTCTACTGGTACATGGACAACTGTTTGTAACTGATGGACTTACCAGTC  120
              |||||||||||||||||||||||||||||||||||||||  |||||||||||||||||||
Sbjct  55874  AGCTGCCGAATCTTCTACTGGTACATGGACAACTGTTTG-GACTGATGGACTTACCAGTC  55932

Query  121    TTGATCGTTACAAAGGACG  139
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```
Sbjct  55933  TTGATCGTTACAAAGGACG  55951
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Diarrhena obovata voucher BH:J.I. Davis 756 plastid, complete genome
Sequence ID: **gb|KM974739.1|** Length: 137421 Number of Matches: 1
Range 1: 55036 to 55173

Score	Expect	Identities	Gaps	Strand	Frame
239 bits(264)	1e-59()	137/139(99%)	1/139(0%)	Plus/Plus	

Features:

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Query  1      GGCAGCATTCCGAGTAACTCCTCAGCCTGGGGTTCCGCCCGAAGAAGCAGGGGCTGCAGT  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  55036  GGCAGCATTCCGAGTAACTCCTCAGCCTGGGGTTCCGCCCGAAGAAGCAGGGGCTGCAGT  55095

Query  61     AGCTGCCGAATCTTCTACTGGTACATGGACAACTGTTTGTAACTGATGGACTTACCAGTC  120
              |||||||||||||||||||||||||||||||||||||||  |||||||||||||||||||
Sbjct  55096  AGCTGCCGAATCTTCTACTGGTACATGGACAACTGTTTG-GACTGATGGACTTACCAGTC  55154

Query  121    TTGATCGTTACAAAGGACG  139
              |||||||||||||||||||
Sbjct  55155  TTGATCGTTACAAAGGACG  55173
```

Neomolinia japonica ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast
Sequence ID: **gb|HQ600431.1|** Length: 751 Number of Matches: 1

See 1 more title(s)
Range 1: 113 to 250

Score	Expect	Identities	Gaps	Strand	Frame
239 bits(264)	1e-59()	137/139(99%)	1/139(0%)	Plus/Plus	

Features:

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Query  1    GGCAGCATTCCGAGTAACTCCTCAGCCTGGGGTTCCGCCCGAAGAAGCAGGGGCTGCAGT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  113  GGCAGCATTCCGAGTAACTCCTCAGCCTGGGGTTCCGCCCGAAGAAGCAGGGGCTGCAGT  172

Query  61   AGCTGCCGAATCTTCTACTGGTACATGGACAACTGTTTGTAACTGATGGACTTACCAGTC  120
            |||||||||||||||||||||||||||||||||||||||  |||||||||||||||||||
Sbjct  173  AGCTGCCGAATCTTCTACTGGTACATGGACAACTGTTTG-GACTGATGGACTTACCAGTC  231

Query  121  TTGATCGTTACAAAGGACG  139
            |||||||||||||||||||
Sbjct  232  TTGATCGTTACAAAGGACG  250
```

Neomolinia fauriei ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast
Sequence ID: **gb|HQ600429.1|** Length: 751 Number of Matches: 1
Range 1: 113 to 250

Score	Expect	Identities	Gaps	Strand	Frame
239 bits(264)	1e-59()	137/139(99%)	1/139(0%)	Plus/Plus	

Features:

```
Query  1    GGCAGCATTCCGAGTAACTCCTCAGCCTGGGGTTCCGCCCGAAGAAGCAGGGGCTGCAGT  60
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Sbjct  113  GGCAGCATTCCGAGTAACTCCTCAGCCTGGGGTTCCGCCCGAAGAAGCAGGGGCTGCAGT  172

Query  61   AGCTGCCGAATCTTCTACTGGTACATGGACAACTGTTTGTAACTGATGGACTTACCAGTC  120
            |||||||||||||||||||||||||||||||||||||||  |||||||||||||||||||
Sbjct  173  AGCTGCCGAATCTTCTACTGGTACATGGACAACTGTTTG-GACTGATGGACTTACCAGTC  231

Query  121  TTGATCGTTACAAAGGACG  139
            |||||||||||||||||||
Sbjct  232  TTGATCGTTACAAAGGACG  250
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Phaenosperma globosa chloroplast partial rbcL gene for ribulose bisphosphate carboxylase large chain
Sequence ID: **emb|AJ784824.1|** Length: 1357 Number of Matches: 1
Range 1: 98 to 235

Score	Expect	Identities	Gaps	Strand	Frame
239 bits(264)	1e-59()	137/139(99%)	1/139(0%)	Plus/Plus	

Features:

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Query  1    GGCAGCATTCCGAGTAACTCCTCAGCCTGGGGTTCCGCCCGAAGAAGCAGGGGCTGCAGT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  98   GGCAGCATTCCGAGTAACTCCTCAGCCTGGGGTTCCGCCCGAAGAAGCAGGGGCTGCAGT  157

Query  61   AGCTGCCGAATCTTCTACTGGTACATGGACAACTGTTTGTAACTGATGGACTTACCAGTC  120
            |||||||||||||||||||||||||||||||||||||||  |||||||||||||||||||
```

```
Sbjct  158  AGCTGCCGAATCTTCTACTGGTACATGGACAACTGTTTG-GACTGATGGACTTACCAGTC  216

Query  121  TTGATCGTTACAAAGGACG  139
            |||||||||||||||||||
Sbjct  217  TTGATCGTTACAAAGGACG  235
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BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BT764JVC015**

Formatting options
Download

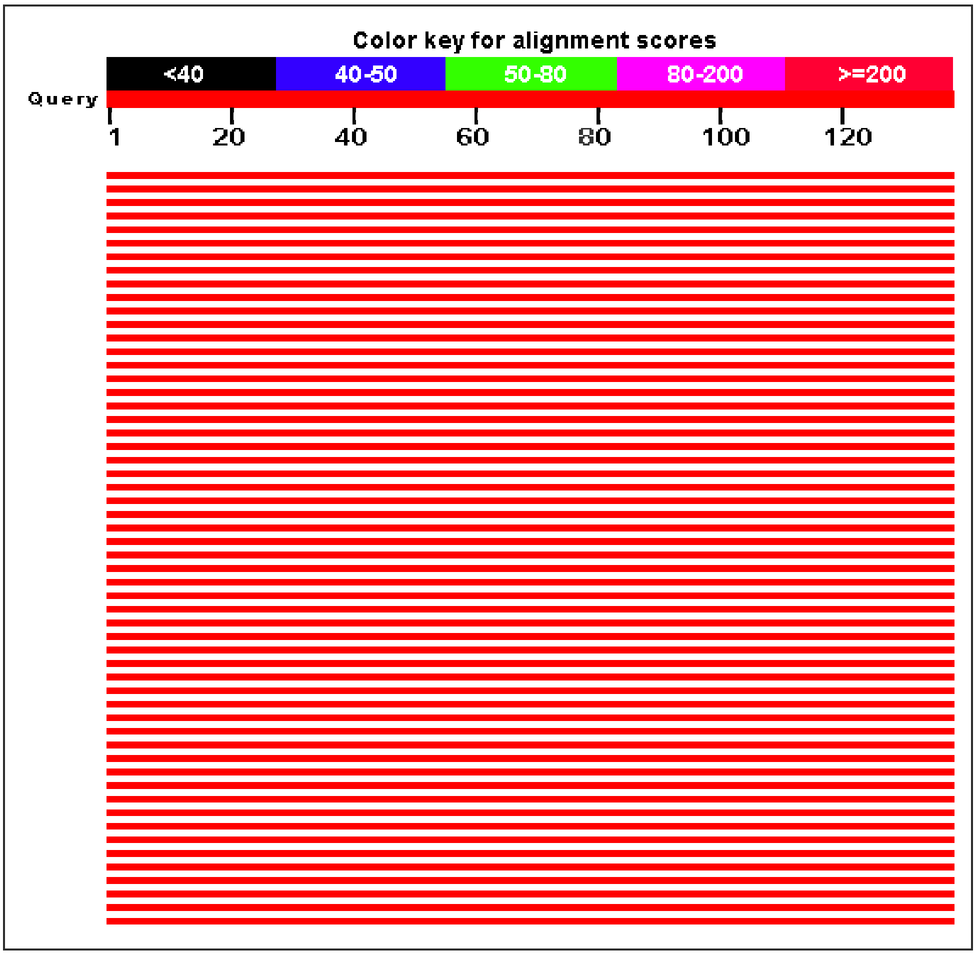
Blast report description

YK10D11.3l_RbcL_Clones5,6

RID	BT764JVC015 (Expires on 02-12 21:37 pm)		
Query ID	lcl|Query_90621	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	138		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Phaenosperma globosum voucher BH:J.I. Davis 779 plastid, complete genome	235	235	100%	1e-58	98%	KM974745.1
Diarrhena obovata voucher BH:J.I. Davis 756 plastid, complete genome	235	235	100%	1e-58	98%	KM974739.1
Neomolinia japonica ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	235	235	100%	1e-58	98%	HQ600431.1
Neomolinia fauriei ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	235	235	100%	1e-58	98%	HQ600429.1
Phaenosperma globosa chloroplast partial rbcL gene for ribulose bisphosphate carboxylase large chain	235	235	100%	1e-58	98%	AJ784824.1
Diarrhena obovata ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gene, partial cds; chloroplast	235	235	100%	1e-58	98%	AY622890.1
Hordeum vulgare subsp. vulgare chloroplast, complete genome	232	232	100%	2e-57	97%	KT962228.1
Festuca bromoides chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV1607	232	232	100%	2e-57	97%	LN908031.1
Valiha diffusa chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV1487	232	232	100%	2e-57	97%	LN908028.1
Sirochloa parvifolia chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher NOP224	232	232	100%	2e-57	97%	LN908013.1
Nastus aristatus chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV1464	232	232	100%	2e-57	97%	LN907971.1
Humbertochloa bambusiuscula chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV956	232	232	100%	2e-57	97%	LN907952.1
Hickelia madagascariensis chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV724	232	232	100%	2e-57	97%	LN907951.1
Festuca camusiana chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV617	232	232	100%	2e-57	97%	LN907946.1
Bromus leptoclados chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV1617	232	232	100%	2e-57	97%	LN907903.1

Poaceae sp. SERC-1076419263 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KP402760.1
Poaceae sp. SERC-1076419267 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KP402694.1
Panicum virgatum voucher SERC-1076419297 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KP402686.1
Bromus diandrus ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KP149548.1
Lolium sp. KK-0011 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KP149535.1
Protea scolopendriifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KP110421.1
Festuca scabra ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KP110319.1
Bromus kalmii voucher BIOUG24048-E05 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KT695565.1
Bromus inermis voucher BIOUG24048-G05 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KT695423.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KR092108.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KR092107.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KR092106.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KR092105.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KR092104.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KR092103.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KR092102.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KR092101.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds;	232	232	100%	2e-57	97%	KR092100.1

chloroplast						
Triticum turgidum subsp. durum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KR092099.1**
Triticum turgidum subsp. durum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KR092098.1**
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KR092097.1**
Triticum turgidum subsp. durum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KR092096.1**
Medicago truncatula ribulose bisphosphate carboxylase large chain domain protein partial mRNA	232	232	100%	2e-57	97%	**XM_013588237.1**
Hordeum vulgare cultivar NARC 4064 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KP827658.1**
Triticum aestivum cultivar NARC 10727 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KP827657.1**
Pseudostachyum polymorphum isolate J725 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KR529912.1**
Festuca arundinacea voucher CAN:Saarela 331 plastid, complete genome	232	232	100%	2e-57	97%	**KM974751.1**
Melica subulata voucher CAN:Saarela 836 plastid, complete genome	232	232	100%	2e-57	97%	**KM974743.1**
Melica mutica voucher US:W.J. Kress & M. Butts 04-7461 plastid, complete genome	232	232	100%	2e-57	97%	**KM974742.1**
Hordeum jubatum voucher CAN:Saarela 18478 plastid, complete genome	232	232	100%	2e-57	97%	**KM974741.1**
Bromus vulgaris voucher CAN:Saarela 822 plastid, complete genome	232	232	100%	2e-57	97%	**KM974737.1**
Brachyelytrum aristosum voucher BH:J.I. Davis 777 plastid, complete genome	232	232	100%	2e-57	97%	**KM974735.1**
Helictochloa hookeri voucher CAN:Saarela 18359 plastid, complete genome	232	232	100%	2e-57	97%	**KM974734.1**
Thinopyrum ponticum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KR824042.1**
Lolium temulentum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KM538824.1**
Chikusichloa aquatica chloroplast, complete genome	232	232	100%	2e-57	97%	**KR078265.1**
Vulpia octoflora ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KJ773986.1**
Luziola fluitans ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KJ773657.1**
Melica uniflora ribulose-1,5-						

bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid	232	232	100%	2e-57	97%	KM360877.1
Elymus caninus ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid	232	232	100%	2e-57	97%	KM360764.1
Bromus sterilis ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid	232	232	100%	2e-57	97%	KM360634.1
Guadua weberbaueri voucher TULV:XL & MK 582 plastid, complete genome	232	232	100%	2e-57	97%	KP793062.1
Triticum macha chloroplast DNA, complete genome	232	232	100%	2e-57	97%	LC005978.1
Triticum monococcum subsp. monococcum chloroplast DNA, complete genome	232	232	100%	2e-57	97%	LC005977.1
Triticum aestivum chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco, cultivar Cadenza	232	232	100%	2e-57	97%	LN626616.2
Hordeum vulgare chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco	232	232	100%	2e-57	97%	LN626641.1
Secale cereale chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco	232	232	100%	2e-57	97%	LN626639.1
Aegilops tauschii chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco	232	232	100%	2e-57	97%	LN626630.1
Aegilops juvenalis chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco	232	232	100%	2e-57	97%	LN626628.1
Aegilops cylindrica chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco	232	232	100%	2e-57	97%	LN626627.1
Triticum dicoccon chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco, cultivar CI12214 INTRID:CWI47369 ENT:2129	232	232	100%	2e-57	97%	LN626623.1
Triticum monococcum chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco	232	232	100%	2e-57	97%	LN626620.1
Triticum aestivum chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco, cultivar SATYN_II_9428	232	232	100%	2e-57	97%	LN626619.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KM212132.1
Schizachne purpurascens voucher TJD-203 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KJ841556.1
Festuca arundinacea voucher TJD-592 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KJ841555.1
Leersia oryzoides voucher TJD-294 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KJ841375.1

Hordeum jubatum voucher TJD-322 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KJ841357.1**
Festuca subverticillata voucher TJD-316 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KJ841326.1**
Festuca subverticillata voucher TJD-204 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KJ841325.1**
Festuca rubra subsp. rubra voucher TJD-159 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KJ841324.1**
Elymus trachycaulus subsp. trachycaulus voucher TJD-625 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KJ841297.1**
Elymus repens voucher TJD-224 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KJ841296.1**
Bromus inermis voucher TJD-578 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KJ841141.1**
Brachyelytrum erectum voucher TJD-343 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KJ841140.1**
Triticum turgidum subsp. durum cultivar Langdon chloroplast, complete genome	232	232	100%	2e-57	97%	**KM352501.1**
Triticum timopheevii chloroplast DNA, complete genome	232	232	100%	2e-57	97%	**AB976560.1**
Elymus strictus voucher Y2137 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KM017751.1**
Lolium perenne voucher Batianoff 2010513 (MEL 2132634A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KJ599220.1**
Lolium multiflorum voucher Jackson s.n. (MEL 2035113A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KJ599219.1**
Lolium loliaceum voucher Whinray 829 (MEL 0534323A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KJ599218.1**
Festuca rubra voucher Reid 2361 (MEL 2323513A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KJ599217.1**
Festuca pratensis voucher Lepschi 3922 (MEL 2274993A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KJ599216.1**
Festuca plebeia voucher Morris 86664 (MEL 2131516A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	**KJ599215.1**

Festuca muelleri voucher Walsh 6797 (MEL 2314310A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KJ599214.1
Festuca asperula voucher Walsh 6242 (MEL 2275915A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KJ599213.1
Festuca arundinacea voucher McKenzie 07/11 (MEL 2331054A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KJ599212.1
Festuca arundinacea voucher Leeman s.n. (MEL 2105597A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KJ599211.1
Dryopoa dives voucher Cochrane 716 (MEL 2062412A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KJ599210.1
Lolium temulentum f. arvense voucher Gray 1614 (HO 537164) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KJ599185.1
Dryopoa dives voucher Birch 476 (MEL 2355932A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KJ599175.1
Hainardia cylindrica voucher Reid 2754 (MEL 2330507A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KJ599172.1
Parapholis strigosa voucher Stajsic 975 (MEL 2024132A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KJ599171.1
Psilurus incurvus voucher Adair 2157 (MEL 1592359A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KJ599169.1
Lamarckia aurea voucher Stajsic 5306 (MEL 2339294A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	232	232	100%	2e-57	97%	KJ599168.1

Alignments

Phaenosperma globosum voucher BH:J.I. Davis 779 plastid, complete genome

Sequence ID: **gb|KM974745.1|** Length: 137897 Number of Matches: 1

Range 1: 55814 to 55951

Score	Expect	Identities	Gaps	Strand	Frame
235 bits(260)	1e-58()	135/138(98%)	0/138(0%)	Plus/Plus	

Features:

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Sbjct  55814  GGCAGCATTCCGAGTAACTCCTCAGCCTGGGGTTCCGCCCGAAGAAGCAGGGGCTGCAGT  55873

Query  61     AGCTGCCGAATCTTCTACTGGTACATGGACAACTGCTTGGTATGATGGACTTACCAGTCT  120
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Sbjct  55874  AGCTGCCGAATCTTCTACTGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCT  55933
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Query  121    TGATCGTTACAAAGGACG  138
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Sbjct  55934  TGATCGTTACAAAGGACG  55951
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Diarrhena obovata voucher BH:J.I. Davis 756 plastid, complete genome
Sequence ID: **gb|KM974739.1|** Length: 137421 Number of Matches: 1
Range 1: 55036 to 55173

Score	Expect	Identities	Gaps	Strand	Frame
235 bits(260)	1e-58()	135/138(98%)	0/138(0%)	Plus/Plus	

Features:

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Sbjct  55036  GGCAGCATTCCGAGTAACTCCTCAGCCTGGGGTTCCGCCCGAAGAAGCAGGGGCTGCAGT  55095

Query  61     AGCTGCCGAATCTTCTACTGGTACATGGACAACTGCTTGGTATGATGGACTTACCAGTCT  120
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Sbjct  55096  AGCTGCCGAATCTTCTACTGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCT  55155

Query  121    TGATCGTTACAAAGGACG  138
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Sbjct  55156  TGATCGTTACAAAGGACG  55173
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Neomolinia japonica ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast
Sequence ID: **gb|HQ600431.1|** Length: 751 Number of Matches: 1

See 1 more title(s)
Range 1: 113 to 250

Score	Expect	Identities	Gaps	Strand	Frame
235 bits(260)	1e-58()	135/138(98%)	0/138(0%)	Plus/Plus	

Features:

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Sbjct  113  GGCAGCATTCCGAGTAACTCCTCAGCCTGGGGTTCCGCCCGAAGAAGCAGGGGCTGCAGT  172

Query  61   AGCTGCCGAATCTTCTACTGGTACATGGACAACTGCTTGGTATGATGGACTTACCAGTCT  120
            ||||||||||||||||||||||||||||||||||| ||||  ||||||||||||||||||
Sbjct  173  AGCTGCCGAATCTTCTACTGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCT  232

Query  121  TGATCGTTACAAAGGACG  138
            ||||||||||||||||||
Sbjct  233  TGATCGTTACAAAGGACG  250
```

Neomolinia fauriei ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast
Sequence ID: **gb|HQ600429.1|** Length: 751 Number of Matches: 1
Range 1: 113 to 250

Score	Expect	Identities	Gaps	Strand	Frame
235 bits(260)	1e-58()	135/138(98%)	0/138(0%)	Plus/Plus	

Features:

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Query  61   AGCTGCCGAATCTTCTACTGGTACATGGACAACTGCTTGGTATGATGGACTTACCAGTCT  120
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Sbjct  173  AGCTGCCGAATCTTCTACTGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCT  232

Query  121  TGATCGTTACAAAGGACG  138
            ||||||||||||||||||
Sbjct  233  TGATCGTTACAAAGGACG  250
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Phaenosperma globosa chloroplast partial rbcL gene for ribulose bisphosphate carboxylase large chain
Sequence ID: **emb|AJ784824.1|** Length: 1357 Number of Matches: 1
Range 1: 98 to 235

Score	Expect	Identities	Gaps	Strand	Frame
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Features:

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Sbjct  98   GGCAGCATTCCGAGTAACTCCTCAGCCTGGGGTTCCGCCCGAAGAAGCAGGGGCTGCAGT  157
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Sbjct  158  AGCTGCCGAATCTTCTACTGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCT  217

Query  121  TGATCGTTACAAAGGACG  138
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Sbjct  218  TGATCGTTACAAAGGACG  235
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BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BT6RWKB0014**
  Formatting options
  Download
Blast report description

YK10D11.3d_TRNL1_C1-3,5-9

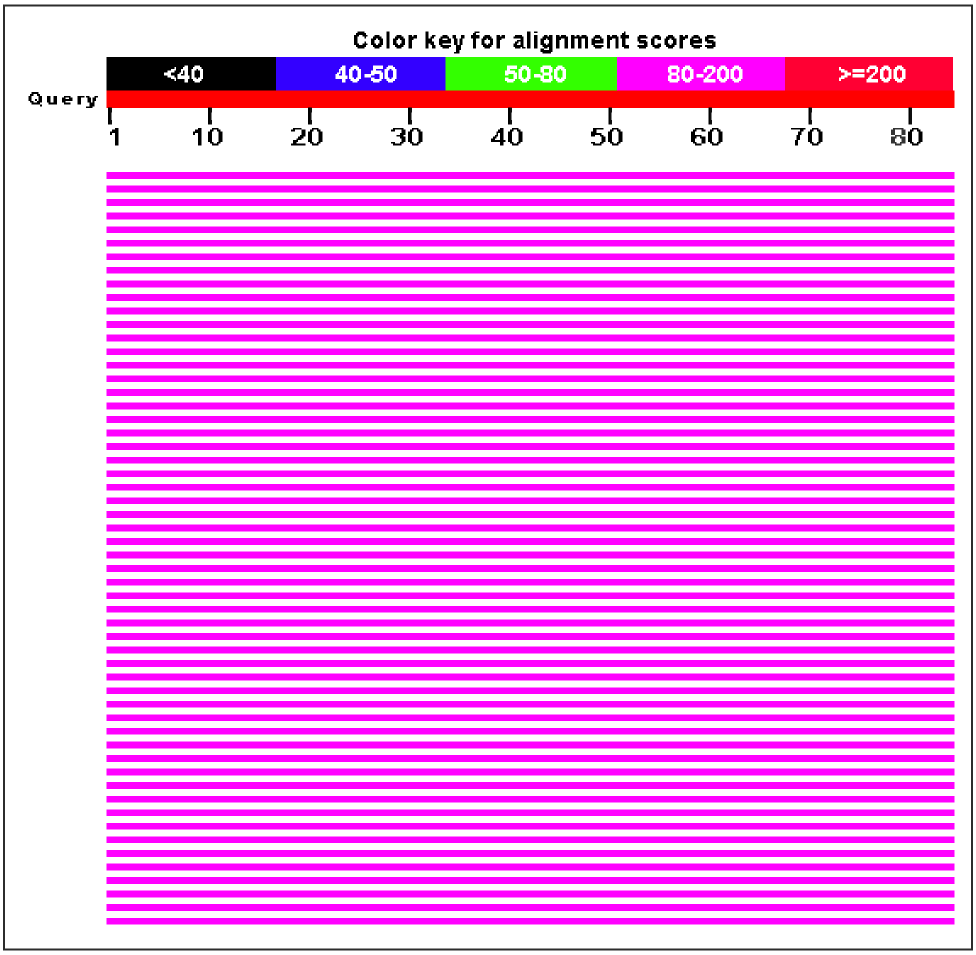
RID BT6RWKB0014 (Expires on 02-12 21:30 pm)

Query ID lcl|Query_107317
Description YK10D11.3d_TRNL1_C5
Molecule type nucleic acid
Query Length 84

Database Name nr
Description Nucleotide collection (nt)
Program BLASTN 2.3.1+

Graphic Summary

Distribution of 102 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Elymus peschkovae voucher 115 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KP325400.1
Elymus scandicus voucher 114 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KP325399.1
Elymus excelsus voucher 1114 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KP325398.1
Elymus pendulinus voucher 113 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KP325397.1
Elymus dahuricus var. cylindricus voucher 5509 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KP325396.1
Elymus excelsus voucher 5513 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KP325395.1
Elymus probatovae voucher 5645 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KP325394.1
Elymus ircutensis voucher Alt 10-198 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KP325393.1
Elymus vassiljevii voucher 5665 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KP325392.1
Elymus peschkovae voucher 5631 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KP325391.1
Elymus charkeviczii voucher 5550 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KP325390.1
Agropyron cristatum var. pectinatum voucher M.Pinar 4412a trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	152	152	100%	6e-34	100%	KP723655.1
Agropyron deweyi voucher M.Pinar 4321a trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene, complete	152	152	100%	6e-34	100%	KP723652.1

sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast						
Aegilops geniculata isolate CRF BGE022746 trnL gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	152	152	100%	6e-34	100%	KR559558.1
Aegilops neglecta bio-material USDA:PI170209 trnL gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	152	152	100%	6e-34	100%	KR559557.1
Elymus nevskii voucher Alt 1124 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KJ744043.1
Agropyron cristatum voucher Alt 11-377 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KJ744042.1
Elymus caninus voucher Alt 1031 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KJ744041.1
Campeiostachys dahurica voucher Xa 09-157 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KJ744040.1
Elymus fedtschenkoi voucher Alt 12-133 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KJ755833.1
Agropyron krylovianum voucher Alt 12-264 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KJ755832.1
Elymus subfibrosus tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KP257587.1
Elymus lanceolatus subsp. lanceolatus isolate CP3 tRNA-Leu (trnL) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KP208327.1
Triticum macha chloroplast DNA, complete genome	152	152	100%	6e-34	100%	LC005978.1
Triticum monococcum subsp. monococcum chloroplast DNA, complete genome	152	152	100%	6e-34	100%	LC005977.1
Triticum turgidum subsp. durum cultivar Langdon chloroplast, complete genome	152	152	100%	6e-34	100%	KM352501.1
Triticum timopheevii chloroplast DNA, complete genome	152	152	100%	6e-34	100%	AB976560.1
Aegilops kotschyi cultivar TA1980 chloroplast, complete genome	152	152	100%	6e-34	100%	KJ614420.1
Aegilops sharonensis cultivar TA1995 chloroplast, complete genome	152	152	100%	6e-34	100%	KJ614419.1
Aegilops bicornis cultivar Clae57 chloroplast, complete genome	152	152	100%	6e-34	100%	KJ614418.1
Aegilops sharonensis cultivar TA1996 chloroplast, complete genome	152	152	100%	6e-34	100%	KJ614417.1
Aegilops longissima cultivar TA1924 chloroplast, complete genome	152	152	100%	6e-34	100%	KJ614416.1
Aegilops searsii cultivar TA1841 chloroplast, complete genome	152	152	100%	6e-34	100%	KJ614415.1
Aegilops searsii cultivar TA1837 chloroplast, complete genome	152	152	100%	6e-34	100%	KJ614414.1
Aegilops searsii cultivar TA1926	152	152	100%	6e-34	100%	KJ614413.1

chloroplast, complete genome						
Aegilops tauschii cultivar AL8/78 chloroplast, complete genome	152	152	100%	6e-34	100%	KJ614412.1
Triticum urartu cultivar PI428335 chloroplast, complete genome	152	152	100%	6e-34	100%	KJ614411.1
Triticum timopheevii cultivar Tim01 chloroplast, complete genome	152	152	100%	6e-34	100%	KJ614410.1
Triticum timopheevii cultivar TA944 chloroplast, complete genome	152	152	100%	6e-34	100%	KJ614409.1
Triticum timopheevii cultivar TA1485 chloroplast, complete genome	152	152	100%	6e-34	100%	KJ614408.1
Triticum timopheevii cultivar TA0941 chloroplast, complete genome	152	152	100%	6e-34	100%	KJ614407.1
Aegilops speltoides var. speltoides cultivar PI487232 chloroplast, complete genome	152	152	100%	6e-34	100%	KJ614406.1
Aegilops speltoides var. ligustica cultivar TA1796 chloroplast, complete genome	152	152	100%	6e-34	100%	KJ614405.1
Aegilops speltoides var. ligustica cultivar AE918 chloroplast, complete genome	152	152	100%	6e-34	100%	KJ614404.1
Triticum aestivum cultivar spleta PI384000 chloroplast, complete genome	152	152	100%	6e-34	100%	KJ614403.1
Triticum turgidum cultivar TA1133 chloroplast, complete genome	152	152	100%	6e-34	100%	KJ614402.1
Triticum turgidum cultivar TA0060 chloroplast, complete genome	152	152	100%	6e-34	100%	KJ614401.1
Triticum turgidum cultivar TA0073 chloroplast, complete genome	152	152	100%	6e-34	100%	KJ614400.1
Triticum turgidum cultivar TA2801 chloroplast, complete genome	152	152	100%	6e-34	100%	KJ614399.1
Triticum turgidum cultivar PI520121 chloroplast, complete genome	152	152	100%	6e-34	100%	KJ614398.1
Triticum aestivum cultivar Chinese Spring TA3008 chloroplast, complete genome	152	152	100%	6e-34	100%	KJ614396.1
Elymus repens isolate xt_plant145 tRNA-Leu (trnL) gene, intron; chloroplast	152	152	100%	6e-34	100%	KJ746409.1
Triticum aestivum chromosome 3B, genomic scaffold, cultivar Chinese Spring	152	315	100%	6e-34	100%	HG670306.1
Triticum aestivum chloroplast, complete genome	152	152	100%	6e-34	100%	KJ592713.1
Elymus sibiricus isolate EI_201311 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905225.1
Elymus dolichatherus isolate EI_201310 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905224.1
Elymus nutans isolate EI_201309 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905223.1
Elymus sibiricus isolate EI_201307 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905221.1
Elymus tangutorum isolate EI_201305 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905219.1
Elymus nutans isolate EI_201302 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905216.1

Elymus nutans isolate EI_201301 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905215.1
Elymus dolichatherus isolate EI_201228 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905214.1
Elymus tangutorum isolate EI_201226 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905212.1
Elymus tangutorum isolate EI_201216 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905202.1
Elymus nutans isolate EI_201224 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905210.1
Elymus dahuricus var. cylindricus isolate EI_201222 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905208.1
Elymus tangutorum isolate EI_201221 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905207.1
Elymus sibiricus isolate EI_201220 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905206.1
Elymus antiquus isolate EI_201219 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905205.1
Elymus excelsus isolate EI_201218 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905204.1
Elymus nutans isolate EI_201217 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905203.1
Elymus excelsus isolate EI_201214 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905200.1
Elymus tangutorum isolate EI_201213 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905199.1
Elymus dolichatherus isolate EI_201212 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905198.1
Elymus dolichatherus isolate EI_201211 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene,	152	152	100%	6e-34	100%	KF905197.1

partial sequence; chloroplast						
Elymus tangutorum isolate EI_201209 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905195.1
Elymus dahuricus isolate EI_201208 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905194.1
Elymus tibeticus isolate EI_201206 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905192.1
Elymus tangutorum isolate EI_201205 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905191.1
Elymus tangutorum isolate EI_201204 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905190.1
Elymus dahuricus var. cylindricus isolate EI_201202 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905188.1
Elymus nutans isolate EI_201102 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905186.1
Elymus sibiricus isolate EI_201101 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF905185.1
Triticum urartu plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	152	152	100%	6e-34	100%	AB732946.1
Triticum spelta plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	152	152	100%	6e-34	100%	AB732945.1
Triticum monococcum plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	152	152	100%	6e-34	100%	AB732944.1
Triticum durum plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	152	152	100%	6e-34	100%	AB732942.1
Triticum monococcum subsp. aegilopoides plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	152	152	100%	6e-34	100%	AB732941.1
Triticum aestivum plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	152	152	100%	6e-34	100%	AB732940.1
Elymus tsukushiensis plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	152	152	100%	6e-34	100%	AB732933.1
Elymus racemifer plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	152	152	100%	6e-34	100%	AB732932.1
Elymus humidus plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	152	152	100%	6e-34	100%	AB732931.1
Elymus dahuricus plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	152	152	100%	6e-34	100%	AB732930.1

Elymus caninus plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	152	152	100%	6e-34	100%	AB732929.1
Aegilops geniculata chloroplast, complete genome	152	152	100%	6e-34	100%	KF534490.1
Aegilops cylindrica chloroplast, complete genome	152	152	100%	6e-34	100%	KF534489.1
Elymus tauri isolate Psetau3 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu (trnL) gene, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF600705.1
Elymus tauri isolate Psetau2 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu (trnL) gene, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF600704.1
Elymus stipifolius isolate Psesti3 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu (trnL) gene, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF600702.1
Elymus stipifolius isolate Psesti2 trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	152	152	100%	6e-34	100%	KF600701.1

Alignments

Elymus peschkovae voucher 115 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast

Sequence ID: **gb|KP325400.1|** Length: 1046 Number of Matches: 1
Range 1: 103 to 186

Score	Expect	Identities	Gaps	Strand	Frame
152 bits(168)	6e-34()	84/84(100%)	0/84(0%)	Plus/Minus	

Features:

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Query  1    GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  186  GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  127

Query  61   AACACGGATTTGGCTCAGGATTGC  84
            ||||||||||||||||||||||||
Sbjct  126  AACACGGATTTGGCTCAGGATTGC  103
```

Elymus scandicus voucher 114 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast

Sequence ID: **gb|KP325399.1|** Length: 1039 Number of Matches: 1
Range 1: 103 to 186

Score	Expect	Identities	Gaps	Strand	Frame
152 bits(168)	6e-34()	84/84(100%)	0/84(0%)	Plus/Minus	

Features:

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Query  1    GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  186  GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  127

Query  61   AACACGGATTTGGCTCAGGATTGC  84
            ||||||||||||||||||||||||
Sbjct  126  AACACGGATTTGGCTCAGGATTGC  103
```

Elymus excelsus voucher 1114 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast

Sequence ID: **gb|KP325398.1|** Length: 1043 Number of Matches: 1
Range 1: 103 to 186

Score	Expect	Identities	Gaps	Strand	Frame
152 bits(168)	6e-34()	84/84(100%)	0/84(0%)	Plus/Minus	

Features:

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Query  1    GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  186  GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  127

Query  61   AACACGGATTTGGCTCAGGATTGC  84
            ||||||||||||||||||||||||
Sbjct  126  AACACGGATTTGGCTCAGGATTGC  103
```

Elymus pendulinus voucher 113 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KP325397.1|** Length: 1049 Number of Matches: 1
Range 1: 103 to 186

Score	Expect	Identities	Gaps	Strand	Frame
152 bits(168)	6e-34()	84/84(100%)	0/84(0%)	Plus/Minus	

Features:

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Query  1    GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  186  GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  127

Query  61   AACACGGATTTGGCTCAGGATTGC  84
            ||||||||||||||||||||||||
Sbjct  126  AACACGGATTTGGCTCAGGATTGC  103
```

Elymus dahuricus var. cylindricus voucher 5509 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KP325396.1|** Length: 1043 Number of Matches: 1
Range 1: 103 to 186

Score	Expect	Identities	Gaps	Strand	Frame
152 bits(168)	6e-34()	84/84(100%)	0/84(0%)	Plus/Minus	

Features:

```
Query  1    GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  186  GAGTCTCTGCACCTATCCTTTTCCTTTGTATTCTAGTTCGAGAACCCCTTGTTTTCTCAA  127

Query  61   AACACGGATTTGGCTCAGGATTGC  84
            ||||||||||||||||||||||||
Sbjct  126  AACACGGATTTGGCTCAGGATTGC  103
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Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BT7C09KD014**

Formatting options

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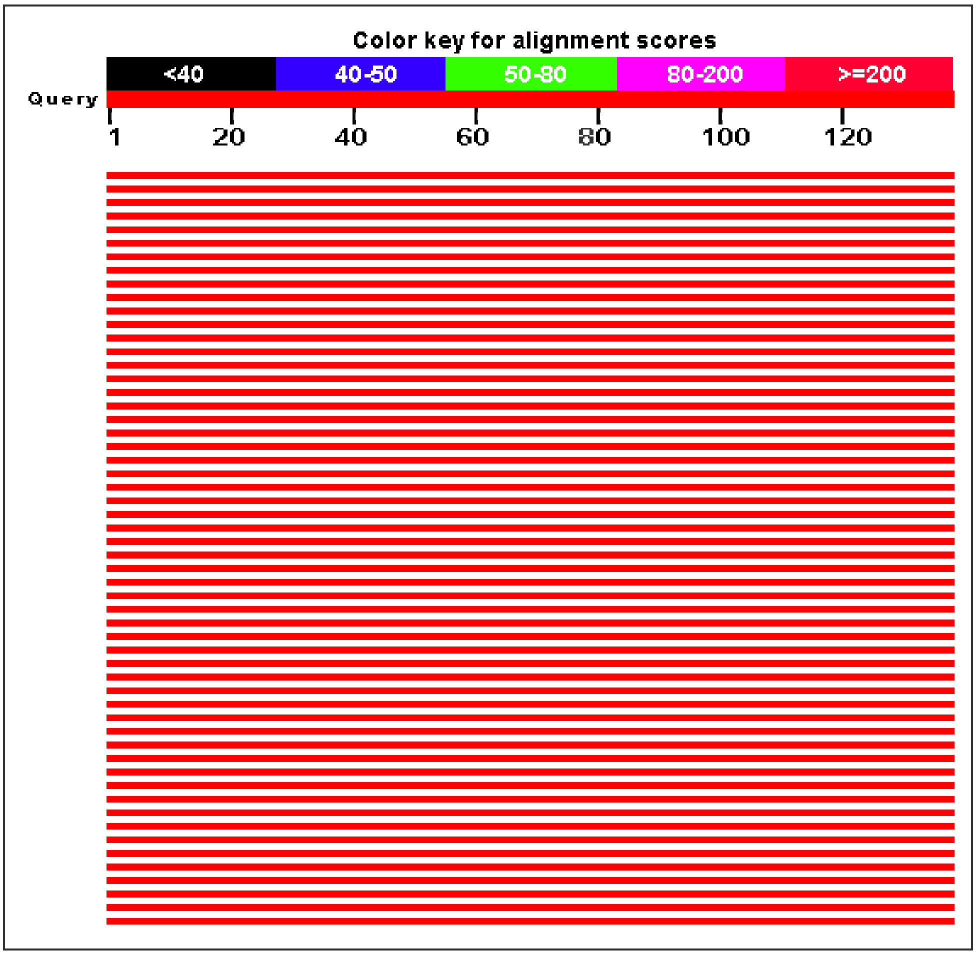
Blast report description

YK10D11.3l_RbcL_Clones8-11

RID	BT7C09KD014 (Expires on 02-12 21:41 pm)		
Query ID	lcl|Query_179257	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	138		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Phaenosperma globosum voucher BH:J.I. Davis 779 plastid, complete genome	250	250	100%	6e-63	100%	KM974745.1
Diarrhena obovata voucher BH:J.I. Davis 756 plastid, complete genome	250	250	100%	6e-63	100%	KM974739.1
Neomolinia japonica ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	250	250	100%	6e-63	100%	HQ600431.1
Neomolinia fauriei ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	250	250	100%	6e-63	100%	HQ600429.1
Phaenosperma globosa chloroplast partial rbcL gene for ribulose bisphosphate carboxylase large chain	250	250	100%	6e-63	100%	AJ784824.1
Diarrhena obovata ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gene, partial cds; chloroplast	250	250	100%	6e-63	100%	AY622890.1
Hordeum vulgare subsp. vulgare chloroplast, complete genome	244	244	100%	2e-61	99%	KT962228.1
Festuca bromoides chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV1607	244	244	100%	2e-61	99%	LN908031.1
Valiha diffusa chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV1487	244	244	100%	2e-61	99%	LN908028.1
Sirochloa parvifolia chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher NOP224	244	244	100%	2e-61	99%	LN908013.1
Nastus aristatus chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV1464	244	244	100%	2e-61	99%	LN907971.1
Humbertochloa bambusiuscula chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV956	244	244	100%	2e-61	99%	LN907952.1
Hickelia madagascariensis chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV724	244	244	100%	2e-61	99%	LN907951.1
Festuca camusiana chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV617	244	244	100%	2e-61	99%	LN907946.1
Bromus leptoclados chloroplast partial rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, specimen voucher MSV1617	244	244	100%	2e-61	99%	LN907903.1

Poaceae sp. SERC-1076419263 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KP402760.1
Poaceae sp. SERC-1076419267 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KP402694.1
Panicum virgatum voucher SERC-1076419297 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KP402686.1
Bromus diandrus ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KP149548.1
Lolium sp. KK-0011 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KP149535.1
Protea scolopendriifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KP110421.1
Festuca scabra ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KP110319.1
Bromus kalmii voucher BIOUG24048-E05 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KT695565.1
Bromus inermis voucher BIOUG24048-G05 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KT695423.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KR092108.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KR092107.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KR092106.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KR092105.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KR092104.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KR092103.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KR092102.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KR092101.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds;	244	244	100%	2e-61	99%	KR092100.1

chloroplast						
Triticum turgidum subsp. durum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KR092099.1
Triticum turgidum subsp. durum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KR092098.1
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KR092097.1
Triticum turgidum subsp. durum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KR092096.1
Medicago truncatula ribulose bisphosphate carboxylase large chain domain protein partial mRNA	244	244	100%	2e-61	99%	XM_013588237.1
Hordeum vulgare cultivar NARC 4064 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KP827658.1
Triticum aestivum cultivar NARC 10727 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KP827657.1
Pseudostachyum polymorphum isolate J725 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KR529912.1
Festuca arundinacea voucher CAN:Saarela 331 plastid, complete genome	244	244	100%	2e-61	99%	KM974751.1
Melica subulata voucher CAN:Saarela 836 plastid, complete genome	244	244	100%	2e-61	99%	KM974743.1
Melica mutica voucher US:W.J. Kress & M. Butts 04-7461 plastid, complete genome	244	244	100%	2e-61	99%	KM974742.1
Hordeum jubatum voucher CAN:Saarela 18478 plastid, complete genome	244	244	100%	2e-61	99%	KM974741.1
Bromus vulgaris voucher CAN:Saarela 822 plastid, complete genome	244	244	100%	2e-61	99%	KM974737.1
Brachyelytrum aristosum voucher BH:J.I. Davis 777 plastid, complete genome	244	244	100%	2e-61	99%	KM974735.1
Helictochloa hookeri voucher CAN:Saarela 18359 plastid, complete genome	244	244	100%	2e-61	99%	KM974734.1
Thinopyrum ponticum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KR824042.1
Lolium temulentum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KM538824.1
Chikusichloa aquatica chloroplast, complete genome	244	244	100%	2e-61	99%	KR078265.1
Vulpia octoflora ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KJ773986.1
Luziola fluitans ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KJ773657.1
Melica uniflora ribulose-1,5-						

bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid	244	244	100%	2e-61	99%	**KM360877.1**
Elymus caninus ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid	244	244	100%	2e-61	99%	**KM360764.1**
Bromus sterilis ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; plastid	244	244	100%	2e-61	99%	**KM360634.1**
Guadua weberbaueri voucher TULV:XL & MK 582 plastid, complete genome	244	244	100%	2e-61	99%	**KP793062.1**
Triticum macha chloroplast DNA, complete genome	244	244	100%	2e-61	99%	**LC005978.1**
Triticum monococcum subsp. monococcum chloroplast DNA, complete genome	244	244	100%	2e-61	99%	**LC005977.1**
Triticum aestivum chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco, cultivar Cadenza	244	244	100%	2e-61	99%	**LN626616.2**
Hordeum vulgare chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco	244	244	100%	2e-61	99%	**LN626641.1**
Secale cereale chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco	244	244	100%	2e-61	99%	**LN626639.1**
Aegilops tauschii chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco	244	244	100%	2e-61	99%	**LN626630.1**
Aegilops juvenalis chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco	244	244	100%	2e-61	99%	**LN626628.1**
Aegilops cylindrica chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco	244	244	100%	2e-61	99%	**LN626627.1**
Triticum dicoccon chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco, cultivar CI12214 INTRID:CWI47369 ENT:2129	244	244	100%	2e-61	99%	**LN626623.1**
Triticum monococcum chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco	244	244	100%	2e-61	99%	**LN626620.1**
Triticum aestivum chloroplast rbcL gene for ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit, Rubisco, cultivar SATYN_II_9428	244	244	100%	2e-61	99%	**LN626619.1**
Triticum aestivum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	**KM212132.1**
Schizachne purpurascens voucher TJD-203 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	**KJ841556.1**
Festuca arundinacea voucher TJD-592 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	**KJ841555.1**
Leersia oryzoides voucher TJD-294 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	**KJ841375.1**

Hordeum jubatum voucher TJD-322 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	**KJ841357.1**
Festuca subverticillata voucher TJD-316 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	**KJ841326.1**
Festuca subverticillata voucher TJD-204 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	**KJ841325.1**
Festuca rubra subsp. rubra voucher TJD-159 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	**KJ841324.1**
Elymus trachycaulus subsp. trachycaulus voucher TJD-625 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	**KJ841297.1**
Elymus repens voucher TJD-224 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	**KJ841296.1**
Bromus inermis voucher TJD-578 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	**KJ841141.1**
Brachyelytrum erectum voucher TJD-343 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	**KJ841140.1**
Triticum turgidum subsp. durum cultivar Langdon chloroplast, complete genome	244	244	100%	2e-61	99%	**KM352501.1**
Triticum timopheevii chloroplast DNA, complete genome	244	244	100%	2e-61	99%	**AB976560.1**
Elymus strictus voucher Y2137 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	**KM017751.1**
Lolium perenne voucher Batianoff 2010513 (MEL 2132634A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	**KJ599220.1**
Lolium multiflorum voucher Jackson s.n. (MEL 2035113A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	**KJ599219.1**
Lolium loliaceum voucher Whinray 829 (MEL 0534323A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	**KJ599218.1**
Festuca rubra voucher Reid 2361 (MEL 2323513A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	**KJ599217.1**
Festuca pratensis voucher Lepschi 3922 (MEL 2274993A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	**KJ599216.1**
Festuca plebeia voucher Morris 86664 (MEL 2131516A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	**KJ599215.1**

Festuca muelleri voucher Walsh 6797 (MEL 2314310A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KJ599214.1
Festuca asperula voucher Walsh 6242 (MEL 2275915A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KJ599213.1
Festuca arundinacea voucher McKenzie 07/11 (MEL 2331054A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KJ599212.1
Festuca arundinacea voucher Leeman s.n. (MEL 2105597A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KJ599211.1
Dryopoa dives voucher Cochrane 716 (MEL 2062412A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KJ599210.1
Lolium temulentum f. arvense voucher Gray 1614 (HO 537164) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KJ599185.1
Dryopoa dives voucher Birch 476 (MEL 2355932A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KJ599175.1
Hainardia cylindrica voucher Reid 2754 (MEL 2330507A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KJ599172.1
Parapholis strigosa voucher Stajsic 975 (MEL 2024132A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KJ599171.1
Psilurus incurvus voucher Adair 2157 (MEL 1592359A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KJ599169.1
Lamarckia aurea voucher Stajsic 5306 (MEL 2339294A) ribulose-1,5-bisphosphate carboxylase/oxgenase large subunit (rbcL) gene, partial cds; chloroplast	244	244	100%	2e-61	99%	KJ599168.1

Alignments

Phaenosperma globosum voucher BH:J.I. Davis 779 plastid, complete genome
Sequence ID: **gb|KM974745.1|** Length: 137897 Number of Matches: 1
Range 1: 55814 to 55951

Score	Expect	Identities	Gaps	Strand	Frame
250 bits(276)	6e-63()	138/138(100%)	0/138(0%)	Plus/Plus	

Features:

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Sbjct  55814  GGCAGCATTCCGAGTAACTCCTCAGCCTGGGGTTCCGCCCGAAGAAGCAGGGGCTGCAGT  55873

Query  61     AGCTGCCGAATCTTCTACTGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCT  120
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Sbjct  55874  AGCTGCCGAATCTTCTACTGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCT  55933
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Query  121    TGATCGTTACAAAGGACG  138
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Sbjct  55934  TGATCGTTACAAAGGACG  55951
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Diarrhena obovata voucher BH:J.I. Davis 756 plastid, complete genome
Sequence ID: **gb|KM974739.1|** Length: 137421 Number of Matches: 1
Range 1: 55036 to 55173

Score	Expect	Identities	Gaps	Strand	Frame
250 bits(276)	6e-63()	138/138(100%)	0/138(0%)	Plus/Plus	

Features:

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Sbjct  55096  AGCTGCCGAATCTTCTACTGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCT  55155

Query  121    TGATCGTTACAAAGGACG  138
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Sbjct  55156  TGATCGTTACAAAGGACG  55173
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Neomolinia japonica ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast
Sequence ID: **gb|HQ600431.1|** Length: 751 Number of Matches: 1

See 1 more title(s)
Range 1: 113 to 250

Score	Expect	Identities	Gaps	Strand	Frame
250 bits(276)	6e-63()	138/138(100%)	0/138(0%)	Plus/Plus	

Features:

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Sbjct  113  GGCAGCATTCCGAGTAACTCCTCAGCCTGGGGTTCCGCCCGAAGAAGCAGGGGCTGCAGT  172

Query  61   AGCTGCCGAATCTTCTACTGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCT  120
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Sbjct  173  AGCTGCCGAATCTTCTACTGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCT  232

Query  121  TGATCGTTACAAAGGACG  138
            ||||||||||||||||||
Sbjct  233  TGATCGTTACAAAGGACG  250
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Neomolinia fauriei ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast
Sequence ID: **gb|HQ600429.1|** Length: 751 Number of Matches: 1
Range 1: 113 to 250

Score	Expect	Identities	Gaps	Strand	Frame
250 bits(276)	6e-63()	138/138(100%)	0/138(0%)	Plus/Plus	

Features:

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Query  61   AGCTGCCGAATCTTCTACTGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCT  120
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Query  121  TGATCGTTACAAAGGACG  138
            ||||||||||||||||||
Sbjct  233  TGATCGTTACAAAGGACG  250
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Phaenosperma globosa chloroplast partial rbcL gene for ribulose bisphosphate carboxylase large chain
Sequence ID: **emb|AJ784824.1|** Length: 1357 Number of Matches: 1
Range 1: 98 to 235

Score	Expect	Identities	Gaps	Strand	Frame
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Features:

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Sbjct  98   GGCAGCATTCCGAGTAACTCCTCAGCCTGGGGTTCCGCCCGAAGAAGCAGGGGCTGCAGT  157
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Sbjct  158  AGCTGCCGAATCTTCTACTGGTACATGGACAACTGTTTGGACTGATGGACTTACCAGTCT  217

Query  121  TGATCGTTACAAAGGACG  138
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Sbjct  218  TGATCGTTACAAAGGACG  235
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Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BTNCZXBC015**
Formatting options
Download
Blast report description

[1]YK11H13H141B_TRNL1_C2-4,6,9-10

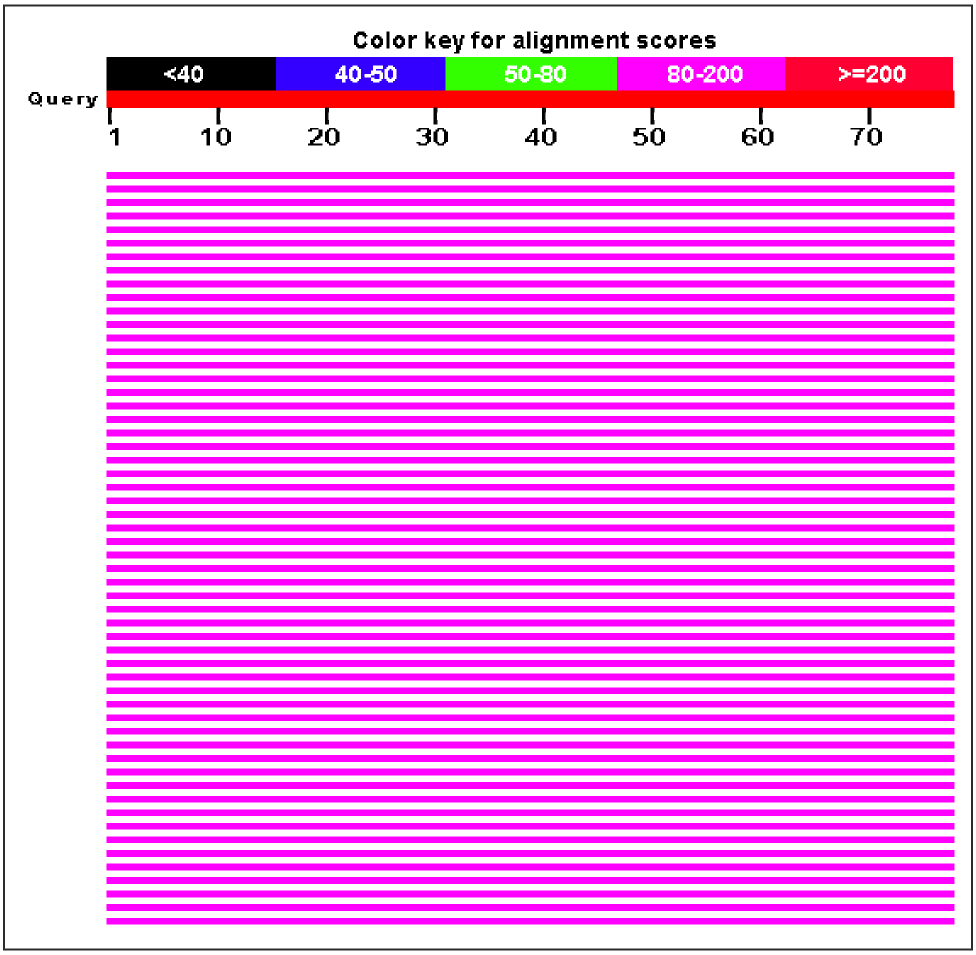
RID BTNCZXBC015 (Expires on 02-13 01:40 am)

Query ID lcl|Query_38467
Description [1]YK11H13H141B_TRNL1_C1
Molecule type nucleic acid
Query Length 78

Database Name nr
Description Nucleotide collection (nt)
Program BLASTN 2.3.1+

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Pinus sibirica chloroplast, complete genome	132	132	100%	5e-28	97%	KT723438.2
Pinus tabuliformis voucher PTAB20150818V5 chloroplast, complete genome	132	132	100%	5e-28	97%	KT740995.1
Pinus bungeana voucher Pbungeana2015 chloroplast, complete genome	132	132	100%	5e-28	97%	KR873010.1
Pinus taiwanensis voucher Ptaiwanensis14 chloroplast, complete genome	132	132	100%	5e-28	97%	KP771703.1
Pinus strobus plastid, complete genome	132	132	100%	5e-28	97%	KP099650.1
Tracheophyta environmental sample clone C6 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KJ015985.1
Tracheophyta environmental sample clone C5 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KJ015984.1
Tracheophyta environmental sample clone C4 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KJ015983.1
Tracheophyta environmental sample clone C3 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KJ015982.1
Tracheophyta environmental sample clone C2 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KJ015981.1
Tracheophyta environmental sample clone C1 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KJ015980.1
Tracheophyta environmental sample clone S5-3 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616492.1
Tracheophyta environmental sample clone S5-2 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616491.1
Tracheophyta environmental sample clone S5-1 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616490.1
Tracheophyta environmental sample clone S4-11 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616487.1
Tracheophyta environmental sample clone S4-10 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616486.1
Tracheophyta environmental sample clone S2-7 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616474.1
Tracheophyta environmental sample clone S2-6 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616473.1
Tracheophyta environmental sample clone S2-2 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616469.1
Tracheophyta environmental sample clone S2-1 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616468.1
Pinus luchuensis chloroplast trnL gene, intron, partial sequence, isolate: OGA0449	132	132	100%	5e-28	97%	AB817641.1
Pinus luchuensis chloroplast trnL gene, intron, partial sequence, isolate:	132	132	100%	5e-28	97%	AB817461.1

OGA0239						
Pinus taeda chloroplast, complete genome	132	132	100%	5e-28	97%	KC427273.1
Pinus massoniana chloroplast, complete genome	132	132	100%	5e-28	97%	KC427272.1
Pinus thunbergii trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504692.1
Pinus bungeana trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504691.1
Pinus koraiensis trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504690.1
Pinus densiflora trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504689.1
Pinus x rigitaeda trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504688.1
Pinus sylvestris trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504686.1
Pinus rigida trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504685.1
Pinus densiflora cultivar Multicaulis trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504684.1
Pinus sylvestris voucher Psy01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739418.1
Pinus peuce voucher Ppe01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739417.1
Pinus halepensis voucher Pha01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739416.1
Pinus brutia voucher Pb01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739415.1
Pinus brutia var. eldarica voucher Pe01.120311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739414.1
Pinus nigra voucher Pn01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739413.1
Pinus pinea voucher Ppi01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739412.1
Pinus heldreichii voucher Phe01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739411.1
Pinus arizonica var. cooperi isolate COOP01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854216.1
Pinus coulteri isolate COUL03 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854215.1
Pinus cubensis isolate CUBE01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854214.1
Pinus culminicola isolate CULM01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854213.1
Pinus fenzeliana var. dabeshanensis isolate DABE01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854212.1
Pinus dalatensis isolate DALA03 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854211.1
Pinus densiflora isolate DENS02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854210.1
Pinus densata isolate DENT01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854209.1
Pinus devoniana isolate DEVO02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854208.1
Pinus discolor isolate DISC02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854207.1

Pinus hartwegii isolate DONN02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854206.1**
Pinus douglasiana isolate DOUG01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854205.1**
Pinus echinata isolate ECHI01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854204.1**
Pinus edulis isolate EDUL08 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854203.1**
Pinus elliottii isolate ELLI01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854202.1**
Pinus engelmannii isolate ENGE02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854201.1**
Pinus fragilissima isolate FRAG01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854200.1**
Pinus glabra isolate GLAB01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854199.1**
Pinus greggii isolate GREG02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854198.1**
Pinus halepensis isolate HALE03 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854197.1**
Pinus hartwegii isolate HART07 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854196.1**
Pinus heldreichii isolate HELD07 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854195.1**
Pinus hwangshanensis isolate HWAN01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854194.1**
Pinus jeffreyi isolate JEFF04 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854193.1**
Pinus johannis chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854192.1**
Pinus kesiya isolate KESI11 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854191.1**
Pinus latteri isolate LATT02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854190.1**
Pinus pringlei isolate PRIN02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854189.1**
Pinus lawsonii isolate LAWS02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854188.1**
Pinus leiophylla isolate LEIO03 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854187.1**
Pinus lumholtzii isolate LUMH07 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854186.1**
Pinus massoniana isolate MASS02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854185.1**
Pinus maximartinezii isolate MAXZ01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854184.1**
Pinus montezumae isolate MONZ01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854183.1**
Pinus morrisonicola isolate MORR01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854182.1**
Pinus mugo isolate MUGO01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854181.1**
Pinus muricata isolate MURI01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854180.1**
Pinus nigra isolate NIGR20 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854179.1**
Pinus pseudostrobus var. apulcensis isolate OAXA02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854178.1**
Pinus occidentalis isolate OCCI02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854177.1**
Pinus palustris isolate PALU02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854176.1**
Pinus patula isolate PATU01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854175.1**
Pinus pinceana isolate PINC13 chloroplast,						

partial genome	132	132	100%	5e-28	97%	JN854174.1
Pinus pinea isolate PINE03 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854173.1
Pinus ponderosa var. benthamiana isolate POND21 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854172.1
Pinus ponderosa var. scopulorum isolate POND59 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854171.1
Pinus pseudostrobus isolate PSEU03 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854169.1
Pinus pumila isolate PUMI07 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854168.1
Pinus pungens isolate PUNG01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854167.1
Pinus quadrifolia isolate QUAD02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854166.1
Pinus radiata isolate RADI01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854165.1
Pinus remota isolate REMO05 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854164.1
Pinus rigida isolate RIGI01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854163.1
Pinus roxburghii isolate ROXB04 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854162.1
Pinus sabiniana isolate SABI04 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854161.1
Pinus serotina isolate SERO01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854160.1
Pinus strobiformis isolate STRF17 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854159.1
Pinus sylvestris isolate SYLV02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854158.1
Pinus taiwanensis isolate TAIW04 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854157.1
Pinus tropicalis isolate TROP02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854156.1

Alignments

Pinus sibirica chloroplast, complete genome
Sequence ID: **gb|KT723438.2|** Length: 116635 Number of Matches: 1
Range 1: 66690 to 66767

Score	Expect	Identities	Gaps	Strand	Frame
132 bits(146)	5e-28()	76/78(97%)	0/78(0%)	Plus/Minus	

Features:

```
Query  1      GGCAATCCTGAGCCAAATCCGGTTCATGAAGACAATGTTTCTTCTCCTAAGATAGGAAGA  60
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  66767  GGTAATCCTGAGCCAAATCCGGTTCATGAAGACAATGTTTCTTCTCCTAAGATAGGAAGG  66708

Query  61     GGATAGGTGCAGAGACTC  78
              ||||||||||||||||||
Sbjct  66707  GGATAGGTGCAGAGACTC  66690
```

Pinus tabuliformis voucher PTAB20150818V5 chloroplast, complete genome
Sequence ID: **gb|KT740995.1|** Length: 119646 Number of Matches: 1
Range 1: 68565 to 68642

Score	Expect	Identities	Gaps	Strand	Frame
132 bits(146)	5e-28()	76/78(97%)	0/78(0%)	Plus/Minus	

Features:

```
Query  1      GGCAATCCTGAGCCAAATCCGGTTCATGAAGACAATGTTTCTTCTCCTAAGATAGGAAGA  60
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  68642  GGTAATCCTGAGCCAAATCCGGTTCATGAAGACAATGTTTCTTCTCCTAAGATAGGAAGG  68583

Query  61     GGATAGGTGCAGAGACTC  78
```

```
              ||||||||||||||||||
Sbjct  68582  GGATAGGTGCAGAGACTC  68565
```

Pinus bungeana voucher Pbungeana2015 chloroplast, complete genome
Sequence ID: **gb|KR873010.1|** Length: 117861 Number of Matches: 1
Range 1: 68182 to 68259

Score	Expect	Identities	Gaps	Strand	Frame
132 bits(146)	5e-28()	76/78(97%)	0/78(0%)	Plus/Minus	

Features:

```
Query  1      GGCAATCCTGAGCCAAATCCGGTTCATGAAGACAATGTTTCTTCTCCTAAGATAGGAAGA  60
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  68259  GGTAATCCTGAGCCAAATCCGGTTCATGAAGACAATGTTTCTTCTCCTAAGATAGGAAGG  68200

Query  61     GGATAGGTGCAGAGACTC  78
              ||||||||||||||||||
Sbjct  68199  GGATAGGTGCAGAGACTC  68182
```

Pinus taiwanensis voucher Ptaiwanensis14 chloroplast, complete genome
Sequence ID: **gb|KP771703.1|** Length: 119741 Number of Matches: 1
Range 1: 68622 to 68699

Score	Expect	Identities	Gaps	Strand	Frame
132 bits(146)	5e-28()	76/78(97%)	0/78(0%)	Plus/Minus	

Features:

```
Query  1      GGCAATCCTGAGCCAAATCCGGTTCATGAAGACAATGTTTCTTCTCCTAAGATAGGAAGA  60
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  68699  GGTAATCCTGAGCCAAATCCGGTTCATGAAGACAATGTTTCTTCTCCTAAGATAGGAAGG  68640

Query  61     GGATAGGTGCAGAGACTC  78
              ||||||||||||||||||
Sbjct  68639  GGATAGGTGCAGAGACTC  68622
```

Pinus strobus plastid, complete genome
Sequence ID: **gb|KP099650.1|** Length: 115576 Number of Matches: 1
Range 1: 65526 to 65603

Score	Expect	Identities	Gaps	Strand	Frame
132 bits(146)	5e-28()	76/78(97%)	0/78(0%)	Plus/Minus	

Features:

```
Query  1      GGCAATCCTGAGCCAAATCCGGTTCATGAAGACAATGTTTCTTCTCCTAAGATAGGAAGA  60
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  65603  GGTAATCCTGAGCCAAATCCGGTTCATGAAGACAATGTTTCTTCTCCTAAGATAGGAAGG  65544

Query  61     GGATAGGTGCAGAGACTC  78
              ||||||||||||||||||
Sbjct  65543  GGATAGGTGCAGAGACTC  65526
```

BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - BTNP4864014**

Formatting options

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Blast report description

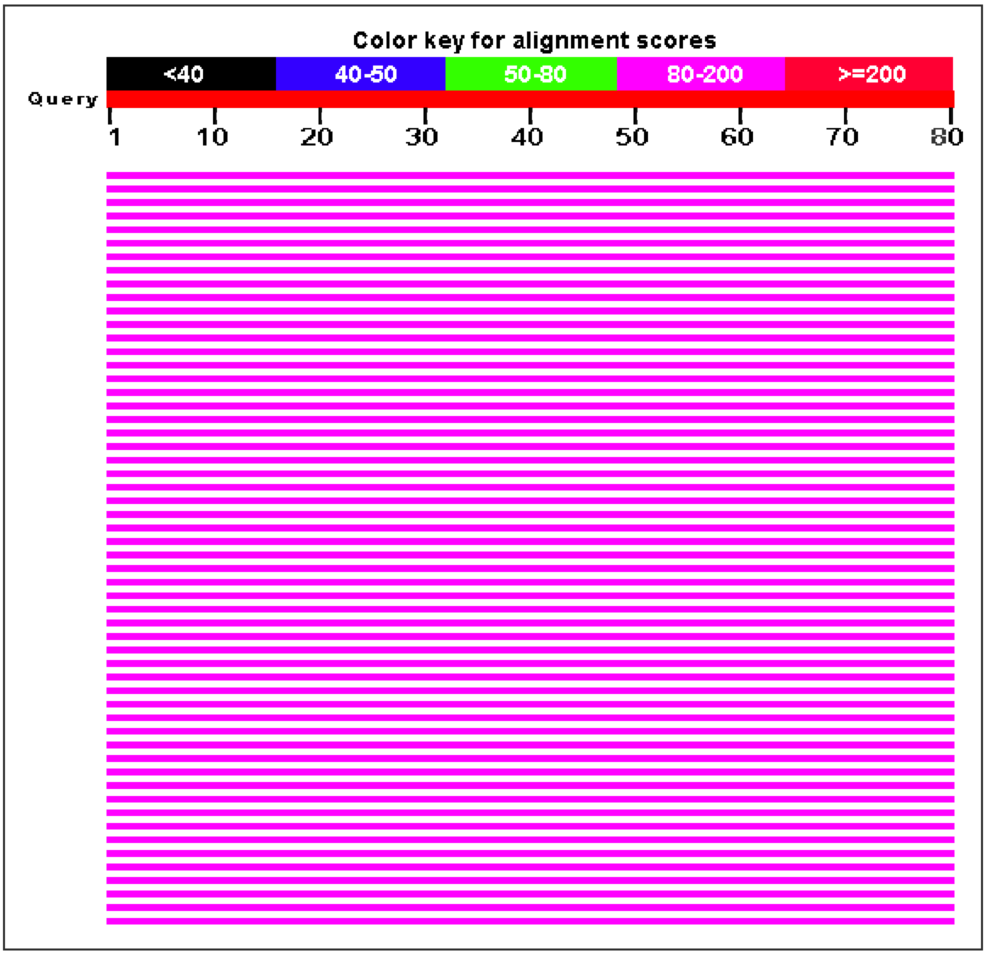
[5]YK11H13H141B_TRNL1_C5

RID BTNP4864014 (Expires on 02-13 01:45 am)

Query ID	lcl|Query_190117	**Database Name**	nr
Description	[5]YK11H13H141B_TRNL1_C5	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.1+
Query Length	80		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Musa yunnanensis isolate SS&JS 473 Montharop Khun Nan tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257604.1
Musella lasiocarpa isolate SS&JS 231 Dararassami tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257602.1
Musa yunnanensis isolate SS&JS 444 Yunnan Namtok Pa Way tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257599.1
Musa yunnanensis isolate SS&JS 349 Yunnan Inthanon tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257598.1
Musa yunnanensis isolate SS&JS 235 Yunnan QSBG tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257597.1
Musa yunnanensis isolate SS&JS 125 Yunnan Huai Nam Dang tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257596.1
Musa laterita isolate SS&JS 412 Bua Si Som Pli Lueang tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257595.1
Musa serpentina isolate SS&JS 353 Nakkharat Huay Hang Pon tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257594.1
Musa serpentina isolate SS&JS 246 Nakkharat Dan Chedi Sam Ong tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257593.1
Musa ornata isolate SS&JS 449 Bua Si Chomphu Luk Khieo tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257592.1
Musa ornata isolate SS&JS 433 Bua Luang tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257591.1
Musa ornata isolate SS&JS 169 Bua Si Muang tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257590.1
Musa laterita isolate SS&JS 308 Bua Si Som Dan Mae Lamao tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic	136	136	100%	4e-29	98%	KT257589.1

spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast						
Musa itinerans isolate SS&JS 175 Hok Khao Soi Dao tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257588.1
Musa balbisiana isolate SS&JS 12 Tani Pa Tat Luang tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257585.1
Musa acuminata var. zebrina isolate SS&JS 155 Thahan Phran tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257584.1
Musa acuminata subsp. truncata isolate SS&JS 368 Pa Cameron tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257583.1
Musa acuminata subsp. siamea isolate SS&JS 450 Pa Kanchanaburi Campus tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257582.1
Musa acuminata subsp. siamea isolate SS&JS 173 Pa Pli Lueang Ban Pa Kluai tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257581.1
Musa acuminata subsp. siamea isolate SS&JS 136 Pa Namtok Kha-On tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257580.1
Musa acuminata subsp. siamea isolate SS&JS 131 Pa La-U tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257579.1
Musa acuminata subsp. siamea isolate SS&JS 1 Khae Phetchabun tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257578.1
Musa acuminata subsp. malaccensis isolate SS&JS 374 Pa Kao Talu tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257577.1
Musa acuminata subsp. malaccensis isolate SS&JS 108 Pa Hat Prapat tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257576.1
Musa acuminata subsp. malaccensis isolate SS&JS 107 Pa Pato tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257575.1
Musa acuminata subsp. malaccensis isolate SS&JS 104 Pa Chumphon tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257574.1
Musa acuminata subsp. malaccensis isolate SS&JS 445 Pa Namtok Pa Way tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and	136	136	100%	4e-29	98%	KT257573.1

tRNA-Phe (trnF) gene, partial sequence; chloroplast						
Musa acuminata subsp. malaccensis isolate SS&JS 202 Pa Tanopute tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	KT257572.1
Musa balbisiana chloroplast, complete genome	136	136	100%	4e-29	98%	KT595228.1
Musa textilis plastid, complete genome	136	136	100%	4e-29	98%	KF601567.1
Musa acuminata subsp. malaccensis chloroplast complete genome, biomaterial CIRAD:930	136	136	100%	4e-29	98%	HF677508.1
Musa environmental sample tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	136	136	100%	4e-29	98%	JX113269.1
Musa sp. Ogasawara06 chloroplast trnL gene, intron, partial sequence, isolate: OGA0508	136	136	100%	4e-29	98%	AB817687.1
Musa basjoo tRNA-Leu (trnL(UAA)) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF(GAA)) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	FJ428188.2
Musella lasiocarpa isolate Kress-GH01-210 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	FJ621287.1
Musa mannii tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	FJ621285.1
Musa nagensium tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	FJ621284.1
Musa rubra tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	FJ621277.1
Musa splendida tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	FJ621282.1
Musa balbisiana isolate Bangladesh tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	FJ621280.1
Musa balbisiana isolate Yunnan tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	FJ621279.1
Musa ornata tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	FJ621278.1
Musa itinerans tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	FJ621276.1
Musa formosana tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	FJ621275.1
Musa sanguinea tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	FJ621274.1
Musa campestris tRNA-Leu (trnL) gene,						

partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	FJ621273.1
Musa beccarii tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	FJ621272.1
Musa basjoo tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	FJ621270.1
Musa maclayi tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	FJ621269.1
Musa laterita tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	FJ621268.1
Musa salaccensis tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	FJ621266.1
Musa velutina tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	FJ621264.1
Musa rosea tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	FJ621263.1
Angiosperm environmental sample chloroplast partial tRNA-Leu gene, intron region, isolated from Cryptorhynchinae sp.34 BMNH:796424	136	136	100%	4e-29	98%	FN398125.1
Musa beccarii tRNA-Leu gene, partial sequence; tRNA-Leu(UAA)-tRNA-Phe(GAA) intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	136	136	100%	4e-29	98%	AF431635.1
Musa gracilis isolate SS&JS 128 Sri Nara QSBG tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	KT257587.1
Musa textilis tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	131	131	96%	2e-27	97%	FJ621281.1
Musa borneensis tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	FJ621265.1
Musa violascens tRNA-Leu (trnL(UAA)) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF(GAA)) gene, partial sequence; chloroplast	131	131	100%	2e-27	96%	FJ428195.1
Musa rosea plastid partial tRNA-Leu gene and trnL-trnF IGS, specimen voucher Asmussen 101 (CP)	131	131	100%	2e-27	96%	AM113703.1
Musella lasiocarpa isolate Yunnan tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	129	129	100%	6e-27	96%	FJ621286.1
Thaumatococcus daniellii plastid, partial genome	127	127	100%	2e-26	95%	KF601575.1
Heliconia collinsiana plastid, complete genome	127	127	100%	2e-26	95%	JX088660.1
Calathea villosa voucher R.Dressler 2912 (COL) tRNA-Leu (trnL) gene, partial	127	127	100%	2e-26	95%	JN413158.1

sequence; chloroplast						
Hypselodelphys hirsuta voucher A.Ley 269 (WAG) tRNA-Leu (trnL) gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	JN413110.1
Heliconia stricta tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	FJ621299.1
Megaphrynium trichogynum voucher Ley 114 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	127	127	100%	2e-26	95%	EU647828.1
Thaumatococcus sp. Ley 179 voucher Ley 179 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	127	127	100%	2e-26	95%	EU647827.1
Thaumatococcus daniellii voucher Ley 96 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	127	127	100%	2e-26	95%	EU647826.1
Hypselodelphys sp. Ley 125 voucher Ley 125 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	127	127	100%	2e-26	95%	EU647825.1
Hypselodelphys scandens voucher Ley 160 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	127	127	100%	2e-26	95%	EU647824.1
Trachyphrynium braunianum voucher Ley 171 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	127	127	100%	2e-26	95%	EU647823.1
Hypselodelphys violacea voucher Ley 28 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	127	127	100%	2e-26	95%	EU647821.1
Hypselodelphys hirsuta voucher Ley 156 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	127	127	100%	2e-26	95%	EU647820.1
Hypselodelphys poggeana voucher Ley 168 (LBV, WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	127	127	100%	2e-26	95%	EU647819.1
Heliconia solomonensis tRNA-Leu gene, partial sequence; tRNA-Leu(UAA)-tRNA-Phe(GAA) intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	AF431634.1
Heliconia rostrata tRNA-Leu gene, partial sequence; tRNA-Leu(UAA)-tRNA-Phe(GAA) intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	127	127	100%	2e-26	95%	AF431633.1
Hypselodelphys velutina voucher Jongkind 4839 (WAG) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence	123	123	100%	3e-25	94%	EU647818.1
Ensete superbum isolate SS&JS 242 Pha Pli Lueang Vachiralongkorn Dam tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence;	122	122	100%	9e-25	92%	KT257601.1

chloroplast						
Ensete glaucum isolate SS&JS 229 Nuan Sae-Lae tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	122	122	100%	9e-25	92%	KT257600.1
Musa coccinea isolate SS&JS 223 Rattakatthali tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	122	122	100%	9e-25	92%	KT257586.1
Costus zingiberoides voucher BTM86-00-01 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	122	122	100%	9e-25	94%	KJ011345.1
Costus talbotii voucher 2003-0109009 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	122	122	100%	9e-25	94%	KJ011343.1
Costus aff. tappenbeckianus SMS-2014 voucher 2005-0100002 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	122	122	100%	9e-25	94%	KJ011342.1
Costus aff. tappenbeckianus SMS-2014 voucher 2005-0100001 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	122	122	100%	9e-25	94%	KJ011341.1
Costus scaber voucher R2253 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	122	122	100%	9e-25	94%	KJ011339.1
Costus ricus voucher R2970 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	122	122	100%	9e-25	94%	KJ011338.1
Costus quasi-appendiculatus voucher CSpecht 99-233 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	122	122	100%	9e-25	94%	KJ011337.1
Costus aff. phyllocephalus SMS-2014 voucher BB870057 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	122	122	100%	9e-25	94%	KJ011334.1
Costus osae voucher M9501 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	122	122	100%	9e-25	94%	KJ011333.1
Costus maboumiensis voucher M10227 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	122	122	100%	9e-25	94%	KJ011330.1
Costus lucanusianus voucher Breteler5297 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	122	122	100%	9e-25	94%	KJ011329.1
Costus aff. ligularis SMS-2014 voucher 2005-0100003 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	122	122	100%	9e-25	94%	KJ011324.1
Costus aff. ligularis SMS-2014 voucher 1998-0923003 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	122	122	100%	9e-25	94%	KJ011323.1

Costus leucanthus voucher 1996-1105001 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	122	122	100%	9e-25	94%	KJ011322.1
Costus lateriflorus voucher M10331 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	122	122	100%	9e-25	94%	KJ011321.1
Costus dubius voucher M10206 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	122	122	100%	9e-25	94%	KJ011314.1
Costus barbatus voucher CSpecht 01-256 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	122	122	100%	9e-25	94%	KJ011308.1
Costus vinosus voucher M9568 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	118	118	100%	1e-23	93%	KJ011344.1
Costus erythrophyllus voucher R2847 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	116	116	100%	4e-23	91%	KJ011315.1

Alignments

Musa yunnanensis isolate SS&JS 473 Montharop Khun Nan tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast

Sequence ID: **gb|KT257604.1|** Length: 1002 Number of Matches: 1
Range 1: 102 to 181

Score	Expect	Identities	Gaps	Strand	Frame
136 bits(150)	4e-29()	78/80(98%)	0/80(0%)	Plus/Plus	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCTTTTATTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  60
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Sbjct  102  GGCAATCCTGAGCCAAATCCTTATTTTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  161

Query  61   AAGGATAGGTGCAGAGACTC  80
            ||||||||||||||||||||
Sbjct  162  AAGGATAGGTGCAGAGACTC  181
```

Musella lasiocarpa isolate SS&JS 231 Dararassami tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast

Sequence ID: **gb|KT257602.1|** Length: 902 Number of Matches: 1
Range 1: 82 to 161

Score	Expect	Identities	Gaps	Strand	Frame
136 bits(150)	4e-29()	78/80(98%)	0/80(0%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTTTATTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  60
            |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  82   GGCAATCCTGAGCCAAATCCTTATTTTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  141

Query  61   AAGGATAGGTGCAGAGACTC  80
            ||||||||||||||||||||
Sbjct  142  AAGGATAGGTGCAGAGACTC  161
```

Musa yunnanensis isolate SS&JS 444 Yunnan Namtok Pa Way tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast

Sequence ID: **gb|KT257599.1|** Length: 971 Number of Matches: 1
Range 1: 102 to 181

Score	Expect	Identities	Gaps	Strand	Frame

136 bits(150)	4e-29()	78/80(98%)	0/80(0%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTTTATTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  60
            |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  102  GGCAATCCTGAGCCAAATCCTTATTTTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  161

Query  61   AAGGATAGGTGCAGAGACTC  80
            ||||||||||||||||||||
Sbjct  162  AAGGATAGGTGCAGAGACTC  181
```

Musa yunnanensis isolate SS&JS 349 Yunnan Inthanon tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KT257598.1|** Length: 971 Number of Matches: 1
Range 1: 102 to 181

Score	**Expect**	**Identities**	**Gaps**	**Strand**	**Frame**
136 bits(150)	4e-29()	78/80(98%)	0/80(0%)	Plus/Plus	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCTTTTATTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  60
            |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  102  GGCAATCCTGAGCCAAATCCTTATTTTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  161

Query  61   AAGGATAGGTGCAGAGACTC  80
            ||||||||||||||||||||
Sbjct  162  AAGGATAGGTGCAGAGACTC  181
```

Musa yunnanensis isolate SS&JS 235 Yunnan QSBG tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KT257597.1|** Length: 971 Number of Matches: 1
Range 1: 102 to 181

Score	**Expect**	**Identities**	**Gaps**	**Strand**	**Frame**
136 bits(150)	4e-29()	78/80(98%)	0/80(0%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCTTTTATTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  60
            |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  102  GGCAATCCTGAGCCAAATCCTTATTTTGAGAAAACAAAGGTTTATAAAACTAGAATTTAA  161

Query  61   AAGGATAGGTGCAGAGACTC  80
            ||||||||||||||||||||
Sbjct  162  AAGGATAGGTGCAGAGACTC  181
```

BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - 9EWF28YV015**
    Formatting options
    Download
Blast report description

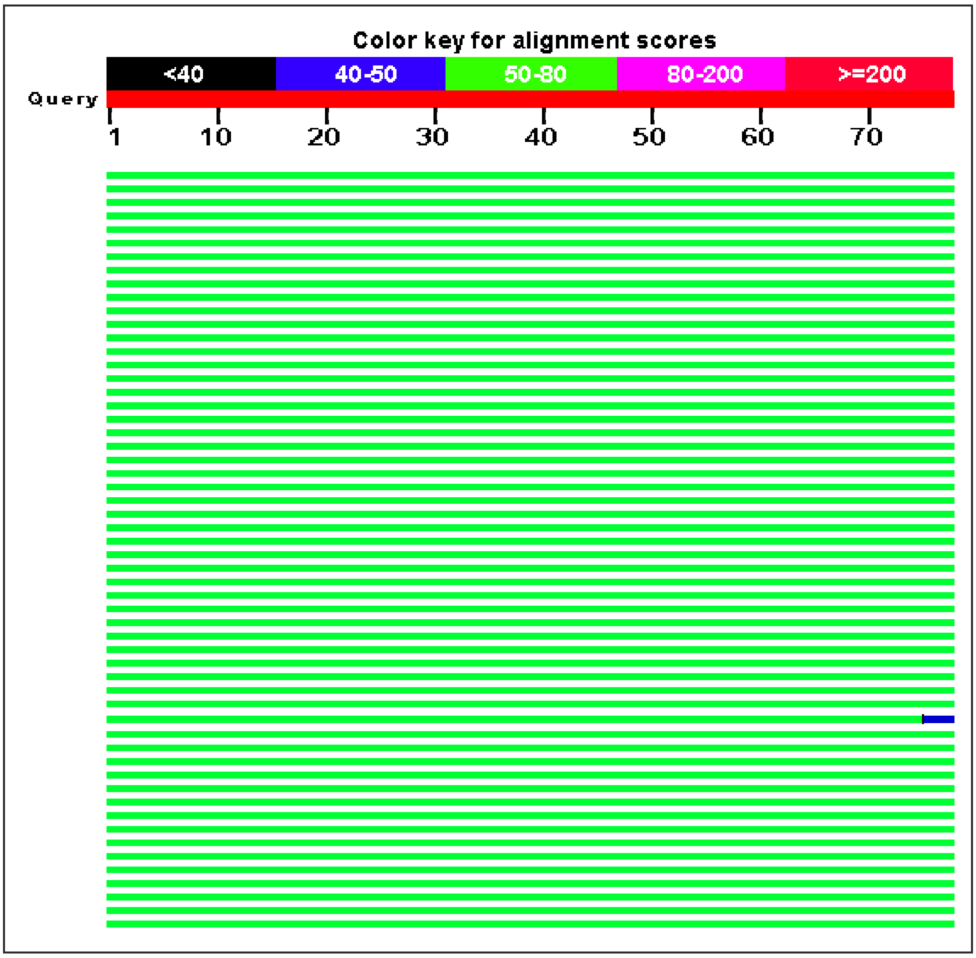
YK072B51A2_TRNL_Clone9

RID 9EWF28YV015 (Expires on 01-15 17:01 pm)

Query ID	lcl|Query_36281	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.0+
Query Length	78		

Graphic Summary

Distribution of 101 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Musa yunnanensis isolate SS&JS 473 Montharop Khun Nan tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257604.1
Musella lasiocarpa isolate SS&JS 231 Dararassami tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257602.1
Musa yunnanensis isolate SS&JS 444 Yunnan Namtok Pa Way tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257599.1
Musa yunnanensis isolate SS&JS 349 Yunnan Inthanon tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257598.1
Musa yunnanensis isolate SS&JS 235 Yunnan QSBG tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257597.1
Musa yunnanensis isolate SS&JS 125 Yunnan Huai Nam Dang tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257596.1
Musa laterita isolate SS&JS 412 Bua Si Som Pli Lueang tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257595.1
Musa serpentina isolate SS&JS 353 Nakkharat Huay Hang Pon tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257594.1
Musa serpentina isolate SS&JS 246 Nakkharat Dan Chedi Sam Ong tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257593.1
Musa ornata isolate SS&JS 449 Bua Si Chomphu Luk Khieo tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257592.1
Musa ornata isolate SS&JS 433 Bua Luang tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257591.1
Musa ornata isolate SS&JS 169 Bua Si Muang tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257590.1
Musa laterita isolate SS&JS 308 Bua Si Som Dan Mae Lamao tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic	75.2	75.2	100%	1e-10	83%	KT257589.1

spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast						
Musa itinerans isolate SS&JS 175 Hok Khao Soi Dao tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257588.1
Musa balbisiana isolate SS&JS 12 Tani Pa Tat Luang tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257585.1
Musa acuminata var. zebrina isolate SS&JS 155 Thahan Phran tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257584.1
Musa acuminata subsp. truncata isolate SS&JS 368 Pa Cameron tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257583.1
Musa acuminata subsp. siamea isolate SS&JS 450 Pa Kanchanaburi Campus tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257582.1
Musa acuminata subsp. siamea isolate SS&JS 173 Pa Pli Lueang Ban Pa Kluai tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257581.1
Musa acuminata subsp. siamea isolate SS&JS 136 Pa Namtok Kha-On tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257580.1
Musa acuminata subsp. siamea isolate SS&JS 131 Pa La-U tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257579.1
Musa acuminata subsp. siamea isolate SS&JS 1 Khae Phetchabun tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257578.1
Musa acuminata subsp. malaccensis isolate SS&JS 374 Pa Kao Talu tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257577.1
Musa acuminata subsp. malaccensis isolate SS&JS 108 Pa Hat Prapat tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257576.1
Musa acuminata subsp. malaccensis isolate SS&JS 107 Pa Pato tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257575.1
Musa acuminata subsp. malaccensis isolate SS&JS 104 Pa Chumphon tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257574.1
Musa acuminata subsp. malaccensis isolate SS&JS 445 Pa Namtok Pa Way tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and	75.2	75.2	100%	1e-10	83%	KT257573.1

tRNA-Phe (trnF) gene, partial sequence; chloroplast						
Musa acuminata subsp. malaccensis isolate SS&JS 202 Pa Tanopute tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KT257572.1
Musa balbisiana chloroplast, complete genome	75.2	75.2	100%	1e-10	83%	KT595228.1
Musa textilis plastid, complete genome	75.2	75.2	100%	1e-10	83%	KF601567.1
Platycaulos galpinii voucher T.Vanderniet 208, Z tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	KF423010.1
Musa acuminata subsp. malaccensis chloroplast complete genome, biomaterial CIRAD:930	75.2	75.2	100%	1e-10	83%	HF677508.1
Musa environmental sample tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	JX113269.1
Musa sp. Ogasawara06 chloroplast trnL gene, intron, partial sequence, isolate: OGA0508	75.2	75.2	100%	1e-10	83%	AB817687.1
Musa basjoo tRNA-Leu (trnL(UAA)) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF(GAA)) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	FJ428188.2
Musella lasiocarpa isolate Kress-GH01-210 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	FJ621287.1
Musa mannii tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	FJ621285.1
Musa nagensium tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	FJ621284.1
Musa rubra tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	FJ621277.1
Musa splendida tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	FJ621282.1
Musa textilis tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	119	100%	1e-10	83%	FJ621281.1
Musa balbisiana isolate Bangladesh tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	FJ621280.1
Musa balbisiana isolate Yunnan tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	FJ621279.1
Musa ornata tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	FJ621278.1
Musa itinerans tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	FJ621276.1

Musa formosana tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	FJ621275.1
Musa sanguinea tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	FJ621274.1
Musa campestris tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	FJ621273.1
Musa beccarii tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	FJ621272.1
Musa basjoo tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	FJ621270.1
Musa maclayi tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	FJ621269.1
Musa laterita tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	FJ621268.1
Musa salaccensis tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	FJ621266.1
Musa velutina tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	FJ621264.1
Musa rosea tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	FJ621263.1
Angiosperm environmental sample chloroplast partial tRNA-Leu gene, intron region, isolated from Cryptorhynchinae sp.34 BMNH:796424	75.2	75.2	100%	1e-10	83%	FN398125.1
Musa beccarii tRNA-Leu gene, partial sequence; tRNA-Leu(UAA)-tRNA-Phe(GAA) intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	75.2	75.2	100%	1e-10	83%	AF431635.1
Costus erythrophyllus voucher R2847 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	73.4	73.4	100%	4e-10	81%	KJ011315.1
Leptocarpus sp. BGB-2013b voucher NSW:784994 tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	73.4	73.4	100%	4e-10	81%	KF179160.1
Leptocarpus canus voucher NSW:870886 tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	73.4	73.4	100%	4e-10	81%	KF179155.1
Meeboldina sp. NSW713871 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	73.4	73.4	100%	4e-10	81%	GQ408973.1
Corypha utan chloroplast tRNA-Leu gene (partial), trnL-trnF intergenic spacer and tRNA-Phe gene (partial), specimen voucher Zona 898 (FTG)	73.4	73.4	100%	4e-10	81%	AM903234.1
Chuniophoenix hainanensis chloroplast tRNA-Leu gene (partial), trnL-trnF intergenic	73.4	73.4	100%	4e-10	81%	AM903232.1

spacer and tRNA-Phe gene (partial), specimen voucher Zona 791 (FTG)						
Meeboldina cana tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	73.4	73.4	100%	4e-10	81%	AF148744.1
Corypha taliera chloroplast partial tRNA-Leu gene, intergenic spacer and partial tRNA-Phe gene	73.4	73.4	100%	4e-10	81%	AJ404893.1
Corypha umbraculifera chloroplast DNA for trnL-trnF intergenic spacer	73.4	73.4	100%	4e-10	81%	AJ241267.1
Musa gracilis isolate SS&JS 128 Sri Nara QSBG tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	KT257587.1
Costus zingiberoides voucher BTM86-00-01 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	KJ011345.1
Costus talbotii voucher 2003-0109009 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	KJ011343.1
Costus aff. tappenbeckianus SMS-2014 voucher 2005-0100002 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	KJ011342.1
Costus aff. tappenbeckianus SMS-2014 voucher 2005-0100001 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	KJ011341.1
Costus scaber voucher R2253 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	KJ011339.1
Costus ricus voucher R2970 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	KJ011338.1
Costus quasi-appendiculatus voucher CSpecht 99-233 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	KJ011337.1
Costus aff. phyllocephalus SMS-2014 voucher BB870057 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	KJ011334.1
Costus osae voucher M9501 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	KJ011333.1
Costus maboumiensis voucher M10227 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	KJ011330.1
Costus lucanusianus voucher Breteler5297 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	KJ011329.1
Costus aff. ligularis SMS-2014 voucher 2005-0100003 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	KJ011324.1

Costus aff. ligularis SMS-2014 voucher 1998-0923003 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	KJ011323.1
Costus leucanthus voucher 1996-1105001 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	KJ011322.1
Costus lateriflorus voucher M10331 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	KJ011321.1
Costus dubius voucher M10206 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	KJ011314.1
Costus barbatus voucher CSpecht 01-256 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	KJ011308.1
Thaumatococcus daniellii plastid, partial genome	71.6	71.6	100%	1e-09	81%	KF601575.1
Costus pulverulentus plastid, partial genome	71.6	71.6	100%	1e-09	81%	KF601573.1
Platycaulos mahonii subsp. mahonii voucher C.Hardy 327, Z tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	KF423059.1
Platycaulos acutus voucher H.P.Linder 7295, Z tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	KF423049.1
Platycaulos cascadensis voucher H.P.Linder 7358, Z tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	KF423034.1
Platycaulos anceps voucher H.P.Linder 7274, Z tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	KF422996.1
Dypsis decaryi chloroplast trnL gene, intron, partial sequence, isolate: OGA0510	71.6	71.6	100%	1e-09	81%	AB817689.1
Clinostigma savoryanum chloroplast trnL gene, intron, partial sequence, isolate: OGA0416	71.6	71.6	100%	1e-09	81%	AB817609.1
Clinostigma savoryanum chloroplast trnL gene, intron, partial sequence, isolate: OGA0244	71.6	71.6	100%	1e-09	81%	AB817466.1
Heliconia collinsiana plastid, complete genome	71.6	71.6	100%	1e-09	81%	JX088660.1
Megaphrynium macrostachyum voucher A.Ley 260 (WAG) tRNA-Leu (trnL) gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	JN413113.1
Hypselodelphys hirsuta voucher A.Ley 269 (WAG) tRNA-Leu (trnL) gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	JN413110.1
Lanaria lanata voucher E.R. Orchard 342 (M) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	HM459536.1
Costus potierae isolate MH1 tRNA-Leu gene, partial sequence; trnL-trnF intergenic	71.6	71.6	100%	1e-09	81%	HQ234747.1

spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast						
Heliconia stricta tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	71.6	71.6	100%	1e-09	81%	FJ621299.1
Costus vinosus voucher M9568 tRNA-Leu gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe gene, partial sequence; chloroplast	68.0	68.0	94%	2e-08	82%	KJ011344.1

Alignments

Musa yunnanensis isolate SS&JS 473 Montharop Khun Nan tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KT257604.1|** Length: 1002 Number of Matches: 1
Range 1: 102 to 181

Score	Expect	Identities	Gaps	Strand	Frame
75.2 bits(82)	1e-10()	66/80(83%)	2/80(2%)	Plus/Minus	

Features:

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Query  1    GAGTCTCTGC-CCTATCCTTTTAA-TTCCAGTTTTATAAAATTTTNTTTTTTCAAAAGGA  58
            |||||||||| ||||||||||||| ||| |||||||||||  ||| |||| ||||||  |
Sbjct  181  GAGTCTCTGCACCTATCCTTTTAAATTCTAGTTTTATAAACCTTTGTTTTCTCAAAATAA  122

Query  59   AGATGTGGGTCGGGATTTCC  78
             ||| ||| || ||||| ||
Sbjct  121  GGATTTGGCTCAGGATTGCC  102
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Musella lasiocarpa isolate SS&JS 231 Dararassami tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KT257602.1|** Length: 902 Number of Matches: 1
Range 1: 82 to 161

Score	Expect	Identities	Gaps	Strand	Frame
75.2 bits(82)	1e-10()	66/80(83%)	2/80(2%)	Plus/Minus	

Features:

```
Query  1    GAGTCTCTGC-CCTATCCTTTTAA-TTCCAGTTTTATAAAATTTTNTTTTTTCAAAAGGA  58
            |||||||||| ||||||||||||| ||| |||||||||||  ||| |||| ||||||  |
Sbjct  161  GAGTCTCTGCACCTATCCTTTTAAATTCTAGTTTTATAAACCTTTGTTTTCTCAAAATAA  102

Query  59   AGATGTGGGTCGGGATTTCC  78
             ||| ||| || ||||| ||
Sbjct  101  GGATTTGGCTCAGGATTGCC  82
```

Musa yunnanensis isolate SS&JS 444 Yunnan Namtok Pa Way tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KT257599.1|** Length: 971 Number of Matches: 1
Range 1: 102 to 181

Score	Expect	Identities	Gaps	Strand	Frame
75.2 bits(82)	1e-10()	66/80(83%)	2/80(2%)	Plus/Minus	

Features:

```
Query  1    GAGTCTCTGC-CCTATCCTTTTAA-TTCCAGTTTTATAAAATTTTNTTTTTTCAAAAGGA  58
            |||||||||| ||||||||||||| ||| |||||||||||  ||| |||| ||||||  |
Sbjct  181  GAGTCTCTGCACCTATCCTTTTAAATTCTAGTTTTATAAACCTTTGTTTTCTCAAAATAA  122

Query  59   AGATGTGGGTCGGGATTTCC  78
             ||| ||| || ||||| ||
Sbjct  121  GGATTTGGCTCAGGATTGCC  102
```

Musa yunnanensis isolate SS&JS 349 Yunnan Inthanon tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KT257598.1|** Length: 971 Number of Matches: 1
Range 1: 102 to 181

Score	Expect	Identities	Gaps	Strand	Frame

75.2 bits(82)	1e-10()	66/80(83%)	2/80(2%)	Plus/Minus	

Features:

```
Query  1    GAGTCTCTGC-CCTATCCTTTTAA-TTCCAGTTTTATAAAATTTTNTTTTTTCAAAAGGA  58
            |||||||||| ||||||||||||| ||| |||||||||||  ||| |||| ||||||  |
Sbjct  181  GAGTCTCTGCACCTATCCTTTTAAATTCTAGTTTTATAAACCTTTGTTTTCTCAAAATAA  122

Query  59   AGATGTGGGTCGGGATTTCC  78
             ||| ||| || ||||| ||
Sbjct  121  GGATTTGGCTCAGGATTGCC  102
```

Musa yunnanensis isolate SS&JS 235 Yunnan QSBG tRNA-Lue (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KT257597.1|** Length: 971 Number of Matches: 1
Range 1: 102 to 181

Score	Expect	Identities	Gaps	Strand	Frame
75.2 bits(82)	1e-10()	66/80(83%)	2/80(2%)	Plus/Minus	

Features:

```
Query  1    GAGTCTCTGC-CCTATCCTTTTAA-TTCCAGTTTTATAAAATTTTNTTTTTTCAAAAGGA  58
            |||||||||| ||||||||||||| ||| |||||||||||  ||| |||| ||||||  |
Sbjct  181  GAGTCTCTGCACCTATCCTTTTAAATTCTAGTTTTATAAACCTTTGTTTTCTCAAAATAA  122

Query  59   AGATGTGGGTCGGGATTTCC  78
             ||| ||| || ||||| ||
Sbjct  121  GGATTTGGCTCAGGATTGCC  102
```

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Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - 9B135E3F016**
Formatting options
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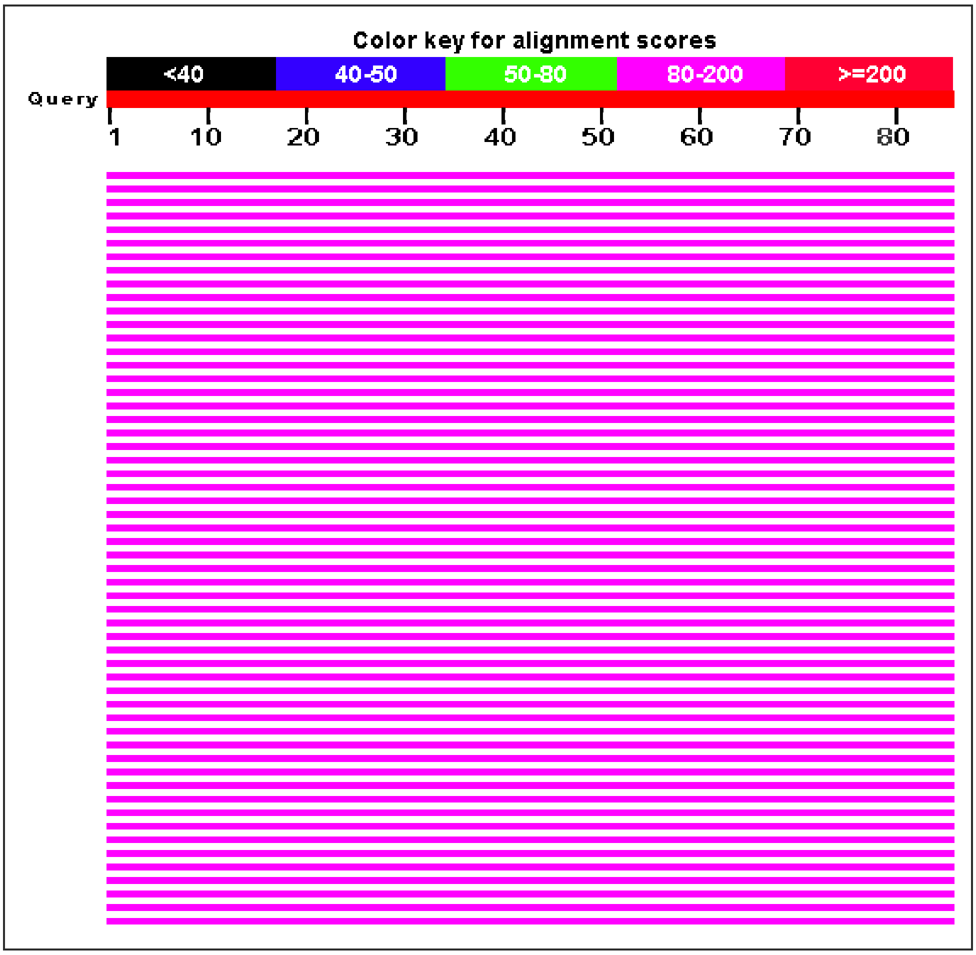
Blast report description

YK07-2-B5-1S_TRNL_Clone3

RID	9B135E3F016 (Expires on 01-14 05:55 am)		
Query ID	lcl|Query_33141	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.0+
Query Length	85		

Graphic Summary

Distribution of 102 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Agropyron cristatum var. pectinatum voucher M.Pinar 4412a trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP723655.1
Agropyron deweyi voucher M.Pinar 4321a trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP723652.1
Aegilops geniculata isolate CRF BGE022746 trnL gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	154	154	100%	2e-34	100%	KR559558.1
Aegilops neglecta bio-material USDA:PI170209 trnL gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	154	154	100%	2e-34	100%	KR559557.1
Elymus nevskii voucher Alt 1124 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KJ744043.1
Agropyron cristatum voucher Alt 11-377 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KJ744042.1
Elymus caninus voucher Alt 1031 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KJ744041.1
Campeiostachys dahurica voucher Xa 09-157 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KJ744040.1
Elymus fedtschenkoi voucher Alt 12-133 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KJ755833.1
Agropyron krylovianum voucher Alt 12-264 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KJ755832.1
Elymus subfibrosus tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP257587.1
Elymus lanceolatus subsp. lanceolatus isolate CP3 tRNA-Leu (trnL) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KP208327.1
Triticum macha chloroplast DNA, complete genome	154	154	100%	2e-34	100%	LC005978.1
Triticum monococcum subsp. monococcum chloroplast DNA, complete genome	154	154	100%	2e-34	100%	LC005977.1
Triticum turgidum subsp. durum cultivar Langdon chloroplast, complete genome	154	154	100%	2e-34	100%	KM352501.1
Triticum timopheevii chloroplast DNA,	154	154	100%	2e-34	100%	AB976560.1

complete genome						
Aegilops kotschyi cultivar TA1980 chloroplast, complete genome	154	154	100%	2e-34	100%	**KJ614420.1**
Aegilops sharonensis cultivar TA1995 chloroplast, complete genome	154	154	100%	2e-34	100%	**KJ614419.1**
Aegilops bicornis cultivar Clae57 chloroplast, complete genome	154	154	100%	2e-34	100%	**KJ614418.1**
Aegilops sharonensis cultivar TA1996 chloroplast, complete genome	154	154	100%	2e-34	100%	**KJ614417.1**
Aegilops longissima cultivar TA1924 chloroplast, complete genome	154	154	100%	2e-34	100%	**KJ614416.1**
Aegilops searsii cultivar TA1841 chloroplast, complete genome	154	154	100%	2e-34	100%	**KJ614415.1**
Aegilops searsii cultivar TA1837 chloroplast, complete genome	154	154	100%	2e-34	100%	**KJ614414.1**
Aegilops searsii cultivar TA1926 chloroplast, complete genome	154	154	100%	2e-34	100%	**KJ614413.1**
Aegilops tauschii cultivar AL8/78 chloroplast, complete genome	154	154	100%	2e-34	100%	**KJ614412.1**
Triticum urartu cultivar PI428335 chloroplast, complete genome	154	154	100%	2e-34	100%	**KJ614411.1**
Triticum timopheevii cultivar Tim01 chloroplast, complete genome	154	154	100%	2e-34	100%	**KJ614410.1**
Triticum timopheevii cultivar TA944 chloroplast, complete genome	154	154	100%	2e-34	100%	**KJ614409.1**
Triticum timopheevii cultivar TA1485 chloroplast, complete genome	154	154	100%	2e-34	100%	**KJ614408.1**
Triticum timopheevii cultivar TA0941 chloroplast, complete genome	154	154	100%	2e-34	100%	**KJ614407.1**
Aegilops speltoides var. speltoides cultivar PI487232 chloroplast, complete genome	154	154	100%	2e-34	100%	**KJ614406.1**
Aegilops speltoides var. ligustica cultivar TA1796 chloroplast, complete genome	154	154	100%	2e-34	100%	**KJ614405.1**
Aegilops speltoides var. ligustica cultivar AE918 chloroplast, complete genome	154	154	100%	2e-34	100%	**KJ614404.1**
Triticum aestivum cultivar spleta PI384000 chloroplast, complete genome	154	154	100%	2e-34	100%	**KJ614403.1**
Triticum turgidum cultivar TA1133 chloroplast, complete genome	154	154	100%	2e-34	100%	**KJ614402.1**
Triticum turgidum cultivar TA0060 chloroplast, complete genome	154	154	100%	2e-34	100%	**KJ614401.1**
Triticum turgidum cultivar TA0073 chloroplast, complete genome	154	154	100%	2e-34	100%	**KJ614400.1**
Triticum turgidum cultivar TA2801 chloroplast, complete genome	154	154	100%	2e-34	100%	**KJ614399.1**
Triticum turgidum cultivar PI520121 chloroplast, complete genome	154	154	100%	2e-34	100%	**KJ614398.1**
Triticum aestivum cultivar Chinese Spring TA3008 chloroplast, complete genome	154	154	100%	2e-34	100%	**KJ614396.1**
Elymus repens isolate xt_plant145 tRNA-Leu (trnL) gene, intron; chloroplast	154	154	100%	2e-34	100%	**KJ746409.1**
Triticum aestivum chromosome 3B, genomic scaffold, cultivar Chinese Spring	154	319	100%	2e-34	100%	**HG670306.1**
Triticum aestivum chloroplast, complete genome	154	154	100%	2e-34	100%	**KJ592713.1**
Elymus sibiricus isolate EI_201311 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	**KF905225.1**
Elymus dolichatherus isolate EI_201310 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	**KF905224.1**
Elymus nutans isolate EI_201309 tRNA-Leu						

(trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905223.1
Elymus sibiricus isolate El_201307 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905221.1
Elymus tangutorum isolate El_201305 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905219.1
Elymus nutans isolate El_201302 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905216.1
Elymus nutans isolate El_201301 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905215.1
Elymus dolichatherus isolate El_201228 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905214.1
Elymus tangutorum isolate El_201226 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905212.1
Elymus tangutorum isolate El_201216 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905202.1
Elymus nutans isolate El_201224 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905210.1
Elymus dahuricus var. cylindricus isolate El_201222 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905208.1
Elymus tangutorum isolate El_201221 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905207.1
Elymus sibiricus isolate El_201220 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905206.1
Elymus antiquus isolate El_201219 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905205.1
Elymus excelsus isolate El_201218 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905204.1
Elymus nutans isolate El_201217 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905203.1

Elymus excelsus isolate EI_201214 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905200.1
Elymus tangutorum isolate EI_201213 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905199.1
Elymus dolichatherus isolate EI_201212 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905198.1
Elymus dolichatherus isolate EI_201211 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905197.1
Elymus tangutorum isolate EI_201209 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905195.1
Elymus dahuricus isolate EI_201208 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905194.1
Elymus tibeticus isolate EI_201206 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905192.1
Elymus tangutorum isolate EI_201205 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905191.1
Elymus tangutorum isolate EI_201204 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905190.1
Elymus dahuricus var. cylindricus isolate EI_201202 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905188.1
Elymus nutans isolate EI_201102 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905186.1
Elymus sibiricus isolate EI_201101 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF905185.1
Triticum urartu plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732946.1
Triticum spelta plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732945.1
Triticum monococcum plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732944.1
Triticum durum plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	AB732942.1

Triticum monococcum subsp. aegilopoides plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	**AB732941.1**
Triticum aestivum plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	**AB732940.1**
Elymus tsukushiensis plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	**AB732933.1**
Elymus racemifer plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	**AB732932.1**
Elymus humidus plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	**AB732931.1**
Elymus dahuricus plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	**AB732930.1**
Elymus caninus plastid DNA, tRNA-Leu (trnL), trnL-trnF intergenic spacer, partial sequence	154	154	100%	2e-34	100%	**AB732929.1**
Aegilops geniculata chloroplast, complete genome	154	154	100%	2e-34	100%	**KF534490.1**
Aegilops cylindrica chloroplast, complete genome	154	154	100%	2e-34	100%	**KF534489.1**
Elymus tauri isolate Psetau3 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu (trnL) gene, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	**KF600705.1**
Elymus tauri isolate Psetau2 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu (trnL) gene, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	**KF600704.1**
Elymus stipifolius isolate Psesti3 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu (trnL) gene, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	**KF600702.1**
Elymus stipifolius isolate Psesti2 trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	**KF600701.1**
Elymus spicatus isolate Psespi6 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu (trnL) gene, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	**KF600700.1**
Elymus breviaristatus isolate Elybre1 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu (trnL) gene, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	**KF600684.1**
Elymus sibiricus isolate Elysib1 trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	**KF600697.1**
Elymus pendulinus isolate Elypen1 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu (trnL) gene, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	**KF600696.1**
Elymus nevskii isolate Elynev1 tRNA-Thr						

(trnT) gene, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu (trnL) gene, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF600695.1
Elymus mutabilis isolate Elymut2 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu (trnL) gene, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF600694.1
Elymus longearistatus isolate Elylon1 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu (trnL) gene, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF600693.1
Elymus gmelinii isolate Elygme1 trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF600692.1
Elymus dentatus isolate Elyden2 trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF600691.1
Elymus ciliaris isolate Elycil5 trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF600690.1
Elymus ciliaris isolate Elycil2 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, tRNA-Leu (trnL) gene, and trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	154	154	100%	2e-34	100%	KF600689.1

Alignments

Agropyron cristatum var. pectinatum voucher M.Pinar 4412a trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|KP723655.1|** Length: 1516 Number of Matches: 1

See 2 more title(s)
Range 1: 682 to 766

Score	Expect	Identities	Gaps	Strand	Frame
154 bits(170)	2e-34()	85/85(100%)	0/85(0%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCGTGTTTTGAGAAAACAAGGGGTTCTCGAACTAGAATACAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  682  GGCAATCCTGAGCCAAATCCGTGTTTTGAGAAAACAAGGGGTTCTCGAACTAGAATACAA  741

Query  61   AGGAAAAGGATAGGTGCAGAGACTC  85
            |||||||||||||||||||||||||
Sbjct  742  AGGAAAAGGATAGGTGCAGAGACTC  766
```

Agropyron deweyi voucher M.Pinar 4321a trnT-trnL intergenic spacer, partial sequence; tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|KP723652.1|** Length: 1517 Number of Matches: 1

See 8 more title(s)
Range 1: 682 to 766

Score	Expect	Identities	Gaps	Strand	Frame
154 bits(170)	2e-34()	85/85(100%)	0/85(0%)	Plus/Plus	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCGTGTTTTGAGAAAACAAGGGGTTCTCGAACTAGAATACAA  60
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  682  GGCAATCCTGAGCCAAATCCGTGTTTTGAGAAAACAAGGGGTTCTCGAACTAGAATACAA  741

Query  61   AGGAAAAGGATAGGTGCAGAGACTC  85
            |||||||||||||||||||||||||
Sbjct  742  AGGAAAAGGATAGGTGCAGAGACTC  766
```

Aegilops geniculata isolate CRF BGE022746 trnL gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|KR559558.1|** Length: 856 Number of Matches: 1
Range 1: 42 to 126

Score	Expect	Identities	Gaps	Strand	Frame
154 bits(170)	2e-34()	85/85(100%)	0/85(0%)	Plus/Plus	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCGTGTTTTGAGAAAACAAGGGGTTCTCGAACTAGAATACAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  42   GGCAATCCTGAGCCAAATCCGTGTTTTGAGAAAACAAGGGGTTCTCGAACTAGAATACAA  101

Query  61   AGGAAAAGGATAGGTGCAGAGACTC  85
            |||||||||||||||||||||||||
Sbjct  102  AGGAAAAGGATAGGTGCAGAGACTC  126
```

Aegilops neglecta bio-material USDA:PI170209 trnL gene and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|KR559557.1|** Length: 841 Number of Matches: 1
Range 1: 42 to 126

Score	Expect	Identities	Gaps	Strand	Frame
154 bits(170)	2e-34()	85/85(100%)	0/85(0%)	Plus/Plus	

Features:

```
Query  1    GGCAATCCTGAGCCAAATCCGTGTTTTGAGAAAACAAGGGGTTCTCGAACTAGAATACAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  42   GGCAATCCTGAGCCAAATCCGTGTTTTGAGAAAACAAGGGGTTCTCGAACTAGAATACAA  101

Query  61   AGGAAAAGGATAGGTGCAGAGACTC  85
            |||||||||||||||||||||||||
Sbjct  102  AGGAAAAGGATAGGTGCAGAGACTC  126
```

Elymus nevskii voucher Alt 1124 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|KJ744043.1|** Length: 1048 Number of Matches: 1
Range 1: 102 to 186

Score	Expect	Identities	Gaps	Strand	Frame
154 bits(170)	2e-34()	85/85(100%)	0/85(0%)	Plus/Plus	

Features:

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Query  1    GGCAATCCTGAGCCAAATCCGTGTTTTGAGAAAACAAGGGGTTCTCGAACTAGAATACAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  102  GGCAATCCTGAGCCAAATCCGTGTTTTGAGAAAACAAGGGGTTCTCGAACTAGAATACAA  161

Query  61   AGGAAAAGGATAGGTGCAGAGACTC  85
            |||||||||||||||||||||||||
Sbjct  162  AGGAAAAGGATAGGTGCAGAGACTC  186
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BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ blastn suite/ **Formatting Results - 9B3V90K0013**
  Formatting options
  Download
Blast report description

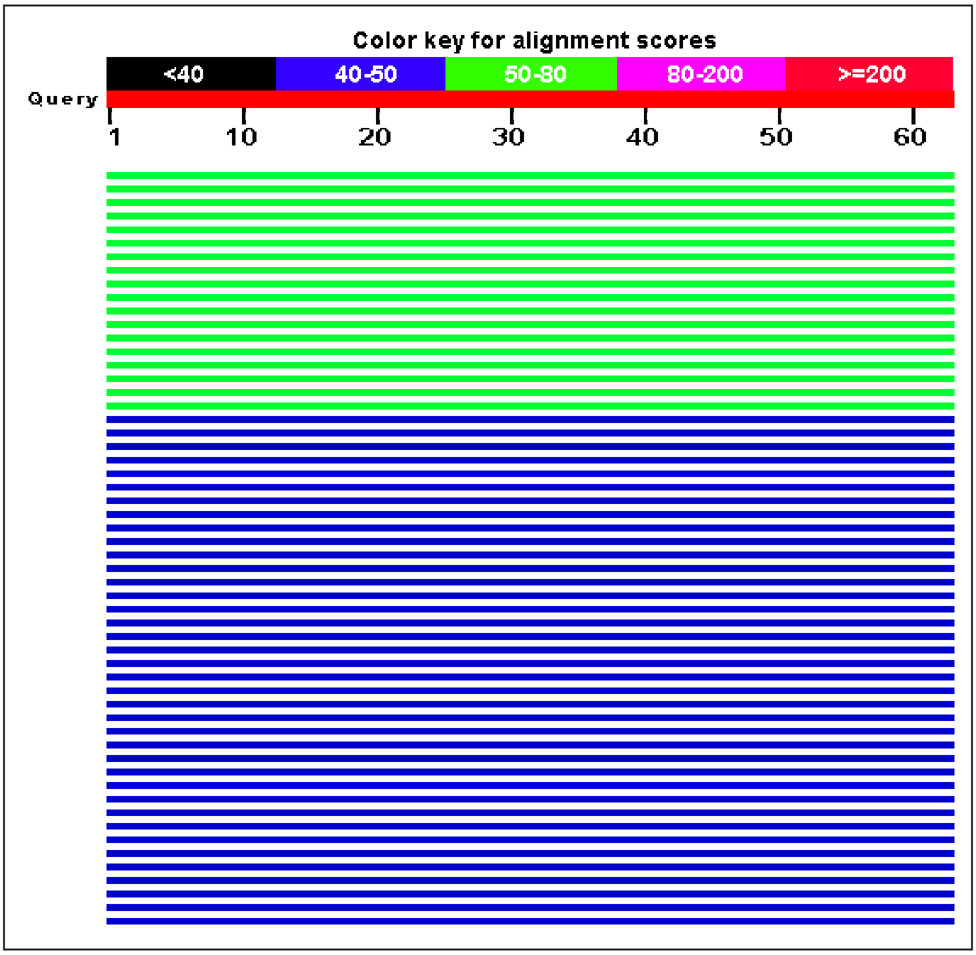
YK07-2-B5-1S_TRNL_Clone9

RID 9B3V90K0013 (Expires on 01-14 06:42 am)

Query ID	lcl|Query_142197	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.0+
Query Length	63		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Paphiopedilum victoria-regina voucher KDAIS Pap-14 tRNA-Leu (trnL) gene, intron; chloroplast	55.4	55.4	100%	7e-05	80%	EF156072.1
Paphiopedilum victoria-mariae voucher KDAIS Pap-84 tRNA-Leu (trnL) gene, intron; chloroplast	55.4	55.4	100%	7e-05	80%	EF156071.1
Paphiopedilum moquetteanum voucher KDAIS Pap-48 tRNA-Leu (trnL) gene, intron; chloroplast	55.4	55.4	100%	7e-05	80%	EF156044.1
Paphiopedilum haynaldianum voucher KDAIS Pap-54 tRNA-Leu (trnL) gene, intron; chloroplast	55.4	55.4	100%	7e-05	80%	EF156025.1
Paphiopedilum glaucophyllum voucher KDAIS Pap-29 tRNA-Leu (trnL) gene, intron; chloroplast	55.4	55.4	100%	7e-05	80%	EF156020.1
Paepalanthus tuberosus isolate FS1641 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	53.6	53.6	100%	2e-04	79%	EU924486.1
Cascadia nuttallii genomic DNA containing trnL(UAA) gene (5' exon, intron and 3' exon), trnL-F IGS, trnF(GAA) gene, specimen voucher R. Olmstead 921 (NY)	51.8	51.8	100%	8e-04	78%	LM654424.1
Cascadia nuttallii genomic DNA containing trnL(UAA) gene (5' exon, intron and 3' exon), trnL-F IGS, trnF(GAA) gene, specimen voucher W.J. Dress 4198 (LE)	51.8	51.8	100%	8e-04	78%	LM654423.1
Ephedra likiangensis isolate H15 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	51.8	51.8	100%	8e-04	78%	KC407792.1
Lomatogonium rotatum isolate 1316o tRNA-Leu (trnL) gene, partial sequence; chloroplast	51.8	51.8	100%	8e-04	78%	GQ245087.1
Paphiopedilum urbanianum voucher KDAIS Pap-106 tRNA-Leu (trnL) gene, intron; chloroplast	51.8	51.8	100%	8e-04	76%	EF156067.1
Paphiopedilum schoseri voucher KDAIS Pap-116 tRNA-Leu (trnL) gene, intron; chloroplast	51.8	51.8	100%	8e-04	76%	EF156059.1
Paphiopedilum papuanum voucher KDAIS Pap-27 tRNA-Leu (trnL) gene, intron; chloroplast	51.8	51.8	100%	8e-04	76%	EF156047.1
Paphiopedilum braemii voucher KDAIS Pap-103 tRNA-Leu (trnL) gene, intron; chloroplast	51.8	51.8	100%	8e-04	76%	EF156004.1
Paphiopedilum argus voucher KDAIS Pap-77 tRNA-Leu (trnL) gene, intron; chloroplast	51.8	51.8	100%	8e-04	76%	EF156000.1
Paphiopedilum acmodontum voucher KDAIS Pap-94 tRNA-Leu (trnL) gene, intron; chloroplast	51.8	51.8	100%	8e-04	76%	EF155996.1
Cascadia nuttallii trnL gene, partial sequence; trnL-trnK intergenic spacer region, complete sequence and trnK, partial sequence; chloroplast genes for chloroplast products	51.8	51.8	100%	8e-04	78%	AF374798.1
Lomatogonium rotatum chloroplast tRNA-	51.8	51.8	100%	8e-04	77%	AJ408011.1

Leu gene, intron						
Ephedra monosperma voucher Freitag 33031 (KAS) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	100%	0.003	77%	KP788797.1
Ephedra likiangensis voucher Boufford 30871 (GH) tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	100%	0.003	77%	KP788795.1
Acanthophippium sylhetense voucher L.Li 124(IBSC) tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	100%	0.003	74%	KM025171.1
Ephedra minuta isolate H10 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	100%	0.003	77%	KC407787.1
Ephedra minuta isolate H6 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	100%	0.003	77%	KC407783.1
Ephedra distachya voucher s.n. (MEXU) tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	100%	0.003	77%	JX217730.1
Apostasia shenzhenica isolate A001 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	50.0	50.0	100%	0.003	76%	JF796889.1
Paphiopedilum wilhelminiae voucher KDAIS Pap-205 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	GQ505313.1
Paphiopedilum supardii voucher KDAIS Pap-189 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	GQ505312.1
Andreaea rupestris var. fauriei isolate CB136 tRNA-Phe (trnF) gene, partial sequence; trnF-trnL intergenic spacer, complete sequence; and tRNA-Leu (trnL) gene, partial sequence; chloroplast	50.0	50.0	100%	0.003	78%	FJ572421.1
Ephedra equisetina chloroplast DNA, complete sequence	50.0	50.0	100%	0.003	77%	AP010819.1
Paphiopedilum wardii voucher KDAIS Pap-18 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156076.1
Paphiopedilum villosum voucher KDAIS Pap-36 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156074.1
Paphiopedilum venustum voucher KDAIS Pap-95 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156070.1
Paphiopedilum venustum voucher KDAIS Pap-32 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156069.1
Paphiopedilum spicerianum voucher KDAIS Pap-28 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156060.1
Paphiopedilum hookerae var. volonteanum voucher KDAIS Pap-125 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156030.1
Paphiopedilum sanderianum voucher KDAIS Pap-46 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156057.1
Paphiopedilum ooii voucher KDAIS Pap-134 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156046.1
Paphiopedilum robinsonii voucher KDAIS Pap-41 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156055.1

Paphiopedilum richardianum voucher KDAIS Pap-68 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156054.1
Paphiopedilum kolopakingii voucher KDAIS Pap-57 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156036.1
Paphiopedilum primulinum voucher KDAIS Pap-45 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156051.1
Paphiopedilum philippinense voucher KDAIS Pap-7 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156050.1
Paphiopedilum philippinense voucher KDAIS Pap-186 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156049.1
Paphiopedilum parishii voucher KDAIS Pap-276 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156048.1
Paphiopedilum liemianum voucher KDAIS Pap-113 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156038.1
Paphiopedilum intaniae voucher KDAIS Pap-96 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156032.1
Paphiopedilum hookerae voucher KDAIS Pap-89 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156031.1
Paphiopedilum hirsutissimum voucher KDAIS Pap-115 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156029.1
Paphiopedilum glanduliferum voucher KDAIS Pap-40 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156019.1
Paphiopedilum gigantifolium voucher KDAIS Pap-101 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156018.1
Paphiopedilum fairrieanum voucher KDAIS Pap-79 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156017.1
Paphiopedilum esquirolei voucher KDAIS Pap-52 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156015.1
Paphiopedilum druryi voucher KDAIS Pap-93 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156013.1
Paphiopedilum dianthum voucher KDAIS Pap-85 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156012.1
Paphiopedilum barbigerum voucher KDAIS Pap-23 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF156003.1
Paphiopedilum appletonianum voucher KDAIS Pap-60 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF155999.1
Paphiopedilum anitum voucher KDAIS Pap-102 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF155998.1
Paphiopedilum adductum voucher KDAIS Pap-25 tRNA-Leu (trnL) gene, intron; chloroplast	50.0	50.0	100%	0.003	78%	EF155997.1
Andreaea rupestris tRNA-Leu (trnL) gene, intron; chloroplast gene for chloroplast product	50.0	50.0	100%	0.003	78%	AY050278.1
Acanthephippium mantinianum tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer region, partial sequence; chloroplast gene for chloroplast product	50.0	50.0	100%	0.003	74%	AF519966.1
Andreaea rupestris trnL gene, partial sequence; chloroplast gene for chloroplast product	50.0	50.0	100%	0.003	78%	AF478294.1

Ephedra equisetina voucher 60821 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	50.0	50.0	100%	0.003	77%	AY423434.1
Ephedra equisetina tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	50.0	50.0	100%	0.003	77%	AY423433.1
Rheum palmatum chloroplast, complete genome	48.2	48.2	100%	0.010	74%	KR816224.1
Asperugo procumbens tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	100%	0.010	75%	KF288033.1
Tulipa uniflora genomic DNA containing partial trnL gene, trnL-trnF IGS and partial trnF gene, specimen voucher K:Chase 751	48.2	48.2	100%	0.010	78%	HF953004.1
Rheum palmatum voucher 0942 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	100%	0.010	74%	KF586494.1
Asperugo procumbens isolate 4 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	48.2	48.2	100%	0.010	75%	KC542472.1
Asperugo procumbens tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	48.2	48.2	100%	0.010	75%	JX976911.1
Asperugo procumbens chloroplast gene for tRNA-Leu (trnL) and trnL-trnF intergenic spacer, partial and complete sequence, specimen_voucher: Tarbiat Modares University Herbarium 2007-3	48.2	48.2	100%	0.010	75%	AB758320.1
Vicia villosa isolate HS1415 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	100%	0.010	79%	JX505776.1
Asperugo procumbens voucher Alm 1283 (WS) tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast	48.2	48.2	100%	0.010	75%	JQ388577.1
Rheum acuminatum tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	100%	0.010	74%	FJ872100.1
Rheum franzenbachii tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	100%	0.010	74%	EU840548.1
Rheum altaicum tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	100%	0.010	74%	EU840547.1
Aeschynomene denticulata chloroplast partial tRNA-Leu gene intron, clone 1	48.2	48.2	100%	0.010	75%	FM211260.1
Aeschynomene sensitiva chloroplast partial tRNA-Leu gene intron, clone 3	48.2	48.2	100%	0.010	75%	FM211244.1
Aeschynomene sensitiva chloroplast partial tRNA-Leu gene intron, clone 1	48.2	48.2	100%	0.010	75%	FM211240.1
Aeschynomene indica chloroplast partial tRNA-Leu gene intron, clone 4	48.2	48.2	100%	0.010	75%	FM211235.1
Aeschynomene evenia chloroplast partial tRNA-Leu gene intron, clone 1	48.2	48.2	100%	0.010	75%	FM211228.1
Aeschynomene hispida chloroplast partial tRNA-Leu gene intron, clone 1	48.2	48.2	100%	0.010	75%	FM211225.1
Tulipa uniflora tRNA-Leu (trnL) gene, trnL-trnF intergenic spacer, and tRNA-Phe (trnF) gene, complete sequence; plastid	48.2	48.2	100%	0.010	78%	EU912325.1
Shorea guiso chloroplast DNA, trnL intron, partial sequence, isolate: 3402	48.2	48.2	100%	0.010	75%	AB452041.1
Anisoptera laevis chloroplast DNA, trnL	48.2	48.2	100%	0.010	75%	AB451993.1

intron, partial sequence, isolate: A0007						
Rheum wittrockii voucher 99059 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	100%	0.010	74%	AY566464.1
Rheum tanguticum voucher 2060 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	100%	0.010	74%	AY566457.1
Rheum palmatum voucher 2082 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	100%	0.010	74%	AY566453.1
Rheum palmatum voucher 1236 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	100%	0.010	74%	AY566451.1
Rheum rhaponticum voucher GG001 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	100%	0.010	74%	AY566446.1
Rheum hotaoense voucher 99130-1 tRNA-Leu (trnL) gene and trnL-trnF intergenic spacer, partial sequence; chloroplast	48.2	48.2	100%	0.010	74%	AY566445.1
Seddera hirsuta tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast genes for chloroplast products	48.2	48.2	100%	0.010	74%	AY101119.1
Cladostigma hildebrandtioides tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast genes for chloroplast products	48.2	48.2	100%	0.010	74%	AY101118.1
Sabaudiella aloysii tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast genes for chloroplast products	48.2	48.2	100%	0.010	74%	AY101117.1
Hildebrandtia africana tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast genes for chloroplast products	48.2	48.2	100%	0.010	74%	AY101116.1
Hildebrandtia sp. Phillipson and Milijaona 3624 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast genes for chloroplast products	48.2	48.2	100%	0.010	74%	AY101115.1
Hildebrandtia promontorii tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast genes for chloroplast products	48.2	48.2	100%	0.010	74%	AY101114.1
Vicia villosa tRNA-Leu (trnL) gene, intron; chloroplast	48.2	48.2	100%	0.010	79%	DQ311955.1
Shorea materialis trnL gene, partial intron sequence	48.2	48.2	100%	0.010	75%	AY026561.1
Shorea guiso trnL gene, partial intron sequence	48.2	48.2	100%	0.010	75%	AY026551.1
Cymopterus nivalis tRNA-Phe gene, partial sequence; tRNA-Leu gene, complete sequence; and tRNA-Thr gene, partial sequence; chloroplast genes for chloroplast products	48.2	48.2	100%	0.010	74%	AF444012.1

Alignments

Paphiopedilum victoria-regina voucher KDAIS Pap-14 tRNA-Leu (trnL) gene, intron; chloroplast
Sequence ID: **gb|EF156072.1|** Length: 564 Number of Matches: 1
Range 1: 81 to 148

Score	Expect	Identities	Gaps	Strand	Frame

55.4 bits(60)	7e-05()	55/69(80%)	7/69(10%)	Plus/Minus	

Features:

```
Query  1    GAGTCTCTGCACCTATCCTGTTTCATG-GAATTTCCTCCTCTTTT-----GATTTGGCTC  54
            ||||||||||||||||||  ||| ||  |||||| | | | ||||     ||||||||||
Sbjct  148  GAGTCTCTGCACCTATCCCTTTTTATTCGAATTTTC-CATTTTTTATAAAGATTTGGCTC  90

Query  55   AGGATTGCC  63
            |||||||||
Sbjct  89   AGGATTGCC  81
```

Paphiopedilum victoria-mariae voucher KDAIS Pap-84 tRNA-Leu (trnL) gene, intron; chloroplast
Sequence ID: **gb|EF156071.1|** Length: 563 Number of Matches: 1
Range 1: 80 to 147

Score	Expect	Identities	Gaps	Strand	Frame
55.4 bits(60)	7e-05()	55/69(80%)	7/69(10%)	Plus/Minus	

Features:

```
Query  1    GAGTCTCTGCACCTATCCTGTTTCATG-GAATTTCCTCCTCTTTT-----GATTTGGCTC  54
            ||||||||||||||||||  ||| ||  |||||| | | | ||||     ||||||||||
Sbjct  147  GAGTCTCTGCACCTATCCCTTTTTATTCGAATTTTC-CATTTTTTATAAAGATTTGGCTC  89

Query  55   AGGATTGCC  63
            |||||||||
Sbjct  88   AGGATTGCC  80
```

Paphiopedilum moquetteanum voucher KDAIS Pap-48 tRNA-Leu (trnL) gene, intron; chloroplast
Sequence ID: **gb|EF156044.1|** Length: 563 Number of Matches: 1
Range 1: 80 to 147

Score	Expect	Identities	Gaps	Strand	Frame
55.4 bits(60)	7e-05()	55/69(80%)	7/69(10%)	Plus/Minus	

Features:

```
Query  1    GAGTCTCTGCACCTATCCTGTTTCATG-GAATTTCCTCCTCTTTT-----GATTTGGCTC  54
            ||||||||||||||||||  ||| ||  |||||| | | | ||||     ||||||||||
Sbjct  147  GAGTCTCTGCACCTATCCCTTTTTATTCGAATTTTC-CATTTTTTATAAAGATTTGGCTC  89

Query  55   AGGATTGCC  63
            |||||||||
Sbjct  88   AGGATTGCC  80
```

Paphiopedilum haynaldianum voucher KDAIS Pap-54 tRNA-Leu (trnL) gene, intron; chloroplast
Sequence ID: **gb|EF156025.1|** Length: 563 Number of Matches: 1
Range 1: 80 to 147

Score	Expect	Identities	Gaps	Strand	Frame
55.4 bits(60)	7e-05()	55/69(80%)	7/69(10%)	Plus/Minus	

Features:

```
Query  1    GAGTCTCTGCACCTATCCTGTTTCATG-GAATTTCCTCCTCTTTT-----GATTTGGCTC  54
            ||||||||||||||||||  ||| ||  |||||| | | | ||||     ||||||||||
Sbjct  147  GAGTCTCTGCACCTATCCCTTTTTATTCGAATTTTC-CATTTTTTATAAAGATTTGGCTC  89

Query  55   AGGATTGCC  63
            |||||||||
Sbjct  88   AGGATTGCC  80
```

Paphiopedilum glaucophyllum voucher KDAIS Pap-29 tRNA-Leu (trnL) gene, intron; chloroplast
Sequence ID: **gb|EF156020.1|** Length: 565 Number of Matches: 1
Range 1: 80 to 147

Score	Expect	Identities	Gaps	Strand	Frame
55.4 bits(60)	7e-05()	55/69(80%)	7/69(10%)	Plus/Minus	

Features:

```
Query  1    GAGTCTCTGCACCTATCCTGTTTCATG-GAATTTCCTCCTCTTTT-----GATTTGGCTC  54
            ||||||||||||||||||  ||| ||  |||||| | | | ||||     ||||||||||
Sbjct  147  GAGTCTCTGCACCTATCCCTTTTTATTCGAATTTTC-CATTTTTTATAAAGATTTGGCTC  89

Query  55   AGGATTGCC  63
            |||||||||
Sbjct  88   AGGATTGCC  80
```

Paepalanthus tuberosus isolate FS1641 tRNA-Leu (trnL) gene, partial sequence; trnL-trnF intergenic spacer, complete sequence; and tRNA-Phe (trnF) gene, partial sequence; chloroplast
Sequence ID: **gb|EU924486.1|** Length: 805 Number of Matches: 1
Range 1: 106 to 172

Score	Expect	Identities	Gaps	Strand	Frame
53.6 bits(58)	2e-04()	53/67(79%)	4/67(5%)	Plus/Minus	

Features:

```
Query  1    GAGTCTCTGCACCTATCCTGTTTCATGG---AATTTCCTCCT-CTTTTGATTTGGCTCAG  56
            ||||||||||||||||||| ||| || |    || | ||| | |||  ||||||||||||
Sbjct  172  GAGTCTCTGCACCTATCCTTTTTTATAGTTTGATATTCTCATACTTAGGATTTGGCTCAG  113

Query  57   GATTGCC  63
            |||| ||
Sbjct  112  GATTACC  106
```

Cascadia nuttallii genomic DNA containing trnL(UAA) gene (5' exon, intron and 3' exon), trnL-F IGS, trnF(GAA) gene, specimen voucher R. Olmstead 921 (NY)
Sequence ID: **emb|LM654424.1|** Length: 843 Number of Matches: 1
Range 1: 26 to 83

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	8e-04()	49/63(78%)	5/63(7%)	Plus/Minus	

Features:

```
Query  1   GAGTCTCTGCACCTATCCTGTTTCATGGAATTTCCTCCTCTTTTGATTTGGCTCAGGATT  60
           ||||||||||||||||||| |||| ||   |||  ||       ||||||||||||||||
Sbjct  83  GAGTCTCTGCACCTATCCTTTTTCTTGTGTTTTGTTC-----AGGATTTGGCTCAGGATT  29

Query  61  GCC  63
           |||
Sbjct  28  GCC  26
```

Cascadia nuttallii genomic DNA containing trnL(UAA) gene (5' exon, intron and 3' exon), trnL-F IGS, trnF(GAA) gene, specimen voucher W.J. Dress 4198 (LE)
Sequence ID: **emb|LM654423.1|** Length: 872 Number of Matches: 1
Range 1: 52 to 109

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	8e-04()	49/63(78%)	5/63(7%)	Plus/Minus	

Features:

```
Query  1    GAGTCTCTGCACCTATCCTGTTTCATGGAATTTCCTCCTCTTTTGATTTGGCTCAGGATT  60
            ||||||||||||||||||| |||| ||   |||  ||       ||||||||||||||||
Sbjct  109  GAGTCTCTGCACCTATCCTTTTTCTTGTGTTTTGTTC-----AGGATTTGGCTCAGGATT  55

Query  61   GCC  63
            |||
Sbjct  54   GCC  52
```

Ephedra likiangensis isolate H15 tRNA-Thr (trnT) gene, partial sequence; trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, complete sequence; and trnL-trnF intergenic spacer, partial sequence; chloroplast
Sequence ID: **gb|KC407792.1|** Length: 665 Number of Matches: 1
Range 1: 294 to 361

Score	Expect	Identities	Gaps	Strand	Frame
51.8 bits(56)	8e-04()	53/68(78%)	5/68(7%)	Plus/Minus	

Features:

```
Query  1    GAGTCTCTGCACCTATC---CTGTTTCATG--GAATTTCCTCCTCTTTTGATTTGGCTCA  55
            |||||||||||||||||   || ||| | |  ||   |||||    ||||||||||||||
Sbjct  361  GAGTCTCTGCACCTATCTACCTTTTTTAGGCAGAGAATCCTCTGACTTTGATTTGGCTCA  302

Query  56   GGATTGCC  63
            ||||||||
Sbjct  301  GGATTGCC  294
```

Lomatogonium rotatum isolate 1316o tRNA-Leu (trnL) gene, partial sequence; chloroplast
Sequence ID: **gb|GQ245087.1|** Length: 409 Number of Matches: 1
Range 1: 84 to 156

Score	Expect	Identities	Gaps	Strand	Frame

51.8 bits(56) 8e-04() 57/73(78%) 10/73(13%) Plus/Minus

Features:

```
Query  1    GAGTCTCTGCACCTATCC--TGTTTCAT--GGA--ATTTCCTCCTCTTTT----GATTTG  50
            ||||||||||||||||||  | |||| |  |||   |||| |  ||||||    ||||||
Sbjct  156  GAGTCTCTGCACCTATCCTTTTTTTCTTTCGGAGCCTTTCTTTTTCTTTTTTAGGATTTG  97

Query  51   GCTCAGGATTGCC  63
            |||||||||||||
Sbjct  96   GCTCAGGATTGCC  84
```

BLAST ®

Basic Local Alignment Search Tool

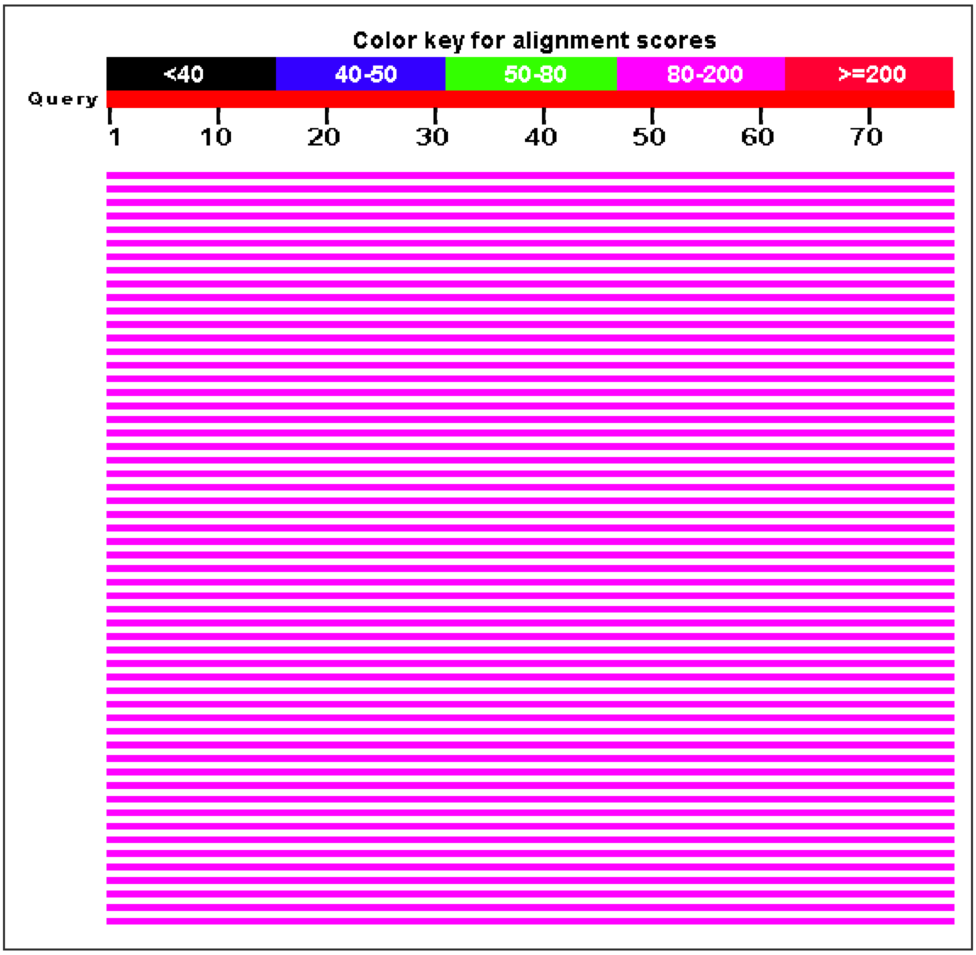
NCBI/ BLAST/ blastn suite/ **Formatting Results - 99WX6DF301R**
 Formatting options
 Download
Blast report description

YK07A41C1_TRNL_Clone1

RID	99WX6DF301R (Expires on 01-13 19:37 pm)		
Query ID	lcl|Query_68415	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.0+
Query Length	78		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Pinus sibirica chloroplast, complete genome	132	132	100%	5e-28	97%	KT723438.2
Pinus tabuliformis voucher PTAB20150818V5 chloroplast, complete genome	132	132	100%	5e-28	97%	KT740995.1
Pinus bungeana voucher Pbungeana2015 chloroplast, complete genome	132	132	100%	5e-28	97%	KR873010.1
Pinus taiwanensis voucher Ptaiwanensis14 chloroplast, complete genome	132	132	100%	5e-28	97%	KP771703.1
Pinus strobus plastid, complete genome	132	132	100%	5e-28	97%	KP099650.1
Tracheophyta environmental sample clone C6 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KJ015985.1
Tracheophyta environmental sample clone C5 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KJ015984.1
Tracheophyta environmental sample clone C4 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KJ015983.1
Tracheophyta environmental sample clone C3 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KJ015982.1
Tracheophyta environmental sample clone C2 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KJ015981.1
Tracheophyta environmental sample clone C1 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KJ015980.1
Tracheophyta environmental sample clone S5-3 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616492.1
Tracheophyta environmental sample clone S5-2 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616491.1
Tracheophyta environmental sample clone S5-1 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616490.1
Tracheophyta environmental sample clone S4-11 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616487.1
Tracheophyta environmental sample clone S4-10 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616486.1
Tracheophyta environmental sample clone S2-7 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616474.1
Tracheophyta environmental sample clone S2-6 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616473.1
Tracheophyta environmental sample clone S2-2 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616469.1
Tracheophyta environmental sample clone S2-1 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616468.1
Pinus luchuensis chloroplast trnL gene, intron, partial sequence, isolate: OGA0449	132	132	100%	5e-28	97%	AB817641.1
Pinus luchuensis chloroplast trnL gene, intron, partial sequence, isolate:	132	132	100%	5e-28	97%	AB817461.1

OGA0239						
Pinus taeda chloroplast, complete genome	132	132	100%	5e-28	97%	KC427273.1
Pinus massoniana chloroplast, complete genome	132	132	100%	5e-28	97%	KC427272.1
Pinus thunbergii trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504692.1
Pinus bungeana trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504691.1
Pinus koraiensis trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504690.1
Pinus densiflora trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504689.1
Pinus x rigitaeda trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504688.1
Pinus sylvestris trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504686.1
Pinus rigida trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504685.1
Pinus densiflora cultivar Multicaulis trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504684.1
Pinus sylvestris voucher Psy01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739418.1
Pinus peuce voucher Ppe01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739417.1
Pinus halepensis voucher Pha01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739416.1
Pinus brutia voucher Pb01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739415.1
Pinus brutia var. eldarica voucher Pe01.120311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739414.1
Pinus nigra voucher Pn01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739413.1
Pinus pinea voucher Ppi01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739412.1
Pinus heldreichii voucher Phe01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739411.1
Pinus arizonica var. cooperi isolate COOP01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854216.1
Pinus coulteri isolate COUL03 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854215.1
Pinus cubensis isolate CUBE01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854214.1
Pinus culminicola isolate CULM01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854213.1
Pinus fenzeliana var. dabeshanensis isolate DABE01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854212.1
Pinus dalatensis isolate DALA03 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854211.1
Pinus densiflora isolate DENS02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854210.1
Pinus densata isolate DENT01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854209.1
Pinus devoniana isolate DEVO02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854208.1
Pinus discolor isolate DISC02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854207.1

Pinus hartwegii isolate DONN02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854206.1**
Pinus douglasiana isolate DOUG01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854205.1**
Pinus echinata isolate ECHI01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854204.1**
Pinus edulis isolate EDUL08 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854203.1**
Pinus elliottii isolate ELLI01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854202.1**
Pinus engelmannii isolate ENGE02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854201.1**
Pinus fragilissima isolate FRAG01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854200.1**
Pinus glabra isolate GLAB01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854199.1**
Pinus greggii isolate GREG02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854198.1**
Pinus halepensis isolate HALE03 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854197.1**
Pinus hartwegii isolate HART07 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854196.1**
Pinus heldreichii isolate HELD07 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854195.1**
Pinus hwangshanensis isolate HWAN01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854194.1**
Pinus jeffreyi isolate JEFF04 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854193.1**
Pinus johannis chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854192.1**
Pinus kesiya isolate KESI11 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854191.1**
Pinus latteri isolate LATT02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854190.1**
Pinus pringlei isolate PRIN02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854189.1**
Pinus lawsonii isolate LAWS02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854188.1**
Pinus leiophylla isolate LEIO03 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854187.1**
Pinus lumholtzii isolate LUMH07 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854186.1**
Pinus massoniana isolate MASS02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854185.1**
Pinus maximartinezii isolate MAXZ01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854184.1**
Pinus montezumae isolate MONZ01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854183.1**
Pinus morrisonicola isolate MORR01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854182.1**
Pinus mugo isolate MUGO01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854181.1**
Pinus muricata isolate MURI01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854180.1**
Pinus nigra isolate NIGR20 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854179.1**
Pinus pseudostrobus var. apulcensis isolate OAXA02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854178.1**
Pinus occidentalis isolate OCCI02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854177.1**
Pinus palustris isolate PALU02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854176.1**
Pinus patula isolate PATU01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854175.1**
Pinus pinceana isolate PINC13 chloroplast,						

partial genome	132	132	100%	5e-28	97%	JN854174.1
Pinus pinea isolate PINE03 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854173.1
Pinus ponderosa var. benthamiana isolate POND21 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854172.1
Pinus ponderosa var. scopulorum isolate POND59 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854171.1
Pinus pseudostrobus isolate PSEU03 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854169.1
Pinus pumila isolate PUMI07 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854168.1
Pinus pungens isolate PUNG01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854167.1
Pinus quadrifolia isolate QUAD02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854166.1
Pinus radiata isolate RADI01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854165.1
Pinus remota isolate REMO05 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854164.1
Pinus rigida isolate RIGI01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854163.1
Pinus roxburghii isolate ROXB04 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854162.1
Pinus sabiniana isolate SABI04 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854161.1
Pinus serotina isolate SERO01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854160.1
Pinus strobiformis isolate STRF17 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854159.1
Pinus sylvestris isolate SYLV02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854158.1
Pinus taiwanensis isolate TAIW04 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854157.1
Pinus tropicalis isolate TROP02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854156.1

Alignments

Pinus sibirica chloroplast, complete genome
Sequence ID: **gb|KT723438.2|** Length: 116635 Number of Matches: 1
Range 1: 66690 to 66767

Score	Expect	Identities	Gaps	Strand	Frame
132 bits(146)	5e-28()	76/78(97%)	0/78(0%)	Plus/Plus	

Features:

```
Query  1      GAGTCTCTGCACCTATCCTCTTCCTATCTTAGGAGAAGAAACATTGTCTTCATGAACCGG  60
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  66690  GAGTCTCTGCACCTATCCCCTTCCTATCTTAGGAGAAGAAACATTGTCTTCATGAACCGG  66749

Query  61     ATTTGGCTCAGGATTGCC  78
              ||||||||||||||| ||
Sbjct  66750  ATTTGGCTCAGGATTACC  66767
```

Pinus tabuliformis voucher PTAB20150818V5 chloroplast, complete genome
Sequence ID: **gb|KT740995.1|** Length: 119646 Number of Matches: 1
Range 1: 68565 to 68642

Score	Expect	Identities	Gaps	Strand	Frame
132 bits(146)	5e-28()	76/78(97%)	0/78(0%)	Plus/Plus	

Features:

```
Query  1      GAGTCTCTGCACCTATCCTCTTCCTATCTTAGGAGAAGAAACATTGTCTTCATGAACCGG  60
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  68565  GAGTCTCTGCACCTATCCCCTTCCTATCTTAGGAGAAGAAACATTGTCTTCATGAACCGG  68624

Query  61     ATTTGGCTCAGGATTGCC  78
```

```
              ||||||||||||||| ||
Sbjct  68625  ATTTGGCTCAGGATTACC  68642
```

Pinus bungeana voucher Pbungeana2015 chloroplast, complete genome
Sequence ID: **gb|KR873010.1|** Length: 117861 Number of Matches: 1
Range 1: 68182 to 68259

Score	Expect	Identities	Gaps	Strand	Frame
132 bits(146)	5e-28()	76/78(97%)	0/78(0%)	Plus/Plus	

Features:

```
Query  1      GAGTCTCTGCACCTATCCTCTTCCTATCTTAGGAGAAGAAACATTGTCTTCATGAACCGG  60
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  68182  GAGTCTCTGCACCTATCCCCTTCCTATCTTAGGAGAAGAAACATTGTCTTCATGAACCGG  68241

Query  61     ATTTGGCTCAGGATTGCC  78
              ||||||||||||||| ||
Sbjct  68242  ATTTGGCTCAGGATTACC  68259
```

Pinus taiwanensis voucher Ptaiwanensis14 chloroplast, complete genome
Sequence ID: **gb|KP771703.1|** Length: 119741 Number of Matches: 1
Range 1: 68622 to 68699

Score	Expect	Identities	Gaps	Strand	Frame
132 bits(146)	5e-28()	76/78(97%)	0/78(0%)	Plus/Plus	

Features:

```
Query  1      GAGTCTCTGCACCTATCCTCTTCCTATCTTAGGAGAAGAAACATTGTCTTCATGAACCGG  60
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  68622  GAGTCTCTGCACCTATCCCCTTCCTATCTTAGGAGAAGAAACATTGTCTTCATGAACCGG  68681

Query  61     ATTTGGCTCAGGATTGCC  78
              ||||||||||||||| ||
Sbjct  68682  ATTTGGCTCAGGATTACC  68699
```

Pinus strobus plastid, complete genome
Sequence ID: **gb|KP099650.1|** Length: 115576 Number of Matches: 1
Range 1: 65526 to 65603

Score	Expect	Identities	Gaps	Strand	Frame
132 bits(146)	5e-28()	76/78(97%)	0/78(0%)	Plus/Plus	

Features:

```
Query  1      GAGTCTCTGCACCTATCCTCTTCCTATCTTAGGAGAAGAAACATTGTCTTCATGAACCGG  60
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  65526  GAGTCTCTGCACCTATCCCCTTCCTATCTTAGGAGAAGAAACATTGTCTTCATGAACCGG  65585

Query  61     ATTTGGCTCAGGATTGCC  78
              ||||||||||||||| ||
Sbjct  65586  ATTTGGCTCAGGATTACC  65603
```

BLAST ®

Basic Local Alignment Search Tool

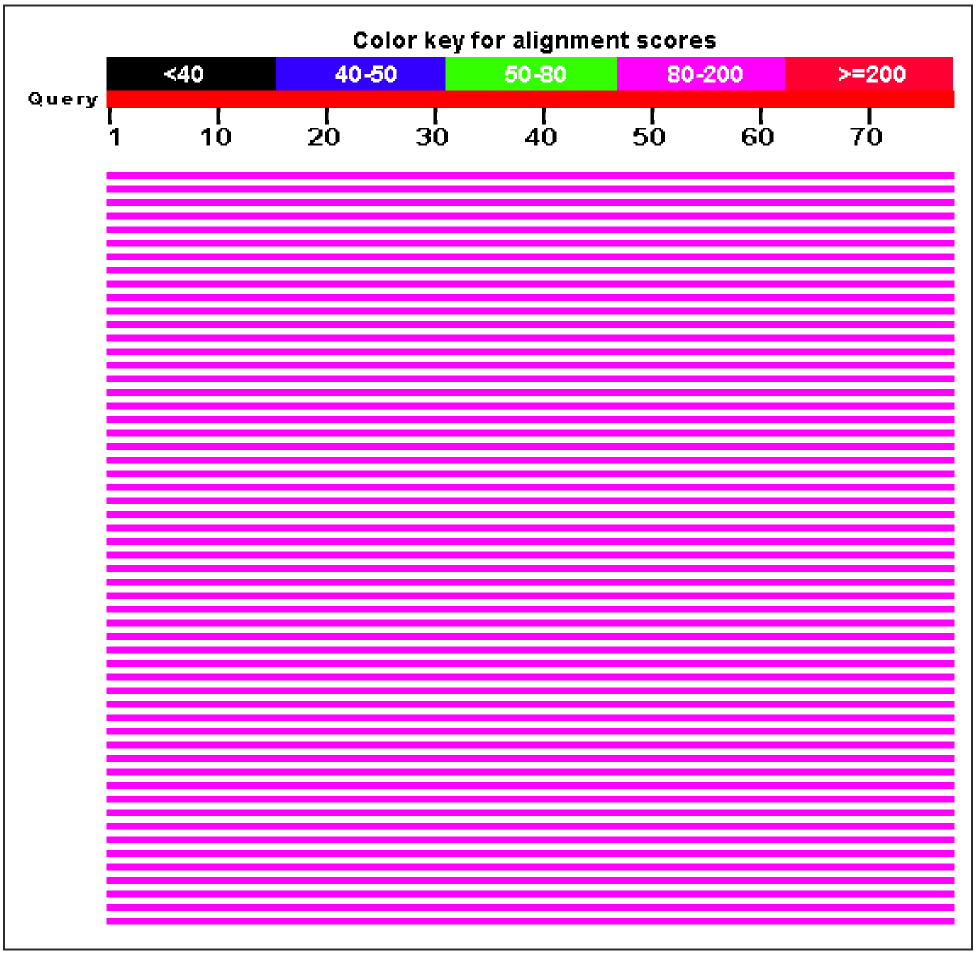
NCBI/ BLAST/ blastn suite/ **Formatting Results - 9ESXNHED013**
  Formatting options
  Download
Blast report description

YK11-H13H14-1131141B_TRNL_Clone9/10

RID	9ESXNHED013 (Expires on 01-15 16:00 pm)		
Query ID	lcl|Query_188163	**Database Name**	nr
Description	None	**Description**	Nucleotide collection (nt)
Molecule type	nucleic acid	**Program**	BLASTN 2.3.0+
Query Length	78		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Pinus sibirica chloroplast, complete genome	132	132	100%	5e-28	97%	KT723438.2
Pinus tabuliformis voucher PTAB20150818V5 chloroplast, complete genome	132	132	100%	5e-28	97%	KT740995.1
Pinus bungeana voucher Pbungeana2015 chloroplast, complete genome	132	132	100%	5e-28	97%	KR873010.1
Pinus taiwanensis voucher Ptaiwanensis14 chloroplast, complete genome	132	132	100%	5e-28	97%	KP771703.1
Pinus strobus plastid, complete genome	132	132	100%	5e-28	97%	KP099650.1
Tracheophyta environmental sample clone C6 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KJ015985.1
Tracheophyta environmental sample clone C5 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KJ015984.1
Tracheophyta environmental sample clone C4 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KJ015983.1
Tracheophyta environmental sample clone C3 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KJ015982.1
Tracheophyta environmental sample clone C2 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KJ015981.1
Tracheophyta environmental sample clone C1 tRNA-Leu (trnL(UAA)) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KJ015980.1
Tracheophyta environmental sample clone S5-3 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616492.1
Tracheophyta environmental sample clone S5-2 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616491.1
Tracheophyta environmental sample clone S5-1 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616490.1
Tracheophyta environmental sample clone S4-11 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616487.1
Tracheophyta environmental sample clone S4-10 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616486.1
Tracheophyta environmental sample clone S2-7 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616474.1
Tracheophyta environmental sample clone S2-6 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616473.1
Tracheophyta environmental sample clone S2-2 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616469.1
Tracheophyta environmental sample clone S2-1 tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	KF616468.1
Pinus luchuensis chloroplast trnL gene, intron, partial sequence, isolate: OGA0449	132	132	100%	5e-28	97%	AB817641.1
Pinus luchuensis chloroplast trnL gene, intron, partial sequence, isolate:	132	132	100%	5e-28	97%	AB817461.1

OGA0239						
Pinus taeda chloroplast, complete genome	132	132	100%	5e-28	97%	KC427273.1
Pinus massoniana chloroplast, complete genome	132	132	100%	5e-28	97%	KC427272.1
Pinus thunbergii trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504692.1
Pinus bungeana trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504691.1
Pinus koraiensis trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504690.1
Pinus densiflora trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504689.1
Pinus x rigitaeda trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504688.1
Pinus sylvestris trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504686.1
Pinus rigida trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504685.1
Pinus densiflora cultivar Multicaulis trnT-trnL intergenic spacer and tRNA-Leu (trnL) gene, partial sequence; chloroplast	132	132	100%	5e-28	97%	JX504684.1
Pinus sylvestris voucher Psy01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739418.1
Pinus peuce voucher Ppe01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739417.1
Pinus halepensis voucher Pha01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739416.1
Pinus brutia voucher Pb01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739415.1
Pinus brutia var. eldarica voucher Pe01.120311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739414.1
Pinus nigra voucher Pn01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739413.1
Pinus pinea voucher Ppi01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739412.1
Pinus heldreichii voucher Phe01.100311 tRNA-Leu (trnL) gene, intron; chloroplast	132	132	100%	5e-28	97%	JQ739411.1
Pinus arizonica var. cooperi isolate COOP01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854216.1
Pinus coulteri isolate COUL03 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854215.1
Pinus cubensis isolate CUBE01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854214.1
Pinus culminicola isolate CULM01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854213.1
Pinus fenzeliana var. dabeshanensis isolate DABE01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854212.1
Pinus dalatensis isolate DALA03 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854211.1
Pinus densiflora isolate DENS02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854210.1
Pinus densata isolate DENT01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854209.1
Pinus devoniana isolate DEVO02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854208.1
Pinus discolor isolate DISC02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854207.1

Pinus hartwegii isolate DONN02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854206.1**
Pinus douglasiana isolate DOUG01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854205.1**
Pinus echinata isolate ECHI01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854204.1**
Pinus edulis isolate EDUL08 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854203.1**
Pinus elliottii isolate ELLI01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854202.1**
Pinus engelmannii isolate ENGE02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854201.1**
Pinus fragilissima isolate FRAG01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854200.1**
Pinus glabra isolate GLAB01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854199.1**
Pinus greggii isolate GREG02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854198.1**
Pinus halepensis isolate HALE03 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854197.1**
Pinus hartwegii isolate HART07 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854196.1**
Pinus heldreichii isolate HELD07 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854195.1**
Pinus hwangshanensis isolate HWAN01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854194.1**
Pinus jeffreyi isolate JEFF04 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854193.1**
Pinus johannis chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854192.1**
Pinus kesiya isolate KESI11 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854191.1**
Pinus latteri isolate LATT02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854190.1**
Pinus pringlei isolate PRIN02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854189.1**
Pinus lawsonii isolate LAWS02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854188.1**
Pinus leiophylla isolate LEIO03 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854187.1**
Pinus lumholtzii isolate LUMH07 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854186.1**
Pinus massoniana isolate MASS02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854185.1**
Pinus maximartinezii isolate MAXZ01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854184.1**
Pinus montezumae isolate MONZ01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854183.1**
Pinus morrisonicola isolate MORR01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854182.1**
Pinus mugo isolate MUGO01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854181.1**
Pinus muricata isolate MURI01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854180.1**
Pinus nigra isolate NIGR20 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854179.1**
Pinus pseudostrobus var. apulcensis isolate OAXA02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854178.1**
Pinus occidentalis isolate OCCI02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854177.1**
Pinus palustris isolate PALU02 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854176.1**
Pinus patula isolate PATU01 chloroplast, partial genome	132	132	100%	5e-28	97%	**JN854175.1**
Pinus pinceana isolate PINC13 chloroplast,						

partial genome	132	132	100%	5e-28	97%	JN854174.1
Pinus pinea isolate PINE03 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854173.1
Pinus ponderosa var. benthamiana isolate POND21 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854172.1
Pinus ponderosa var. scopulorum isolate POND59 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854171.1
Pinus pseudostrobus isolate PSEU03 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854169.1
Pinus pumila isolate PUMI07 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854168.1
Pinus pungens isolate PUNG01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854167.1
Pinus quadrifolia isolate QUAD02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854166.1
Pinus radiata isolate RADI01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854165.1
Pinus remota isolate REMO05 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854164.1
Pinus rigida isolate RIGI01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854163.1
Pinus roxburghii isolate ROXB04 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854162.1
Pinus sabiniana isolate SABI04 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854161.1
Pinus serotina isolate SERO01 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854160.1
Pinus strobiformis isolate STRF17 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854159.1
Pinus sylvestris isolate SYLV02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854158.1
Pinus taiwanensis isolate TAIW04 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854157.1
Pinus tropicalis isolate TROP02 chloroplast, partial genome	132	132	100%	5e-28	97%	JN854156.1

Alignments

Pinus sibirica chloroplast, complete genome
Sequence ID: **gb|KT723438.2|** Length: 116635 Number of Matches: 1
Range 1: 66690 to 66767

Score	Expect	Identities	Gaps	Strand	Frame
132 bits(146)	5e-28()	76/78(97%)	0/78(0%)	Plus/Plus	

Features:

```
Query  1      GAGTCTCTGCACCTATCCTCTTCCTATCTTAGGAGAAGAAACATTGTCTTCATGAACCGG  60
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  66690  GAGTCTCTGCACCTATCCCCTTCCTATCTTAGGAGAAGAAACATTGTCTTCATGAACCGG  66749

Query  61     ATTTGGCTCAGGATTGCC  78
              ||||||||||||||| ||
Sbjct  66750  ATTTGGCTCAGGATTACC  66767
```

Pinus tabuliformis voucher PTAB20150818V5 chloroplast, complete genome
Sequence ID: **gb|KT740995.1|** Length: 119646 Number of Matches: 1
Range 1: 68565 to 68642

Score	Expect	Identities	Gaps	Strand	Frame
132 bits(146)	5e-28()	76/78(97%)	0/78(0%)	Plus/Plus	

Features:

```
Query  1      GAGTCTCTGCACCTATCCTCTTCCTATCTTAGGAGAAGAAACATTGTCTTCATGAACCGG  60
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  68565  GAGTCTCTGCACCTATCCCCTTCCTATCTTAGGAGAAGAAACATTGTCTTCATGAACCGG  68624

Query  61     ATTTGGCTCAGGATTGCC  78
```

```
                  ||||||||||||||| ||
Sbjct  68625  ATTTGGCTCAGGATTACC  68642
```

Pinus bungeana voucher Pbungeana2015 chloroplast, complete genome
Sequence ID: **gb|KR873010.1|** Length: 117861 Number of Matches: 1
Range 1: 68182 to 68259

Score	Expect	Identities	Gaps	Strand	Frame
132 bits(146)	5e-28()	76/78(97%)	0/78(0%)	Plus/Plus	

Features:

```
Query  1      GAGTCTCTGCACCTATCCTCTTCCTATCTTAGGAGAAGAAACATTGTCTTCATGAACCGG  60
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  68182  GAGTCTCTGCACCTATCCCCTTCCTATCTTAGGAGAAGAAACATTGTCTTCATGAACCGG  68241

Query  61     ATTTGGCTCAGGATTGCC  78
              ||||||||||||||| ||
Sbjct  68242  ATTTGGCTCAGGATTACC  68259
```

Pinus taiwanensis voucher Ptaiwanensis14 chloroplast, complete genome
Sequence ID: **gb|KP771703.1|** Length: 119741 Number of Matches: 1
Range 1: 68622 to 68699

Score	Expect	Identities	Gaps	Strand	Frame
132 bits(146)	5e-28()	76/78(97%)	0/78(0%)	Plus/Plus	

Features:

```
Query  1      GAGTCTCTGCACCTATCCTCTTCCTATCTTAGGAGAAGAAACATTGTCTTCATGAACCGG  60
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  68622  GAGTCTCTGCACCTATCCCCTTCCTATCTTAGGAGAAGAAACATTGTCTTCATGAACCGG  68681

Query  61     ATTTGGCTCAGGATTGCC  78
              ||||||||||||||| ||
Sbjct  68682  ATTTGGCTCAGGATTACC  68699
```

Pinus strobus plastid, complete genome
Sequence ID: **gb|KP099650.1|** Length: 115576 Number of Matches: 1
Range 1: 65526 to 65603

Score	Expect	Identities	Gaps	Strand	Frame
132 bits(146)	5e-28()	76/78(97%)	0/78(0%)	Plus/Plus	

Features:

```
Query  1      GAGTCTCTGCACCTATCCTCTTCCTATCTTAGGAGAAGAAACATTGTCTTCATGAACCGG  60
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  65526  GAGTCTCTGCACCTATCCCCTTCCTATCTTAGGAGAAGAAACATTGTCTTCATGAACCGG  65585

Query  61     ATTTGGCTCAGGATTGCC  78
              ||||||||||||||| ||
Sbjct  65586  ATTTGGCTCAGGATTACC  65603
```