

Sequence ID: [KC179735.1](#) Length: 796 Number of Matches: 1

Range 1: 39 to 796 [GenBank](#) [Graphics](#)

[▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Identities	Gaps	Strand
1310 bits(709)	0.0	746/762(98%)	10/762(1%)	Plus/Plus
Query 3	TTG-ACGCTTGTGGCTTCAGGCTGTTGCTGACGGGACCTTCACGGGTTTCGTACGTGCAC	61		
Sbjct 39	TTGAACGCTTGTGGCTTCAGGCTGTTGCTGACGGGACCTTCACGGGTTTCGTACGTGCAC	98		
Query 62	GTCGTAGTTGCAACTTTCTTCGTCCACCTGTGCACACTCTGTAGGTCGGATAACCCCA-	120		
Sbjct 99	GTCGTAGTTGCAACTTTCTTCGTCCACCTGTGCACACTCTGTAGGTCGGATA-CCCCAT	157		
Query 121	TTTGAAGGGTGCACGTC-TTCAAAAGCGCGCTCCCTTTGCCTTCCAGGCCTATGTCCTAT	179		
Sbjct 158	TTTGAAGGGTGCACGTCCTTTAAAAAGCGCGCTCCCTTTGCCTTCCAGGCCTATGTCCTAT	217		
Query 180	AAACACTTTTGTATGTAATGAATGTCATTGATTATTGGACCTCACGTCCTTTAAACTAA	239		
Sbjct 218	AAACACTTTTGTATGTAACGAATGTCATTGATTATTGGACCTCACGTCCTTTAAACTAA	277		
Query 240	ATACAACCTTTCAACAACGGATCTCTGGCTCTCGCATCGATGAAGAACGCAGCGAAATGC	299		
Sbjct 278	ATACAACCTTTCAACAACGGATCTCTGGCTCTCGCATCGATGAAGAACGCAGCGAAATGC	337		
Query 300	GATAACTAATGTGAATTGCAGAAATTCAGTGAATCATCGAGTCTTTGAACGCACCTTGCGC	359		
Sbjct 338	GATAACTAATGTGAATTGCAGAAATTCAGTGAATCATCGAGTCTTTGAACGCACCTTGCGC	397		
Query 360	CCTTCGGCACTCCGAAGGGCATGCCTGTTTGAGTGTGAGTAACTTCTCAACCTCCCTCAC	419		
Sbjct 398	CCTTTGGCACTCCGAAGGGCATGCCTGTTTGAGTGTGAGTAACTTCTCAACCTCCCTCAC	457		
Query 420	TTTGTGTGAGCTGGCGGATTGGATGGTGGGGCTTGCTGGACCTCTCTGGTTCAGCTC	479		
Sbjct 458	TTTGTGTGAGCTGGCGGATTGGAT-GTGGGGCTTGCTGGACCTATCTTGGTTCAGCTC	516		
Query 480	CCCTGAAATGCATTAGCAGAAACCGTTACCTTTTGGCGCGCTGCAGCTGTGATAATTATC	539		
Sbjct 517	CCCTGAAATGCATTAGCAGAAACCGTTACCTTTTGGCGCGCTGCAGCTGTGATAATTATC	576		
Query 540	TACGGCTATGGCTGGGCTGACTGTGTTGTAGCGCTTGTCTCTGAAGGGTTTGGCCC	599		
Sbjct 577	TACGGCTATGGCTGGGCTGACTGTGTTGTAGCGCTTGTCTCTGAAGGG-TTTGGCCC	635		
Query 600	TAGTGGCCCTCCCTTTGCCTTCTCTCAGAGAGATACCTGTGACGCGAGTGCGCGGGC	659		
Sbjct 636	TAGTGGCCCTCCCTTTGCCTTCTCTCAGAGAGATACCTGTGACGCGAGTGCGCGGGC	695		
Query 660	TATTCAGCTTCTAACCGTCCCTTTGGGGACAACCTTATTGACCATTTGACCTCAAAATCAGG	719		
Sbjct 696	TATTCAGCTTCTAACCGTCCCTTTGGGGACAAC-TATTGACCATTTGACCTCAAAATCAGG	754		
Query 720	TAGGACTACCGCTGAACCTTAAGCATATCA-TAA-CGG-GGA 758			
Sbjct 755	TAGGACTACCGCTGAACCTTAAGCATATCAATAAGCGGAGGA 796			

Figure S1. Results of ITS sequence alignment (Compared with *Flammulina rossica* GenBank: KC179735.1 on NCBI, the similarity was over 99%, and it was identified as *Flammulina rossica*.)