

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	G T C T G A G T T G C A A C T T T C T T C G T C C A C C T G T G C A C A C T C T G T A G G T C T G G A T A A C C C C A -	120		
Sbjct 99	G T C T G A G T T G C A A C T T T C T T C G T C C A C C T G T G C A C A C T C T G T A G G T C T G G A T A - C C C C A T	157		
Query 121	T T T G A A G G G T G C A C G T C - T T C A A A A G C G C G C T C C C T T T G C C T T C C A G G C C T A T G T C T T A T	179		
Sbjct 158	T T T G A A G G G T G C A C G T C T T T A A A A A G C G C G C T C C C T T T G C C T T C C A G G C C T A T G T C T T A T	217		
Query 180	A A A C A C T T T T G T A T G T A A T G A A T G I C A T T G A T T A T T G G A C C T C A C G T C C T T T A A A C T A A	239		
Sbjct 218	A A A C A C T T T T G T A T G T A A C G A A T G T C A T T G A T T A T T G G A C C T C A C G T C C T T T A A A C T A A	277		
Query 240	A T A C A A C T T T C A A C A A C G G A T C T C T T G G C T C T G C A T C G A T G A A G A A C G C A G C G A A A T G C	299		
Sbjct 278	A T A C A A C T T T C A A C A A C G G A T C T C T T G G C T C T G C A T C G A T G A A G A A C G C A G C G A A A T G C	337		
Query 300	G A T A A C T A A T G T G A A T T G C A G A A T T C A G T G A A T C A T C G A G T C T T T G A A C G C A C C T T G C G C	359		
Sbjct 338	G A T A A C T A A T G T G A A T T G C A G A A T T C A G T G A A T C A T C G A G T C T T T G A A C G C A C C T T G C G C	397		
Query 360	C C T T C G G C A C T C C G A A G G G C A T G C C T G T T T G A G T G T C A G T A A C T T C T C A A C C T C C C T C A C	419		
Sbjct 398	C C T T T G G C A C T C C G A A G G G C A T G C C T G T T T G A G T G T C A G T A A C T T C T C A A C C T C C C T C A C	457		
Query 420	T T T G T T G T G A G T G G C G G A T T G G A T G G T G G G G G C T T G C T G G A C C T C T C T T G G T T C A G C T C	479		
Sbjct 458	T T T G C T G T G A G T G G C G G A T T G G A T - G T G G G G C T T G C T G G A C C T A T C T T G G T T C A G C T C	516		
Query 480	C C C T G A A A T G C A T T A G C A G A A A C C G T T A C C T T T T G G C G C G C T G C A G C T G T G A T A A T T A T C	539		
Sbjct 517	C C C T G A A A T G C A T T A G C A G A A A C C G T T A C C T T T T G G C G C G C T G C A G C T G T G A T A A T T A T C	576		
Query 540	T A C G G C T A T G G C T G G G C T G A C T G T G T T G T A G C G C T T G T T C G T C T C T G A A G G G T T T T G C C C	599		
Sbjct 577	T A C G G C T A T G G C T G G G C T G A C T G T G T T G T A G C G C T T G T T C G T C T C T G A A G G G - T T T G C C C	635		
Query 600	T A G T G G C C T T C C C T T T G C C T T C T C T C A C G A G A G A T A C C T G T G A C G C G A G T G C G C G G G C	659		
Sbjct 636	T A G T G G C C T T C C C T T T G C C T T C T C T T T C A C G A G A G A T A C C T G T G A C G C G A G T G C G C G G G C	695		
Query 660	T A T T C A G C T T T C T A A C C G T C C C T T T G G G G A C A A C T T A T T G A C C A T T T G A C C T C A A A T C A G G	719		
Sbjct 696	T A T T C A G C T T T C T A A C C G T C C C T T T G G G G A C A A C - T A T T G A C C A T T T G A C C T C A A A T C A G G	754		
Query 720	T A G G A C T A C C C G T G A A C T T A A G C A T A T C A - T A A - C G G - G G A	758		
Sbjct 755	T A G G A C T A C C C G T G A A C T T A A G C A T A T C A A T A A G C G G A G G A	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*.)