

## Quercus cerris internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence

GenBank: AY226832.1

[FASTA](#) [Graphics](#) [PopSet](#)

[Go to:](#)

LOCUS AY226832 592 bp DNA linear PLN 29-DEC-2004  
 DEFINITION Quercus cerris internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence.  
 ACCESSION AY226832  
 VERSION AY226832.1 GI:29424088  
 KEYWORDS .  
 SOURCE Quercus cerris (Turkey oak)  
 ORGANISM Quercus cerris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae; Pentapetalae; rosids; fabids; Fagales; Fagaceae; Quercus.  
 REFERENCE 1 (bases 1 to 592)  
 AUTHORS Bellarosa,R., Simeone,M.C., Papini,A. and Schirone,B.  
 TITLE Utility of ITS sequence data for phylogenetic reconstruction of Italian Quercus spp  
 JOURNAL Mol. Phylogenet. Evol. 34 (2), 355-370 (2005)  
 PUBMED [15619447](#)  
 REFERENCE 2 (bases 1 to 592)  
 AUTHORS Bellarosa,R. and Simeone,M.C.  
 TITLE Direct Submission  
 JOURNAL Submitted (29-JAN-2003) Dipartimento di Tecnologia, Ingegneria e Scienze dell'Ambiente e Foreste, Universita' della Tuscia, Via S. Camillo de' Lellis, Viterbo 01100, Italy  
 FEATURES Location/Qualifiers

source

Feature type

Annotation

```

1..592
/organism="Quercus cerris"
/mol_type="genomic DNA"
/db_xref="taxon:39468"
/country="Italy: natural population, Latium"

1..221
/product="internal transcribed spacer 1"

222..384
/product="5.8S ribosomal RNA"

385..592
/product="internal transcribed spacer 2"
    
```

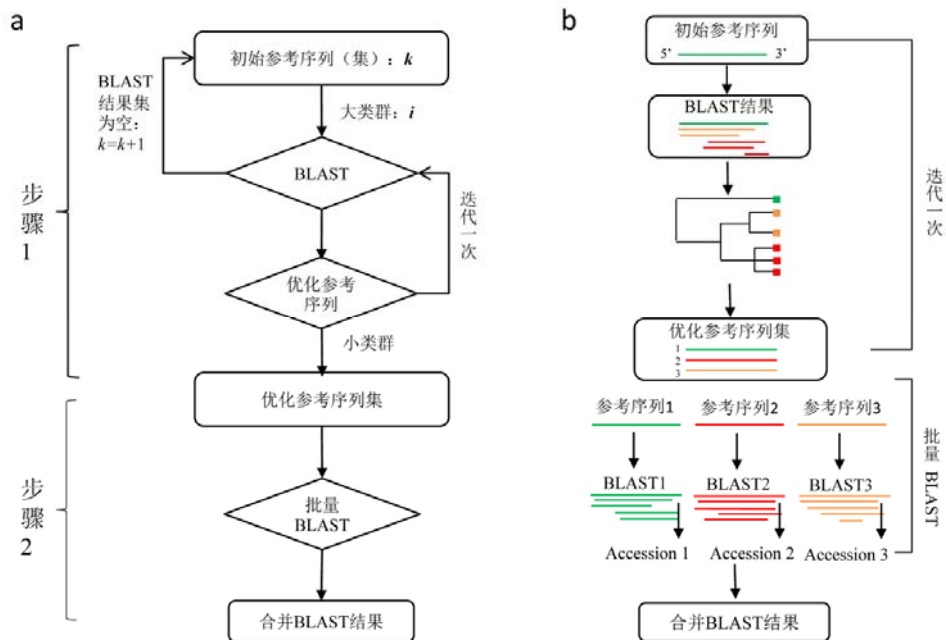
ORIGIN

```

1 tcgaaacctg cacagcagaa cgaccgcgca atgggtgaca accgacgggg ggcggggggc
61 gctcgtcgtt ccctcgcccc tcacgcagcg ggggacctcg cgtctcttgc ctgcaaacgg
121 aaccccgccg cggaaacgcg caaggaatc gaaccaagag agccgcgccg gaggccccgg
181 acacgggtgc cccccggcgt cggcgtctta cgaattattt aaacgactc tcggcaacgg
241 atatctagcg tctcgatcgc atgaagaacg tagcgaaatg cgatacttgg tgtgaattgc
301 agaatcccgc gaatcatcga gtttttgaac gcaagttgcg ccgaaacct ttcggccgag
361 ggcacgtctg cctgggtgtc acgcatcgtt gcccccacca aactccggtt cggcgccggc
421 ggaagtggc ctcctgtgcg tgcttgcgcg cgcggttagc ccaaaagcga gtcctcgccg
481 acgagcgcga cgacaatcgg tggtttttgc accctcgttc cagctcgtgc gcgccccgct
541 gcgcaaacgc gctcttgcca cccttaacgc ttgcctcggc gacgctccca ac
//
    
```

附录1 GenBank中的序列数据格式。左侧方框中是GenBank定义的基因类型(feature type), 右侧方框中为该序列的相关注释信息。

Appendix 1 Data format for a sequence in GenBank. The items in the left box are feature types defined in GenBank, while those in the right box are GenBank annotation information.



附录2 NCBIminer的工作流程。a为NCBIminer工作的主要流程，b详细解释了优化参考序列集建立和多查询归并算法的步骤。根据Xu *et al.* (2015)修改。

Appendix 2 NCBIminer workflow. a, Major steps of the NCBIminer's work flow; b, The algorithms for the establishment of improved reference sequences and sequence combination of multiple queries. Modified from Xu *et al.* (2015).