Nucleotide sequence of a ligninase gene from *Phanerochaete chrysosporium*

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Lignin biodegradation is catalyzed in part by ligninases, also known as lignin peroxidases (1-4). We have cloned and sequenced the gene encoding ligninase isozyme H8 from the white-rot fungus *Phanerochaete chrysosporium.* The gene is interrupted by eight introns, ranging in size from 49 to 69 bp, which are distributed throughout the gene. Putative transcriptional control signals (underlined) include a CAAT at position -110 and a TATA box at -81 relative to the translational initiation codon. The nucleotide sequence of the coding region is identical to the cDNA sequence published previously (5), except for a GC at positions 591-592 instead of CG, resulting in an Arg to Ala substitution.

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-260  GGCCCAAATGTGAGACGAGTCGGTGATGGTTGCCGGCACCGCACCAACTCGCTCACAGGCTGCGTTTTGGCAGCGTCCTCATTGGCTGGCGCAGTGTCGT -161
-160  GCATGTCCGCCGCACCGCGTCACGTCGATTCGACACTGTTCTACGGCGAACAATACCAGGACGTCGACCACGCCTAGGGTATAAAAGGGCGACAGGACCA  -61
 -60  CCGCAGTCCCTCAGACATCCAGTCTCTTCAGTCCCACTCAGCACCAGCAACACAGCGGACATGGCCTTCAAGCAGCTCTTCGCAGCTATCTCTCTCGCTC   40
                                                                                MetAlaPheLysGlnLeuPheAlaAlaIleSerLeuAlaL
  41  TCTTGCTCTCGGCTGCGAACGGTATGCCCATCGCAGTTAGCGTTGACCAGTGGACTGCATGCTGAACGTCGTCTTGTGCAGCGGCTGCGGTGATCGAGAA  140
      euLeuLeuSerAlaAlaAsnA                                                                    laAlaAlaValIleGluLy
 141  GCCGCCACCTGTTCCAACGGCAAGACCGTCGGCGATGCGTCGTGCTGCTTGGTTCGACGTCCTGGATGATATCCAGCAGAACCTGTTCCACGGCGGC  240
      sArgAlaThrCysSerAsnGlyLysThrValGlyAspIleSerCysCysAlaTrpPheAspValLeuAspAspIleGlnGlnAsnLeuPheHisGlyGly
 241  CAGTGCGGCGCTGAGGCGCACGAGTCGATTCGTCTGTGAGTGATCCCGTCGCGATCTCCTCCTATGCATGTTTGAACACCCCGCCCAGCGTCTTCCACGA  340
      GlnCysGlyAlaGluAlaHisGluSerIleArgLe                                                      uValPheHisAs
 341  CTCCATCGCAATTTCGCCCCGCCATGGAGGCACAGGGCAAGTTCGGGTAAGTTGCCACCCGCGTTGCGCCACCTAGTCGTTTGCTGATCCCTCCTTGCAGC  440
      pSerIleAlaIleSerProAlaMetGluAlaGlnGlyLysPheGl                                                        y
 441  GGCGGTGGTGCTGACGGCTCCATCATGATCTTCGACGATATCGAGACTGCGTTCCACCCTAACATCGGTCTCGACGAGATCGTCAAGCTCCAGAAGCCAT  540
      GlyGlyGlyAlaAspGlySerIleMetIlePheAspAspIleGluThrAlaPheHisProAsnIleGlyLeuAspGluIleValLysLeuGlnLysProP
 541  TCGTTCAGAAGCACGGTGTCACCCCTGGTGACTTCATCGCCTTCGCTGGTGCTGTCGCGCTCAGCAACTGCCCTGGTGCCCCGCAGATGAACTTCTTCAC  640
      heValGlnLysHisGlyValThrProGlyAspPheIleAlaPheAlaGlyAlaValAlaLeuSerAsnCysProGlyAlaProGlnMetAsnPhePheTh
 641  TGGTCGTGCACCTGGTATACCTGCAAAACTCGCTTTGCGGATGGTACGAACTAACTGTCTGCTTTAGCTACCCAGCCCGCTCCTGATGGCCTTGTCCCCG  740
      rGlyArgAlaProA                                                                    laThrGlnProAlaProAspGlyLeuValProG
 741  AGCCCTTCCGTAAGTGGTCTTATCCAAGCAGTTAGGTGCGGTCTATACTGACTAGCATGCAGACACTGTCGACCAAATCATCAACCGTGTCAACGACGCA  840
      luProPheH                                                                        isThrValAspGlnIleIleAsnArgValAsnAspAla
 841  GGCGAGTTCGATGAGCTCGAGCTTGTCTGGATGCTCTCCGCGTAAGTCACTCACTGTTGACTTCGACACTCCCTTCCTGAGACCTCGACAGGCACTCCGT  940
      GlyGluPheAspGluLeuGluLeuValTrpMetLeuSerAl                                                        aHisSerVa
 941  CGCAGCGGTGAACGACGTCGACCCGACCGTCCAGGGTCTGCCCTTTGACTCGACCCCCGGAATCTTCGACTCCCAGTTCTTCGTCGAGACTCAGCTTCGT 1040
      lAlaAlaValAsnAspValAsnProThrValGlnGlyLeuProPheAspSerThrProGlyIlePheAspSerGlnPhePheValGluThrGlnLeuArg
1041  GGTACCGCCTTCCCCGGCTCTGGTGGCAACCAAGGCGAGGTCGAGTCGCCGCTCCCTGGCGAAATTCGCATCCAGTCCGACCACACTATCGCCCGCGACT 1140
      GlyThrAlaPheProGlySerGlyGlyAsnGlnGlyGluValGluSerProLeuProGlyGluIleArgIleGlnSerAspHisThrIleAlaArgAsp5
1141  CGCGCACGGCGTGTGAATGGCAGTCCTTCGTCAACAACCAGTCCAAGCTCGTCGATGACTTCCAGTTCATCTTCCTCGCCCTCACCCAGCTCGGCCAGGA 1240
      erArgThrAlaCysGluTrpGlnSerPheValAsnAsnGlnSerLysLeuValAspAspPheGlnPheIlePheLeuAlaLeuThrGlnLeuGlyGlnAs
1241  CCCGAACGCGATGACCGACTGCTCGGATGTTATCCCGCAGTCCAAGCCCATCCCTGGCAACCTCCCATTCTCGTTCTTCCCCGCTGGCAAGACCATCAAG 1340
      pProAsnAlaMetThrAspCysSerAspValIleProGlnSerLysProIleProGlyAsnLeuProPheSerPhePheProAlaGlyLysThrIleLys
1341  GACGTTGAGCAGGCGGTGCGTATTTCACCCCACCATGCAGTAGAGTGGCTGCTGAACATCGCATGACAGTGTGCGGAGACCCCCTTCCCGACTCTCACCA 1440
      AspValGluGlnAla                                                                  CysAlaGluThrProPheProThrLeuThrT
1441  CTCTCCCGGGCCCCGAGACGTCCGTCCAGCGCATGTGAGTACAATCCATGAGATCTTTCAGGAAATGCAATCTGGGCTGACATGCTCCTCTCCAGCCCT 1540
      hrLeuProGlyProGluThrSerValGlnArgIl                                                               ePro
1541  CCGCCTCCGGGTGCTTAAATGATGCCATACAGAATACTCCTCAAACCGACTGTAACCGTGGCCGGCTAACTCGTGACGGAACTTCGGCTTTACTAGATTT 1640
      ProProProGlyAlaEnd
1641  CATTCATCGTATCTCTGCACCTAACTACGAATCTCATTCGTCTACTCTCTTACGATATCTGCCGTGGGCTTATGAAATATCGGTGCACATCCTCTTCTTC 1740
1741  CGATCATGATTGAGGGTCTTGGAAGGTAACTAGCTATTGAGATACCACTCGTGCCCTTCGCATTGCGTCCGCGTGGTGAAAGTGGTGATGTCCTATTGCC 1840
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