

# Nucleotide and derived amino acid sequence of a pectinesterase cDNA isolated from *Aspergillus niger* strain RH 5344

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Pectinesterase belongs to the group of pectic enzymes and catalyzes the hydrolysis of methyl ester groups of galacturonic acid residues of pectin (1).

Pectinesterase from *Aspergillus niger* strain RH 5344 was purified to homogeneity and partially sequenced. An oligonucleotide derived from a peptide fragment was synthesized and used as a specific probe to identify a pectinesterase cDNA from *Aspergillus niger* RH 5344. The complete nucleotide sequence of this gene has been determined on both strands and contains a 993-bp coding region, which comprises a mature protein of 314 amino acids and an N-terminal signal peptide of 17 amino acids.

Sequencing of several peptides of the isolated protein by Edman

degradation confirmed the sequence information obtained from the cDNA.

## ACKNOWLEDGEMENT

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## REFERENCE

1. Rexova-Benkova, L. and Markovic, C. (1976) *Advan. Carbohydr. Chem. Biochem.* 33, 323–385.

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1 CGCCGATCAGTCGATCCTTAACAGCAATC
ATG GTT AAG TCA ATT CTT GCA TCC GTT CTC TTT GCA GCG ACC GCG CTG GCC GCG AGC CGC 60
M V K S I L A S V L F A A T A L A A S R
ATG ACG GCT CCT TCC GGT GCG ATT GTT GTT GCC AAG TCC GGA GGT GAC TAC GAC ACG ATC 120
M T A P S G A I V V A K S G G D Y D T I
AGC GCT GCC GTT GAT GCT CTC AGC ACG ACT TCG ACC GAG ACC CAG ACC ATC TTC ATT GAG 180
S A A V D A L S T T S T E T Q T I F I E
GAG GGA TCC TAC GAC GAG CAG GTG TAT ATT CCC GCC CTC AGT GGA AAG CTG ATT GTC TAC 240
E G S Y D E Q V Y I P A L S G K L I V Y
GGT CAG ACT GAG GAC ACT ACC ACC TAC ACC AGC AAC CTG GTC AAC ATC ACC CAC GCC ATC 300
G Q T E D T T T Y T S N L V N I T H A I
GCT TTG GCC GAT GTC GAC AAT GAC GAT GAG ACT GCA ACC CTC CGT AAC TAC GCT GAA GGC 360
A L A D V D N D D E T A T L R N Y A E G
TCG GCC ATC TAC AAC CTC AAC ATT GCC AAC ACC TGC GGT CAG GCC TGC CAC CAG GCT CTC 420
S A I Y N L N I A N T C G Q A C H Q A L
GCC GTG AGC GCC TAT GCC AGC GAG CAG GGA TAC TAC GCC TGC CAG TTC ACC GGA TAC CAG 480
A V S A Y A S E Q G Y Y A C Q F T G Y Q
GAC ACC CTT CTG GCT GAG ACC GGC TAC CAG GTT TAC GCC GGA ACC TAC ATC GAG GGT GCC 540
D T L L A E T G Y Q V Y A G T Y I E G A
GTC GAC TTC ATC TTT GGA CAG CAC GCC CGC GCC TGG TTC CAC GAG TGC GAC ATC CGC GTC 600
V D F I F G Q H A R A W F H E C D I R V
CTC GAG GGC CCC AGC TCC GCC TCC ATC ACC GCC AAC GGC CGC TCC TCC GAG TCG GAC GAC 660
L E G P S S A S I T A N G R S S E S D D
TCT TAC TAC GTG ATC CAC AAG TCC ACC GTC GCT GCT GAT GGC AAC GAT GTT TCC TCC 720
S Y Y V I H K S T V A A A D G N D V S S
GGC ACC TAC TAC CTC GGC CGC CCC TGG TCC CAG TAC GCT CGC GTC TGC CAG AAG ACC 780
G T Y Y L G R P W S Q Y A R V C F Q K T
TCC ATG ACC GAT GTG ATC AAC CAC CTC GGC TGG ACT GAG TGG TCG ACC TCC ACC CCC AAC 840
S M T D V I N H L G W T E W S T S T P N
ACC GAG AAC GTC ACC TTT GTT GAA TAC GGC AAC ACC GGC ACT GGC GCT GAG GGT CCC CGT 900
T E N V T F V E Y G N T G T G A E G P R
GCT AAC TTC TCT TCT GAG CTG ACT GAG CCC ATC ACT ATC TCT TGG CTT CTC GAG TCT GAC 960
A N F S S E L T E P I T I S W L L G S D
TGG GAG GAC TGG GTT GAT ACT AGC TAC ATC AAC TAA ACTTGTGTGAAAGTTGTAAGCTGGTTGGAGA 1027
W E D W V D T S Y I N STOP
AGGGTCGTATATAGTGTGTGGATCTGTATATATGTGAGATGGAGATATAGCTAATTGTGGTTAGTTAATCACTGCTCA 1106
ATTCATTTCGAAGCAACTTTTTATTGGAAAAA

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