



(86) **Date de dépôt PCT/PCT Filing Date:** 2007/04/12
(87) **Date publication PCT/PCT Publication Date:** 2007/10/25
(45) **Date de délivrance/Issue Date:** 2015/11/24
(85) **Entrée phase nationale/National Entry:** 2008/10/09
(86) **N° demande PCT/PCT Application No.:** FI 2007/050196
(87) **N° publication PCT/PCT Publication No.:** 2007/118935
(30) **Priorités/Priorities:** 2006/04/13 (US11/404,065);
2006/04/13 (FI20065234)

(51) **Cl.Int./Int.Cl. C12N 9/42** (2006.01),
A23K 1/165 (2006.01), **C11D 3/386** (2006.01),
C12N 15/56 (2006.01), **C12N 15/62** (2006.01),
C12N 15/63 (2006.01), **D06M 16/00** (2006.01)

(72) **Inventeurs/Inventors:**
ALAPURANEN, MARIKA, FI;
VALTAKARI, LEENA, FI;
KALLIO, JARNO, FI;
OJAPALO, PENTTI, FI;
VEHMAANPERAE, JARI, FI

(73) **Propriétaire/Owner:**
AB ENZYMES OY, FI

(74) **Agent:** NORTON ROSE FULBRIGHT CANADA
LLP/S.E.N.C.R.L., S.R.L.

(54) **Titre : PROTEINES DE FUSION DE CELLULASE ET LEUR UTILISATION**

(54) **Title: CELLULASE FUSION PROTEINS AND THEIR USE**

(57) **Abrégé/Abstract:**

Cellulase fusion proteins comprising an endoglucanase core region and a heterologous cellulose binding domain are described. The fusion proteins may be produced by recombinant techniques using appropriate polynucleotides, expressing vectors and host cells. The fusion proteins and enzyme preparations thereof are useful in treating cellulosic material, such as textile material, and they are particularly useful in biostoning denim or in biofinishing fabrics and garments. In addition the fusion proteins may be used in pulp and paper industry, oil extraction from plants, detergent compositions, or for improving the quality of animal feed.



(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
25 October 2007 (25.10.2007)

PCT

(10) International Publication Number
WO 2007/118935 A1

(51) International Patent Classification:

C12N 9/42 (2006.01) *D06M 16/00* (2006.01)
C12N 15/62 (2006.01) *C11D 3/386* (2006.01)
C12N 15/56 (2006.01) *A23K 1/165* (2006.01)
C12N 15/63 (2006.01)

(21) International Application Number:

PCT/FI2007/050196

(22) International Filing Date: 12 April 2007 (12.04.2007)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

20065234 13 April 2006 (13.04.2006) FI
11/404,065 13 April 2006 (13.04.2006) US

(71) Applicant (for all designated States except US): **AB ENZYMES OY** [FI/FI]; Tykkimäentie 15, FI-05200 Rajamäki (FI).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **ALAPURANEN, Marika** [FI/FI]; c/o Roal Oy, Tykkimäentie 15, FI-05200 Rajamäki (FI). **VALTAKARI, Leena** [FI/FI]; Pinnintie 24, FI-05200 Rajamäki (FI). **KALLIO, Jarno** [FI/FI]; Muorinpolku 8 A 12, FI-04400 Järvenpää (FI). **OJAPALO, Pentti** [FI/FI]; Daalintie 202, FI-04360 Tuusula (FI). **VEHMAANPERÄ, Jari** [FI/FI]; Lepsämäentie 359, FI-01800 Klaukkala (FI).

(74) Agent: **KOLSTER OY AB**; Iso Roobertinkatu 23, P.O. Box 148, FI-00121 Helsinki (FI).

(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BH, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, SV, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, LV, MC, MT, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

- with international search report
- with (an) indication(s) in relation to deposited biological material furnished under Rule 13bis separately from the description
- with sequence listing part of description published separately in electronic form and available upon request from the International Bureau

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: ENZYME FUSION PROTEINS AND THEIR USE

(57) Abstract: Cellulase fusion proteins comprising an endoglucanase core region and a heterologous cellulose binding domain are described. The fusion proteins may be produced by recombinant techniques using appropriate polynucleotides, expressing vectors and host cells. The fusion proteins and enzyme preparations thereof are useful in treating cellulosic material, such as textile material, and they are particularly useful in biostoning denim or in biofinishing fabrics and garments. In addition the fusion proteins may be used in pulp and paper industry, oil extraction from plants, detergent compositions, or for improving the quality of animal feed.

WO 2007/118935 A1

Cellulase fusion proteins and their use

Field of the Invention

The present invention relates to enzyme technology, and more precisely to cellulase fusion proteins comprising a catalytic domain and a cellulose binding domain. The fusion proteins may be produced by recombinant techniques using appropriate polynucleotides, expressing vectors and host cells, which are also encompassed by the invention. The fusion proteins and enzyme preparations thereof are useful in treating cellulosic material, such as textile material. In addition the fusion proteins may be used in pulp and paper industry, oil extraction from plants, detergent compositions, or for improving the quality of animal feed. The invention thus further relates to a process for treating cellulosic material with the fusion protein, and especially to processes for biostoning or biofinishing fabrics or garments, especially denim. The invention still further relates to detergent compositions and animal feed containing the fusion proteins.

Background of the Invention

Cellulose is the major structural component of higher plants and occurs naturally in almost pure form only in cotton fiber. It provides plant cells with high tensile strength helping them to resist mechanical stress and osmotic pressure. Cellulose is a linear polysaccharide of glucose residues connected by β -1,4-linkages. In nature cellulose is usually associated with lignin and hemicelluloses. Cellulosic material is degraded in nature by a number of various organisms including bacteria and fungi. The biological conversion of cellulose to glucose generally requires three major groups of enzymes: cellobiohydrolases (CBH), endoglucanases (EG) and beta-glucosidases (BG).

There is a wide spectrum of industrial applications of cellulases. In the textile industry, cellulases are used in denim finishing to create a fashionable stone washed appearance in denim cloths in a biostoning process. Cellulases are also used, for instance, to clean fuzz and prevent formation of pills on the surface of cotton garments. In detergent industry cellulases are used to brighten colors and to prevent graying and pilling of garments. Cellulases are further used in food industry and animal feed manufacturing, and they have a great potential in the pulp and paper industry, for instance, in deinking to release ink from fiber surfaces and in improving pulp drainage.

Industrially used cellulases are often mixtures of enzymes having a variety of activities and substrate specificities. The commercial enzyme preparations often comprise all three cellulase activities i.e. CBH, EG and BG. In addition the unique properties of each cellulase make some more suitable for certain purposes than others, and therefore efforts have also been made to obtain and use cellulases having only the desired activities. The most widely used cellulases of fungal origin are derived from *Trichoderma reesei*. However, also other fungal sources have been suggested e.g. in US 5,457,046.

Cellulases applied in denim treatment are usually divided into two main groups: acid and neutral cellulases. Acid cellulases typically operate at pH 4.0 to 5.5 and neutral cellulases in the range of pH 6 to 8. Cellulases having characteristics of both the acid and neutral group can be called hybrid cellulases. Acid cellulases used in biostoning mainly originate from *Trichoderma reesei* (sexual form *Hypocrea jecorina*) and the neutral cellulases come from a variety of fungi, including genera of *Melanocarpus*, *Humicola*, *Myceliophthora*, *Fusarium*, *Acremonium*, and *Chrysosporium* (Haakana *et al.* 2004). *T. reesei* enzymes include, e.g., cellulases from the glycosyl hydrolase family 5 (endoglucanase II, EGII), family 7 (cellobiohydrolase I, CBHI) and family 12 (endoglucanase III, EGIII; Ward *et al.* 1993), and the neutral cellulases, most often endoglucanases, from family 45 and family 7 (Henrissat, 1991; Henrissat and Bairoch, 1993, 1996).

US 5,874,293 discloses an improved cellulase composition comprising elevated amounts of EGII endoglucanase of *T. reesei* for treating cellulose-containing textiles. The composition improved color properties, increased lightness and visual appearance and reduced pilling tendencies. WO97/14804 discloses one 20 kDa and one 50 kDa cellulase with endoglucanase activity derived from *Melanocarpus* sp. that are especially useful in the textile and detergent industry. Fusion proteins containing the 20K- or 50K-proteins linked to a cellulose binding domain preferably from *Trichoderma reesei* are suggested for creating new enzyme properties. No specific examples are given, nor are the desired properties described.

However, there is still a need for improved cellulases, including endoglucanases that are more efficient in fabric treatment and in other fields, where cellulases traditionally are used. In particular, there is a continuous need for more efficient cellulases to improve the process economics. The present invention aims to meet these needs.

In textile industry a "stone washed" look or an abraded look has been denim producers' interest in recent years. Traditional stone washing with pumice stones reduces the strength of fabric and burdens the laundering apparatuses. There is a trend towards enzymatic denim finishing processes, and cellulases have replaced or are being used together with pumice stones to give the fabric its desired "worn" look. Controlled enzyme treatments result in less damage to the garments and machines and eliminate the need for disposal of stones.

A general problem associated with enzymatic stone washing is backstaining caused by redeposition of removed Indigo dye during or after abrasion. The redepositioning of Indigo dye reduces the desired contrast between the white and indigo dyed yarns and it can be most easily noted on the reverse side of denim and the interior pockets (as increased blueness). On the face side this may be seen as reduced contrast between dyed areas and areas from which dye has been removed during biostoning. Backstaining can be reduced by using antibackstaining agents such as nonionic ethoxylated alcohols during the treatment or adding bleaching agents during rinsing steps. The nature of the enzyme has an impact on backstaining. Generally neutral cellulases backstain less than acid cellulases.

WO97/09410 describes that the addition of a certain type of cellulase to another cellulase having abrading activity reduces backstaining. The additional cellulase belongs to family 5 or 7, but it has no significant abrading effect in itself. Preferably said additional cellulase originates from *Bacillus* or *Clostridium*.

US 5,916,799 discloses cellulase compositions containing both cellobiohydrolases and endoglucanases that have been subjected to limited proteolysis to separate the core and binding domains of the enzymes. The obtained enzyme compositions were found to reduce backstaining. WO94/07983 relates to the finding that redeposition of colorant onto fabric during the stone washing process can be reduced by employing a fungal cellulase composition, which is substantially free of cellobiohydrolase type components. WO96/23928 discloses treatment of cellulose containing fabrics with truncated cellulase enzymes. The truncated enzymes lacking cellulose binding domain (CBD) were found to reduce redeposition of dye and increase abrasion.

The general conclusion of the three references cited above could be that the cellulose binding domain has a negative effect on backstaining.

However, the present invention now provides a cellulase construction with low backstaining property, despite the presence of a cellulose binding domain.

Summary of the Invention

The present invention is based on the surprising finding that the effect of endoglucanases could be significantly enhanced by coupling thereto a particular cellulose binding domain without impairing the backstaining properties.

One object of the present invention is to provide novel endoglucanase fusion proteins having improved hydrolytic properties for use in textile industry, especially in stone washing denim. The fusion proteins of the invention have the advantage of being active at both acid and neutral pH values, and they have highly improved performance in biostoning applications. When used in treating denim, the fusion proteins provide a low backstaining effect. With the improved efficiency of the endoglucanases of the invention, the use of the enzymes is significantly more economical. Additional advantages are achieved also in terms of logistics and the storage of the enzyme products, because smaller amounts of the enzyme product are needed. The fusion proteins are also useful in detergent compositions, as well as in other fields such as feed industry, oil extraction from plants, or pulp and paper industry.

A further object of the present invention is to provide polynucleotides encoding the novel endoglucanase fusion proteins.

A still further object of the present invention is to provide a method for producing the fusion proteins.

A still further object of the present invention is to provide novel expression vectors containing such polynucleotides, useful for the production of the endoglucanase fusion proteins, as well as novel hosts transformed with said expression vectors.

A still further object of the present invention is to provide enzyme preparations, which contain one or more novel endoglucanase fusion proteins.

A still further object of the present invention is to provide methods of treating cellulosic material with the fusion protein e.g for use in textile, detergent, animal feed, oil extraction from plants, or pulp and paper industry, and particularly for finishing of textiles, especially for biostoning and biofinishing of denim.

A still further object of the present invention is to provide animal feed or detergent compositions containing the fusion proteins.

The present invention relates to a cellulase fusion protein comprising a first amino acid sequence of an endoglucanase core, and a second amino acid sequence comprising a linker and cellulose binding domain (CBD) having at least 75% identity to SEQ ID NO: 15, or a variant or fragment thereof
5 having cellulose binding activity.

The invention is further directed to an isolated polynucleotide selected from the group consisting of:

- a) a nucleotide sequence of SEQ ID NO: 3 or 5, or a sequence encoding a cellulase fusion protein as defined herein,
- 10 b) a complementary strand of a),
- c) a sequence that is degenerate as a result of the genetic code to anyone of the sequences of a) or b).

The invention still further relates to an expression vector comprising said nucleotide sequence, and to a host cell comprising the expression vector,
15 as well as to an enzyme preparation comprising the fusion protein.

The invention also encompasses a method of producing the fusion protein, comprising the steps of transforming a host cell with an expression vector encoding said fusion protein and culturing said host cell under conditions enabling expression of said fusion protein, and optionally recovering and
20 purifying the fusion protein produced.

The invention still further encompasses a process for treating cellulosic material, wherein said process comprises contacting the cellulosic material with the fusion protein.

The invention is also directed to a process for biostoning, which
25 process comprises the step of contacting the cellulase fusion protein or the enzyme preparation with denim fabric or garments, and to a process for biofinishing, which comprises the step of contacting the cellulase fusion protein or the enzyme preparation with textile materials like fabrics or garments or yarn.

Eventually the invention is directed to a detergent composition comprising the fusion protein and detergent auxiliaries, to animal feed comprising
30 the fusion protein, and to an *Escherichia coli* strain having accession number E. coli DSM 18159.

Specific embodiments of the invention are set forth herein.

Other objects, details and advantages of the present invention will become apparent from the following drawings, detailed description and examples.

Brief Description of the Drawings

Figure 1 illustrates a schematic picture of the expression cassette used in transformation of *T. reesei* protoplasts for production of *T. aurantiacus* EG28 or EG28+CtCBD cellulase. The *cel5A* or *cel5A_Ct cel7A* linkerCBD gene is under control of *T. reesei cbhl* promoter (*cbhl* prom) and transcription termination is ensured with the addition of the *cbhl* terminator (*cbhl* term). The *amdS* gene (*amdS*) is included for selection of transformants. The expression cassette for EG28 and EG28+CtCBD production was isolated as a 8.6 kb *NotI* fragment from pALK1930 or as a 8.9 kb *NotI* fragment from pALK1948, respectively.

Figure 2 illustrates the pH dependency of the heterologously produced *T. aurantiacus* EG28 cellulase by determining from the culture supernatant using CMC as substrate in a 10 min reaction at 50°C (A). Temperature optimum of EG28 cellulase was determined at optimal pH (6.0). The reaction containing CMC as substrate was performed for 10 min (B). The pH and temperature optimum of the EG28+CtCBD fusion protein was determined to be the same as those of the wild-type EG28 cellulase.

Figure 3 shows the biostoning effect of EG28 cellulase, by measuring the color, at different temperatures and pH 6.

Figure 4 shows the biostoning effect of EG28+CtCBD cellulase, by measuring the color, at different pH-values at 50°C.

Figure 5 shows the biostoning effect of EG28+CtCBD cellulase, by measuring the color, at different pH-values at 60°C.

Figure 6 shows the biostoning effect of EG28+CtCBD cellulase, by measuring the color, at different temperatures (pH 6).

Figure 7 shows the Influence of the pelleting temperature on beta-glucanase activity recovery of feeds supplemented with EG28 cellulase.

Figure 8 shows the Influence of the pelleting temperature on cellulase activity recovery of feeds supplemented with EG28+CtCBD cellulase.

Detailed Description of the Invention

Cellulases comprise a catalytic domain/core (CD) expressing cellulase activity. In addition to the catalytic domain the cellulase molecule may

comprise one or more "cellulose binding domains" ("CBDs"), also named as carbohydrate binding domains/modules (CBD/CBM), which can be located either at the N- or C-terminus of the catalytic domain. CBDs have carbohydrate-binding activity and they mediate the binding of the cellulase to crystalline cellulose but have little or no effect on hydrolytic activity of the enzyme on soluble substrates. These two domains are typically connected via a flexible and highly glycosylated linker region, herein called "linker". Such constructs are described e.g. in Srisodsuk et al., 1993. Some of the naturally occurring endoglucanases and cellobiohydrolases have a cellulose binding domain (CBD), while others do not.

Endoglucanases (EGs) are one of the three types of cellulases generally needed for the biological conversion of cellulose to glucose. Endoglucanases cut internal beta-1,4-glucosidic bonds, whereas cellobiohydrolases cut the disaccharide cellobiose from the end of the cellulose polymer chain and beta-1,4-glucosidases hydrolyze the cellobiose and other short cello-oligosaccharides to glucose. "Endoglucanase" ("EG") in connection with the present invention refers to enzymes classified as E.C. 3.2.1.4. They are 1,4-beta-D-glucan 4-glucanohydrolases and catalyze endohydrolysis of 1,4-beta-D-glycosidic linkages in polymers of glucose such as cellulose. Some endoglucanases may also hydrolyse e.g. 1,4-linkages in beta-D-glucans also containing 1,3-linkages. They may therefore also be classified as endo-1,3(4)-beta-glucanases (E.C. 3.2.1.6). Thus, an enzyme may catalyze reactions on several substrates and can belong to multiple classes.

Cellulases including endoglucanases can also be classified into various glycosyl hydrolase families according their primary sequence, supported by analysis of the three dimensional structure of some members of the family (Henrissat 1991, Henrissat and Bairoch 1993, 1996). For example family 45 (formerly celK) contains endoglucanases (EC 3.2.1.4), and family 5 (formerly known as celA) consists mainly of endoglucanases (EC 3.2.1.4). Family 7 (formerly cellulase family celC) contains both endoglucanases and cellobiohydrolases. Some glycosyl hydrolases are multifunctional enzymes that contain catalytic domains that belong to different glycosyl hydrolase families. For the present purposes the endoglucanase part of the fusion protein preferably belongs to the glycoside hydrolase family 45 or family 5, and more preferably to family 5.

According to a preferred embodiment of the invention the endoglucanase part of the fusion protein is derived from a fungus, preferably of the genus *Thermoascus*, and more preferably from *Thermoascus aurantiacus*. Such an endoglucanase has been described e.g. by Hong et al. 2003. WO03/062409 suggests using this enzyme for feed applications, because in addition to endoglucanase it also has beta-glucanase activity. Most preferably the endoglucanase is derived from *T. aurantiacus* strain ALKO4242 deposited as CBS 116239. The endoglucanase gene of said strain has been inserted into plasmid pALK1926 and deposited as DSM 17326. The protein encoded by this gene is herein referred to as "Ta EG28" or simply "EG28".

Alternatively the endoglucanase part of the fusion protein may be obtained from *Acremonium* sp. preferably from *A. thermophilum*, and more preferably from a strain having the characteristics of the strain ALKO4245 deposited as CBS 116240. The endoglucanase obtainable from this strain and encoded by the gene *ce/45A* is herein referred to as "At EG40" or simply "EG40".

Endoglucanase "core" as used herein, means the catalytic domain/core (CD) of an enzyme expressing at least endoglucanase activity. Such a catalytic domain may be in its naturally occurring form (i.e. intact) or, it may be modified.

According to one embodiment of the invention, the endoglucanase core has at least 75, 80, 85, 90, 95, 98 or 99% identity to SEQ ID NO: 2 (Ta EG28). Preferably the core comprises at least the mature protein, which corresponds to amino acids 19 to 334 of SEQ ID NO: 2. The prediction on the signal sequence was made using the program SignalP V3.0 (Nielsen *et al.*, 1997; Bendtsen *et al.*, 2004); the NN value was obtained using neural networks and HMM value using hidden Markov models. Alternatively the endoglucanase part of the fusion protein has at least 75, 80, 85, 90, 95, 98 or 99% identity to the endoglucanase core of At EG40, encoded by a polynucleotide comprised in SEQ ID NO: 8. Preferably the core comprises at least the mature protein, which corresponds to amino acids 22 to 297 of EG40.

"Cellobiohydrolase" or "CBH" as used herein refers to enzymes that cleave cellulose from the end of the glucose chain and produce mainly cellobiose. They are also called 1,4-beta-D-glucan cellobiohydrolases or cellulose 1,4-beta-cellobiosidases. They hydrolyze the 1,4-beta-D-glucosidic linkages

from the reducing or non-reducing ends of a polymer containing said linkages, such as cellulose, whereby cellobiose is released.

The CBD including the linker is preferably derived from *Chaetomium thermophilum*, and especially from the cellobiohydrolase (CBHI/Cel7A) encoding gene of strain ALKO4265, deposited as CBS 730.95. This CBD including the linker is referred to as "CtCBD". According to a preferred embodiment of the invention, the linker plus the cellulose binding domain has a sequence that has at least 80, 85, 90, 95, 98 or 99% identity to SEQ ID NO: 15, (which corresponds to amino acids 335-415 of SEQ ID NO: 4). According to another preferred embodiment the second amino acid sequence comprises amino acids 335 - 379 of SEQ ID NO: 4.

The term "derived from" in connection with a microorganism source means that the polypeptide may naturally be produced by said specific microorganism source, or the polynucleotide encoding the polypeptide maybe isolated from said microorganism source, or the term means a host cell into which the polynucleotide from said microorganism source encoding the polypeptide has been introduced. However it does not exclude minor modifications of the sequence e.g. by substitution, deletion, inversion and/or insertion of one or a few amino acids/codons as long as the biological activity of the encoded protein is retained.

The core, and the linker+CBD, respectively, may also be a fragment or a variant of said sequences, wherein said fragment or variant has cellulase activity and/or cellulose binding activity. For example the first amino acid sequence may comprise a fragment or variant of an amino acid sequence having at least 75% identity to SEQ ID NO: 2 or 8, and the second amino acid sequence may comprise a fragment or variant of an amino acid sequence having at least 75% identity to SEQ ID NO: 15.

In the present context "cellulase activity" means catalytic ability to hydrolyse cellulose or derivatives thereof, such as endoglucanase or beta-glucanase activity. In addition to endoglucanase and/or beta-glucanase activity, some of the cellulases may further have hemicellulase and/or xylanase activity.

As used in the present context the term "identity" refers to the global identity between two amino acid sequences compared to each other from the first amino acid encoded by the corresponding gene to the last amino acid. The identity of the full-length sequences is measured by using Needleman-Wunsch

global alignment program at EMBOSS (European Molecular Biology Open Software Suite; Rice et al., 2000) program package, version 3.0.0, with the following parameters: EMBL0SUM62, Gap penalty 10.0, Extend penalty 0.5. The algorithm is described in Needleman and Wunsch (1970). The man skilled in the art is aware of the fact that results using Needleman-Wunsch algorithm are comparative only when aligning corresponding domains of the sequence. Consequently comparison of e.g. cellulase sequences including CBD or signal sequences with sequences lacking those elements are excluded as not being meaningful.

According to one embodiment of the invention the fusion protein contains an endoglucanase core encoded by a gene equivalent to that included in *E. coli* DSM 17326. Preferably the fusion protein is encoded by a fusion gene equivalent to that included in *E. coli* DSM 18159. "Equivalent" as used herein means essentially similar or similar. According to a specific embodiment of the invention the fusion protein contains an endoglucanase core comprising the sequence of SEQ ID NO:2 and a linker and CBD comprising the sequence of SEQ ID NO: 15. Especially it comprises the amino acid sequence of SEQ ID NO: 4 or 6, or a variant or fragment thereof having cellulase and cellulose binding activity.

A "fragment" is understood to be part of a specific amino acid sequence that is long enough to have the desired biological activity. In other words the fragment may be e.g. only the mature part of the amino acid sequence or even a subsequence of the mature part. By an amino acid sequence that is a "variant" of a specific amino acid sequence is meant an amino acid sequence that is not identical to the specific amino acid sequence, but rather contains at least some amino acid changes i.e. deletions, substitutions, inversions, insertions etc. that do not essentially affect the biological activity of the protein as compared to a similar activity of the specific amino acid sequence, when used for the desired purpose. Biological activity in this context thus refers to cellulase activity, cellulose binding activity or both.

The fusion protein of the invention may be prepared by attaching the endoglucanase core part to the linker and CBD part in the appropriate encoding DNA using generally known recombinant DNA techniques for producing the desired recombinant protein. Briefly the polynucleotides encoding the fusion partners are amplified and cloned, nucleotides may also be synthesized. The fused polynucleotide is inserted into an expression vector, transformed

into a host cell and expressed. Preferably the linker and CBD is attached at the C-terminus of the endoglucanase core.

An "expression vector" is a cloning plasmid or vector capable of expressing DNA encoding the endoglucanase fusion proteins after transformation into a desired host. When a fungal host is used, the gene of interest is preferably provided to a fungal host as part of a cloning or expression vehicle that integrates into the fungal chromosome, or allows the gene of interest to integrate into the host chromosome. Other sequences that are part of the cloning vehicle or expression vehicle may also be integrated with said DNA during the integration process. In addition, in fungi the expression vector or parts thereof can be targeted into predetermined loci. Alternatively, the desired fusion gene is provided as an autonomously replicating plasmid.

The DNA encoding the endoglucanase fusion proteins is preferably placed under the control of (i.e., operably linked to) certain control sequences such as promoter sequences provided by the vector. Upon transformation these control sequences integrate into the host genome with the gene of interest. Alternatively, the control sequences can be those at the integration site.

The expression control sequences of an expression vector will vary depending on whether the vector is designed to express a certain gene in a prokaryotic or in a eukaryotic host (for example, a shuttle vector may provide a gene for selection in bacterial hosts). Expression control sequences can contain transcriptional regulatory elements such as promoters, enhancer elements, and transcriptional termination sequences, and/or translational regulatory elements, such as translational initiation and termination sites.

A polynucleotide molecule, such as DNA, is said to be capable of expressing a polypeptide, if it contains expression control sequences, which contain transcriptional regulatory information and such sequences are operably linked to the nucleotide sequence, which encodes the polypeptide.

An operable linkage is a linkage in which a sequence is connected to a regulatory sequence (or sequences) in such a way as to place expression of the sequence under the influence or control of the regulatory sequence. Two DNA sequences (such as a promoter region sequence linked to the 5' end of the protein encoding sequence) are said to be operably linked if function of promoter results in the transcription.

The vectors of the invention may further comprise other operably linked regulatory elements, such as enhancer sequences.

In a preferred embodiment, genetically stable transformants are constructed, whereby the DNA encoding the fusion proteins is integrated into the host chromosome by transformation with a vector, which may harbor sequences promoting integration of said vector into the chromosome.

Cells that have stably integrated DNA encoding the endoglucanase fusion proteins into their chromosomes may be selected e.g. by introduced marker(s), homologous or heterologous, which allow for selection of host cells which contain the expression vector in the chromosome, for example the marker may provide biocide resistance, e.g., resistance to antibiotics, or heavy metals, such as copper, or markers complementing an auxotrophic mutation in the host chromosome, and the like. The selectable marker can for example be a selection gene directly linked to the DNA gene sequences to be expressed, or introduced into the same cell by co-transformation. Also other selection systems can be used.

Once the expression vector containing the DNA encoding the fusion protein is prepared, it is introduced into an appropriate host cell by any of a variety of suitable means, including transformation as known in the art. After transformation, recipient cells are grown in an appropriate selective medium, which selects for the growth of transformed cells.

Suitable expression and production host systems are for example the production system developed for fungal hosts *Trichoderma* (EP 244 234), or *Aspergillus*, such as *A. oryzae* or *A. niger* (WO 97/08325 and WO 95/33386, U.S. Patent No. 5,843,745, U.S. Patent No. 5,770,418), or the production system developed for *Fusarium*, such as *F. oxysporum* (Malardier et al., 1989). Suitable production systems developed for bacteria include a production system developed for *Bacillus*, for example *B. subtilis*, *B. licheniformis*, *B. amylo-liquefaciens* or for *E. coli*, or for an actinomycete *Streptomyces*. Suitable production systems developed for yeasts are systems developed for *Saccharomyces*, *Shizosaccharomyces* or *Pichia pastoris*. Production systems in other microbes or in mammalian cells or in plants are also possible.

Expression of the cloned gene sequence(s) results in the production of the desired protein, or in the production of a fragment of this protein. This expression can take place in a continuous manner in the transformed cells, or in a controlled manner.

To obtain the enzyme preparations of the invention, the hosts having the desired properties (that is, hosts capable of expressing economically

feasible quantities of the endoglucanase fusion proteins) are cultivated under suitable conditions, and the desired enzymes are preferably secreted from the hosts into the culture medium, and optionally recovered from said culture medium by methods known in the art. Preferably the host for such production is a filamentous fungus, such as *Trichoderma* or *Aspergillus*, and especially *T. reesei*.

As used in the present context the "enzyme preparation" refers to any enzyme product, which contains at least one endoglucanase fusion protein of the invention. Thus, such an enzyme preparation may be a spent culture medium or filtrate. Spent culture medium means the culture medium of the host comprising the produced enzymes. Preferably the host cells are separated from said medium after the production. If desired, such preparations may be lyophilized or the enzymatic activity otherwise concentrated and/or stabilized for storage. If required, a desired enzyme may be further purified in accordance with conventional methods, such as extraction, precipitation, chromatography, affinity chromatography, electrophoresis, or the like.

However, it is an advantage of the invention that the culture medium with or without host cells may be utilized as an enzyme preparation as such without further purification, because the endoglucanase fusion proteins can be secreted into the culture medium, and they display activity in the ambient conditions of the spent culture medium. The enzyme preparations are very economical to provide and use, because isolation of a specific enzyme from the culture medium is unnecessary.

In addition to the endoglucanase fusion protein, the enzyme preparations may comprise one or more other enzymes, which may be for example other cellulases, amylases, lipases, proteases, hemicellulases, xylanases, pectinases and/or oxidases such as laccases and peroxidases. Alternatively, before, during or after the treatment with the endoglucanase fusion protein another enzyme treatment may be carried out. The enzyme treatment may comprise, for example, one or more amylase treatments (e.g. for desizing of denim), one or more cellulase treatments and/or one or more peroxidase and/or laccase treatments. It depends on the application what other enzymes are included in the enzyme preparation or used in the enzyme treatment.

In addition to the fusion protein, the enzyme preparation may contain additives, such as stabilizers, buffers, preservatives, surfactants and/or culture medium components. Preferred additives are such, which are com-

monly used in enzyme preparations intended for the application, where the enzyme preparation is used.

The enzyme preparations may be provided as a liquid or as a solid, for example, as a dried powder or granular, especially non-dusting granules, or a stabilized liquid. It is envisioned that the enzyme preparations can be further enriched, or made partially or completely deficient in specific enzymatic activities, so as to satisfy the requirements of a specific utility in various applications e.g. in the textile industry. A mixture of enzyme activities secreted by a host can be advantageous in a particular industrial application, for example in biofinishing and biostoning.

The endoglucanase fusion proteins and the preparations thereof are useful e.g. in textile, feed, plant oil, detergent, and pulp and paper industry. They may be used for treating any cellulosic material, such as textile material, plants used in animal feed, plant material for oil extraction, or wood-derived mechanical or chemical pulp or secondary fiber. They may also be added into detergents, which normally contain auxiliaries, such as surface-active agents, surfactants, bleaching agents and/or builders. In the present context "cellulosic material" refers to any material comprising cellulose or derivatives thereof as a significant component. The cellulosic material is contacted with an effective amount of the fusion protein under suitable conditions, such as appropriate pH, and temperature, and the reaction is allowed to continue for a time sufficient for the enzymatic reaction to take place.

The fusion enzymes are especially useful in the treatment of textile materials, such as fabrics and garments. The textile material may be manufactured of natural cellulose containing fibers or man-made cellulose containing fibers or mixtures thereof, or a blend of synthetic fibers and cellulose containing fibers. Preferably the cellulose containing material is cotton, especially denim. By "denim" is meant, in connection of this invention, denim fabric, usually denim garments, particularly jeans. Advantageously the denim is Indigo dyed denim. Denim can also be treated with derivatives of Indigo or with Indigo together with some other dye, for example Indigo-dyed denim with sulphur bottom.

The fusion endoglucanases are especially useful in biostoning and biofinishing of textiles.

Stone washing has three steps: desizing, abrasion and after-treatment. The first step, the desizing process is normally the first wet treat-

ment of jeans and means removal of starch or other sizing agents usually applied to the warp yarns to prevent damage during the weaving process. Alpha-amylases are used to remove starch-based sizing agents for improved and uniform wet processing. After desizing the jeans are normally rinsed with water or passed directly to the abrasion step.

The second step, abrasion, can be performed with enzymes or pumice stones or both. In all cases mechanical action is needed to remove the dye, and the treatment is usually carried out in washing machines, like drum washers. The term "abraded" means the appearance of denim fabric, when it has been treated by cellulase enzymes or stones, or both. Synonymous expressions are "stone washed look" or "worn look". As a result of uneven dye removal there are contrasts between dyed areas and areas from which dye has been removed.

Abrasion is generally followed by the third step, after-treatment that includes washing and rinsing steps during which detergents, optical brighteners, bleaching agents or softeners may be used. After the enzymatic treatment the reaction must be stopped in order to prevent damage of the treated materials, for example by temperature and/or pH inactivation, the latter comprising a thorough rinsing and/or detergent wash-off. This ensures that the mechanical strength of the fiber is not further compromised by the continued presence of the enzyme.

As used in the present context the expression "biostoning" of fabric or garment means the use of enzymes in place of, or in addition to, pumice stones for the treatment of fabric or garment, especially denim.

As stated above, treatment with cellulase can completely replace treatment with pumice stones (for example, 1 kg commercial enzyme vs. 100 kg stones). However, cellulase treatment can also be combined with pumice stone treatment, when it is desired to produce a heavily abraded finish. A peach skin effect in which a fine protruding hair-like covering is created is also achieved by a wash combining a neutral cellulase with pumice stones. The fusion proteins described are especially useful to efficiently provide an abraded look and to minimize backstaining in biostoning.

Biostoning is typically performed at about pH 3.0 to 8.0, and preferably at pH 5.0 to 7.0. The temperature of the reaction can range from about 30°C to 80°C and is preferably between 50 to 60°C. The liquor ratio (the ratio of the volume of liquid per weight of fabric) may range from about 3:1 to 20:1,

preferably 5:1 to 10:1. The treatment time can range between 15 min to 90 min and preferably 30 min to 60 min. It should be emphasized that the enzyme dosage greatly depends on the type of the fabrics, machinery, process conditions (pH, temperature, liquor ratio, treatment time, denim load, process scale) and type of enzyme preparation and like. If desired, pumice stones can be used in combination with the endoglucanase fusion proteins. The enzyme dosage required will then be significantly lower. A person skilled in art is capable in defining suitable dosages and conditions.

The endoglucanase fusion proteins of the present invention provide unexpected advantages in that the enzyme performance is high and the back-staining is low resulting in very good contrast. In addition the fusion proteins are easily manufactured, and they may be used in a relatively broad range of temperature and pH.

Further, the endoglucanase fusion proteins are useful in biofinishing of fabrics and garments. "Biofinishing" refers to the use of enzymes in a controlled hydrolysis of cellulosic fibers in order to modify the fabric or yarn surface in a manner that prevents permanently pilling, improves fabric handle like softness and smoothness, clears the surface structure by reducing fuzzing, which results in clarification of colors, improves the drapability of the fabric, improves moisture absorbency and which may improve also the dyeability.

Enzymatic depilling can be carried out at any stage during textile wet processing, preferably after optional desizing and/or bleaching, and similar conditions as in biostoning can be used.

The endoglucanase fusion proteins possessing also beta-glucanase, hemicellulase or xylanase activity are further useful for improving the quality of animal feed, whereby plant material is treated with the enzymes.

Starch, proteins and lipids can be easily degraded by the digestive system of monogastric animals such as poultry and pigs, whereas the major part of non starch polysaccharides (NSP) including mixed-linked beta-glucans of e.g. barley and oats remain intact due to the lack of such enzyme activities within the animal. Furthermore, the digestibility of other components, particularly animal-based fats, is reduced in the presence of NSP.

Beta-glucanases have been commercially used to alleviate problems caused by mixed-linked beta-glucans of barley and oats. Beta-glucanases are known to reduce intestinal viscosity caused by soluble beta-glucans as well as to release nutrients encapsulated by cell-walls rich in beta-

glucans. The use of beta-glucanases improves animal performance, which can be seen as improved weight gain and feed conversion ratio. Also, incidences of sticky droppings in poultry are typically reduced.

Steam pelleting is the main feed processing technology throughout the world. Its advantages over production of mash feeds include easier handling, decrease of toxic substances and organisms, and above all improved feed efficiency. The thermotolerance and high performance of the fusion proteins described herein make them suitable for feed applications.

The invention is illustrated by the following non-limiting examples. It should be understood, however, that the embodiments given in the description above and in the examples are for illustrative purposes only, and that various changes and modifications are possible within the scope of the invention.

Example 1. Production of *Thermoascus aurantiacus* ALKO4242 EG28 cellulase in *Trichoderma reesei*

Standard molecular biology methods were used in the isolation and enzyme treatments of DNA (plasmids, DNA fragments), in *E. coli* transformations, etc. The basic methods used are described in the standard molecular biology handbooks, e.g. Sambrook et al. (1989) and Sambrook and Russell (2001).

The *Thermoascus aurantiacus* *cel5A* gene (SEQ ID NO: 1) encoding EG28 cellulase (SEQ ID NO: 2) was amplified by PCR directly from the *T. aurantiacus* ALKO4242 genomic DNA, isolated by the method of Raeder and Broda (1985). The forward (SEQ ID NO: 9) and reverse (SEQ ID NO: 10) primers were designed on the basis of the published *T. aurantiacus* endoglucanase sequence (AF487830). The amplified 1.3 kb product containing the exact gene (from START to STOP codon) was cloned as a *SacII*-*PstI* fragment into the pBluescript II KS+ vector. Two independent clones were sequenced and one clone was selected and designated as pALK1926. The deposit number of the *E. coli* strain containing pALK1926 in the Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH culture collection is DSM 17326.

An expression plasmid (pALK1930, Fig. 1) was constructed for production of recombinant *T. aurantiacus* cellulase EG28/Cel5A (SEQ ID NO: 2). The *cel5A* gene, including its own signal sequence, was exactly fused to the *T. reesei* *cbh1* (*cel7A*) promoter by PCR. The *cbh1* promoter, *cbh1* terminator and *amdS* marker gene were included as described in Paloheimo et al. (2003). The linear expression cassette (Fig. 1) was isolated from the vector backbone

by restriction enzyme digestion, transformed into *T. reesei* A96, and transformants were selected with acetamide as sole nitrogen source. The host strain lacks four major endogenous cellulases: CBHI/Cel7A, CBHII/Cel6A, EGI/Cel7B and EGII/Cel5A. Transformations were performed according to Penttilä *et al.* (1987) with the modifications described in Karhunen *et al.* (1993). The transformants were purified on selection plates through single conidia prior to sporulating them on PD.

The cellulase production of the transformants was analyzed from the culture supernatants of shake flask cultivations (50 ml). Transformants were grown for 7 days in a complex cellulose-inducing medium (Joutsjoki *et al.* 1993) buffered with 5% KH_2PO_4 at pH 5.5. The enzyme activity of the recombinant protein was measured from the culture supernatant as the release of reducing sugars from carboxymethylcellulose (2% CMC) at 50°C in 50 mM Citrate buffer pH 4.8 essentially as described by Bailey and Nevalainen 1981; Haakana *et al.* 2004. Activity against barley beta-glucan (1%) was also determined by measuring the release of reducing sugars at 50°C in 50 mM acetate buffer pH 4.8 as described by Stålbrand *et al.* 1993. Production of the recombinant protein was also detected from the culture supernatant by SDS-polyacrylamide gel electrophoresis. The genotypes of the chosen transformants were analysed by Southern blotting using the expression cassette as a probe.

The pH optimum of the heterologously produced Ta EG28/Cel5A cellulase was determined in the universal McIlvaine's buffer within a pH range of 4.0 to 8.0 using carboxymethylcellulose as substrate. As shown in Figure 2A the pH optimum for EG28/Cel5A cellulase activity is at pH 6.0. The optimal temperature for the enzymatic activity of EG28/Cel5A cellulase was determined to be 75°C (Figure 2B).

The chosen transformant (RF6188) was cultivated in a bioreactor to obtain material for the application tests (see Example 4).

Example 2. Production of the recombinant *Thermoascus aurantiacus* ALKO4242 EG28+CtCBD fusion protein

To produce a recombinant *Thermoascus aurantiacus* EG28+CtCBD fusion protein (SEQ ID NO: 4), the cellulose binding domain (CBD) of the CBHI/Cel7A cellulase of *Chaetomium thermophilum* ALKO4265 was linked to the EG28/Cel5A cellulase. The construct contains the catalytic domain of

EG28 (amino acids 1-334 of the full-length polypeptide) attached to the linker region and CBD of *C. thermophilum* CBHI/ Cel7A CtCBD (SEQ ID NO: 15).

Standard molecular biology methods were used as described in Example 1. First, a unique *Sna*BI restriction site near the C-terminal end of the EG28/Cel5A sequence was introduced by PCR. This enables direct fusion of any blunt-ended DNA after amino acid Y334 of the EG28/Cel5A polypeptide. The linker and CBD region of the *C. thermophilum* CBHI/Cel7A encoding gene (*cel7A*, SEQ ID NO: 7) was amplified by PCR using forward (SEQ ID NO: 11) and reverse (SEQ ID NO: 12) primers and *C. thermophilum* ALKO4265 genomic DNA as template. The amplified 1.6 kb product was ligated to the *cel5A* gene (after Y334) to create Ta *cel5A*_Ct *cel7A*linkerCBD (SEQ ID NO: 3). The resulting plasmid was designated as pALK1946. The deposit number of the *E. coli* strain containing pALK1946 in the Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH culture collection is DSM 18159.

An expression plasmid (pALK1948, Fig 1) for production of the EG28+CtCBD cellulase was constructed as described in Example 1. The linear 8.9 kb expression cassette (Figure 1) was isolated from the vector backbone by *Not*I restriction enzyme digestion, transformed into *T. reesei* A33 (the strain has the genes encoding the four major cellulases CBHI/Cel7A, CBHII/Cel6A, EGI/Cel7B and EGII/Cel5A deleted), and transformants selected as described in Example 1. The pH and temperature optimum of the fusion protein was determined to be the same as those of the wild-type EG28 protein.

The chosen transformant (RF6377) was cultivated in a bioreactor to obtain material for the application tests (see Examples 5 to 10).

Example 3. Production of the recombinant *Acremonium thermophilum* ALKO4245 EG40+CtCBD fusion protein

For production of a recombinant *Acremonium thermophilum* ALKO4245 EG40+CtCBD fusion protein (SEQ ID NO: 6), the cellulose binding domain of EG40 cellulase is replaced with that of the *Chaetomium thermophilum* ALKO4265 CBHI/Cel7A. The construct contains the catalytic domain of EG40 cellulase (amino acids 1 to 234 of the full-length polypeptide) attached to the linker region and CBD of *C. thermophilum* CBHI/Cel7A (CtCBD, SEQ ID NO: 15).

Standard molecular biology methods are used as described in Example 1. The *Acremonium thermophilum cel45A* gene (SEQ ID NO: 8) is amplified by PCR from the *A. thermophilum* ALKO4245 genomic DNA using prim-

mers (SEQ ID NO: 13) and (SEQ ID NO: 14). The 1.1 kb PCR fragment is cloned as a *SacII*-*PstI* fragment into the pBluescript II KS+ vector. After this, a unique *NruI* restriction site near the C-terminal end of the EG40 sequence is introduced by PCR. This enables direct fusion of any blunt-ended DNA after amino acid S234 of the EG40 polypeptide. The linker plus CBD region of the CBHI/Cel7A cellulase of *Chaetomium thermophilum* (*cel7A*) is amplified by PCR as described in Example 2 and a restriction fragment thereof ligated to the *cel45A* gene (after S234) to create At *cel45A*_Ct *cel7A*linkerCBD (SEQ ID NO: 5). An expression plasmid for production of the EG40+CtCBD cellulase is constructed and the recombinant protein (SEQ ID NO: 6) is produced in *Trichoderma* as described in Example 1.

Example 4. Performance of EG28 cellulase in denim finishing at different temperatures

Thermoascus aurantiacus EG28 cellulase produced in *Trichoderma* (strain RF6188) as described in Example 1 was tested for its ability to create an abraded look similar to that provided by pumice stones in biostoning of denim at different temperatures. An efficient denim finishing enzyme, a commercial EGII enriched acid cellulase preparation produced in *Trichoderma* (US. 5,874,293) was used as a reference.

Jeans made of Indigo dyed denim twill were used as test material after desizing with ECOSTONE® A200 alpha-amylase. The cellulase treatments were performed with Electrolux's Wascator™ FOM 71 CLS washer extractor under conditions described in Table 1.

The endoglucanase activity (ECU) of the enzyme preparations used was measured as the release of reducing sugars from hydroxyethyl cellulose as previously described (Bailey and Nevalainen, 1981). The EGII enriched enzyme concentrate and EG28 preparation were dosed at 220 ECU/g and ca. 380 ECU/g fabric, respectively. The enzymes were tested at their optimal pH range, the EGII preparation at pH 5 and the EG28 preparation at pH 6. After draining, the enzyme was inactivated (for 10 minutes at 40°C) by raising the pH above 11 with sodium hydroxide. The jeans were then rinsed three times with water and dried in a tumbler.

The biostoning effect/abrasion level was evaluated by measuring the color as reflectance values with a Minolta CM 2500 spectrophotometer using L*a*b* color space coordinates (illuminant D65/ 2°). The color from the face and the reverse side of denim and of the pockets was measured after de-

sizing (i.e. before cellulase treatment) and after the cellulase treatment. Each measurement on the face side, reverse side or pockets was the average of approximate 40, 20, or 12 measurements, respectively. Two pairs of jeans were used in each test and the final result was the average thereof. The results are shown in Table 2 and Figure 3.

Table 1. Test conditions/process parameters used in cellulase treatments.

Process parameter	
Denim load	1.3 kg
Water	19 liter
pH control (pH 5 - 5.3)	35 g Na ₂ HPO ₄ 2H ₂ O + 22 g citric acid
pH control (pH 6.1 - 6.3)	35.5 g Na ₂ HPO ₄ 2H ₂ O + 15 g citric acid
Time	45 min
Temperature	40, 50, 60 or 70°C
Cellulase dosage	220 or ca. 380 ECU/g fabric

Table 2. Color measurements of denim treated with EG28 cellulase at different temperatures.

Treatment with EGII enriched preparation was used as reference. L* indicates the lightness, -b* is the blue direction, +b* is the yellow direction.

Enzyme preparation	ECU/g garment	Conditions	Before cellulase Treatment		After cellulase Treatment		deltaL*	deltab*
			L*	b*	L*	b*		
Face side:								
EG28	380	70°C, pH 6.1 - 6.3	23.67	-16.07	32.63	-16.94	8.96	-0.87
EG28	370	60°C, pH 6.1 - 6.3	23.67	-16.38	31.94	-17.09	8.27	-0.71
EG28	380	50°C, pH 6.1 - 6.3	23.62	-16.24	31.91	-16.86	8.30	-0.63
EG28	380	40°C, pH 6.1 - 6.3	23.75	-16.07	30.57	-17.32	6.82	-1.25
EGII enriched	220	60°C, pH 5.2 - 5.3	23.45	-16.10	32.90	-17.29	9.46	-1.19
Reverse side:								
EG28	380	70°C, pH 6.1 - 6.3	49.76	-6.95	49.60	-10.43	-0.16	-3.48
EG28	370	60°C, pH 6.1 - 6.3	49.55	-6.87	50.78	-9.57	1.24	-2.71
EG28	380	50°C, pH 6.1 - 6.3	49.92	-7.05	50.49	-9.83	0.57	-2.78
EG28	380	40°C, pH 6.1 - 6.3	49.89	-6.93	49.73	-9.73	-0.16	-2.80
EGII enriched	220	60°C, pH 5.2 -5.3	49.75	-6.82	48.28	-12.26	-1.47	-5.45
Pockets:								
EG28	380	70°C, pH 6.1 - 6.3	77.40	-8.14	68.53	-12.60	-8.86	-4.47
EG28	374	60°C, pH 6.1 - 6.3	77.91	-7.71	70.29	-12.34	-7.62	-4.63
EG28	380	50°C, pH 6.1 - 6.3	78.11	-7.62	70.63	-12.02	-7.49	-4.40
EG28	380	40°C, pH 6.1 - 6.3	77.51	-7.60	70.47	-11.91	-7.04	-4.32
EGII enriched	220	60°C, pH 5.2 -5.3	77.46	-7.68	66.18	-14.17	-11.29	-6.49

The results in Table 2 and Fig. 3 show that the best abrasion effect with the EG28 preparation (strain RF6188) was obtained at the range of 50 to 70°C. Using a dosage of 380 ECU/g fabric of the EG28 preparation at 70°C a similar abrasion level (lightness L*) was obtained compared to using the dosage of 220 ECU/g fabric of an EGII enriched preparation at 60°C. However, the back-staining effect (re-deposition of Indigo-dye) on the reverse side of the denim and pockets was lower with the EG28 preparation (higher lightness, less blue) than with the EGII enriched preparation. Also the contrast on the face side of the denim looked better.

Example 5. Performance of EG28+CtCBD fusion protein compared to EG28 cellulase in denim finishing

Recombinant *Thermoascus aurantiacus* EG28+CtCBD fusion protein produced in *Trichoderma* (strain RF6377) as described in Example 2 was compared to the EG28 preparation from strain RF6188 in biostoning of denim at pH 6, 60°C. The denim and test system for biostoning were as in Example 4, except that the amount of denim was leveled to 1430 g with an extra piece of different denim that was not included in the measurements. The effect of the cellulase treatment was evaluated as in Example 4.

The results in Table 3 show that the biostoning effect of the EG28+CtCBD preparation was very good at a low dosage. With strain RF6377 a similar abrasion level (lightness L*) was obtained with 6.5 times lower dosage compared to RF6188. Linking of cellulose binding domain (CBD) to EG28 cellulase did not increase the undesirable backstaining effect, but increased the desired washing performance greatly.

Table 3. Color measurements of denim treated with EG28 and EG28+CtCBD cellulases at 60 °C, pH 6.

L* indicates the lightness, -b* is the blue direction, +b* is the yellow direction.

Enzyme preparation	ECU/g garment	Before cellulase treatment		After cellulase Treatment		deltaL*	deltab*
		L*	b*	L*	b*		
Face side:							
EG28	325	23.40	-16.02	31.01	-17.12	7.62	-1.10
EG28+CtCBD	50	23.81	-16.21	31.60	-16.92	7.80	-0.71
Reverse side:							
EG28	325	49.46	-6.83	50.03	-9.62	0.57	-2.79
EG28+CtCBD	50	49.36	-7.03	50.62	-9.61	1.27	-2.58
Pockets:							
EG28	325	76.11	-8.36	68.53	-12.46	-7.58	-4.10
EG28+CtCBD	50	76.02	-8.45	68.81	-12.39	-7.21	-3.94

Example 6. Performance of EG28+CtCBD cellulase compared to EGII cellulase in denim finishing

Recombinant *Thermoascus aurantiacus* EG28+CtCBD fusion protein produced in *Trichoderma* (strain RF6377) was compared to the commercial EGII enriched acid cellulase preparation (US. 5,874,293) in biostoning of denim.

The test system for biostoning was as in Example 4, except that pieces (legs) of several different Denim types from Ukos Sport (Belgium) and Vicunha (Brazil) were used (total 1.2 kg). The conditions for EG28+CtCBD and EGII treatment were as in Table 4. The effect of the cellulase treatment was evaluated as in Example 4.

The results of the experiments performed with four different denim fabrics are shown in Tables 4 and 5. Using an enzyme dosage of 500 ECU/g fabric of EG28+CtCBD preparation a similar lightness level was obtained compared to using a dosage of 1000 ECU/g of the EGII enriched preparation. The performance of the EG28+CtCBD preparation required roughly only half of the ECU-activity of that of EGII enriched cellulase. Also the culture medium of EG28+CtCBD produced by the recombinant host is volumetrically about two-fold as effective as that of the EGII producing recombinant host in biostoning. Considerably less backstaining was observed on the reverse side of the denim when EG28+CtCBD preparation was used. The performance of the EG28+CtCBD preparation at 50°C was better at pH 6 than at pH 5.

Table 4. Color measurements on the face side of denim treated with EG28+CtCBD cellulase at pH 5 and 6. Treatment with EGII enriched preparation was used for comparison. L* indicates the lightness, -b* is the blue direction, +b* is the yellow direction.

Enzyme preparation	Denim	ECU/g garment	Conditions	Before cellulase Treatment		After cellulase treatment		deltaL*	deltab*
				L*	b*	L*	b*		
EGII Enriched	Atlanta, Ukos sport	1000	pH adj. with acetic acid 55 min, 50°C, pH 5	19.96	-15.91	27.44	-18.49	7.48	-2.58
	Mathew, Ukos sport			18.28	-7.97	21.87	-11.71	3.59	-3.74
	Nostalg, Ukos sport			19.12	-8.78	23.90	-13.50	4.78	-4.72
	Vicunha, Savana			17.24	-10.49	21.51	-14.93	4.27	-4.44
	Average			18.65	-10.79	23.68	-14.66	5.03	-3.87
EG28+CtCBD	Atlanta, Ukos sport	500	pH adj. with acetic acid 55 min, 50°C, pH 5	19.79	-16.02	25.88	-18.44	6.09	-2.42
	Mathew, Ukos sport			18.07	-8.58	21.45	-11.80	3.38	-3.22
	Nostalg, Ukos sport			19.05	-8.73	22.65	-12.69	3.60	-3.96
	Vicunha, Savana			17.38	-10.11	20.75	-14.18	3.37	-4.07
	Average			18.57	-10.86	22.68	-14.28	4.11	-3.42
EG28+CtCBD	Atlanta, Ukos sport	500	pH adj. with acetic acid 55 min, 50°C, pH 6	19.98	-16.18	27.35	-18.20	7.37	-2.02
	Mathew, Ukos sport			17.51	-8.84	21.40	-11.62	3.89	-2.78
	Nostalg, Ukos sport			18.58	-8.65	22.96	-12.75	4.38	-4.10
	Vicunha, Savana			17.50	-10.16	21.49	-14.06	3.99	-3.90
	Average			18.39	-10.96	23.30	-14.16	4.91	-3.20

Table 5. Color measurements on the reverse side of denim treated with EG28+CtCBD cellulase at pH 5 and 6. Treatment with EGII enriched preparation was used for comparison. L* indicates the lightness, -b* is the blue direction.

Enzyme preparation	Denim	ECU/g garment	Conditions	Before cellulase treatment		After cellulase treatment		deltaL*	deltab*
				L*	b*	L*	b*		
EGII Enriched	Atlanta, Ukos sport	1000	pH adj. with acetic acid 55 min, 50°C, pH 5	47.98	-7.25	40.18	-14.63	-7.80	-7.38
	Mathew, Ukos sport			38.41	-7.17	36.11	-10.93	-2.30	-3.76
	Nostalgia, Ukos sport			46.70	-6.06	41.87	-11.73	-4.83	-5.67
	Vicunha, Savana			35.65	-9.24	33.48	-12.44	-2.17	-3.20
	Average			42.19	-7.43	37.91	-12.43	-4.28	-5.00
EG28+CtCBD	Atlanta, Ukos sport	500	pH adj. with acetic acid 55 min, 50°C, pH 5	48.01	-7.29	41.82	-13.25	-6.19	-5.96
	Mathew, Ukos sport			37.60	-7.27	35.59	-10.50	-2.01	-3.23
	Nostalgia, Ukos sport			46.79	-5.99	44.75	-9.37	-2.04	-3.38
	Vicunha, Savana			35.08	-9.48	33.72	-11.80	-1.36	-2.32
	Average			41.87	-7.51	38.97	-11.23	-2.90	-3.72
EG28+CtCBD	Atlanta, Ukos sport	500	pH adj. with acetic acid 55 min, 50°C, pH 6	47.55	-7.43	42.41	-13.30	-5.14	-5.87
	Mathew, Ukos sport			37.27	-7.58	36.01	-10.27	-1.26	-2.69
	Nostalgia, Ukos sport			47.02	-6.01	44.61	-10.13	-2.41	-4.12
	Vicunha, Savana			34.84	-9.39	33.53	-11.20	-1.31	-1.81
	Average			41.67	-7.60	39.14	-11.23	-2.53	-3.62

Example 7. Effect of pH on the performance of EG28+CtCBD cellulase preparation at 50°C and 60°C

Recombinant *Thermoascus aurantiacus* EG28+CBD fusion protein produced in *Trichoderma* (strain RF6377) was tested for its performance in biostoning of denim at different pH values at 50°C and 60°C.

Indigo dyed denim twill (different from the previous examples) that was desized and cut into pieces was used as test material. Cellulase treatments were performed in LP-2 Launder Ometer as follows. About 7.2 g of denim fabric (ca. 12 cm x 12 cm swath), 200 ml of Mc Ilvaine's citrate phosphate buffer, and 90 steel balls (diameter 0.6 cm) were loaded into 1.2 liter containers. The Launder Ometer was run for 120 min at different pH values of 4 to 8 using temperatures 50°C and 60°C. After removing the swathes from the containers they were rinsed with water and soaked in water containing NaOH (pH>11) for 10 min with mixing. Thereafter, the swathes were soaked in warm water containing liquid detergent (OMO Color) and mixed for 10 min, followed by careful rinsing with warm water for several times. The swathes were dried at room temperature. The biostoning effect was evaluated by measuring the color as reflectance units as described in Example 4. Each measurement value on the face side of denim swath was the average of at least 20 measurements.

The results shown in Tables 6 and 7 and Figures 4 and 5 show that the most optimal pH range for the EG28+CtCBD cellulase at 50° is 5.5 to 6.5 and at 60°C 5 to 7.

Table 6. Color measurements on the face side of denim treated with EG28+CtCBD cellulase at different pH values in Launder at 50°C.

L* indicates the lightness, -b* is the blue direction.

Enzyme preparation	ECU/g garment	Conditions	Before cellulase Treatment		After cellulase treatment		Increase of L*
			L*	b*	L*	b*	
Buffer Control	0	pH 6	17.28	-13.07	18.77	-14.13	1.49
Buffer Control	0	pH 8	17.01	-13.4	18.18	-14.45	1.17
EG28+CtCBD	1000	pH 4	16.79	-13.59	20.86	-16.40	4.07
EG28+CtCBD	1000	pH 5	17.34	-13.18	21.59	-16.44	4.25
EG28+CtCBD	1000	pH 5.5	17.30	-13.25	22.06	-16.39	4.76
EG28+CtCBD	1000	pH 6	17.35	-13.42	22.29	-16.47	4.94
EG28+CtCBD	1000	pH 6.5	17.31	-13.41	22.48	-16.65	5.17
EG28+CtCBD	1000	pH 7	17.34	-13.25	21.55	-16.23	4.21
EG28+CtCBD	1000	pH 8	16.91	-13.63	19.62	-15.72	2.71

Table 7. Color measurements on the face side of denim treated with EG28+CtCBD cellulase at different pH values in Launder at 60°C.

L* indicates the lightness, -b* is the blue direction.

Enzyme preparation	ECU/g garment	Conditions	Before cellulase		After cellulase		Increase of L*
			L*	b*	L*	b*	
EG28+CtCBD	1000	pH 4	17.19	-13.58	20.48	-15.77	3.29
EG28+CtCBD	1000	pH 5	17.10	-13.24	22.74	-16.59	5.64
EG28+CtCBD	1000	pH 5.5	17.10	-13.54	22.66	-16.61	5.56
EG28+CtCBD	1000	pH 6	17.10	-13.65	22.83	-16.74	5.73
EG28+CtCBD	1000	pH 6.5	17.19	-13.47	22.65	-11.72	5.46
EG28+CtCBD	1000	pH 7	16.99	-13.72	22.10	-16.66	5.11
EG28+CtCBD	1000	pH 8	17.13	-13.68	19.35	-15.15	2.22
Buffer Control	0	pH 6	17.36	-13.6	18.95	-14.28	1.59

Example 8. Performance of EG28+CtCBD cellulase preparation in denim finishing at different temperatures

Recombinant *Thermoascus aurantiacus* EG28+CtCBD fusion protein produced in *Trichoderma* (strain RF6377) as described in Example 1 was tested for its ability to create an abraded look similar to that provided by pumice stones in biostoning of denim at different temperatures. Efficient denim finishing enzymes, commercial EGII enriched acid cellulase preparation (US. 5,874,293) and neutral cellulase preparation ECOSTONE[®] C1 were used as reference.

The test system for biostoning was as in Example 4, except that different Denim twill and a washing time of 55 min were used. The enzymatic activity (endoglucanase unit, ECU) of the EG28+CtCBD and EGII enriched enzyme preparations was measured as in Example 4. The activity (neutral cellulase unit, NCU) of the neutral cellulase preparation ECOSTONE[®] C1 was measured as the release of reducing sugars from carboxymethyl cellulose as previously described (Bailey and Nevalainen, 1981; Haakana et al. 2004). The ECOSTONE[®] C1, EG28+CtCBD, or EGII enriched preparations were dosed at 250 NCU/g, 500 ECU/g, or 1000 ECU/g fabric, respectively. The effect of the cellulase treatment was evaluated as in Example 4.

The performance of EG28+CtCBD at temperatures of 40 to 70°C, pH 6 is shown in Table 8 and Figure 6. The preferred temperature range for the enzyme is 50 to 70°C. Lower temperatures like 40°C can be used to obtain an abrasion effect with less colorpull if a darker look is desirable.

The results are also in agreement with those obtained in Example 6, where the performance of EG28+CtCBD in biostoning was shown to be about two times more effective than that of the commercial EGII enriched acid cellulase preparation. Acid cellulases generally have a tendency of backstaining. Neutral cellulases, like ECOSTONE[®] C1, typically cause low backstaining therefore resulting in good contrast. The results obtained here show that a similar effect was obtained with the EG28+CtCBD cellulase as with the neutral cellulases (Table 8).

Table 8. Color measurements of denim treated with EG28+CtCBD cellulase at different temperatures.

Treatment with EGII enriched acid cellulase and ECOSTONE® C1 neutral cellulase preparation was used as reference. L* indicates the lightness, -b* is the blue direction, +b* is the yellow direction.

Enzyme preparation	Activity/g garment	Conditions	Before cellulase Treatment		After cellulase Treatment		deltaL*	deltab*
			L*	b*	L*	b*		
Face side:								
EG28+CBD	500 ECU/g	70C°, pH 6.2	17.38	-13.49	27.42	-17.27	10.05	-3.78
EG28+CBD	500 ECU/g	60C°, pH 6.2	16.76	-13.31	26.01	-17.49	9.25	-4.18
EG28+CBD	500 ECU/g	50C°, pH 6.2	16.78	-13.40	25.00	-17.44	8.22	-4.04
EG28+CBD	500 ECU/g	40C°, pH 6.2	16.76	-13.21	22.86	-17.25	6.11	-4.04
EGII enriched	1000 ECU/g	60C°, pH 5.1	17.24	-13.38	26.59	-17.64	9.35	-4.26
ECOSTONE C1	250 NCU/g	60C°, pH 6.5	17.38	-13.53	26.91	-16.98	9.53	-3.45
Reverse side:								
EG28+CBD	500 ECU/g	70C°, pH 6.2	45.67	-6.33	41.78	-13.83	-3.90	-7.51
EG28+CBD	500 ECU/g	60C°, pH 6.2	45.60	-5.95	42.72	-13.05	-2.88	-7.10
EG28+CBD	500 ECU/g	50C°, pH 6.2	45.67	-5.92	41.81	-13.35	-3.86	-7.44
EG28+CBD	500 ECU/g	40C°, pH 6.2	45.80	-5.72	41.66	-12.52	-4.14	-6.81
EGII enriched	1000 ECU/g	60C°, pH 5.1	46.10	-6.19	39.89	-15.24	-6.21	-9.06
ECOSTONE C1	250 NCU/g	60C°, pH 6.5	45.63	-6.46	42.49	-12.76	-3.14	-6.31

Example 9. Performance of EG28 and EG28+CtCBD cellulases in biofinishing (depilling)

The performance of EG28 cellulase from strain RF6188 and EG28+CtCBD preparation from strain RF6377 in depilling of cotton knitwear was tested. The cellulase treatments were performed with Electrolux's Wasca-tor FOM 71 CLS washer extractor under conditions described in Table 9.

Pieces of two kinds of low quality Polo-neck sweaters with fuzzy surface, made of 100% cotton jersey-based fabric or rib made of 95% cotton and 5% of lycra were used as test material with filling material. Samples were first prewashed for 10 min at 60°C with 1 ml/l surfactants/wetting agents (Sandoclean PCJ from Sandos and Imacol CN from Clariant) and rinsed three

times with water. After that the cotton knits were treated with cellulase at 60°C for 60 minutes, in the presence of the same textile auxiliaries as used in pre-wash. The enzyme was inactivated as described in Example 4, except for the temperature, which was 60°C during the alkaline rinse. The pieces of knitwear were rinsed three times and thereafter dried in the dumber.

Table 9. Test conditions/process parameters used in biofinishing treatments.

Process parameter	
Fabric load	1.0 kg
Water	15 liter
Sandoclean PCJ and Imacol CN	1 ml/l
Buffer/pH control (pH 5 -5.3)	ca. 3 ml Acetic acid (80 %)
Time	60 min
Temperature	60°C
Cellulase dosage	1200 ECU/g fabric

The effect of the cellulase treatment was evaluated visually with the naked eye and with a loupe. A prewashed sample without enzyme was used as control.

The results showed that the EG28+CtCBD preparation improved depilling properties. The surface fuzzing of the knitwear was considerably reduced after treatment with the EG28+CtCBD preparation compared to the control (treatment without enzyme). Also the EG28 preparation had a depilling effect.

Example 10. Feed pelleting stability test

Two cellulose preparations, EG28 (strain RF6188) and EG28+CtCBD (strain RF6377) were separately tested in an experiment, which simulates an industrial feed production process. Prior to testing the spray-dried EG28 or EG28+CtCBD preparations were ground with wheat flour in order to improve homogeneity at feed level. EG28 or EG28+CtCBD enzymes premixed with flour were added at a dosage of 200 g/t and at 500 g/t of feed, respectively. Enzyme overdosing was used to facilitate analysis from samples pelleted at high temperatures, where activity may have been substantially reduced.

The mill and mixer are used for producing meal mixtures as part of a semi-industrial feed plant with a nominal pelleting capacity of 5 t/h. The mill is a Champion hammer mill equipped with Ø 3.0 mm die. The ground raw material is mixed in a 2,500 litre horizontal mixer at 27 rpm before being transferred to the mini feed milling plant. The plant comprises a horizontal mixer (volume 700 L, speed 48 rpm, mixing batches of 300 kg), a Skjold TR dozing screw and a Kahl cascade mixer (length 130 cm, diameter 30 cm, speed 155 rpm, equipped with 37 adjustable pallets). The dwell time for 300 kg/h is approx. 30 sec. Mounted on the side of the cascade mixer is a manifold with a water discharger and 3 steam valves from which steam is lead to the meal. Steam is provided by a high-pressure boiler with a maximum capacity of 400 kg steam/h. Tests are conducted with 2 atmospheres overpressure and the steam is led via a pressure reduction valve, which controls the addition of steam to the cascade mixer. Three valves on the manifold are used for fine adjustment of the desired meal temperature. Meal temperature is measured by a digital thermometer placed in the outlet of the cascade mixer, just before the meal entered to pellet die. The pellet press is a Simon Heesen, type labor (monoroll) with a Ø 3 mm * 35 mm die and a 7.5 kW motor. Internal diameter of die: 173 mm, height of press roll: 50 mm, diameter of press roll: 140 mm, run rate 500 rpm and nominal capacity: 300 kg/h. Samples are taken after the pellet press and cooled in a partitioned cooling box with perforated bottom, ventilator: 1500 m³ air/h.

A 300 kg batch of a wheat-based mash feed was produced. A pre-mix was produced from 10 kg of this meal and 200 g (or 500 g) of the test enzyme in a 70 litre compulsory mixer. Mixer speed: 45 rpm. Mixing time: 10 min. This premix was added with 290 kg of the feed into the horizontal mixer in the mini feed milling plant and mixed for 10 minutes. After sampling of the mash, the feed was pelleted through the pellet press (die Ø 3 mm). The meal was heated to the target temperature (65 to 90°C) by adjusting steam addition to the cascade mixer. For each temperature, a sample was first taken 10 minutes after the target pelleting temperature (as measured in the meal just prior to pelleting) was achieved. Samples were taken during 1.0 min. corresponding to 5.0 kg of pelleted feed. The sample was taken as sub-samples of approx. 500 grams and placed in a cooling box for 10-15 seconds after the pellets had left the pellet press. All samples were aerated and cooled at ambient temperature

for 15 minutes. The samples were homogeneously sub-sampled on a riffler sample divider and filled into plastic bags.

The samples were analysed as follows: 2.5 g of well ground sample and 20 ml of acetate buffer (0.05 M, pH 5.0) buffer were stirred for 30 min at room temperature, centrifuged (10 min, 4000 rpm) and diluted. 1.0 ml of cleared sample in triplicate was equilibrated for 5 min in a water bath at 40°C. The reaction was initiated by addition of a Beta-Gluczyme tablet (Megazyme, Ireland) without stirring. After exactly 30 min the reaction was stopped by adding 5.0 ml of Trizma Base 1% (w/v) (Sigma-Aldrich) with vigorous stirring on a vortex mixer. The tube was left at room temperature for about 5 min; the slurry was stirred again and filtered through Whatman™ 1 filter paper. The absorbance of the filtrate was measured at 590 nm. The results were analyzed using a standard curve.

Enzyme activity recoveries before and after pelleting are presented in Table 10. The influence of pelleting temperature on the recovery of the beta-glucanase activity has also been presented in Figures 7 and 8. The EG28 and EG28+CtCBD cellulases were stable up to 80°C. The EG28+CtCBD cellulase tended to be more stable than EG28 at the pelleting temperature of 90°C.

Table 10. Enzyme activity recoveries before (meal from horizontal mixer) and after pelleting at temperatures ranging from 65 to 90°C.

Pelleting temperature	Beta-Glucanase activity (FBU/kg of feed)	
	(EG28)	(EG28+CtCBD)
Meal from horizontal mixer	239 000 ± 9 000 (100%)	1 148 000 ± 48 000 (100%)
Pellet (65°C)	227 000 ± 16 000 (95%)	1 007 000 ± 67 000 (88%)
Pellet (70°C)	217 000 ± 5 000 (91%)	1 012 000 ± 54 000 (88%)
Pellet (75°C)	227 000 ± 14 000 (95%)	993 000 ± 49 000 (86%)
Pellet (80°C)	215 000 ± 6 000 (90%)	1 030 000 ± 87 000 (90%)
Pellet (85°C)	188 000 ± 7 000 (79%)	904 000 ± 56 000 (79%)
Pellet (90°C)	149 000 ± 8 200 (62%)	861 000 ± 32 000 (75%)

List of deposited organisms

Strain	Plasmid contained	Deposition authority	Deposition date	Deposition number
<i>Acremonium thermophilum</i> ALKO4245	-	CBS ⁽¹⁾	Sep 20, 2004	CBS 116240
<i>Thermoascus aurantiacus</i> ALKO4242	-	CBS ⁽¹⁾	Sep 20, 2004	CBS 116239
<i>Chaetomium thermophilum</i> ALKO4265	-	CBS ⁽²⁾	Nov 8, 1995	CBS 730.95
<i>Escherichia coli</i>	pALK1946	DSMZ ⁽³⁾	Apr 7, 2006	DSM 18159
<i>Escherichia coli</i>	pALK1926	DSMZ	May 13, 2005	DSM 17326

⁽¹⁾ the Centraalbureau Voor Schimmelcultures at Uppsalalaan 8, 3584 CT, Utrecht, the Netherlands

⁽²⁾ the Centraalbureau Voor Schimmelcultures at Oosterstraat 1, 3742 SK BAARN, The Netherlands

⁽³⁾ Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (DSMZ), Mascheroder Weg 1 b, D-38124 Braunschweig, Germany

References

Altschul SF, W Gish, W Miller, EW Myers and DJ Lipman. 1990. Basic local alignment search tool. J. Mol. Biol. 215:403-410.

Bailey MJ and KMH Nevalainen 1981. Induction, isolation and testing of stable *Trichoderma reesei* mutants with improved production of solubilizing cellulase. Enz Microbiol Technol. 3: 153-157.

Bendtsen J.D., Nielsen H., von Heijne G. and Brunak S. (2004) Improved prediction of signal peptides: SignalP 3.0. J. Mol. Biol. 340: 783-795.

Gasteiger, E, A Gattiker, C Hoogland, I Ivanyi, RD Appel and A Bairoch. 2003. ExPASy: the proteomics server for in-depth protein knowledge and analysis. Nucleic Acids Res. 31:3784-3788.

Haakana H, A Miettinen-Oinonen, V Joutsjoki, A Mäntylä, P Suominen, and J Vehmaanperä. 2004. Cloning of cellulase genes from *Melanocarpus albomyces* and their efficient expression in *Trichoderma reesei*. Enz Microbiol Technol. 34: 159-167.

Henrissat B. (1991) A classification of glycosyl hydrolases based on amino acid sequence similarities. Biochem. J. 280: 309-316.

Henrissat B. and Bairoch A. (1993) New families in the classification of glycosyl hydrolases based on amino acid sequence similarities. Biochem. J. 293: 781-788.

Henrissat B. and Bairoch A. (1996). Updating the sequence-based classification of glycosyl hydrolases. Biochem. J. 316: 695-696.

Hong J., H. Tamaki, K. Yamamoto, and H. Kumagai. 2003. Cloning of a gene encoding a thermo-stabile endo- β -1,4-glucanase from *Thermoascus aurantiacus* and its expression in yeast. Biotech. Letters 25:657-661.

IUPAC (International Union of Pure and Applied Chemistry) (1987). Measurement of cellulase activities. *Pure and Appl. Chem.* 59:257-268.

Joutsjoki, VV, TK Torkkeli and KMH Nevalainen. 1993. Transformation of *Trichoderma reesei* with the *Hormoconis resinae* glucoamylase P (*gamP*) gene: production of a heterologous glucoamylase by *Trichoderma reesei*. Curr. Genet. 24:223-228.

Karhunen T, A Mäntylä, KMH Nevalainen and PL Suominen. 1993. High frequency one-step gene replacement in *Trichoderma reesei*. I. Endoglucanase I overproduction. Mol. Gen. Genet. 241:515-522.

Malardier L, Daboussi MJ, Julien J, Roussel F, Scazzocchio C and Brygoo Y. 1989. Cloning of the nitrate reductase gene (*niaD*) of *Aspergillus*

nidulans and its use for transformation of *Fusarium oxysporum*. *Gene* 15:147-156.

Needleman S. and Wunsch C. (1970) A general method applicable to the search for similarities in the amino acid sequence of two proteins. *Journal of Molecular Biology* 48, 443-453.

Nielsen H., Engelbrecht J., Brunak S. and von Heijne G. (1997) Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites. *Protein Engineering* 10: 1-6.

Paloheimo M, A Mäntylä, J Kallio, and P Suominen. 2003. High-yield production of a bacterial xylanase in the filamentous fungus *Trichoderma reesei* requires a carrier polypeptide with an intact domain structure. *Appl. Env. Microbiol.* 69:7073-7082.

Penttilä M, H Nevalainen, M Rättö, E Salminen and J Knowles. 1987. A versatile transformation system for the cellulolytic filamentous fungus *Trichoderma reesei*. *Gene* 61:155-164.

Raeder U and P Broda. 1985. Rapid preparation of DNA from filamentous fungi. *Lett. Appl. Microbiol.* 1:17-20.

Rice P, Longden I and Bleasby A. (2000). EMBOSS: The European Molecular Biology Open Software Suite. *Trends in Genetics* 16:276-277.

Sambrook J, EF Fritsch and T Maniatis. 1989. *Molecular cloning, a laboratory manual*. Cold Spring Harbor Laboratory, New York, US.

Sambrook J and DW Russell. 2001. *Molecular cloning, a laboratory manual*. Cold Spring Harbor Laboratory, New York, US.

Srisodsuk M, Reinikainen T, Penttilä M and Teeri T. (1993) Role of the interdomain linker peptide of *Trichoderma reesei* cellobiohydrolase I in its interaction with crystalline cellulose. *J. Biol. Chem.* Oct 5;268(28): 20756-61.

Stålbrand H, Siika-aho M, Tenkanen M and L Viikari. 1993. *J. Biotechnol.* 29:229-242.

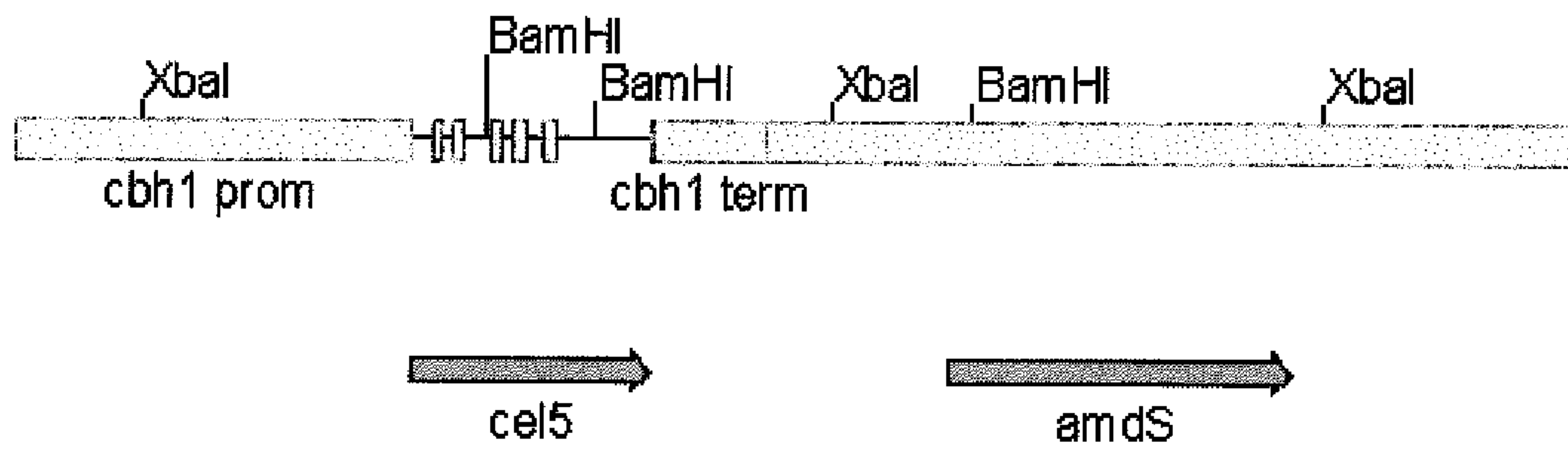
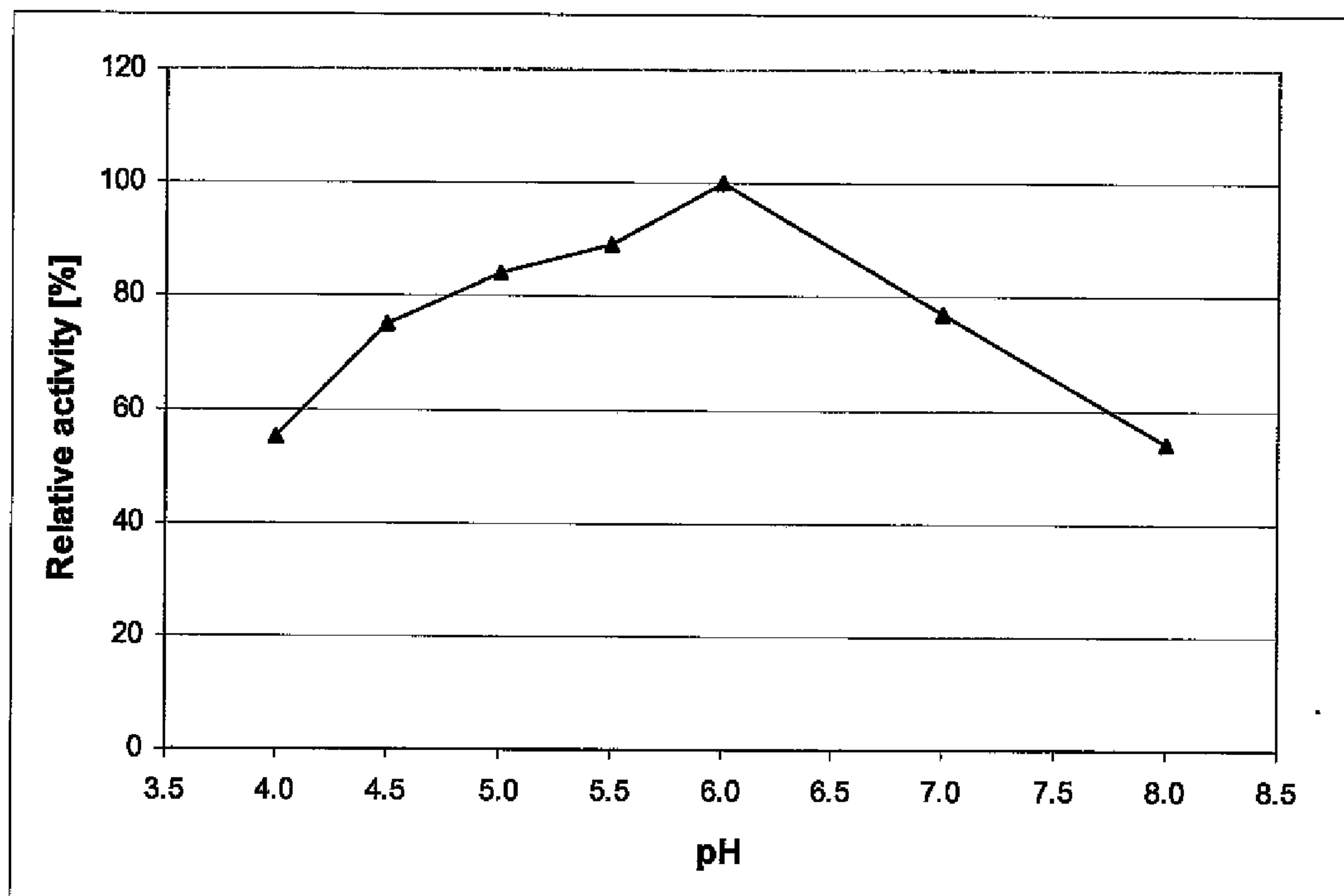
Ward M, Shan W, Dauberman J, Weiss G, Larenas E, Bower B, Rey M, Clarkson K and Bott R. (1993) Cloning, sequence and preliminary structural analysis of a small, high pI endoglucanase (EGIII) from *Trichoderma reesei*. *Proceedings of the second TRICEL symposium on TRICHODERMA REESEI CELLULASES AND OTHER HYDROLASES*, Espoo, Finland, 1993, ed. by P. Suominen and T. Reinikainen. *Foundation for Biotechnical and Industrial Fermentation Research* 8 (1993): 153-158.

Claims

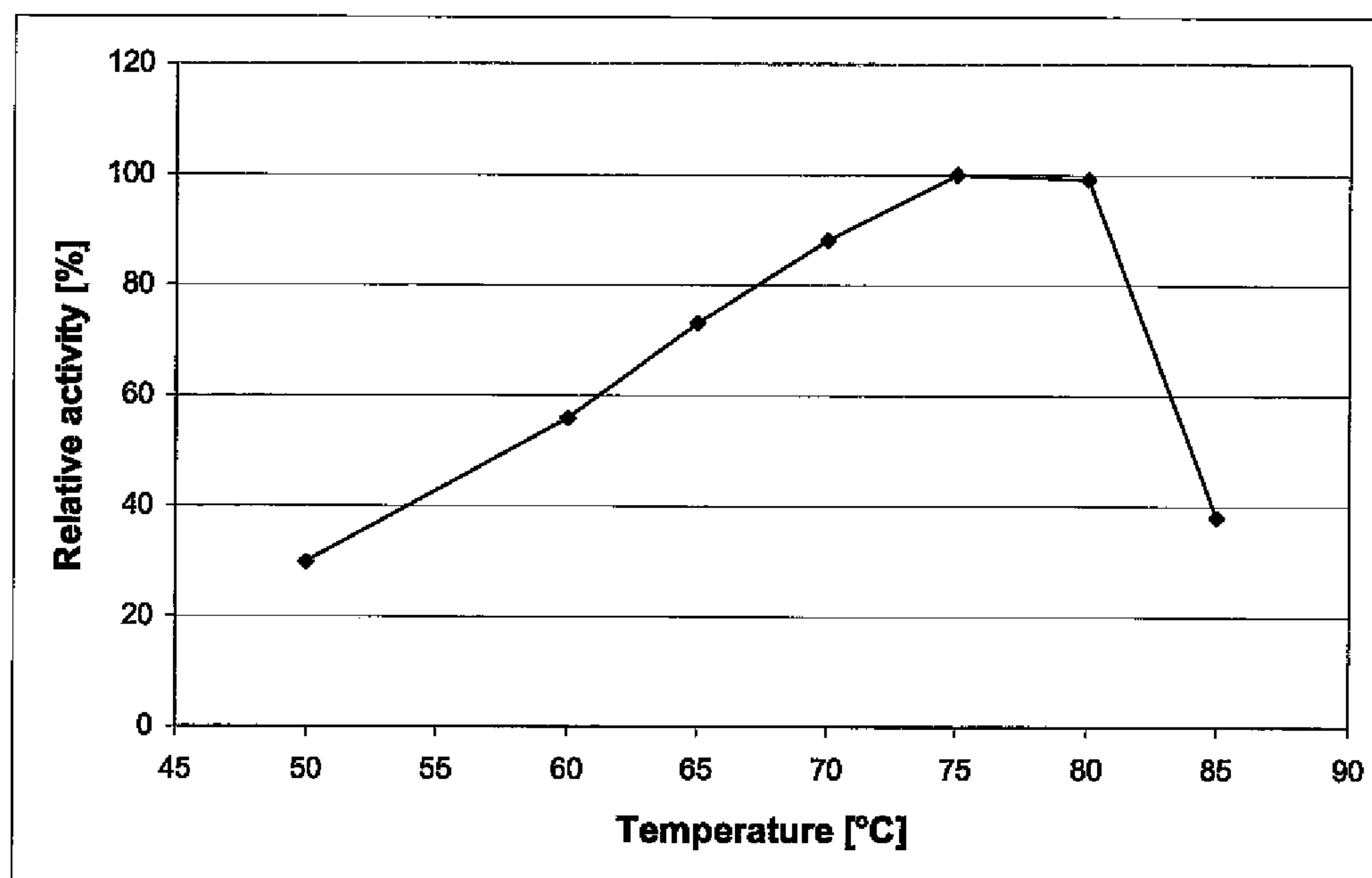
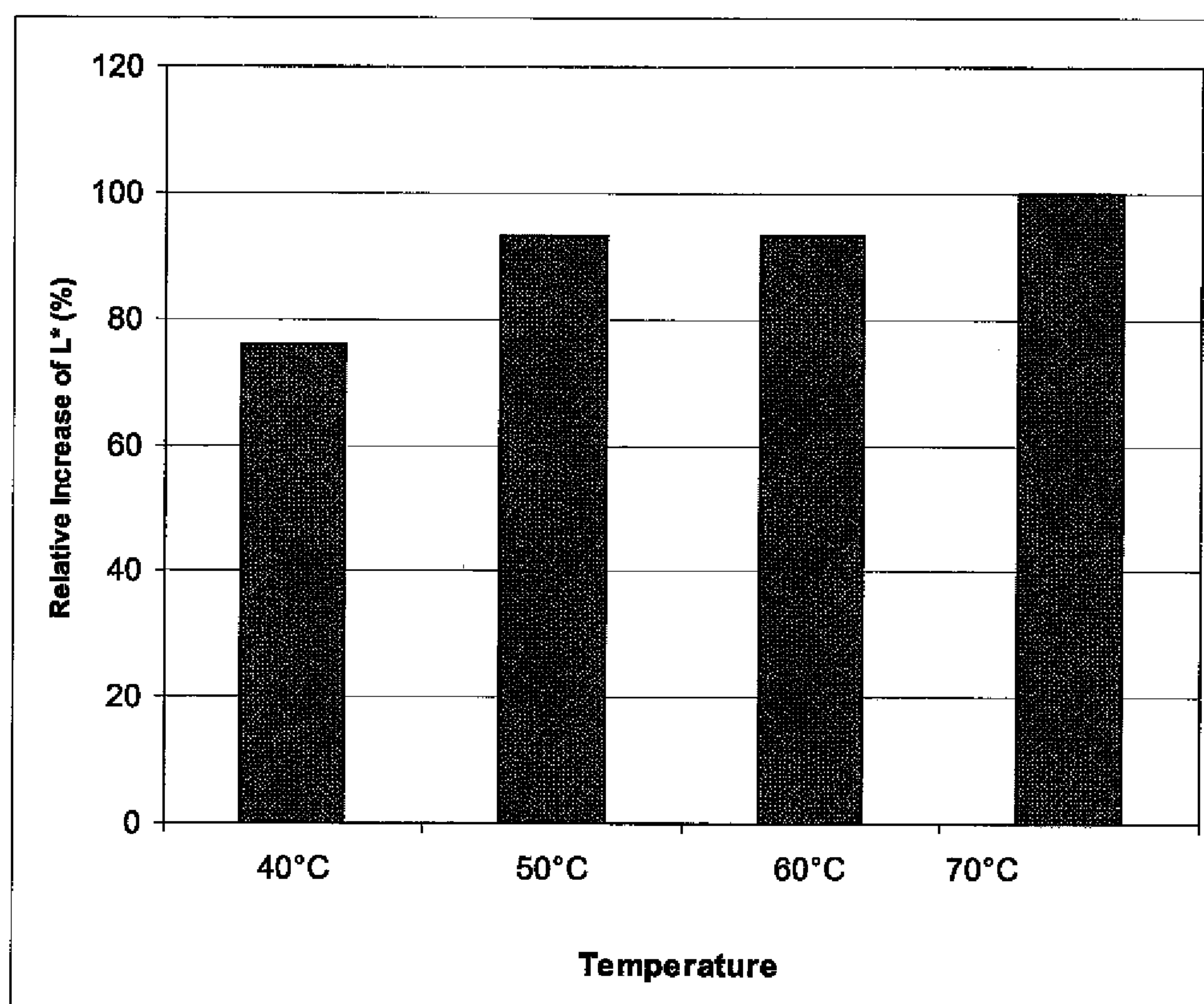
1. A cellulase fusion protein comprising a first amino acid sequence of an endoglucanase core having at least 75% identity to SEQ ID NO:2, a mature part thereof corresponding to amino acids 19 to 334 of SEQ ID NO:2, or a fragment of SEQ ID NO:2 having cellulase activity, and a second amino acid sequence comprising a linker and cellulose binding domain (CBD) having at least 75% identity to SEQ ID NO: 15, or a fragment of SEQ ID NO:15 having cellulose binding activity.
2. The fusion protein of claim 1, wherein the endoglucanase belongs to glycosyl hydrolase family 5.
3. The fusion protein of claim 1 or 2, wherein the endoglucanase core is from *Thermoascus aurantiacus*.
4. The fusion protein of claim 3, wherein the *Thermoascus aurantiacus* is *T. aurantiacus* CBS 116239.
5. The fusion protein of claim 4, wherein the endoglucanase core consists of amino acids 19 to 334 of SEQ ID NO: 2.
6. The fusion protein of claim 1, wherein the linker and CBD are from cellobiohydrolase of *Chaetomium thermophilum*.
7. The fusion protein of claim 6, wherein the *Chaetomium thermophilum* is *C. thermophilum* CBS 730.95.
8. The fusion protein of claim 1, wherein the endoglucanase core comprises the sequence of SEQ ID NO: 2, and the linker and CBD comprise the sequence of SEQ ID NO: 15.
9. The fusion protein of claim 1 comprising the amino acid sequence of SEQ ID NO: 4, or a fragment thereof having cellulase and cellulose binding activity.
10. The fusion protein of claim 1, wherein the endoglucanase core is encoded by a gene identical to that included in *E. coli* DSM 17326.
11. The fusion protein of claim 1, which is encoded by a fusion gene identical to that included in *E. coli* DSM 18159.
12. An isolated polynucleotide selected from the group consisting of:
 - a) the nucleotide sequence of SEQ ID NO: 3 , or a sequence encoding a cellulase fusion protein of claim 1, and
 - b) a complementary strand of a).
13. The polynucleotide of claim 12, which comprises a fusion gene identical to that included in strain *E. coli* DSM 18159.

14. An expression vector comprising the polynucleotide of claim 12.
15. A host cell comprising the expression vector of claim 14.
16. The host cell of claim 15, which is a fungus.
- 5 17. The host cell of claim 16, wherein the fungus is of the genus *Trichoderma*.
18. A method of producing a fusion protein of any one of claims 1 - 11, comprising the steps of transforming a host cell with an expression vector encoding said fusion protein and culturing said host cell under conditions
- 10 enabling expression of said fusion protein, and optionally recovering and purifying the fusion protein produced.
19. An enzyme preparation comprising the fusion protein of any one of claims 1 - 11, and an additive or culture medium components.
20. A process for treating cellulosic material, wherein said process
- 15 comprises contacting the cellulosic material with the fusion protein of any one of claims 1 - 11, or the enzyme preparation of claim 19.
21. The process of claim 20, wherein the cellulosic material is textile material, plants used in animal feed, or wood-derived pulp or secondary fiber.
22. The process of claim 20, wherein the cellulosic material is plant
- 20 material for oil extraction.
23. A process for biostoning, which process comprises the step of contacting a cellulase fusion protein of any one of claims 1 to 11, or an enzyme preparation of claim 19 with denim fabric or garments.
24. A process for biofinishing, which comprises the step of contact-
- 25 ing a cellulase fusion protein of any one of claims 1 to 11 or the enzyme preparation of claim 19 with textile materials.
25. The process of claim 24, wherein the textile material is fabrics or garments or yarn.
26. A detergent composition comprising the fusion protein of any
- 30 one of claims 1 to 11 and detergent auxiliaries.
27. Animal feed comprising the fusion protein of any one of claims 1 to 11.
28. An *Escherichia coli* strain having accession number DSM 18159.

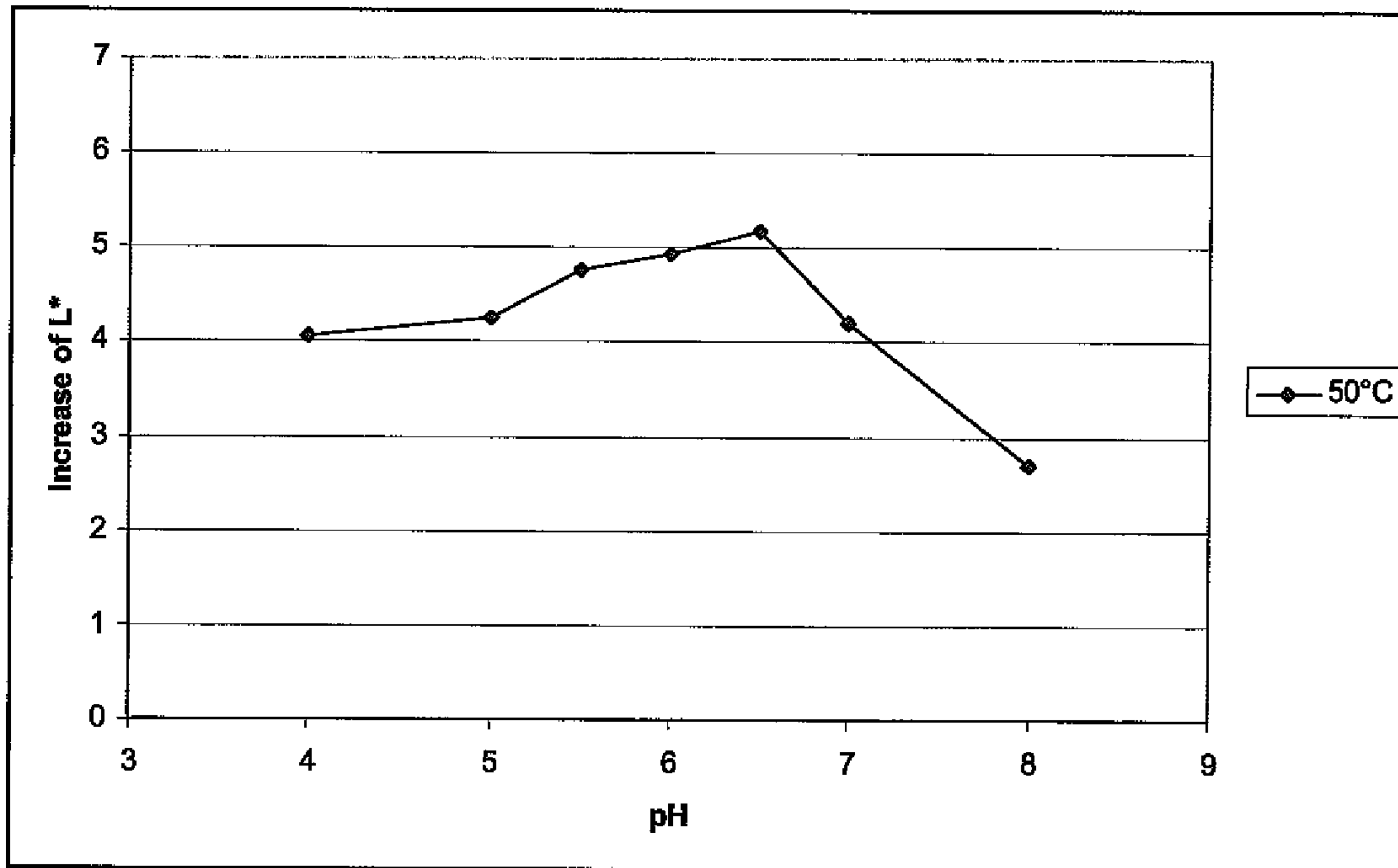
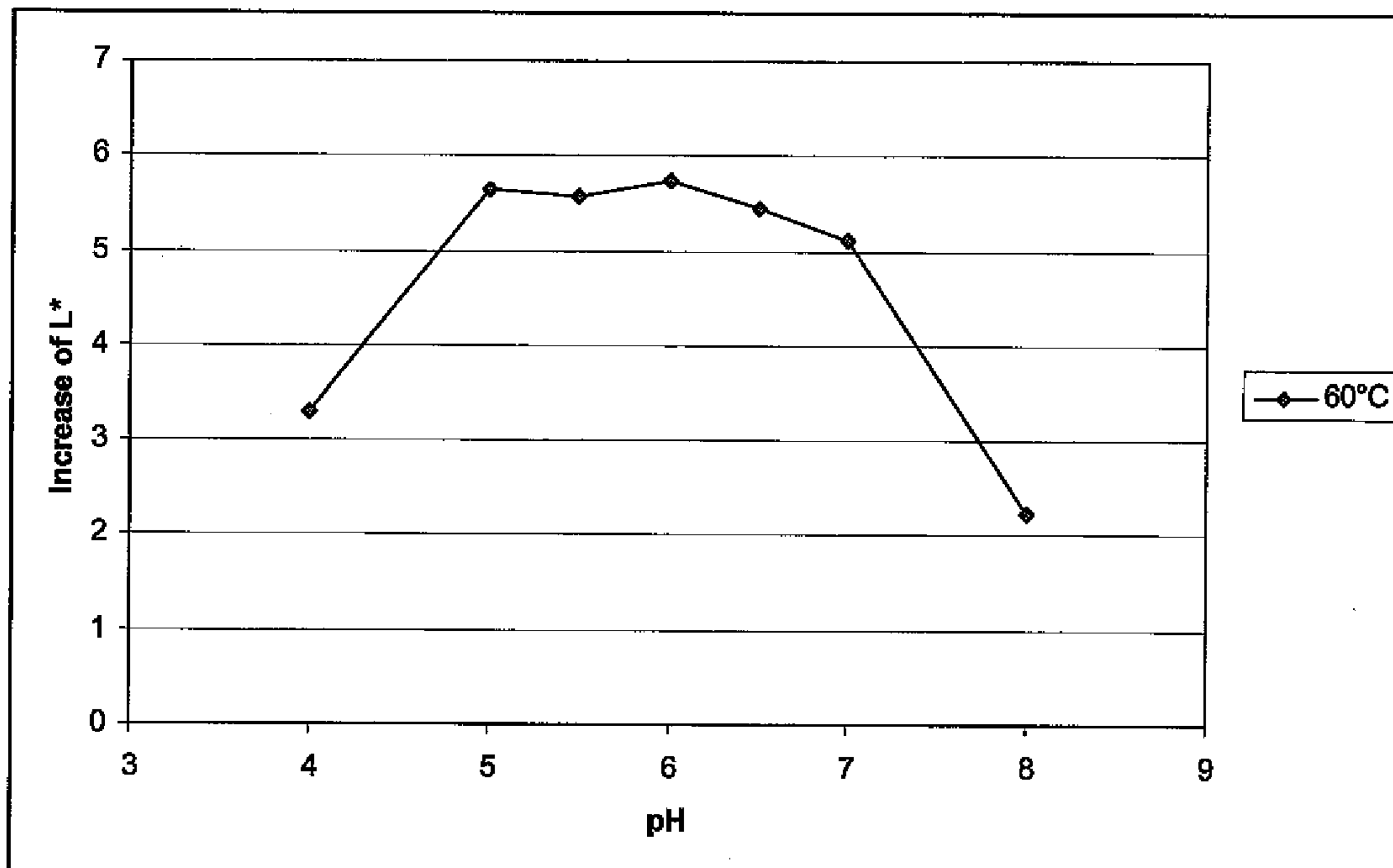
1/5

Figure 1**Figure 2 (A)**

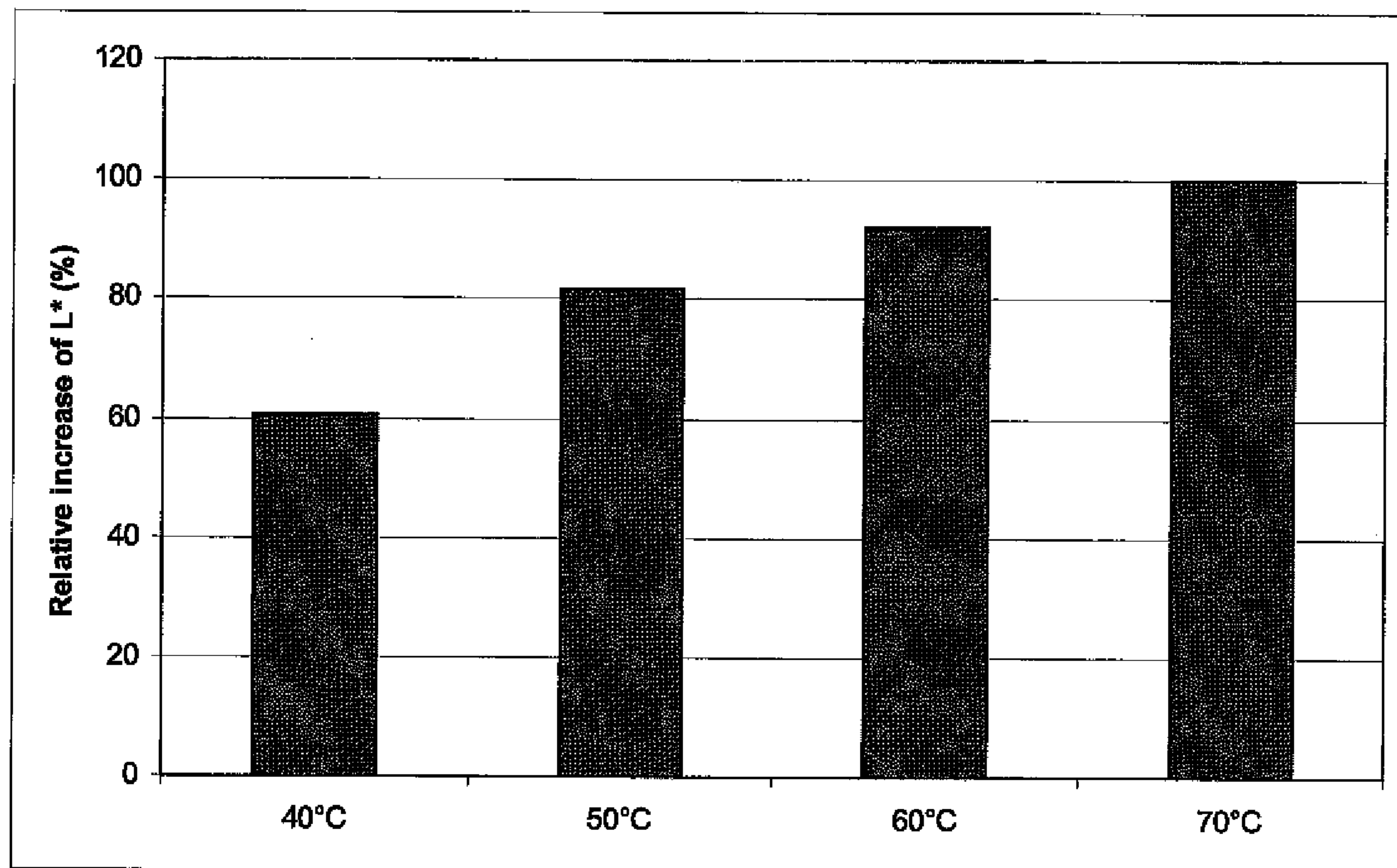
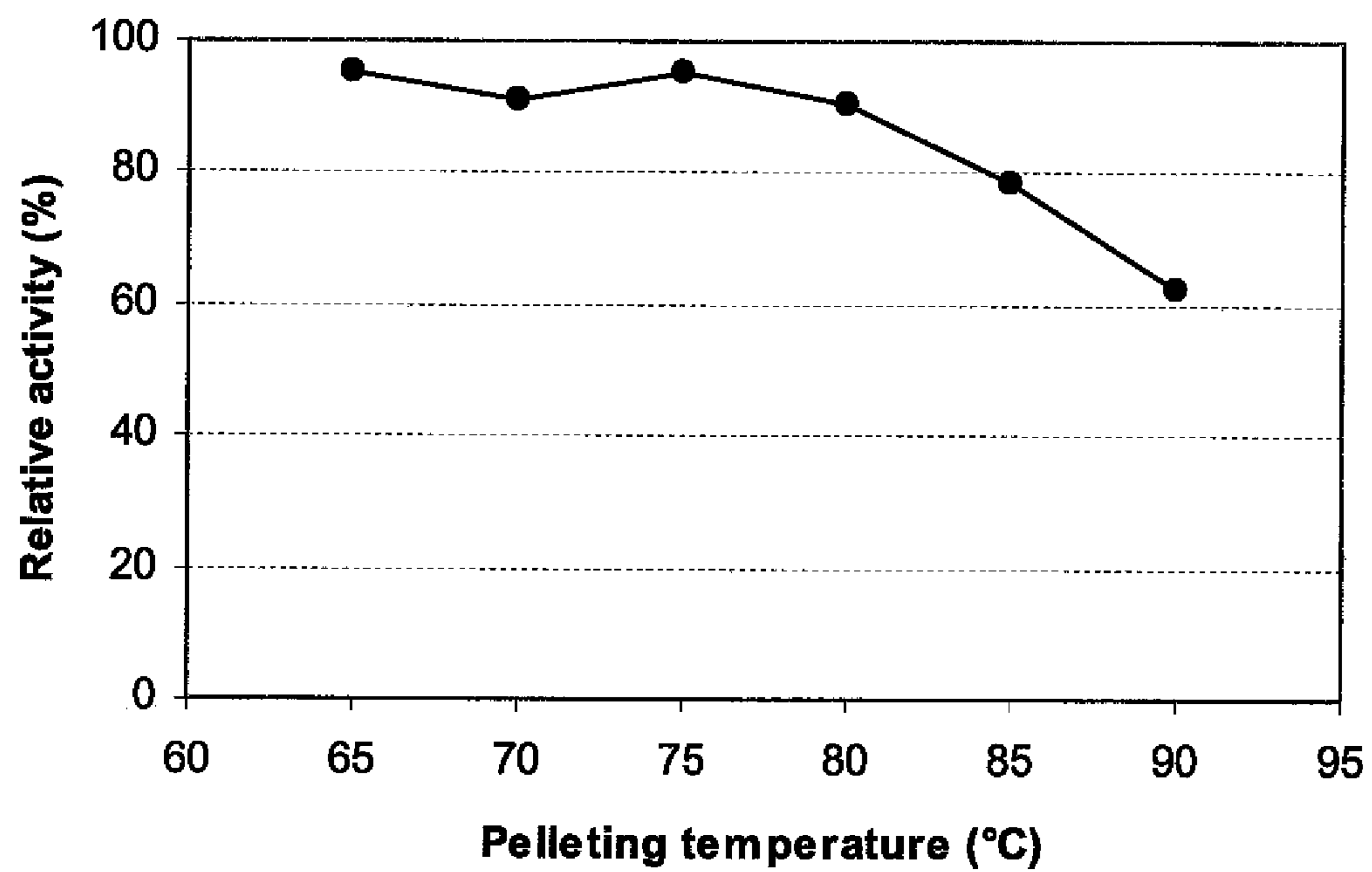
2/5

Figure 2 (B)**Figure 3**

3/5

Figure 4**Figure 5**

4/5

Figure 6**Figure 7**

5/5

Figure 8