



Cold-active beta-galactosidase, a method of producing same and use of such enzyme

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(12) **United States Patent**
Stougaard et al.(10) **Patent No.:** **US 8,288,143 B2**
(45) **Date of Patent:** **Oct. 16, 2012**(54) **COLD-ACTIVE BETA-GALACTOSIDASE, A METHOD OF PRODUCING SAME AND USE OF SUCH ENZYME**(75) Inventors: **Peter Stougaard**, Kirke Hyllinge (DK);
Mariane Schmidt, Frederiksberg (DK)(73) Assignee: **Kobenhavns Universitet**, Copenhagen (DK)

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(51) **Int. Cl.****C07K 1/00** (2006.01)**C12N 9/38** (2006.01)**C07H 21/04** (2006.01)**C12N 15/00** (2006.01)**C12N 1/20** (2006.01)(52) **U.S. Cl.** **435/207**; 435/252.3; 435/320.1;
530/350; 536/23.2(58) **Field of Classification Search** 435/252.3,
435/320.1, 207; 530/350; 536/23.2
See application file for complete search history.(56) **References Cited**FOREIGN PATENT DOCUMENTS
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Primary Examiner — Maryam Monshipouri(74) *Attorney, Agent, or Firm* — Merchant & Gould P.C.(57) **ABSTRACT**

A novel cold-active beta-galactosidase is enzyme specific for lactose. The enzyme is thus useful in e.g. the food industry for catalyzing at low temperatures the hydrolysis of lactose disaccharide into its constituent monosaccharides, glucose and galactose. A method produces the cold-active beta-galactosidase by recombinant DNA technology.

23 Claims, 17 Drawing Sheets

Figure 1

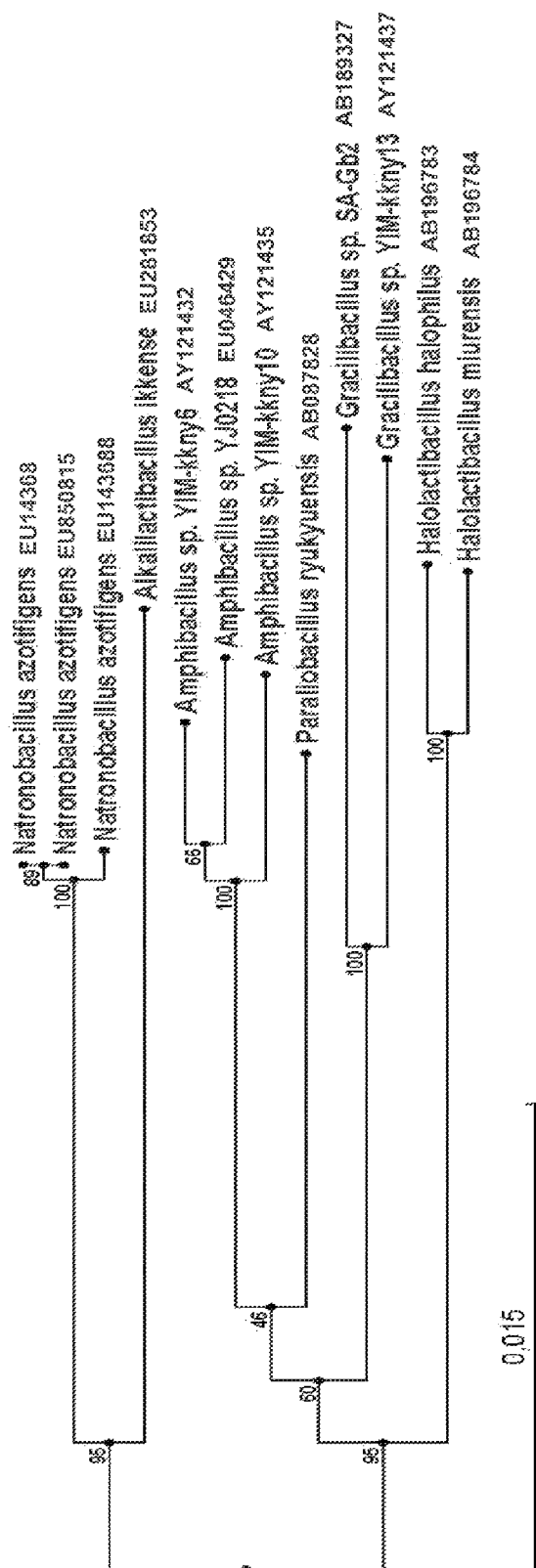


Figure 2

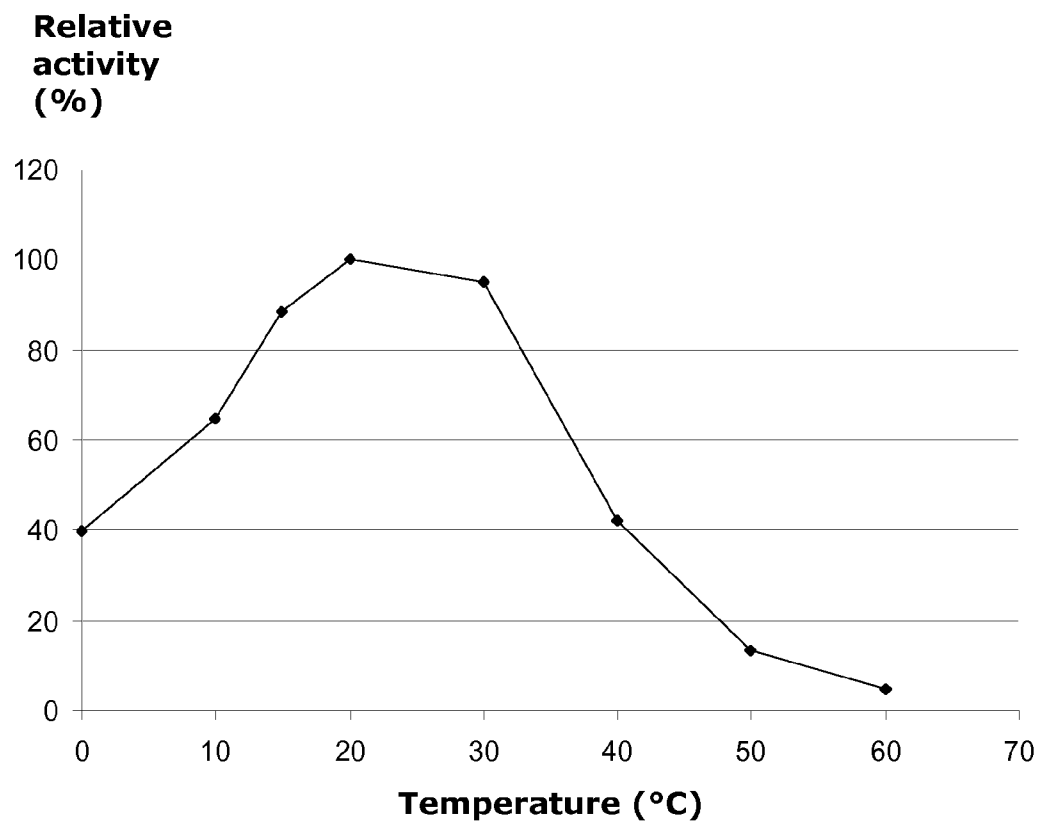


Figure 3

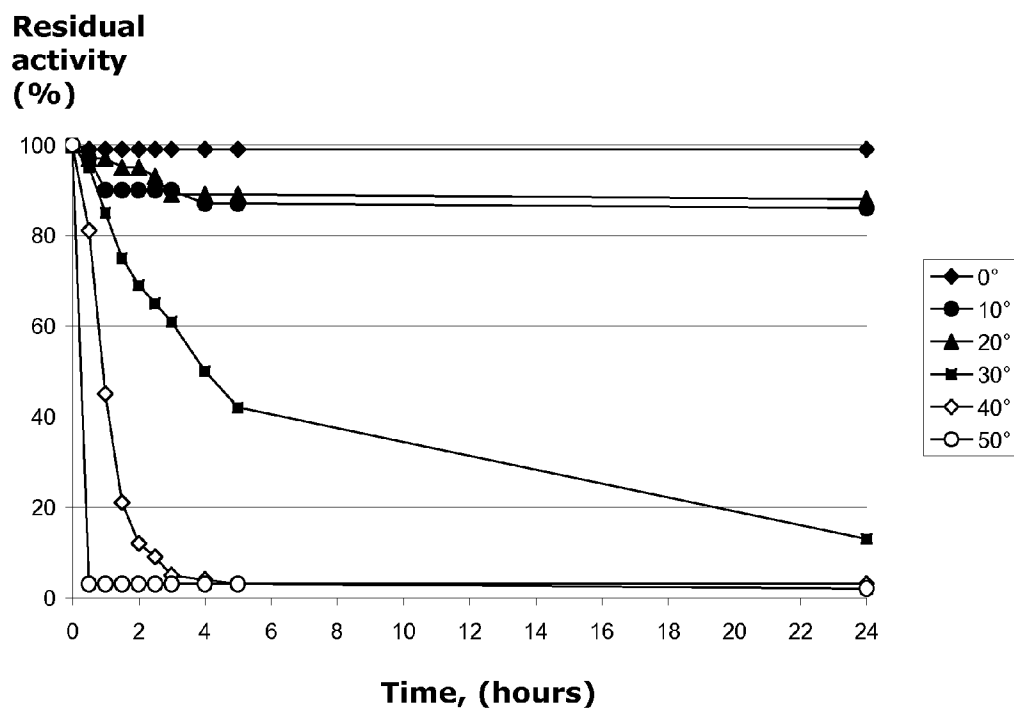


Figure 4

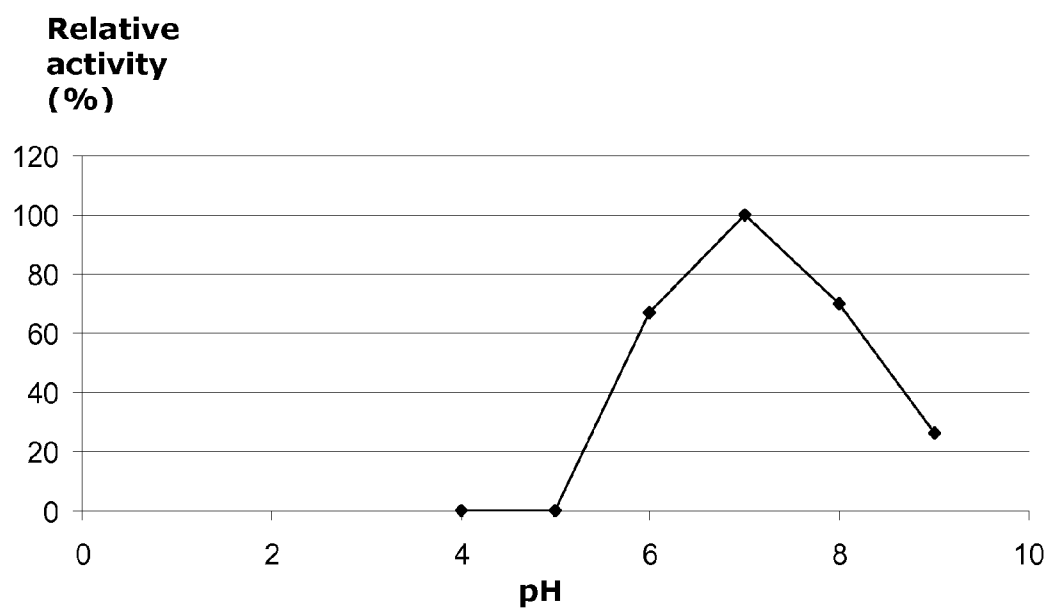


Figure 5

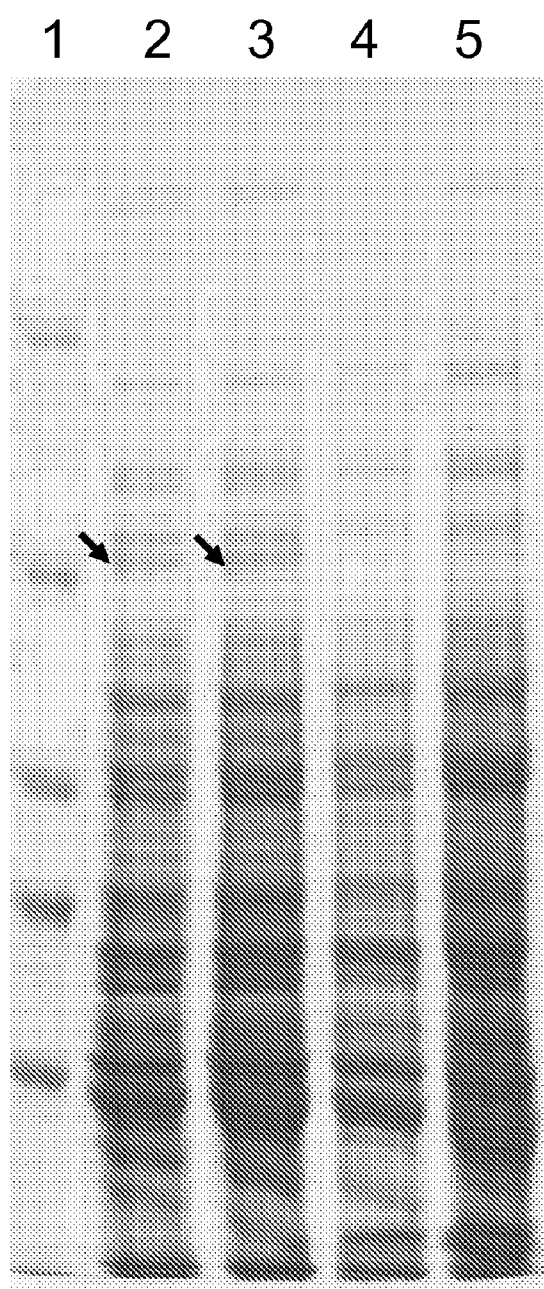


Figure 6

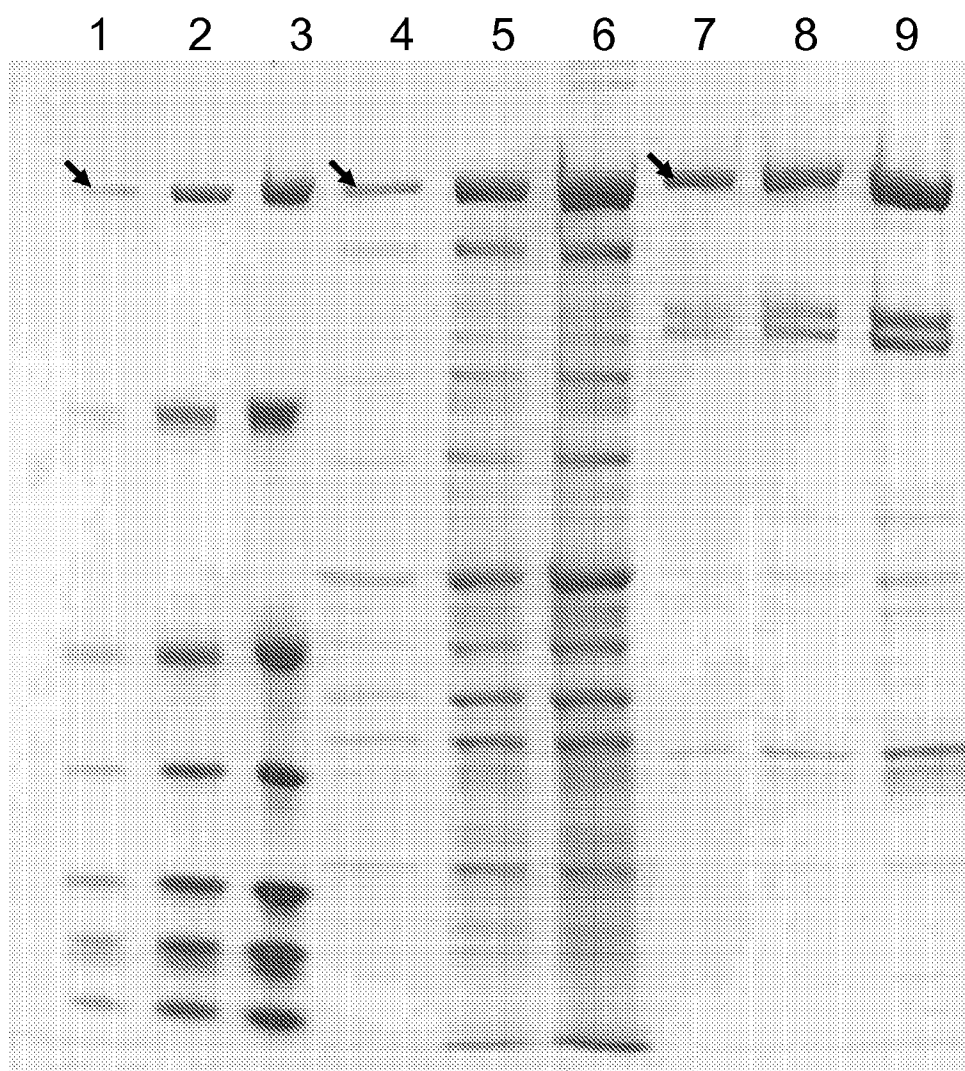


Figure 7

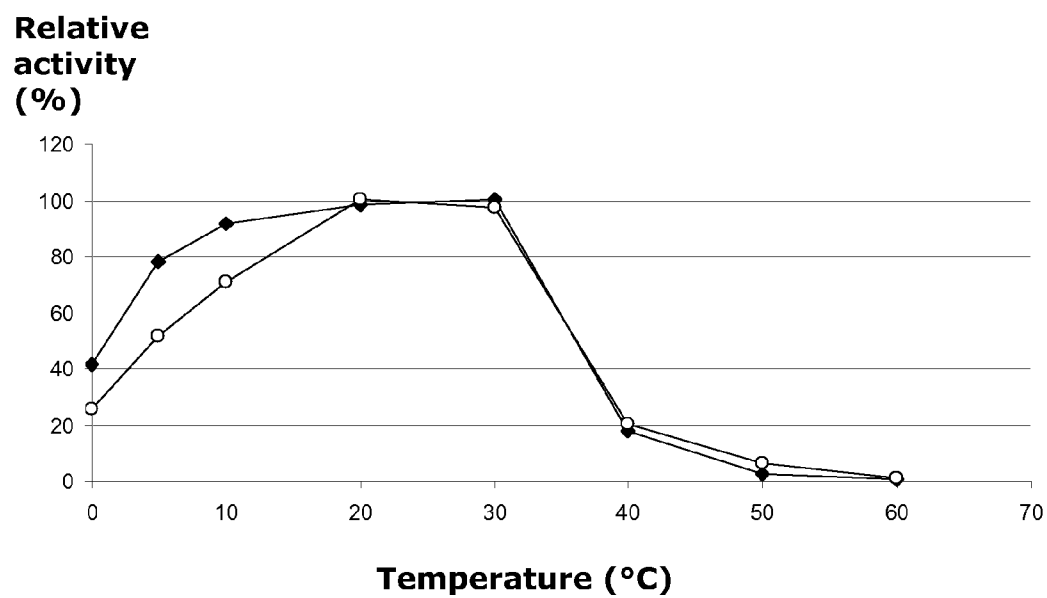


Figure 8

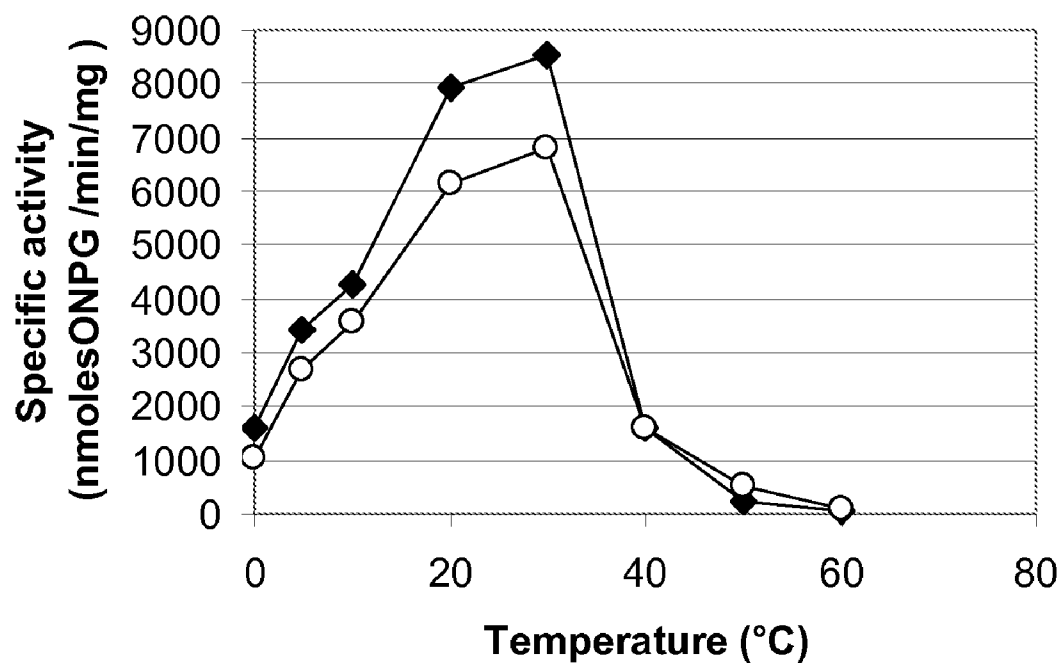


Figure 9

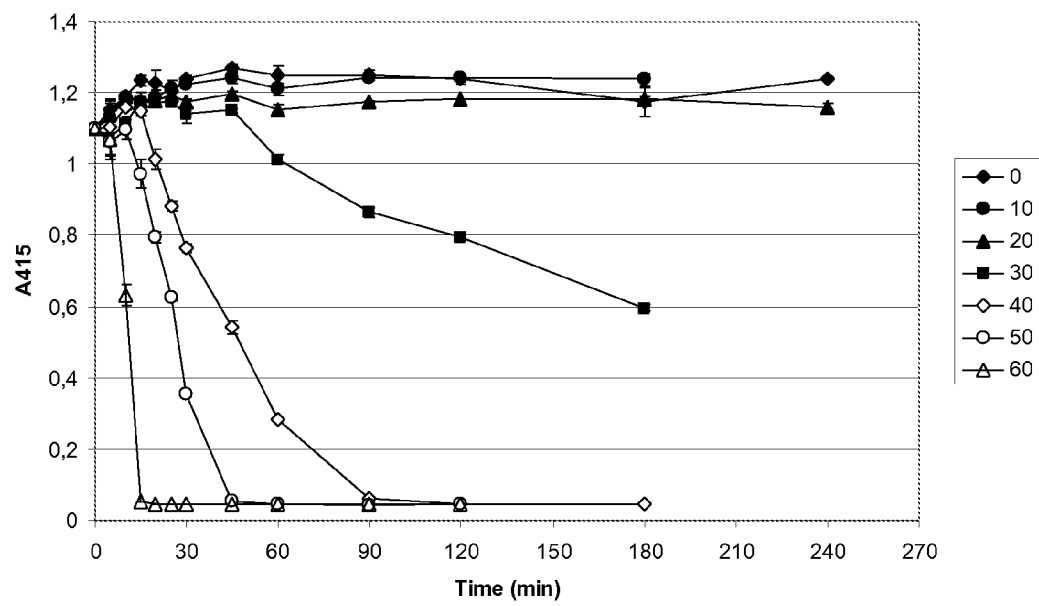


Figure 10

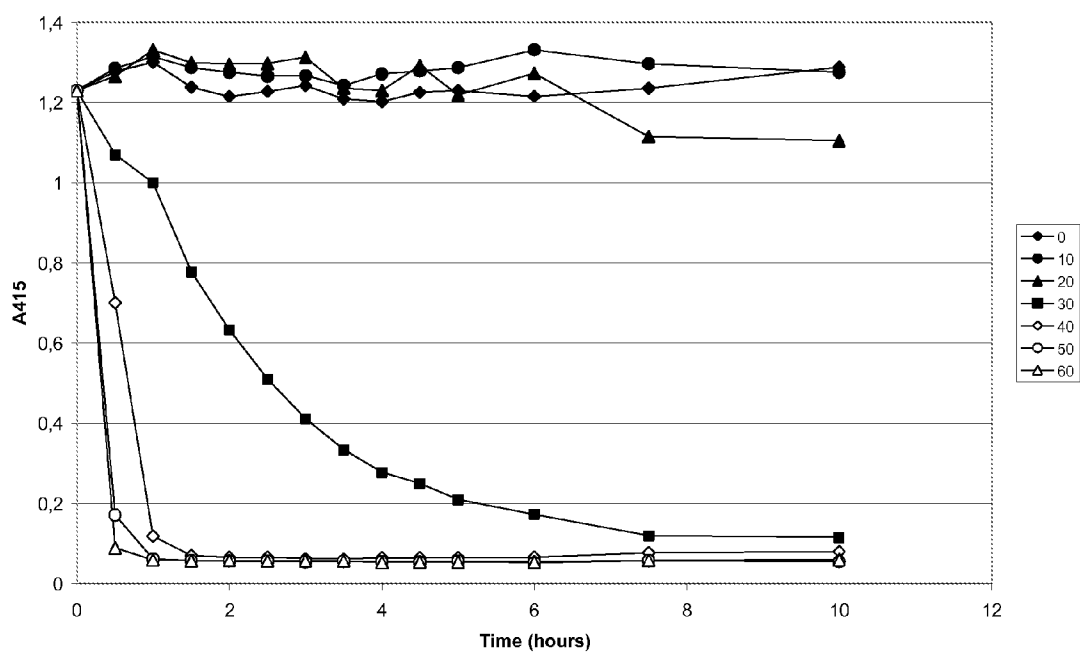


Figure 11

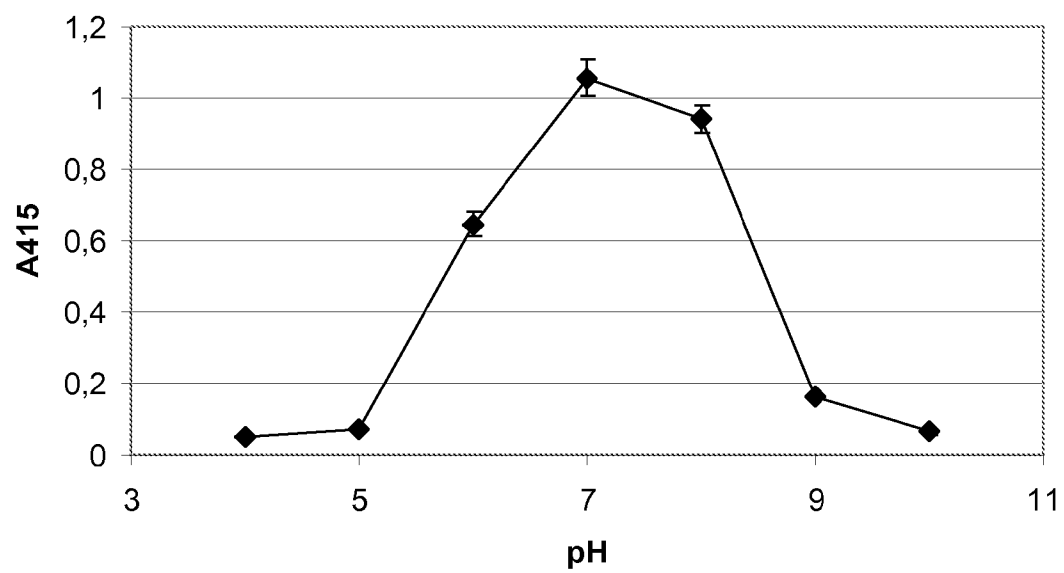


Figure 12

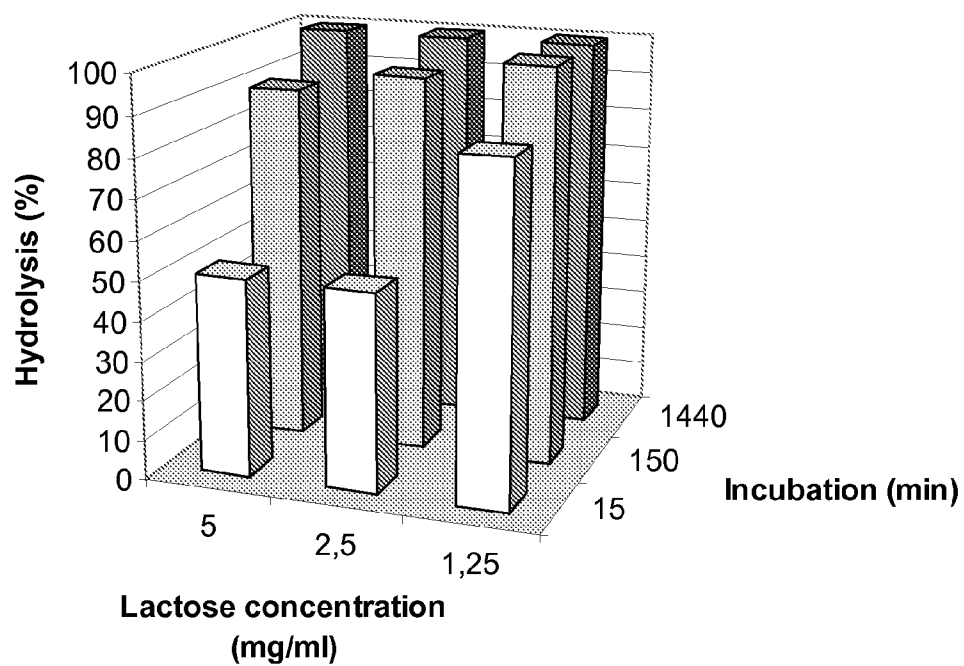
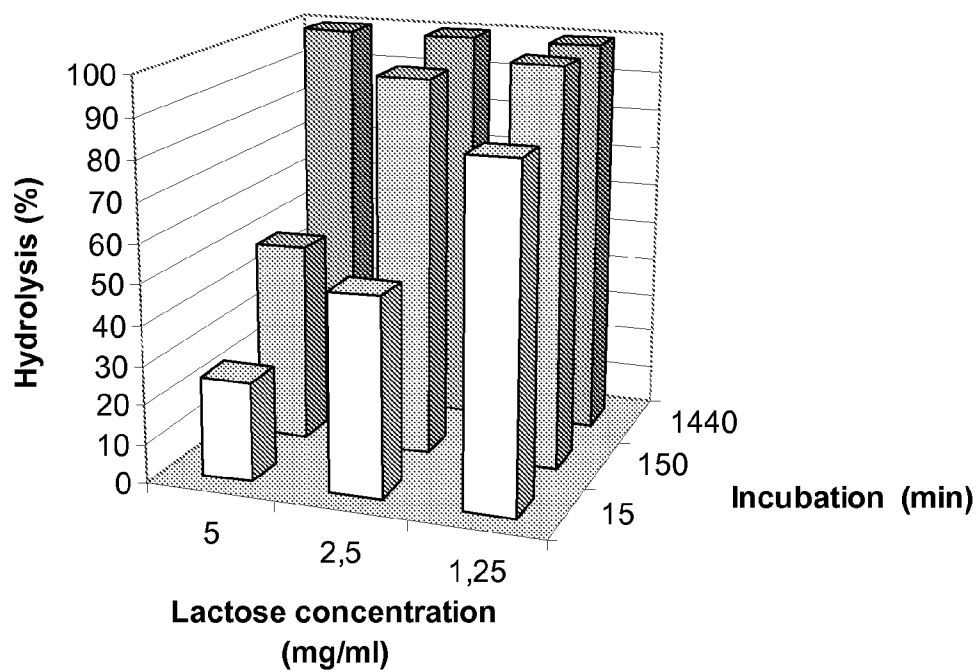


Figure 13

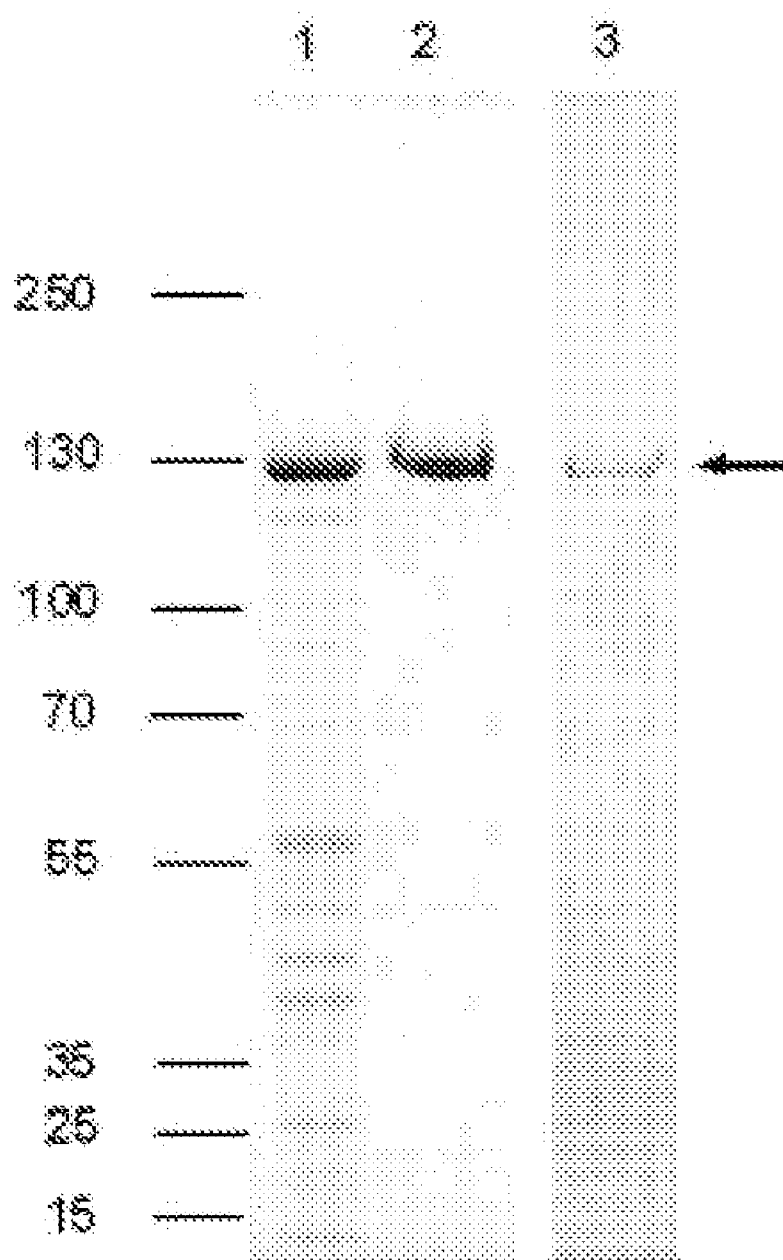


Figure 14

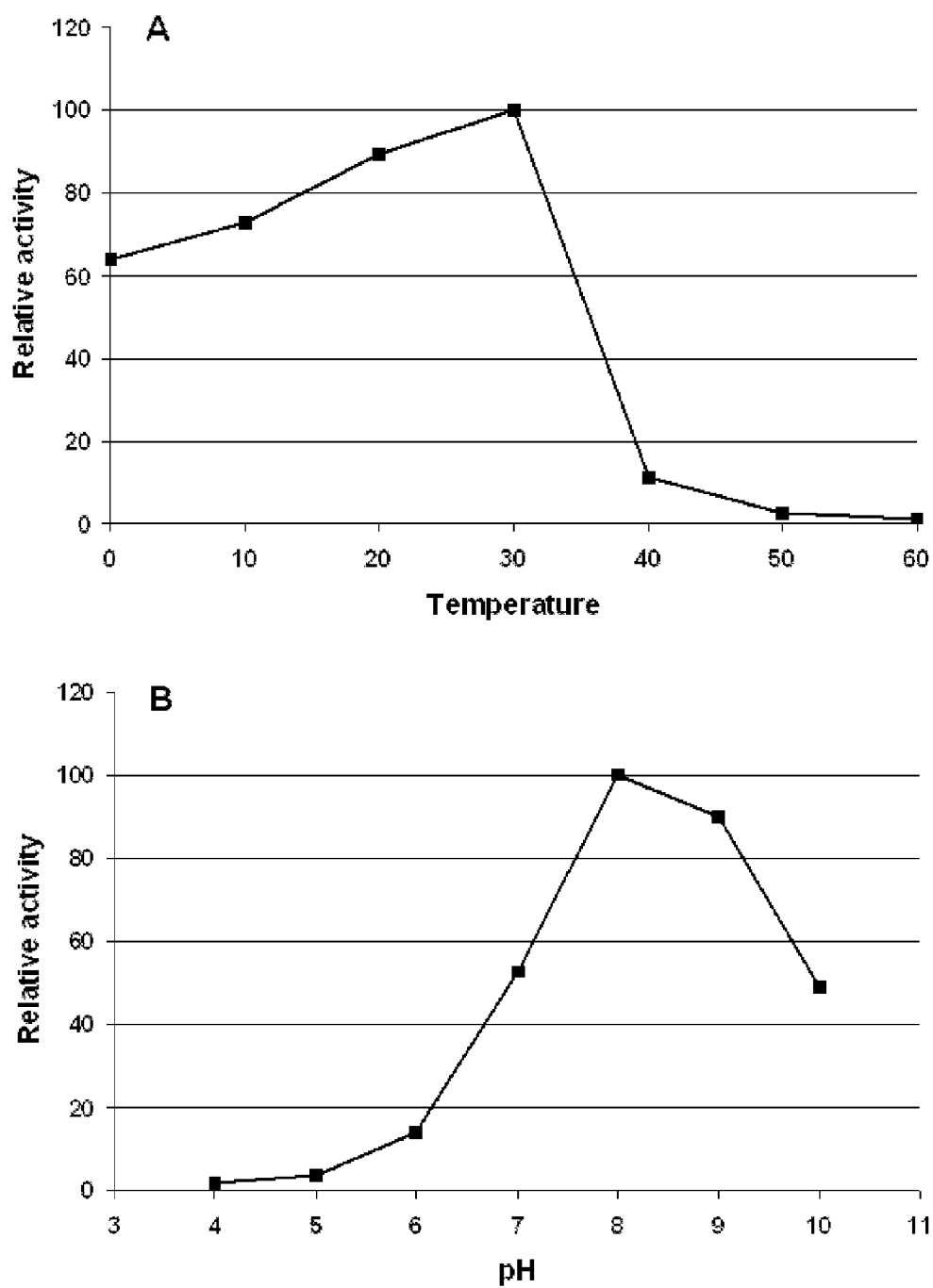


Figure 15

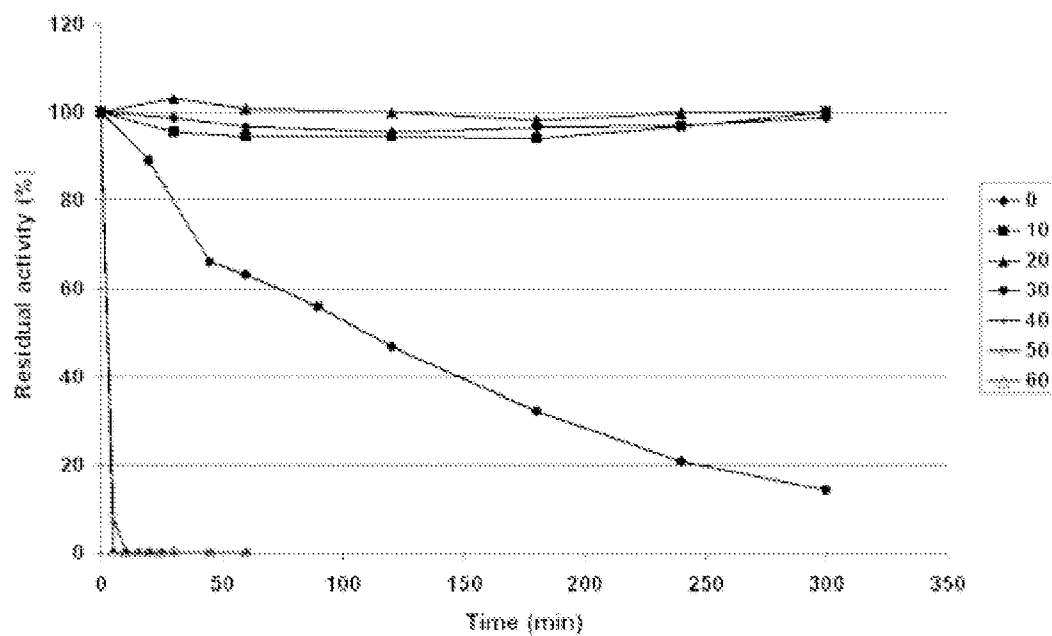


Figure 16

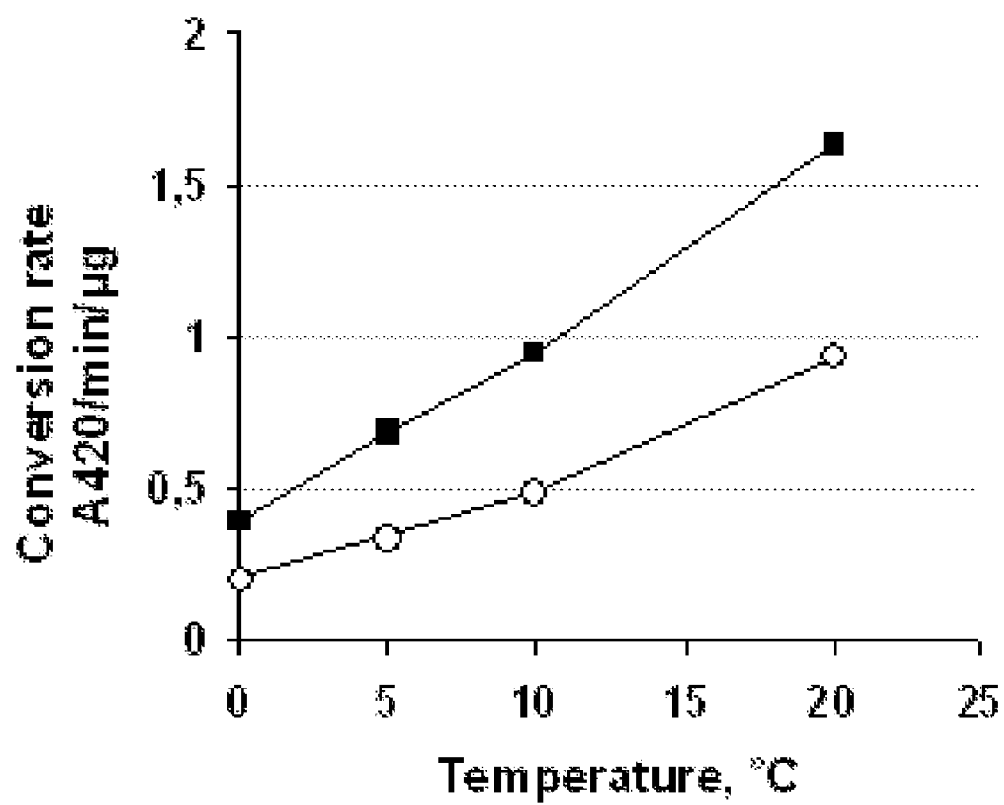
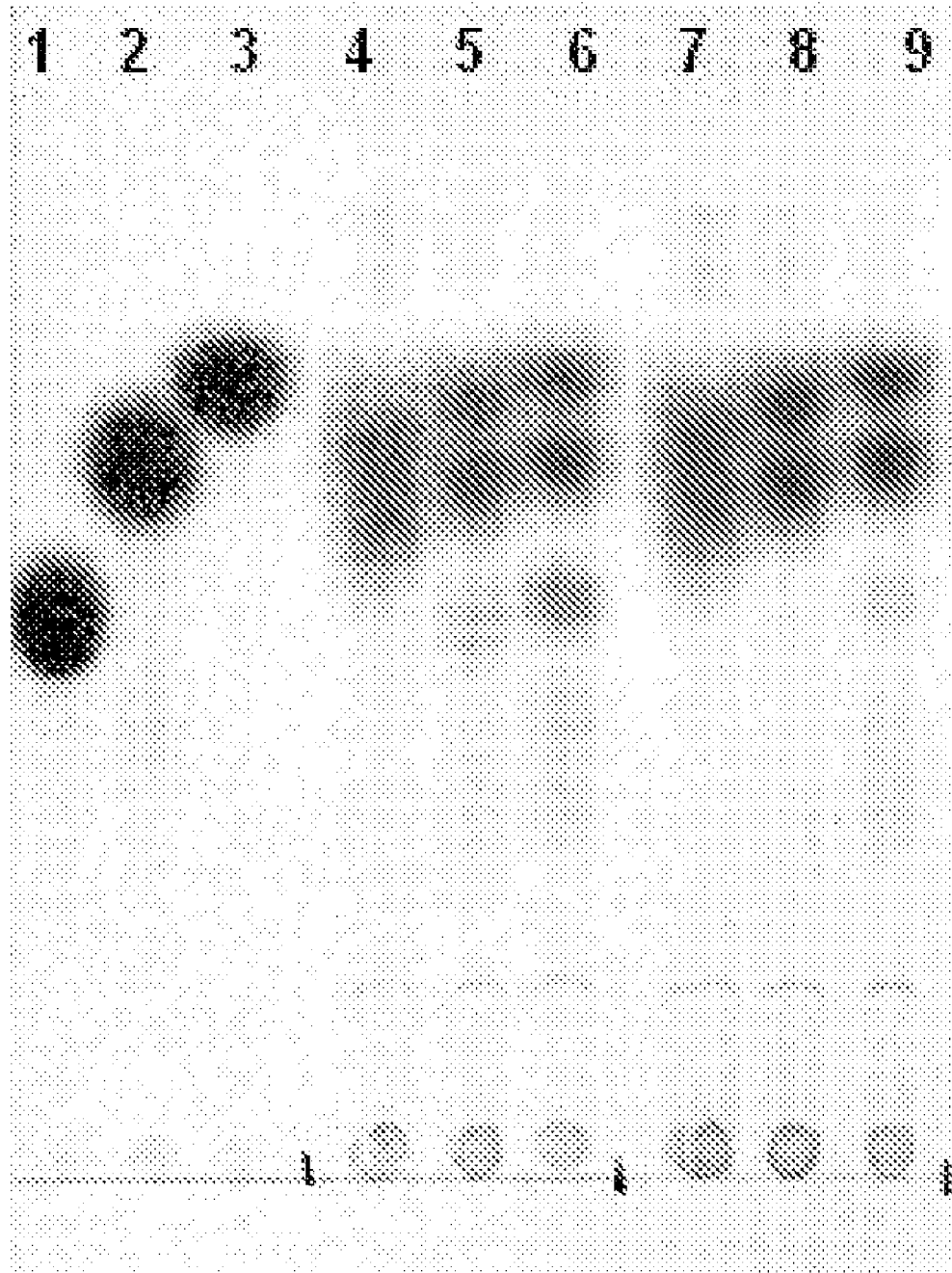


Figure 17



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COLD-ACTIVE BETA-GALACTOSIDASE, A METHOD OF PRODUCING SAME AND USE OF SUCH ENZYME

This application is a National Stage Application of PCT/EP2010/051596, filed 9 Feb. 2010, which claims benefit of Ser. No. 61/176,956, filed 11 May 2009 in the United States, and which also claims benefit of Ser. No. 61/151,208, filed 10 Feb. 2009 in the United States, and which applications are incorporated herein by reference. To the extent appropriate, a claim of priority is made to each of the above disclosed applications.

FIELD OF THE INVENTION

The present invention relates to a novel cold-active beta-galactosidase enzyme specific for lactose. The enzyme is thus useful in e.g. the food industry for catalyzing at low temperatures the hydrolysis of lactose disaccharide into its constituent monosaccharides, glucose and galactose. The present invention further provides a method of producing the cold-active beta-galactosidase by recombinant DNA technology.

BACKGROUND OF THE INVENTION

Beta-galactosidase (beta-D-galactoside galactohydrolase, EC 3.2.1.23) is an enzyme capable of hydrolyzing the disaccharide lactose to its monosaccharide constituents, D-glucose and D-galactose. Beta-galactosidases are found in a large variety of organisms, like mammals, plants, fungi, yeasts, and bacteria. In Nature, beta-galactosidases hydrolyze lactose and other D-galactose-containing carbohydrates. In the industry, beta-galactosidases have been used primarily within the food industry. Beta-galactosidase hydrolysis of lactose and lactose-containing dairy products are used throughout in the dairy industry in the preparation of lactose-free or low-lactose products, which may be consumed by humans suffering from lactose intolerance. Hydrolysis of lactose by beta-galactosidases may also be used in applications where the removal of lactose is required, i.e. prevention of crystallisation of lactose in food and removal of D-galactose moieties in glycosylated proteins. Other applications of beta-galactosidases comprise hydrolysis of lactose into D-galactose and D-glucose with the subsequent modification of the monosaccharides to high value products, like the sweetener D-tagatose (Jorgensen et al. 2004).

Application of beta-galactosidases could be used to produce lactose-free and low-lactose dairy products for lactose intolerant humans.

The major applications for lactose hydrolysis are listed below.

- a) Liquid milk. Lactose hydrolysis in liquid milk improves digestibility for lactose intolerant consumers. In flavoured milks, lactose hydrolysis increases sweetness and enhances flavours.
- b) Milk powders. Lactose hydrolysed milk powders for dietetic uses, especially for infants with temporary beta-galactosidase deficiency.
- c) Fermented milk products. In some cases, lactose hydrolysis in milk used for the manufacture of cheese and yoghurt can increase the rate of acid development and thus reduce processing time.
- d) Concentrated milk products. Lactose hydrolysis in concentrated milk products (e.g. sweetened condensed milk, ice cream) prevents crystallisation of lactose.

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- e) Whey for animal feed. Lactose hydrolysis in whey enables more whey solids to be fed to pigs and cattle and also prevents crystallisation in whey concentrate.
- f) Whey. Lactose hydrolysed whey is concentrated to produce a syrup containing 70-75 percent solids. This syrup provides a source of functional whey protein and sweet carbohydrate and is used as a food ingredient in ice cream, bakery and confectionery products.

The conventional approach in food processing is to carry out the hydrolysis of lactose at 40° C. during approximately four hours.

However, milk or lactose solution as a raw material is a preferable nutrition source for bacteria. As the result, the putrefaction owing to the saprophyte contamination during the treatment is a serious problem in the food production. Thus, the fact is that the conventional beta-galactosidase is of limited use.

Most beta-galactosidases in practical use are active only at temperatures above 20-30° C., temperatures where food spoiling bacteria thrive at best.

Attempts to use thermophilic beta-galactosidases have been used but the products have suffered from off flavours and reduced organoleptic properties due to the heat treatment, and the processes have demanded high energetic costs.

A number of cold-active beta-galactosidases have been described from *Arthrobacter* (Coker, et al. 2003; Karasová-Lipová, et al. 2003; Nakagawa et al. 2003; Nakagawa et al. 2006), from *Carnobacterium piscicola* (Coombs and Brenchley, 1999) and from *Pseudoalteromonas* (Cieslinski, et al. 2005; Fernandes, et al. 2002; Hoyoux, et al. 2001; Turkiewicz, et al. 2003). Furthermore, Nakagawa et al. (2006) described a cold-active beta-galactosidase from the yeast *Guehomyces pullulans*. However, the activity of cold-active beta-galactosidases described so far is low at the low temperatures, which is wanted by the dairy industry. The beta-galactosidase from the yeast *Guehomyces pullulans* had approximately 17% at 0° C. (Nakagawa et al. 2005), the beta-galactosidases from *Carnobacterium piscicola* BA showed approximately 24% activity at 10° C. (Coombs and Brenchley, 1999) and the enzymes from *Pseudoalteromonas* isolates showed 39% activity (Fernandes et al. 2002), 22% activity (Cieslinski et al. 2005), and 12% activity (Hoyoux et al. 2001) at 10° C. So far, the beta-galactosidases with highest activity at low temperatures have been isolated from Antarctic *Arthrobacter* isolates. Karasová-Lipová, et al. (2003) showed that a psychrotolerant *Arthrobacter* sp. C2-2 isolate produced beta-galactosidase, which displayed 19% of its maximal activity at 10° C., Coker et al. (2003) described an enzyme from an Antarctic *Arthrobacter* isolate with approximately 50% at 0° C., and Nakagawa et al. (2003, 2006) described a beta-galactosidase from *A. psychrolactophilus* F2, which had its temperature optimum at 10° C.

However, the cold-active beta-galactosidase from the Antarctic *Arthrobacter* was produced in low amounts in native cells and attempts to produce the enzyme recombinantly in *E. coli* were unsuccessful since about 90% of the enzyme was located in insoluble inclusion bodies (Coker et al. 2003). The cold-active beta-galactosidase from *A. psychrolactophilus* F2 could be produced heterologously, but had lower activity than the other *Arthrobacter* beta-galactosidases (Nakagawa et al. 2006).

Therefore, in order to develop a low-temperature process for hydrolysis of lactose there is a need for a novel cold-active beta-galactosidase and a method for producing such enzyme.

SUMMARY OF THE INVENTION

The present invention has, by using recombinant DNA technology, for the first time made it possible to provide a

cold-active beta-galactosidase with high specific activity in industrially appropriate quantities for the manufacturing of food products and pharmaceuticals.

Accordingly, the present invention provides a purified cold-active beta-galactosidase, specific for lactose, having a stable enzymatic activity at temperatures less than 8° C., and specifically at 4° C., which corresponds to refrigerating conservation temperature for dairy products. The enzyme of the present invention is consequently able to hydrolyse lactose in dairy products and milk processing at such a low temperature that saprophytes are hindered to proliferate. The hydrolysis of lactose can be carried out in these refrigeration conditions with no need of a particular treatment to the dairy product concerned.

Specifically, the present invention provides a cold active beta-galactosidase having the sequence as defined in SEQ ID NO. 1, or one having at least 80% homology to the amino acid sequence as defined in SEQ ID NO. 1, the amino acid sequence being selected so that the enzyme has a stable enzymatic activity at temperatures less than 8° C. Preferably the amino acid sequence has at least 90%, and more preferably 95%, homology to the amino acid sequence as defined in SEQ ID NO. 1.

In order to obtain the cold-active beta-galactosidase of the present invention there is further provided a DNA sequence, which

- a) encodes a protein with an amino acid sequence as given in SEQ ID NO. 1, or
- b) hybridises under stringent or very stringent conditions to the sequence of a), or
- c) is degenerative of the sequence of a) or b)

Preferably the DNA sequence is derived from the genus *Alkalilactibacillus*, such as the species *Alkalilactibacillus ikkense*, and has a nucleotide sequence as given in SEQ ID NO. 2.

In a further embodiment, the present invention provides a recombinant vector comprising a DNA sequence that encodes a protein with an amino acid sequence as given in SEQ ID NO. 1, or one having at least 80% homology to the amino acid sequence as defined in SEQ ID NO. 1, the amino acid sequence being selected so that the enzyme has a stable enzymatic activity at temperatures less than 8° C. Preferably the amino acid sequence has at least 90%, and more preferably 95%, homology to the amino acid sequence as defined in SEQ ID NO. 1.

Another object of the present invention is a strain of an isolated *Alkalilactibacillus* bacterium capable of producing a cold-active beta-galactosidase according to the present invention. A preferable strain is *Alkalilactibacillus ikkense* deposited on the 3rd of Mar., 2009, under the Budapest Treaty at the BCCM/LMG-Collection (Belgian Coordinated Collections of Microorganisms) with the Accession No LMG P-24866 and variants and mutants derived therefrom.

To purify the cold-active beta-galactosidase according to the present invention, a bacterium living in the Greenland area was isolated and characterised in order to study how its enzymes, and particularly, the beta-galactosidase was adapted to cold. These studies led to the purification of the beta-galactosidase, meaning that this protein was obtained substantially free of other proteins using protein purification steps known in the art.

Thus, another object of the present invention is a strain of an isolated *Alkalilactibacillus* bacterium capable of producing a cold-active beta-galactosidase according to the present invention. A preferable strain is *alkalilactibacillus ikkense*.

Another object of the invention is a recombinant plasmid or vector suited for transformation of a host, capable of directing

the expression of a DNA sequence according to the invention in such a manner that the host expresses the cold-active beta-galactosidase of the present invention in recoverable form.

According to the invention, another object is the so transformed host. A variety of host-expression systems may be conceived to express the cold-active beta-galactosidase coding sequence, for example bacteria, yeast, insect cells, plant cells, mammalian cells, etc. Particularly, in yeast and in bacteria, a number of vectors containing constitutive or inducible promoters may be used.

It is also an object of the present invention to provide a process for purifying the cold-active beta-galactosidase according to the present invention from a bacterium as well as to provide a process for producing cold-active beta-galactosidase according to the invention in a transformed host.

Accordingly, the invention pertains to a method of producing a polypeptide having cold-active beta-galactosidase activity, comprising isolating a DNA fragment encoding the polypeptide, inserting said DNA fragment into an appropriate host organism, cultivating the host organism under conditions, which lead to expression of the a polypeptide with cold-active beta-galactosidase activity and recovering said polypeptide from the cultivation medium or the host organism.

An appropriate host organism is preferably selected from the group consisting of *Escherichia*, *Bacillus*, *Bifidobacterium*, *Lactococcus*, *Lactobacillus*, *Streptomyces*, *Leuconostoc*, *Streptomyces*, *Saccharomyces*, *Kluyveromyces*, *Candida*, *Torula*, *Torulopsis* and *Aspergillus*.

In a further aspect, the invention relates to a recombinant DNA molecule comprising a DNA fragment encoding a polypeptide having cold-active beta-galactosidase activity and to a microbial cell comprising such recombinant DNA molecule.

In another aspect, the invention pertains to the use of the above polypeptide with cold-active beta-galactosidase activity or a microbial cell expressing such polypeptide in the manufacturing of a food product or a pharmaceutical product.

In another useful aspect, there is provided a method for reducing the lactose content of a food product, comprising adding to the food product an amount of the polypeptide or the microbial cell as disclosed herein, which is sufficient to remove at least part of the lactose present in said food product.

In a practical aspect, the invention pertains to the inactivation of the beta-galactosidase activity of the polypeptide by a moderate increase of the temperature.

In a further interesting aspect, there is provided a method using the polypeptide harbouring a cold-active beta-galactosidase activity or a microbial cell according to the invention in the hydrolysis of lactose, whereby the polypeptide and/or the microbial cell is applied to a reactor containing lactose, which is hydrolyzed under low-temperature conditions.

These and other objects of the present invention will be apparent from the following disclosure.

Other characteristics of the present invention are listed in the annexed claims.

BRIEF DESCRIPTION OF THE FIGURES

FIG. 1 discloses a phylogenetic tree of 16S rRNA gene sequences from *Alkalilactibacillus ikkense* strain 517 and its closest relatives within the rRNA group 1 in the phyletic assemblage classically defined as the genus *Bacillus*. Bootstrap (n=100) values are shown. Bar, 0.015 substitutions per nucleotide position.

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FIG. 2 shows temperature dependence of native Ikka-beta-galactosidase. Y-axis is the relative activity in percent of the maximal activity. X-axis is the incubation temperature.

FIG. 3 shows temperature stability of native Ikka-beta-galactosidase. Y-axis is the residual activity left after incubation at the time indicated on the X-axis. ♦, ●, ▲, ■, ◇, ○, indicate incubation temperatures at 0, 10, 20, 30, 40, and 50° C., respectively.

FIG. 4 discloses pH dependence of native Ikka-beta-galactosidase. Y-axis is the relative activity in percent of the maximal activity. X-axis is pH in the beta-galactosidase assay.

FIG. 5 shows SDS-PAGE of extracts from native *A. ikkense* cells induced with 1 mM IPTG (lanes 2 and 3) and from uninduced, native *A. ikkense* (lanes 4 and 5). Arrows in lanes 2 and 3 indicate the 120 kDa beta-galactosidase band. Lane 1 is molecular weight marker. The marker at 120 kDa is beta-galactosidase from *E. coli*.

FIG. 6 shows SDS-PAGE of three extract dilutions from recombinant *E. coli* cells expressing Ikka-beta-galactosidase (lanes 4, 5, and 6). For comparison, enzyme extract dilutions with beta-galactosidase from *Kluyveromyces lactis* (lanes 7, 8, and 9) and a molecular weight marker with native *E. coli* beta-galactosidase (marker at 120 kDa) were co-electrophoresed with the recombinant Ikka-beta-galactosidase. Arrows show the position of the 120 kDa beta-galactosidase bands

FIG. 7 discloses temperature dependence of recombinant Ikka-beta-galactosidase produced in *E. coli*. Y-axis is the relative activity in percent of the maximal activity. X-axis is the incubation temperature. ♦, indicate recombinant Ikka-beta-galactosidase; ○, indicate *Kluyveromyces lactis* beta-galactosidase.

FIG. 8 shows specific activity of recombinant Ikka-beta-galactosidase produced in *E. coli*. Y-axis is specific activity in nmoles ONP released/hour/mg enzyme. X-axis is temperature in ° C. ♦ is recombinant Ikka-beta-galactosidase, ○ is *Kluyveromyces lactis* beta-galactosidase.

FIG. 9 discloses thermal stability of recombinant Ikka-beta-galactosidase enzyme. An equal amount of enzyme was incubated at the temperature indicated and samples were withdrawn at different time intervals. Y-axis is absorbancy at wavelength 415 nm. X-axis is time in minutes.

FIG. 10 also discloses thermal stability of recombinant Ikka-beta-galactosidase enzyme, while the X-axis is time in hours.

FIG. 11 shows pH dependence of recombinant Ikka-beta-galactosidase. Y-axis is absorbancy measured at wavelength 415. X-axis is pH in the beta-galactosidase assay.

FIG. 12 shows hydrolysis of lactose by recombinant Ikka-beta-galactosidase produced in *E. coli*. The reaction mixture contained lactose in three concentrations, 1.25 mg/ml, 2.5 mg/ml and 5 mg/ml. Samples were withdrawn after incubation for 15, 150, and 1440 minutes. The reactions were incubated at 5° C. (A) or 20° C. (B) and analysed by thin layer chromatography (TLC). The TLC plates were sprayed with an orcinol reagent, and hydrolysis of lactose was estimated by the disappearance of the lactose spots on TLC plates and the concomitant appearance of glucose and galactose spots.

FIG. 13 shows SDS polyacrylamide gel electrophoresis of crude extract of *E. coli* cells expressing *A. ikkense* beta-galactosidase, Lane 1. The beta-galactosidase in the crude extract was further purified on ion exchange chromatography, Lane 2, or on affinity chromatography, Lane 3. The arrow indicates the position of the *E. coli* 120 kDa beta-galactosidase band. Numbers to the left indicate the position of protein bands in the PageRuler™ Plus Prestained Protein Ladder (Fermentas).

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FIG. 14 shows temperature dependence (A) and pH dependence (B) of the purified, recombinant *A. ikkense* beta-galactosidase and of a crude extract containing recombinant enzyme. Y-axis is the relative activity in percent of maximal activity. X-axis is the incubation temperature (A) or pH (B). The relative activity of the purified, recombinant enzyme with ONPG as substrate is illustrated by black squares. Assays were performed in triplicates, and standard error was below 0.05.

FIG. 15 shows thermal stability of the purified, recombinant *A. ikkense* beta-galactosidase enzyme. An equal amount of enzyme was incubated at the temperatures indicated and samples were withdrawn at different time intervals. Y-axis is the residual activity in percent of maximal activity. Enzyme samples were incubated at temperatures from 0° C. to 60° C. and at the time points indicated (X-axis), samples were withdrawn and assayed for active beta-galactosidase at 20° C. Assays were performed in triplicates, and standard error was below 0.05.

FIG. 16 shows benchmarking the *A. ikkense* beta-galactosidase (black squares) with commercially available Lactozyme® 3 3000 L from *K. lactis* (open circles). An equal amount of enzyme (2 mg/ml) was incubated with ONPG as substrate at temperatures from 0° C. to 20° C. Samples were withdrawn at different time intervals and hydrolyzed ONP was measured at A420 nm. Hydrolysis efficiency was calculated as increase in A420 nm per min per microgram active enzyme. Assays were performed in triplicates, and standard error was below 0.05.

FIG. 17 shows thin-layer chromatography (TLC) of the hydrolysis of lactose by the *A. ikkense* beta-galactosidase. Lanes 4-6: samples incubated at 5° C. for 2½ h (4: 1.25 mg/ml lactose, 5: 2.5 mg/ml lactose, 6: 5 mg/ml lactose). Lanes 7-9: samples incubated at 20° C. for 2½ h (7: 1.25 mg/ml lactose, 8: 2.5 mg/ml lactose, 9: 5 mg/ml lactose). Lanes 1-3: Controls, 0.0125 µg of each of the carbohydrates 13 lactose (lane 1), galactose (lane 2) and glucose (lane 3).

DETAILED DESCRIPTION OF THE INVENTION

“Beta-galactosidase” (beta-D-galactoside galactohydrolase, EC 3.2.1.23) is defined as an enzyme capable of hydrolysing lactose to the monosaccharides D-glucose and D-galactose.

“Cold-active” is defined as having activity at temperatures at 15° C. and below, preferably at 10° C. and below and most preferably at 5° C. and below.

A “host cell” is selected from a group of microorganisms comprising fungi, yeasts, and prokaryotes. The microorganism is more preferably a prokaryote and most preferably a bacterium.

Conditions of incubating beta-galactosidase with lactose are defined by performing incubation at a temperature between 0° C. and 20° C., preferably between 5° C. and 15° C.

The term “stringent condition” refers to a condition such that a hybridization is conducted in a solution containing 6×SSC (20×SSC represents 333 mM Sodium citrate, 333 mM NaCl), 0.5% SDS and 50% formamide at 42° C., and then the hybridized products are washed in a solution of 0.1×SSC, 0.5% SDS at 68° C., or to conditions as described in Nakayama, et al., Bio-Jikken-Illustrated, vol. 2, “Idenshi-Kaiseki-No-Kiso (A Basis for Gene Analysis)”, pp. 148-151, Shujunsha, 1995.

EXAMPLES

Example 1

Isolation of Bacteria Producing Cold-Active
Beta-Galactosidases

1.1 Sampling of Bacteria

Ikaite material was collected by scuba divers in the Ikka Fjord, South West Greenland (61° 11'N, 48° 01'W) from a depth of approximately six to ten meters. The columns were between 36-70 cm in length and between 5 and 30 cm in diameter. The columns were kept cold during transportation to the field laboratory.

1.2 Screening Bacteria for Beta-Galactosidase Production

Approximately 3 cm³ of ikaite material from a slice 15-18 cm from the top of an ikaite column was drilled out and suspended in 250 ml R2 broth (Schmidt et al. 2006) buffered to pH 10 with 0.2 M Na₂CO₃/NaHCO₃ buffers as described by Stoll and Blanchard (1990). After incubation at 5° C. for 2 months the culture was inoculated onto R2 medium, pH 10 without glucose but supplemented with lactose (1% w/v), 5-bromo-4-chloro-3-indolyl-β-D-galactopyranoside (X-gal) (40 µg/ml), 10 mM isopropyl-beta-D-thiogalactopyranoside (IPTG) and agar (1.5%, w/v). The plates were incubated at 5° C. for one to two weeks. A total of 17 blue colonies indicating production of beta-galactosidase were detected. Since 16S rRNA gene analyses of the seventeen isolates showed identical sequences only one of the isolates, strain 517, was chosen for further characterization.

Example 2

Taxonomical Analysis of Isolate 517 and Description
of a New Genus and Species, *Alkalilactibacillus*
ikkense

2.1 Phylogenetic Analysis of 16S rRNA Gene Sequences

DNA for phylogenetic analysis was extracted from cells of isolate 517 using FastDNA SPIN Kit for Soil as described by the manufacturer (BIO 101, Irvine, Calif.). 16S rRNA gene amplification was carried out using the primers 27F and 1492R (Lane 1991), and DNA sequencing was carried out at MWG Biotech AG (Ebersberg, Germany) using the same two primers plus additional primers 519R, 532F, 907F, and 907R (Lane 1991). The near full length DNA sequence of the 16S rRNA gene from isolate 517 was submitted to GenBank/EMBL/DBJ with the accession number EU281853. Related sequences were retrieved from public databases using BLASTn at the NCBI server (<http://www.ncbi.nlm.nih.gov/blast/>). The closest related 16S rRNA gene sequences were aligned using the Clustal W multiple alignment program MegAlign 5.03 (DNASTAR, Inc., Madison, Wis.). The Clustal W analysis showed that the closest relatives were *Natronobacillus azotifigens* (accession no. EU850815) (Sorokin et al. 2008), *Paraliobacillus ryukyuensis* (accession no. AB087828) (Ishikawa et al. 2002), *Halolactibacillus halophiles* (accession no. AB196783) (Ishikawa et al. 2005), *Halolactibacillus miurensis* (accession no. AB196784) (Ishikawa et al. 2005), *Amphibacillus tropicus* (accession no. AF418602) (Zhilina et al. 2001, 2002), and *Gracilibacillus halotolerans* (accession no. AF036922) (Wainø et al. 1999). Isolate 517 was most closely related to *N. azotifigens*, *P. ryukyuensis* and *A. tropicus* with 95.9%, 94.4% and 93.9% sequence similarity, respectively. The sequence similarity between isolate 517 and both *H. halophiles*, *H. miurensis*, and *G. halotolerans* was 93.4%. Thus, the distance in 16S rRNA

gene sequence similarity between isolate 517 and the closest related is below the 97% similarity, which is often used as a preliminary guideline for species separation. A phylogenetic tree was created by neighbour-joining analysis (bootstrap=100) using TREECON 1.3b software (Van de Peer and De Wachter, R. 1994) FIG. 1.

2.2 DNA-DNA Hybridization and Base Composition Analysis of Genomic DNA

DNA-DNA hybridization and DNA base composition (G+C content) was carried out at DSMZ (Braunschweig, Germany). DNA was isolated using a French pressure cell (Thermo Spectronic) and was purified by chromatography on hydroxyapatite as described by Cashion et al. (1977). DNA-DNA hybridization was carried out as described by De Ley et al. (1970) under consideration of the modifications described by Huss et al. (1983) using a model Cary 100 Bio UV/VIS-spectrophotometer equipped with a Peltier-thermostatted 6×6 multicell changer and a temperature controller with in-situ temperature probe (Varian). DNA-DNA hybridization between isolate 517 and the closest related based on 16S rRNA sequence similarity *P. ryukyuensis* was 28.8%, and between isolate 517 and *H. miurensis* it was 24.7%.

For determination of GC content, the DNA was hydrolyzed with P1 nuclease and the nucleotides dephosphorylated with bovine alkaline phosphatase (Mesbah et al. 1989). The resulting deoxyribonucleotides were analyzed by HPLC. The DNA G+C content of isolate 517 was 38.4 mol %, which is fairly similar to the closest related species. The G+C content of *N. azotifigens* is 36.1-38.5 mol % (Sorokin et al. 2008), *H. halophiles* and *H. miurensis* is reported to be 38.5-40.7 mol % (Ishikawa et al. 2005), for *P. ryukyuensis* it is 35.6 mol % (Ishikawa et al. 2002), and for *G. halotolerans* it is reported to be 38 mol % (Wainø et al. 1999).

The phylogenetic results and data on GC content indicate that isolate 517 represent a new species within a new genus, since the threshold value for DNA-DNA hybridization to separate two species is 70% (Wayne et al., 1987). Thus, we propose that isolate 517 represents a new genus *Alkalilactibacillus* gen. nov. comprising the species *Alkalilactibacillus ikkense* sp. nov.

Example 3

Characterization of Native Ikka-Beta-Galactosidase
from *Alkalilactobacillus ikkense*

3.1 Beta-Galactosidase Assay.

Beta-galactosidase activity was assayed by hydrolysis of o-nitrophenyl-beta-D-galactopyranoside (ONPG) and measuring the absorbancy of the released o-nitrophenyl (ONP) compound in a spectrophotometer at 415 nm. In the assay, the release of ONP from 1 mM ONPG by the recombinant beta-galactosidase activity was measured at 415 nm at 20° C. and pH 7.0 (0.1 M NaH₂PO₄/Na₂HPO₄). The reactions were stopped by adding 300 µl 0.6 M Na₂CO₃. Assays were performed at 0, 5, 10, 20, 30, 40, 50, and 60° C. for 30 minutes. The sodium phosphate buffers were pre-heated to the respective temperatures prior to assay start.

Thermostability analysis of the enzyme was carried out by placing an aliquot of enzyme at temperatures 0, 10, 20, 30, 40, and 50° C. and taking samples at t=0 to t=24 hours. Immediately after taking the samples, they were cooled and assayed at 20° C. as described above.

The pH activity profile was studied using a mixed pH buffer (250 mM Tris, 250 mM MES, 250 mM acetic acid)

adjusted from pH 4 to pH 10 with HCl or NaOH. The samples were incubated at 20° C. for 1 hour and assayed as described above.

3.2 Production of Native Ikka-Beta-Galactosidase.

Alkalilactobacillus ikkense cells were cultivated in liquid R2 medium supplemented with lactose and IPTG at 15° C. for 3 days on a rotary shaker. Cells were harvested by centrifugation in a Sigma® 3-18M centrifuge at 4,700 rpm and the pellet was resuspended in 2 ml of 0.1 M NaH₂PO₄/Na₂HPO₄, pH 7. Cells were lysed by bead beating in a FastPrep FP120 instrument (Bio101/Savant) for 3 times 25 sec at speed 5.5. The supernatant was then removed from the glass beads and centrifuged for 15 min at 10,000*g at 4° C. The cell free supernatant was then used for assaying.

3.3 Characterization of Temperature Optimum of Native Ikka-Beta-Galactosidase.

The native Ikka-beta-galactosidase displayed maximal activity at 20° C., 40% of the maximal activity was obtained at 0° C., and more than 60% of the maximal activity was observed at 10° C. (FIG. 2). Above 30° C. the enzyme was only moderately active and virtually no activity was observed at 60° C.

The temperature stability of the Ikka-beta-galactosidase was investigated. FIG. 3 shows that almost 100% of the residual activity was observed after 24 hours incubation at 0° C. and that more than 80% activity was left after 24 hours at 20° C. At temperatures above 20° C., the native Ikka-beta-galactosidase rapidly lost activity (FIG. 3). The inactivation at high temperatures was shown to be irreversible.

The pH dependence of the native Ikka-beta-galactosidase was investigated. FIG. 4 shows that maximal activity of the native Ikka-beta-galactosidase was observed at pH 7, and that the enzyme displayed approximately 70% of the maximal activity at pH 6 and at pH 8. At pH 9, approximately 25% of maximal activity was observed. The enzyme showed no activity at pH 5 and below or at pH 10 and above (FIG. 4).

3.4 SDS-PAGE of Native Ikka-Beta-Galactosidase.

Extracts from cells of *A. ikkense* induced with 1 mM IPTG and uninduced were analysed in SDS-PAGE (sodium dodecyl sulfate-polyacrylamide gel electrophoresis) (FIG. 5). Intracellular extracts were prepared by lysing the cells using bead-beating as described above in 3.2. The extracts (0.5-5 µl) were mixed with 12.5 µl 4*LDs sample buffer, 5 µl 10*DTT and 0.1 M NaH₂PO₄/Na₂HPO₄ to a final volume of 50 µl. The samples were heated to 70° C. for 10 minutes and 30 µl was loaded onto a 4-12% SDS gel. The gel was run in a XCell SureLoc™ Mini-Cell (Invitrogen, CA, USA) at 150 V for 1 hour at room temperature. After electrophoresis, the gel was stained using Coomassie Brilliant Blue R-250 (0.1% Coomassie Brilliant Blue R-250 (Serva, Heidelberg, Germany) in 40% EtOH and 10% acetic acid). FIG. 5 shows that a strong 120 kDa band was observed in the lanes with extracts from *A. ikkense* cells induced with IPTG and that this band was missing in lanes with extracts from non-induced cells. Thus, the 120 kDa band was assumed to be the native Ikka-beta-galactosidase.

Example 4

Isolation and Characterization of the Ikka-Beta-Galactosidase Gene from *Alkalilactobacillus Ikkense*

4.1 Isolation of the Ikka-Beta-Galactosidase Gene

DNA from *A. ikkense* was isolated from a culture of 50 ml. The cells were harvested by centrifugation and the chromosomal DNA was isolated using conventional phenol-chloro-

form extraction methods (Maniatis et al., 1982). The DNA was partially digested using Sau3AI (New England Biolabs, MA, USA), and fragments with the lengths between 3 kb and 10 kb were purified from an agarose gel using the QIAquick Gel Extraction Kit (Qiagen, Hilden, Germany) as described by the producer.

The vector for cloning chromosomal DNA from *A. ikkense* was a modified pUC18 plasmid (Stratagene, CA, USA). Plasmid pUC18 was restricted by NdeI and HindIII endonucleases (New England Biolabs). The sticky ends were refilled using Klenow fragment of DNA polymerase (New England Biolabs) and the blunt ends were ligated using T4 DNA ligase (New England Biolabs). DNA sequencing of the modified pUC18 plasmids, denoted pUC18dlacZ, at GATC Biotech AG (Konstanz, Germany) and analysis of the DNA sequence in the CLC Workbench 4 software (CLC bio, Aarhus, Denmark) confirmed that the α-subunit sequence of pUC18 was deleted in plasmid pUC18dlacZ. Thus, plasmid pUC18dlacZ was not able to mediate α-complementation when introduced into *E. coli* cells harbouring the beta-galactosidase ΔZ15 mutation.

Sau3AI restricted and gel-purified chromosomal DNA from *A. ikkense* was ligated into plasmid pUC18dlacZ treated with the restriction endonuclease BamHI and Antarctic Phosphatase (New England Biolabs). The ligation mixture was transformed into chemically competent *E. coli* TOP10 cells. Transformed cells were plated onto LB agar (10 g/l Bacto tryptone, 5 g/l yeast extract, 10 g/l NaCl) containing 20 µg/ml X-gal, 0.1 mM IPTG, and 100 µg/ml ampicillin and incubated over night at 37° C. After a 16 hours over night incubation, the plates were transferred to 20° C. and incubated for another 20 hours. A total of 580 colonies were screened and 1 blue colony was detected. The colony that turned blue during incubation at 20° C. was selected and transferred to 10 ml LB broth and grown at 37° C. over night. Recombinant *E. coli* cells from over night cultures were harvested by centrifugation, and plasmid DNA was purified using the QIAprep Spin Miniprep Kit (Qiagen). Plasmid DNA was analysed for inserts by digestion with restriction endonucleases EcoRI and PstI (New England Biolabs). The insert in the plasmid, denoted pUCIkka-bgal, was sequenced at GATC Biotech AG (Konstanz, Germany) using primer walking with the primer M13 reverse and custom made primers specific for the insert in pUCIkka-bgal (SEQ ID 3: 5'CCGTCATCCATATCACC3'; SEQ ID 4: 5'CCTTTGCCCAAGAGCCAACC3'; SEQ ID 5: 5'GCTATATACAGACTTGGCACC3'; SEQ ID 6: 5'GTAAT-TCAAT GTTCCAACGTG3'; Seq ID 7: 5'CGCTTATGGT-GTGAAG3') and a sequence just downstream of the multiple cloning site in pUC18dlacZ, (SEQ ID 8: 5'GGGCTGGCT-TAACTATGCGG3'). The Ikka-beta-galactosidase gene sequence harboured by the DNA insert is shown as SEQ ID NO 2.

4.2 Characterization of the Ikka-Beta-Galactosidase Gene Sequence

Analysis of the DNA sequence, SEQ ID NO 2, using the CLC Workbench 4 software (CLC bio, Aarhus, Denmark) showed an open reading frame with the coding capacity of 1,041 amino acids, SEQ ID NO 1. The NCBI search tool Blastp was used to search for related sequences in databases.

The closest related sequences were beta-galactosidases from *Bacillus megaterium* (accession no ABN13675) 56.7% identity, *Paenibacillus* sp. JDR-2 (accession no ZP_02849115) 55.3% identity, and *Geobacillus* sp. Y412MC10 (accession no ZP_03036811) 54% identity, all of which belong to the Glycosyl Hydrolase Family 2. Thus, it is concluded that the Ikka-beta-galactosidase belongs to this family. The calculated subunit molecular weight and pI of the Ikka-beta-galac-

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tosidase was 119 kDa and pI 5.0, respectively (ExPASy ProtParam tool). The calculated subunit molecular weight was confirmed by SDS-PAGE, FIGS. 5 and 6. Alignment of the Ikka-beta-galactosidase with structurally resolved enzymes showed that the conserved active site region in *E. coli* (ILCEYAHAMGN) (pos. 534-544) (Gebler et al. 1992) is well conserved in the Ikka-beta-galactosidase (ILCEFSHAMGN) (pos. 547-557), and the active site nucleophile Glu-537 is probably found as Glu-550.

Example 5

Production of Recombinant Ikka-Beta-Galactosidase in *Escherichia coli*

Native *Alkalilactibacillus ikkense* was shown to produce only moderate amounts of Ikka-beta-galactosidase. Therefore, in order to produce larger amounts of the beta-galactosidase, subcloning of the Ikka-beta-galactosidase gene into expression plasmids was carried out.

5.1 Construction of a Vector for the Expression of Recombinant Ikka-Beta-Galactosidase in *Escherichia coli*.

The Ikka-beta-galactosidase gene was subcloned further using chromosomal DNA from *A. ikkense* as template and the PCR primers bGa15': 5'CTGAATTTCGCATATGGCAAAAAAATTAAAAAATTC3' (EcoRI restriction site underlined) (SEQ ID 9), and bGa13': 5'CCAAGCTTATCTGTTTAAACTATTCAACATG3' (HindIII site double underlined) (SEQ ID 10). The polymerase used was the proofreading polymerase Phusion® High-Fidelity DNA Polymerase (New England BioLabs). The PCR reaction was analyzed by gel electrophoresis on a 0.8% agarose gel (Seakem GTG) and the 3.9 kb fragment was ligated into pJET1.2/blunt cloning vector (Fermentas, Helsingborg, Sweden) and transformed into *E. coli* TOP10 cells. *E. coli* transformants containing pJET1.2/blunt were isolated on ampicillin containing LB agar plates and plasmid DNA was prepared as described above. Plasmid DNA was restricted with the enzymes EcoRI and HindIII and analysed on 0.8% (w/v) agarose gels as described. The 3.9 kb DNA fragment was purified from the gel using the QIAquick Gel Extraction Kit as described by the producer. The purified DNA fragment was ligated into plasmid pUC18dlacZ similar restricted with the enzymes EcoRI and HindIII and gel purified as described above. The ligation mixture was transformed into *E. coli* TOP10 cells and recombinant cells harbouring the plasmid pUC18dlacZ with the Ikka-beta-galactosidase gene were selected as blue colonies on LA plates containing 100 µg/ml ampicillin, 1 mM IPTG, and 40 µg/ml X-gal. Transformants were selected and analysed for plasmids and inserts. Plasmid DNA was prepared from a 10 ml culture and the DNA was sent for sequencing at GATC biotech (Konstanz, Germany) using the primers described above in 4.1. The entire Ikka-beta-galactosidase gene was sequenced on both strands in order to ensure that no mutations were introduced during PCR. One of the recombinant clones, which contained plasmid pUC18dlacZ with the Ikka-beta-galactosidase gene, denoted plasmid pUCIkka-bgal_exp, was selected for further expression studies.

5.2 Expression of Recombinant Ikka-Beta-Galactosidase in *Escherichia Coli*.

E. coli TOP10 cells harbouring plasmid pUCIkka-bgal and pUCIkka-bgal_exp were cultivated in 30 ml LB broth containing 100 µg/ml ampicillin over night at 37° C. After an over night incubation, the cells were supplemented with 0.1 mM IPTG and incubated at 20° C. for further 20 hours. Cells were harvested by centrifugation for 30 min at 4,700 rpm at 10° C.

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and resuspended in 1 ml 0.1 M NaH₂PO₄/Na₂HPO₄, pH 7. The cells were lysed by bead beating in a Fast Prep instrument (Fast Prep FP120, Bio101/Savant Instruments Inc., Holbrook, N.Y.) at speed 5.5 for 3 times 25 sek. The samples were cooled on ice in between the beating/shaking. The lysate was centrifuged at 10,000 g for 15 min at 4° C., and the supernatant containing the Ikka-beta-galactosidase enzyme was transferred to a clean tube. This crude extract was used for subsequent analyses.

5.3 Properties of Recombinant Ikka-Beta-Galactosidase Produced in *Escherichia coli*.

5.3.1. SDS-PAGE of Recombinant Ikka-Beta-Galactosidase and Determination of Yield Produced.

Intracellular extracts from recombinant *E. coli* cells harbouring plasmid pUCIkka-bgal were analysed on SDS-PAGE (SDS gel 4-12%, PAGEgel, CA, USA) as described above in 3.4. Cultures induced with 1 mM IPTG and control cultures not induced were analysed.

The protein bands in extracts from cultures grown with and without IPTG were identical apart from a band of approximately 120 kDa in cultures induced with IPTG (arrow in FIG. 6). Thus, as the calculated molecular mass of the Ikka-beta-galactosidase is 119 kDa, and since the strong band at 120 kDa was observed only in cultures induced with IPTG, it is assumed that the 120 kDa band represent the Ikka-beta-galactosidase.

Extracts from cultures of plasmid pUCIkka-bgal harbouring *E. coli* were prepared as described above and diluted before electrophoresis on SDS-PAGE. Beta-galactosidases from *E. coli* (Sigma-Aldrich, MO, USA) and *K. lactis* (Novozymes, Bagsvaerd, Denmark) with known molecular mass and in defined concentrations were co-electrophoresed on the same gel for comparison (arrows in FIG. 6). By comparing the migration and Coomassie Brilliant Blue staining of the known beta-galactosidases with that of the Ikka-beta-galactosidase an estimate of the amount of the Ikka-beta-galactosidase was obtained. The extract, which was used for the subsequent analyses was estimated to have a concentration of Ikka-beta-galactosidase of 2 mg/ml.

5.3.2 Temperature Dependence of Recombinant Ikka-Beta-Galactosidase.

The temperature optimum of recombinant Ikka-beta-galactosidase was determined as described above for the native enzyme using ONPG as a substrate. The temperature profile was determined at 0, 5, 10, 20, 30, 40, 50, and 60° C. for 30, 60 and 120 minutes for the recombinant Ikka-beta-galactosidase and, as controls, for the beta-galactosidases from *E. coli* and *K. lactis*. The optimal temperature for activity of the recombinant Ikka-beta-galactosidase was determined to be 20-30° C. (FIG. 7). However, the Ikka-beta-galactosidase also showed high activity at low temperatures with more than 40% activity at 0° C., approximately 80% activity at 5° C. and more than 90% at 10° C. Compared to the *K. lactis* beta-galactosidase, the specific activity of the Ikka-beta-galactosidase was almost twice as high at temperatures between 0° C. and 30° C. (FIG. 8). Both enzymes showed close to zero activity at 40° C. and above (FIG. 8).

The thermostability of the Ikka-beta-galactosidase was determined at 0, 10, 20, 30, 40, 50, and 60° C. Samples were taken from t=0 hours to t=123 hours with increasing intervals from 5 minutes during the first hour to several hours at the end of the experiment (FIG. 9). FIGS. 9 and 10 show that the Ikka-beta-galactosidase showed high stability at 0° C. and 5° C., at 10° C. the enzyme was stable for approximately 100 hours and at temperatures above 20° C. the Ikka-beta-galactosidase was rather unstable. Treatment at 40° C. for 40 min-

utes resulted in complete inactivation. The inactivation of the Ikka-enzyme was irreversible.

5.3.3 pH Dependence of Recombinant Ikka-Beta-Galactosidase.

The pH activity profile was studied using a mixed pH buffer (250 mM Tris, 250 mM MES, 250 mM acetic acid) adjusted from pH 4 to pH 10 with HCl or NaOH. The samples were incubated at 20° C. for 2 hours. The optimal pH value for the Ikka-beta-galactosidase was shown to be approximately pH 7.0. At pH 6.0 the enzyme showed 60% of maximal activity and at pH 8.0 the Ikka-enzyme displayed 90% activity. At pH 9.0 15% activity was observed whereas no activity could be detected at pH 5.0 or below or at pH 10 and above.

5.3.3 pH Dependence of Recombinant Ikka-Beta-Galactosidase.

The substrate specificity of the Ikka-beta-galactosidase was determined in assays performed at pH 7.0 and 20° C. for 20 minutes using nine different chromogenic substrates, o-nitrophenyl-beta-D-galactopyranoside, p-nitrophenyl-alpha-D-galactopyranoside, o-nitrophenyl-beta-D-glucopyranoside, p-nitrophenyl-beta-D-glucopyranoside, p-nitrophenyl-beta-D-arabinopyranoside, p-nitrophenyl-beta-D-cellobioside, p-nitrophenyl-beta-D-fucopyranoside, p-nitrophenyl-beta-D-lactopyranoside, and p-nitrophenyl-beta-D-mannopyranoside. Each substrate was used at a concentration of 10 mM. The assays showed that the Ikka-beta-galactosidase was only able to hydrolyze o-nitrophenyl-beta-D-galactopyranoside (ONPG) and p-nitrophenyl-beta-D-fucopyranoside (4% of the relative activity compared to hydrolysis of ONPG). The utilization of the remaining substrates was below detection.

Hydrolysis of lactose was determined in a solution of lactose in water. Three different lactose concentrations were tested: 1.25 mg/ml, 2.5 mg/ml, and 5 mg/ml. Total reaction volume was 0.2 ml and each reaction contained 0.2 mg/ml of recombinant Ikka-beta-galactosidase enzyme. The enzyme reactions were incubated at 5° C. and 20° C., and samples were collected after 15 minutes, 2½ hour, and 24 hours. After incubation, the reactions were stopped by heating at 95° C. for 20 minutes. Visualization of the products was carried out by thin-layer chromatography (TLC) on a TLC Silica gel 60 (Merck, Darmstadt, Germany) in a solvent containing 1-butanol, 2-propanol, and water (3:12:4). Volumes containing 0.005 mg lactose were run on the TLC. Controls were 0.5 µl lactose (2.5%), 0.5 µl galactose (2.5%) and 0.5 µl glucose (2.5%). After being dried, the sugars were visualized by spraying with an orcinol reagent followed by incubation for 5-10 min at 100° C.

Hydrolysis of lactose was observed both at 5° C. and at 20° C. At 5° C., approximately 75-85% lactose was hydrolysed in the 1.25 mg/ml reaction after 15 minutes and 100% was hydrolysed within 2½ hours, (FIG. 12 A). Similar hydrolysis efficiency was observed in the 1.25 mg/ml reaction incubated at 20° C. (FIG. 12 B). Hydrolysis effectiveness in the 2.5 mg/ml lactose reaction showed approximately 90-95% hydrolysis within 2½ hours at both temperatures. After 24 hours, 100% hydrolysis was observed for all three lactose concentrations at both temperatures (FIG. 12).

5.3.4 Purification of Recombinant Ikka-Beta-Galactosidase.

Beta-galactosidase was purified from crude extracts by ion exchange chromatography. Portions of two ml were subjected to chromatography on a 1 ml High Q cartridge on a BioLogic LP System (Bio-Rad).

The column was washed with 10 ml of 50 mM phosphate buffer (pH 7) and eluted by a gradient from 0 to 1 M of NaCl in 50 mM phosphate buffer (pH 7) at a flow rate of 0.5 ml/min.

Fractions of 1 ml were collected. Crude extracts were also subjected to affinity chromatography on a 2 ml column of agarose coupled with p-aminobenzyl-1-thio-beta-D-galactopyranoside (PABTG-agarose, Sigma). The column was washed with 10 ml of 50 mM phosphate buffer (pH 7) before it was eluted by 100 mM NaCl in 50 mM phosphate buffer (pH 7) at a flow rate of 0.5 ml/min. Fractions of 1 ml were collected.

The fractions were analysed for the presence of proteins using a BCA Protein Assay Kit (Pierce), and beta-galactosidase was measured in o-nitrophenyl (ONP)-beta-D-galactopyranoside assays as described above. Fractions containing beta-galactosidase activity were analysed by SDS polyacrylamide gel electrophoresis (4-20%, PAGEgel, CA, USA). Purified beta-galactosidase was used for subsequent stability and activity experiments.

FIG. 13 shows that the crude extract from *E. coli* contained recombinant beta-galactosidase with a monomeric molecular weight of approximately 115-120 kDa. Ion exchange chromatography resulted in pure beta-galactosidase (FIG. 13, lane 2), whereas affinity chromatography (FIG. 13, lane 3) only resulted in partially purified recombinant enzyme. Thus, for the subsequent analyses, pure beta-galactosidase from ion exchange was used, unless otherwise specified.

5.3.5 Characterization of Native and Recombinant *A. ikkense* Beta-Galactosidase.

The molecular weight of the *A. ikkense* beta-galactosidase was determined to be approximately 115-120 kDa when analyzed on SDS-PAGE using known beta-galactosidases from *E. coli* and *K. lactis* as references. This result is in agreement with the calculated molecular weight as determined from the DNA sequence (119 kDa). The crude extract from *E. coli* was estimated to contain 10 mg/ml *A. ikkense* beta-galactosidase.

The specific activity, calculated on the basis of purified beta-galactosidase from ion exchange chromatography was 8.4 micromoles/min/mg protein at 20° C. with ONPG as substrate (Table 1).

TABLE 1

Purification	Volume (ml)	Protein (mg)	Specific activity (U mg ⁻¹)	Total activity (U)	Purification (fold)	Recovery (%)
Cell extract	10	30	1.6	48.0	1	100
Ion exchange	10	2.5	8.4	21.1	12	44

A culture of 200 ml *E. coli* cells expressing recombinant *A. ikkense* beta-galactosidase was harvested resulting in a 280 mg wet weight cell pellet. The cells were lysed in a Fast Prep apparatus, and the extract was subjected to ion exchange chromatography. One U is 1 micromole per min at 20° C. with ONPG as substrate.

Extract of *E. coli* expressing recombinant *A. ikkense* beta-galactosidase was analyzed for beta-galactosidase activity.

The thermal stability of the purified, recombinant *A. ikkense* beta-galactosidase enzyme was tested as shown in FIG. 15. An equal amount of enzyme was incubated at the temperatures indicated and samples were withdrawn at different time intervals. Y-axis is the residual activity in percent of maximal activity. Enzyme samples were incubated at temperatures from 0° C. to 60° C. and at the time points indicated (X-axis), samples were withdrawn and assayed for active beta-galactosidase at 20° C. Assays were performed in triplicates, and standard error was below 0.05.

At 0° C. the enzyme displayed more than 60% of the maximal activity, and at 10° C., more than 70% of the maximal activity was observed both for purified recombinant enzyme. Analysis of enzyme stability showed that purified, recombinant beta-galactosidase was 100% stable at 0° C. to

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20° C. for at least 5 hours (FIG. 15), and that the residual activity after 5 days storage at 0° C. to 20° C. was 50-60% (data not shown). At 30° C., the purified beta-galactosidase lost more than 80% of its activity within 5 hours. Complete, irreversible inactivation was achieved within 5 minutes at 50° C. and within 10 minutes at 40° C. (FIG. 15).

The Temperature dependence (A) and pH dependence (B) of the purified, recombinant *A. ikkense* beta-galactosidase was tested (FIG. 14). Y-axis is the relative activity in percent of maximal activity. X-axis is the incubation temperature (A) or pH (B). The relative activity of the purified, recombinant enzyme with ONPG as substrate is illustrated by black squares. Assays were performed in triplicates, and standard error was below 0.05.

Maximal activity of the purified, recombinant enzyme was observed at pH 8 (FIG. 14B). About 60% of the maximal activity was maintained at pH 7, and at pH 9 approximately 90% activity was observed (FIG. 14B).

The recombinant *A. ikkense* beta-galactosidase was benchmarked with Lactozyme 3000® 13 from *K. lactis*. At temperatures between 0° C. and 20° C. the *A. ikkense* beta-galactosidase showed a twofold increase in conversion rate, when compared to the *K. lactis* beta-galactosidase (FIG. 16); *A. ikkense* beta-galactosidase (black squares) compared with commercially available Lactozyme® 3000 L from *K. lactis* (open circles). Specially the experiment was conducted in the following way: An equal amount of enzyme (2 mg/ml) was incubated with ONPG as substrate at temperatures from 0° C. to 20° C. Samples were withdrawn at different time intervals and hydrolyzed ONP was measured at A420 nm. Hydrolysis efficiency was calculated as increase in A420 nm per min per microgram active enzyme. Assays were performed in triplicates, and standard error was below 0.05.

Investigation of substrate specificity of the *A. ikkense* β-galactosidase was carried out using nine different chromogenic substrates. Hydrolysis was only observed with ONPG and with p-nitrophenyl-beta-D-fucopyranoside (4% of the relative activity compared to hydrolysis of ONPG). Thin-layer chromatography (TLC) was used to demonstrate the hydrolysis of lactose by the *A. ikkense* beta-galactosidase (FIG. 17). Lanes 4-6: samples incubated at 5° C. for 2½ h (4: 1.25 mg/ml lactose, 5: 2.5 mg/ml lactose, 6: 5 mg/ml lactose). Lanes 7-9: samples incubated at 20° C. for 2½ h (7: 1.25 mg/ml lactose, 8: 2.5 mg/ml lactose, 9: 5 mg/ml lactose). Lanes 1-3: Controls, 0.0125 mg of each of the carbohydrates lactose (lane 1), galactose (lane 2) and glucose (lane 3).

Hydrolysis of the remaining substrates was below detection limit. Hydrolysis of lactose was observed at both 5° C. and at 20° C. (FIG. 17). At 5° C., approximately 75-85% of the lactose was hydrolyzed in the 1.25 mg/ml reaction after 15 minutes, and 100% of the lactose was hydrolyzed within 2½ hours (FIG. 17, lane 4). Similar hydrolysis efficiency was observed in the 1.25 mg/ml reaction incubated at 20° C. for 2½ hours (FIG. 17, lane 7). Hydrolysis effectiveness in the 2.5 mg/ml lactose reaction showed approximately 90-95% hydrolysis within 2½ hours at both temperatures (FIG. 17, lanes 5 and 8). After 24 hours, 100% hydrolysis was observed for all three lactose concentrations at both temperatures (not shown). At the highest lactose concentration (27 mg/ml), the TLC gel indicated the formation of oligosaccharides (FIG. 17, lanes 6 and 9).

Example 6

Production of Recombinant Ikka-Beta-Galactosidase in *Bacillus Subtilis*

The Ikka-beta-galactosidase was further subcloned in a *Bacillus subtilis* expression vector, pAL10 (MoBiTech,

16

GmbH). PCR was performed using chromosomal DNA from *Alkalilactibacillus ikkense* as template and the PCR primers Bs_pAL_bGa15':

5'GGCCATGGATCCATGGCAAAAAAATTAAAAAAATTC3' (BamHI restriction site underlined) (SEQ ID NO 11) and

Bs_pAL_bGa13': 5'GGCCATCCCGGGTTATCTGTTTAACTATTCAACATG3' (XmaI restriction site double underlined) (SEQ ID NO 12). PCR,

subsequent isolation of the fragment encoding the Ikka-beta-galactosidase, ligation into pUC18dLacZ and transformation of *E. coli* was as described above in 5.1. Plasmid pUC18dLacZ carrying the Ikka-beta-galactosidase gene was prepared and sequenced, before the plasmid DNA was restricted with restriction endonucleases BamHI and XmaI. The 3.1 kb fragment encoding Ikka-beta-galactosidase was purified, inserted into plasmid pAL10 similarly restricted with BamHI and XmaI, and transformed into *E. coli* as described in 5.1. Recombinant *E. coli* harbouring pAL10 containing the Ikka-beta-galactosidase gene was isolated on LB agar plates containing 100 µg/ml ampicillin. Plasmid pAL10_Ikka-bGal was purified and transformed into *B. subtilis* cells using an electroporation protocol for *B. subtilis* from Eppendorf (Germany) (Protocol No. 4308 915.504-08/2003). Recombinant cells harbouring plasmid pAL10 were selected on LB agar containing 5 µg/ml chloramphenicol.

Production of recombinant Ikka-beta-galactosidase in *B. subtilis* was carried out by growing *B. subtilis* pAL10_Ikka-bGal cells in LB containing 5 µg/ml of chloramphenicol at 37° C. for 16 hours. Induction of Ikka-beta-galactosidase synthesis was carried out by changing the temperature to 20° C. *B. subtilis* pAL10_Ikka-bGal cells were cultivated at 20° C. for another 5 hours after which, the cells were harvested, and intracellular enzyme was isolated by Fast Prep as described in 5.2.

A crude, intracellular extract from *B. subtilis* pAL10_Ikka-bGal cells was analysed in ONPG assays as described in 5.3. ONPG assays showed the presence of a cold-active Ikka-beta-galactosidase with an activity similar to the native enzyme, to the recombinant enzyme in crude *E. coli* extracts, and to the pure enzyme produced in *E. coli* cells.

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SEQ ID NO: 1

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: University of Copenhagen

(B) STREET:

(C) CITY:

(D) COUNTRY:

(E) POSTAL CODE:

(ii) TITLE OF INVENTION: Cold-active beta-galactosidase, a method of producing same and use of such enzyme

(iii) NUMBER OF SEQUENCES: 10

(2) INFORMATION FOR SEQ ID NO: 1

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1,041 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: Not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION SEQ ID NO: 1

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1              10
Met Ala Lys Lys Leu Lys Lys Phe Asn Tyr Leu Pro Pro Lys Asn

          20              30
Gly Tyr Pro Glu Trp Asn Asn Asn Pro Glu Ile Phe Gln Leu Asn

          40
Arg Arg Glu Ala His Ala Thr Leu Val Pro Tyr Ser Asn Leu Glu

          50              60
Leu Ala Leu Lys Gly Glu Arg Thr Ala Ser Ser Phe Tyr Gln Ser

          70
Leu Asn Gly Ser Trp Gln Phe Ala Phe Ala Gln Glu Pro Thr Lys

          80              90
Arg Val Ile Asp Phe Tyr Arg Lys Asp Phe Asp His Arg Asp Trp

          100
Asp Ser Ile Lys Val Pro Ser His Trp Gln Leu Glu Gly Tyr Asp

          110              120
Tyr Pro Gln Tyr Thr Asn Thr Thr Tyr Pro Trp Val Glu Lys Glu

          130
Thr Ile Lys Pro Pro Phe Ala Pro Thr Asn Tyr Asn Pro Val Gly

          140              150
Gln Tyr Val Arg Thr Phe Glu Leu Pro Thr Asp Trp Asn Gly Ala

          160
Pro Val Tyr Leu Asn Phe Gln Gly Val Glu Ser Ala Phe Tyr Val

          170              180
Trp Ile Asn Gly Asp Leu Val Gly Tyr Ser Glu Asp Thr Phe Thr

          190
Pro Ala Glu Phe Asp Ile Thr Pro Tyr Leu Ile Glu Gly Glu Asn

          200              210
Lys Leu Ala Val Glu Val Tyr Arg Trp Ser Asp Ala Ser Trp Leu

          220
Glu Asp Gln Asp Phe Trp Arg Leu Ser Gly Ile Phe Arg Asp Val

          230              240
Tyr Leu Tyr Ala Thr Pro Ala Gln His Ile Asp Asp Phe Phe Val

          250
Thr His Glu Leu Asp Ala Asp Tyr Arg Asn Ala Thr Leu Lys Ile

          260              270
Asp Met Lys Val Arg Asp Tyr Phe Glu Ile Gly Glu Pro Val Thr

          280
Val Asn Ala Met Leu Phe Asp Leu Asn Gly Asn Pro Val Leu Lys

          290              300
Gln Pro Leu Leu Ser Ala Val Asp Phe Ser Gly Lys Glu Val Ala

          310
Asp Val Ser Val Ile Thr Thr Ile Asp Asn Pro Leu Lys Trp Ser

          320              330
Ala Glu Asp Pro Asn Leu Tyr Thr Leu Val Leu Ser Leu Val Asp

          340
Gln Asn Gly Lys Leu Leu Glu Thr Glu Ser Cys Arg Val Gly Phe

          350              360
Arg Lys Phe Glu Arg Lys Asp Gly Leu Met Gln Ile Asn Gly Lys

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 370
 Lys Gly Arg Ala Ile Thr Ile Asp Asp Met Val Asn Asp Ile Gln
 380 390
 Leu Met Lys Gln His Asn Ile Asn Ala Val Arg Thr Ser His Tyr
 400
 Pro Asn His Pro Leu Trp Tyr Glu Leu Cys Asp Thr Tyr Gly Leu
 410 420
 Tyr Val Ile Asp Glu Thr Asn Leu Glu Thr His Gly Thr Trp Val
 430
 Tyr Gly Gln Lys Gly Leu Ala Glu Thr Ile Pro Gly Ser Leu Pro
 440 450
 Lys Trp Thr Glu Asn Val Leu Asp Arg Cys Asn Ser Met Phe Gln
 460
 Arg Asp Lys Asn His Pro Ser Ile Leu Asp Trp Ser Leu Gly Asn
 470 480
 Glu Ser Phe Gly Gly Asp Asn Phe Leu Lys Met His Asp Phe Phe
 490
 Thr Glu Gln Asp Pro Ala Arg Leu Val His Tyr Glu Gly Ile Phe
 500 510
 His Tyr Arg Glu Ser Glu Arg Ala Ser Asp Met Glu Ser Thr Met
 520
 Tyr Ile Ser Pro Glu Gly Ile Glu Asp Tyr Ala Lys Lys Ala Thr
 530 540
 Lys Glu Thr Lys Pro Tyr Ile Leu Cys Glu Phe Ser His Ala Met
 550
 Gly Asn Ser Leu Gly Asn Phe Tyr Lys Tyr Thr Glu Leu Phe Asp
 560 570
 Gln Tyr Pro Ile Leu Gln Gly Gly Phe Ile Trp Asp Trp Lys Asp
 580
 Gln Ser Leu Leu Thr Lys Thr Ala Gly Gly Thr Pro Tyr Leu Ala
 590 600
 Tyr Gly Gly Asp Phe Gly Glu Ser Pro His Asp Gly Asn Phe Ala
 610
 Gly Asn Gly Leu Ile Phe Gly Asp Gly Lys Val Ser Pro Lys Ile
 620 630
 Phe Glu Val Lys Arg Cys Tyr Gln Asn Val Asp Phe Lys Ala Ile
 640
 Asp Leu Val His Gly Gln Ile Glu Leu Thr Asn Lys Tyr Leu Phe
 650 660
 Thr Asn Leu Ala Asp Tyr Gln Leu Asn Trp Val Ile Thr Arg Asn
 670
 Gly Asp Ala Ile Glu Ser Gly Ala Thr Asn Ile Asn Val Leu Pro
 680 690
 Gly Glu Lys Arg Glu Val Ile Leu Asp Tyr Thr Phe Pro Thr Gly
 700
 Val Cys Met Thr Asp Glu Tyr Ile Leu Thr Leu Arg Phe Ser Glu
 710 720
 Lys Gly Asp Arg Leu Trp Cys Glu Ala Gly His Glu Val Ala Phe
 730
 Asn Gln Phe Val Leu Pro Thr Lys Val Thr Lys Leu Arg Glu Lys
 740 750
 Thr Gln Asp Thr Lys Thr Leu Ser Val Glu Val Met Gln Asp Arg
 760

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      770                               780
Leu Val Thr Ser Gly Ala Gly Phe Ser Val Gly Phe Asp Thr Lys

      790
Ser Gly Met Leu Val Ser Tyr Gln Val Gly Gly Asn Glu Leu Val

      800                               810
Lys Glu Ala Leu Val Pro Asn Phe Trp Arg Ala Met Thr Asp Asn

      820
Asp Arg Gly Asn Gly Leu Asp Gln Arg Ser Gln Ile Trp Arg Asp

      830                               840
Ala Asn Glu Val Arg Glu Leu Val Ser Phe Gln Tyr Glu Val Leu

      850
Thr Asn Arg Val Ser Ile Ser Thr Val Phe Leu Tyr Glu Asp Leu

      860                               870
Asn His Ser Arg Val Glu Leu Asn Phe Leu Ile Thr Gly Thr Gly

      880
Glu Ile Lys Val Asp Tyr Val Leu Lys Pro Gly Glu Asp Leu Pro

      890                               900
Glu Ile Pro Glu Ile Gly Leu Met Leu Thr Met Pro Lys Ser Phe

      910
Asp Gln Leu Ser Trp Tyr Gly Lys Gly Pro His Glu Ser Tyr Trp

      920                               930
Asp Lys Gln Lys Gly Ala Lys Ile Gly Leu Tyr Gln Gly Phe Val

      940
Gly Asp Gln Tyr Val Pro Tyr Leu Lys Pro Gln Glu Cys Gly Asn

      950                               960
Lys Val Gly Val Arg Ser Ala Glu Leu Val Asn Asp Val Gly Val

      970
Gly Leu Ile Ile Ser Gly Leu Pro Thr Leu Glu Leu Asn Val Leu

      980                               990
Pro Tyr Thr Pro Val Gln Leu Glu Ser Ala Asp His Ser Tyr Gln

      1000
Leu Pro Glu Thr Asp Gln Thr Val Val Arg Ile Asn Leu Gly Gln

      1010                               1020
Met Gly Val Gly Gly Asp Asp Ser Trp Gly Gln Arg Thr His Gln

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      1040
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SEQ ID NO: 2

(2) INFORMATION FOR SEQ ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3,123 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION SEQ ID NO: 2

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ATGGCAAAAA AATTAAAAA ATTCAACTAC CTCCCACCAA AAAACGGGTA      50
CCGAGAGTGG AATAATAATC CGGAAATTTT TCAACTTAAT CGAAGAGAGG      100
CGCATGCAAC ATTGGTGCCA TATTCTAATT TGAATTGGC ACTTAAAGGG      150
GAGCGGACAG CATCATCATT TTATCAATCT TTAAATGGTA GTTGGCAGTT      200
TGCCTTTGCC CAAGAGCCAA CCAAGCGAGT GATAGATTTT TATCGGAAAG      250
ATTTTGATCA TCGCGATTGG GATTGCGATTA AAGTACCAAG TCATTGGCAG      300

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TTAGAAGGCT	ATGACTACCC	GCAATACACC	AACACAACGT	ACCCATGGGT	350
AGAAAAAGAA	ACGATTAAAC	CTCCATTTGC	ACCAACAAAT	TATAATCCAG	400
TCGGACAATA	TGTTTCGCACG	TTTGAATTAC	CGACTGATTG	GAATGGAGCT	450
CCCGTTTATC	TGAATTTCCA	AGGTGTTGAA	TCAGCTTTCT	ACGTCTGGAT	500
AAATGGTGAT	TTGGTCGGAT	ACAGTGAGGA	CACTTTCACA	CCAGCTGAAT	550
TTGATATAAC	TCCCTATTTA	ATAGAGGGTG	AAAATAAGCT	AGCGGTAGAA	600
GTCTATCGTT	GGAGTGATGC	GAGCTGGCTT	GAAGACCAGG	ATTTCTGGAG	650
GTTAAGCGGG	ATTTTTCGTG	ACGTCTATCT	ATATGCAACA	CCAGCTCAGC	700
ACATTGATGA	TTTCTTTGTC	ACACACGAAC	TTGATGCAGA	CTATCGAAAT	750
GCAACGTTGA	AGATTGATAT	GAAAGTGC GC	GATTATTTTCG	AGATTGGCGA	800
GCCTGTCACA	GTTAATGCGA	TGCTCTTTGA	TCTTAATGGG	AATCCGGTTC	850
TCAAGCAACC	GCTTTTATCG	GCAGTAGATT	TTTCAGGTAA	AGAAGTTGCT	900
GATGTGAGCG	TAATAACAAC	AATTGATAAT	CCATTGAAAT	GGAGTGCGGA	950
AGATCCCAAT	CTGTACACTT	TGGTTTAAAG	TTTAGTTGAT	CAGAATGGCA	1000
AGTTGCTTGA	AACAGAAAGC	TGTCGCGTTG	GATTTCGTAA	ATTTGAACGC	1050
AAGGACGGAT	TGATGCAAAT	TAATGGAAAG	CGGATTGTCT	TTAAAGGGAC	1100
AAATCGTCAC	GAATTCGCTT	CTGATAAAGG	TCGGGCGATA	ACGATAGATG	1150
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CGAACCTCAC	ATTATCCGAA	TCATCCGCTT	TGGTATGAGT	TGTGTGATAC	1250
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GGGTTTATGG	TCAAAAAGGA	TTGGCTGAGA	CAATACCAGG	TAGTCTACCA	1350
AAGTGGA CTG	AAAACGTCTT	GGATCGTTGT	AATTCAATGT	TCCAACGTGA	1400
TAAAAACCAC	CCATCGATTG	TGGATTGGTC	ACTTGGTAAT	GAATCTTTTG	1450
GTGGCGATAA	CTTCTTGAAG	ATGCATGACT	TCTTTACGGA	ACAAGATCCA	1500
GCTCGTCTGG	TGCACTATGA	GGGGATTTTT	CATTATCGTG	AATCTGAACG	1550
GGCATCTGAT	ATGGAGAGTA	CCATGTATAT	TTCGCCAGAA	GGCATTGAGG	1600
ACTATGCAAA	GAAAGCGACC	AAGGAGACGA	AACCATATAT	TTTATGCGAA	1650
TTCAGCCATG	CGATGGGCAA	CTCGCTAGGA	AACTTTTATA	AGTATACCGA	1700
GCTATTTGAT	CAATATCCGA	TCTTACAAGG	AGGCTTCATT	TGGGATTGGA	1750
AGGATCAATC	GCTGCTAACG	AAGACAGCAG	GAGGCACACC	GTATCTTGCT	1800
TATGGTGGTG	ATTTTGGTGA	ATCGCCACAC	GACGGCAACT	TTGCTGGTAA	1850
TGGTTTGATT	TTTGGAGATG	GCAAGGTTAG	CCCGAAGATT	TTTGAAGTGA	1900
AGCGTTGTTA	CCAAAATGTT	GATTTCAAAG	CAATAGACTT	AGTGCACGGA	1950
CAAAATCGAAT	TGACCAATAA	ATACTTGTTT	ACCAATCTCG	CTGACTACCA	2000
ACTAAATTGG	GTTATCACTC	GAAACGGTGA	TGCAATAGAG	TCGGGTGCTA	2050
CTAACATCAA	TGTCTTACCA	GGTGAAAAAA	GAGAGGTTAT	ACTTGACTAC	2100
ACGTTCCCAA	CAGGCGTTTG	CATGACGGAT	GAATATATTT	TGACCCTTTCG	2150
TTTTTCTGAG	AAAGTGATC	GCTTATGGTG	TGAAGCGGGA	CATGAAGTTG	2200
CATTTAATCA	GTTTGTTTTA	CCAACAAAAG	TTACGAAATT	ACGTGAGAAG	2250
ACACAAGATA	CCAAGACGCT	TTCAGTTGAA	GTAATGCAAG	ATCGACTTGT	2300
TACATCTGGT	GCTGATTTTA	GCGTCGGATT	TGACACTAAA	TCGGGTATGC	2350

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CCAAACTTCT GCGTGCAAT GACTGATAAT GATCGCGGGA ACGGACTCGA	2450
TCAACGGAGT CAGATTGGC GTGATGCAA TGAGGTACGT GAATTGGTTT	2500
CATTTCAGTA TGAAGTGTG ACCAATAGAG TAAGCATATC AACGGTTTTC	2550
TTATATGAAG ACCTCAACCA TTCACGCGTT GAACTTAACT TTTGATTAC	2600
TGGAAGTGGT GAAATAAAG TGGATTATGT ACTGAAACCG GGAGAAGATT	2650
TACCAGAAAT ACCAGAGATA GGTTCGATGT TAACGATGCC TAAGTCGTTT	2700
GATCAGTTAA GTTGGTATGG AAAAGGCCCA CATGAATCGT ATTGGGATAA	2750
ACAAAAAGGC GCGAAATAG GTCTTTATCA AGGATTTGTC GCGATCAGT	2800
ATGTGCCGTA TTGAAACCA CAAGAATGTG GCAACAAAGT AGGAGTTCGT	2850
TCAGCAGAAT TGGTTAATGA TGTTGGTGTT GGTTCGATTA TAAGTGGACT	2900
TCCAACGCTG GAGTTAAATG TCTTACCATA CACACCAGTG CAACTGGAAT	2950
CAGCTGATCA TAGCTATCAA TTACCAGAAA CAGATCAGAC TGTGTGCGT	3000
ATTAATTTAG GACAAATGGG AGTTGGTGGT GATGATAGTT GGGGACAGCG	3050
AACACACCAA GACTTTACCT TATTTGCAA TAAACCTAT CACTATAGCT	3100
TCATGTTGAA TAGTTTAAAC AGA	3123

SEQ ID NO: 3

(2) INFORMATION FOR SEQ ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION SEQ ID NO: 3

CCGTCATCCA TATCACC

SEQ ID NO: 4

(2) INFORMATION FOR SEQ ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION SEQ ID NO: 4

CCTTTGCCCC AGAGCCAACC

SEQ ID NO: 5

(2) INFORMATION FOR SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION SEQ ID NO: 5

GCTATTATCA GACTTGGCAC C

SEQ ID NO: 6

(2) INFORMATION FOR SEQ ID NO: 6

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 nucleotides

(B) TYPE: nucleic acid

-continued

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION SEQ ID NO: 6
GTAATTCAAT GTTCCAACGT G

SEQ ID NO: 7
(2) INFORMATION FOR SEQ ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION SEQ ID NO: 7
CGCTTATGGT GTGAAG

SEQ ID NO: 8
(2) INFORMATION FOR SEQ ID NO: 8

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION SEQ ID NO: 8
GGGCTGGCTT AACTATGCGG

SEQ ID NO: 9
(2) INFORMATION FOR SEQ ID NO: 9

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION SEQ ID NO: 9
CTGAATTCGC ATATGGCAAA AAAATTAAAA AAATTC

SEQ ID NO: 10
(2) INFORMATION FOR SEQ ID NO: 10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION SEQ ID NO: 10
CCAAGCTTAT CTGTTTAAAC TATTCAACAT G

SEQ ID NO: 11
(2) INFORMATION FOR SEQ ID NO: 11

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION SEQ ID NO: 11
GGCCATGGAT CCATGGCAAA AAAATTAAAA AAATTC

SEQ ID NO: 12
(2) INFORMATION FOR SEQ ID NO: 12

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(xi) SEQUENCE DESCRIPTION SEQ ID NO: 12

GGCCATCCCG GGTATCTGT TTAACTATT CAACATG

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 12

<210> SEQ ID NO 1

<211> LENGTH: 1041

<212> TYPE: PRT

<213> ORGANISM: Alkalilactibacillus ikkense

<400> SEQUENCE: 1

Met Ala Lys Lys Leu Lys Lys Phe Asn Tyr Leu Pro Pro Lys Asn Gly
 1 5 10 15

Tyr Pro Glu Trp Asn Asn Asn Pro Glu Ile Phe Gln Leu Asn Arg Arg
 20 25 30

Glu Ala His Ala Thr Leu Val Pro Tyr Ser Asn Leu Glu Leu Ala Leu
 35 40 45

Lys Gly Glu Arg Thr Ala Ser Ser Phe Tyr Gln Ser Leu Asn Gly Ser
 50 55 60

Trp Gln Phe Ala Phe Ala Gln Glu Pro Thr Lys Arg Val Ile Asp Phe
 65 70 75 80

Tyr Arg Lys Asp Phe Asp His Arg Asp Trp Asp Ser Ile Lys Val Pro
 85 90 95

Ser His Trp Gln Leu Glu Gly Tyr Asp Tyr Pro Gln Tyr Thr Asn Thr
 100 105 110

Thr Tyr Pro Trp Val Glu Lys Glu Thr Ile Lys Pro Pro Phe Ala Pro
 115 120 125

Thr Asn Tyr Asn Pro Val Gly Gln Tyr Val Arg Thr Phe Glu Leu Pro
 130 135 140

Thr Asp Trp Asn Gly Ala Pro Val Tyr Leu Asn Phe Gln Gly Val Glu
 145 150 155 160

Ser Ala Phe Tyr Val Trp Ile Asn Gly Asp Leu Val Gly Tyr Ser Glu
 165 170 175

Asp Thr Phe Thr Pro Ala Glu Phe Asp Ile Thr Pro Tyr Leu Ile Glu
 180 185 190

Gly Glu Asn Lys Leu Ala Val Glu Val Tyr Arg Trp Ser Asp Ala Ser
 195 200 205

Trp Leu Glu Asp Gln Asp Phe Trp Arg Leu Ser Gly Ile Phe Arg Asp
 210 215 220

Val Tyr Leu Tyr Ala Thr Pro Ala Gln His Ile Asp Asp Phe Phe Val
 225 230 235 240

Thr His Glu Leu Asp Ala Asp Tyr Arg Asn Ala Thr Leu Lys Ile Asp
 245 250 255

Met Lys Val Arg Asp Tyr Phe Glu Ile Gly Glu Pro Val Thr Val Asn
 260 265 270

Ala Met Leu Phe Asp Leu Asn Gly Asn Pro Val Leu Lys Gln Pro Leu
 275 280 285

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Leu Ser Ala Val Asp Phe Ser Gly Lys Glu Val Ala Asp Val Ser Val
 290 295 300
 Ile Thr Thr Ile Asp Asn Pro Leu Lys Trp Ser Ala Glu Asp Pro Asn
 305 310 315 320
 Leu Tyr Thr Leu Val Leu Ser Leu Val Asp Gln Asn Gly Lys Leu Leu
 325 330 335
 Glu Thr Glu Ser Cys Arg Val Gly Phe Arg Lys Phe Glu Arg Lys Asp
 340 345 350
 Gly Leu Met Gln Ile Asn Gly Lys Arg Ile Val Phe Lys Gly Thr Asn
 355 360 365
 Arg His Glu Phe Ala Ser Asp Lys Gly Arg Ala Ile Thr Ile Asp Asp
 370 375 380
 Met Val Asn Asp Ile Gln Leu Met Lys Gln His Asn Ile Asn Ala Val
 385 390 395 400
 Arg Thr Ser His Tyr Pro Asn His Pro Leu Trp Tyr Glu Leu Cys Asp
 405 410 415
 Thr Tyr Gly Leu Tyr Val Ile Asp Glu Thr Asn Leu Glu Thr His Gly
 420 425 430
 Thr Trp Val Tyr Gly Gln Lys Gly Leu Ala Glu Thr Ile Pro Gly Ser
 435 440 445
 Leu Pro Lys Trp Thr Glu Asn Val Leu Asp Arg Cys Asn Ser Met Phe
 450 455 460
 Gln Arg Asp Lys Asn His Pro Ser Ile Leu Asp Trp Ser Leu Gly Asn
 465 470 475 480
 Glu Ser Phe Gly Gly Asp Asn Phe Leu Lys Met His Asp Phe Phe Thr
 485 490 495
 Glu Gln Asp Pro Ala Arg Leu Val His Tyr Glu Gly Ile Phe His Tyr
 500 505 510
 Arg Glu Ser Glu Arg Ala Ser Asp Met Glu Ser Thr Met Tyr Ile Ser
 515 520 525
 Pro Glu Gly Ile Glu Asp Tyr Ala Lys Lys Ala Thr Lys Glu Thr Lys
 530 535 540
 Pro Tyr Ile Leu Cys Glu Phe Ser His Ala Met Gly Asn Ser Leu Gly
 545 550 555 560
 Asn Phe Tyr Lys Tyr Thr Glu Leu Phe Asp Gln Tyr Pro Ile Leu Gln
 565 570 575
 Gly Gly Phe Ile Trp Asp Trp Lys Asp Gln Ser Leu Leu Thr Lys Thr
 580 585 590
 Ala Gly Gly Thr Pro Tyr Leu Ala Tyr Gly Gly Asp Phe Gly Glu Ser
 595 600 605
 Pro His Asp Gly Asn Phe Ala Gly Asn Gly Leu Ile Phe Gly Asp Gly
 610 615 620
 Lys Val Ser Pro Lys Ile Phe Glu Val Lys Arg Cys Tyr Gln Asn Val
 625 630 635 640
 Asp Phe Lys Ala Ile Asp Leu Val His Gly Gln Ile Glu Leu Thr Asn
 645 650 655
 Lys Tyr Leu Phe Thr Asn Leu Ala Asp Tyr Gln Leu Asn Trp Val Ile
 660 665 670
 Thr Arg Asn Gly Asp Ala Ile Glu Ser Gly Ala Thr Asn Ile Asn Val
 675 680 685
 Leu Pro Gly Glu Lys Arg Glu Val Ile Leu Asp Tyr Thr Phe Pro Thr
 690 695 700
 Gly Val Cys Met Thr Asp Glu Tyr Ile Leu Thr Leu Arg Phe Ser Glu

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705	710	715	720
Lys Gly Asp Arg Leu Trp Cys Glu Ala Gly His Glu Val Ala Phe Asn	725	730	735
Gln Phe Val Leu Pro Thr Lys Val Thr Lys Leu Arg Glu Lys Thr Gln	740	745	750
Asp Thr Lys Thr Leu Ser Val Glu Val Met Gln Asp Arg Leu Val Thr	755	760	765
Ser Gly Ala Gly Phe Ser Val Gly Phe Asp Thr Lys Ser Gly Met Leu	770	775	780
Val Ser Tyr Gln Val Gly Gly Asn Glu Leu Val Lys Glu Ala Leu Val	785	790	795
Pro Asn Phe Trp Arg Ala Met Thr Asp Asn Asp Arg Gly Asn Gly Leu	805	810	815
Asp Gln Arg Ser Gln Ile Trp Arg Asp Ala Asn Glu Val Arg Glu Leu	820	825	830
Val Ser Phe Gln Tyr Glu Val Leu Thr Asn Arg Val Ser Ile Ser Thr	835	840	845
Val Phe Leu Tyr Glu Asp Leu Asn His Ser Arg Val Glu Leu Asn Phe	850	855	860
Leu Ile Thr Gly Thr Gly Glu Ile Lys Val Asp Tyr Val Leu Lys Pro	865	870	875
Gly Glu Asp Leu Pro Glu Ile Pro Glu Ile Gly Leu Met Leu Thr Met	885	890	895
Pro Lys Ser Phe Asp Gln Leu Ser Trp Tyr Gly Lys Gly Pro His Glu	900	905	910
Ser Tyr Trp Asp Lys Gln Lys Gly Ala Lys Ile Gly Leu Tyr Gln Gly	915	920	925
Phe Val Gly Asp Gln Tyr Val Pro Tyr Leu Lys Pro Gln Glu Cys Gly	930	935	940
Asn Lys Val Gly Val Arg Ser Ala Glu Leu Val Asn Asp Val Gly Val	945	950	955
Gly Leu Ile Ile Ser Gly Leu Pro Thr Leu Glu Leu Asn Val Leu Pro	965	970	975
Tyr Thr Pro Val Gln Leu Glu Ser Ala Asp His Ser Tyr Gln Leu Pro	980	985	990
Glu Thr Asp Gln Thr Val Val Arg Ile Asn Leu Gly Gln Met Gly Val	995	1000	1005
Gly Gly Asp Asp Ser Trp Gly Gln Arg Thr His Gln Asp Phe Thr	1010	1015	1020
Leu Phe Ala Asn Lys Thr Tyr His Tyr Ser Phe Met Leu Asn Ser	1025	1030	1035
Leu Asn Arg	1040		

<210> SEQ ID NO 2

<211> LENGTH: 3123

<212> TYPE: DNA

<213> ORGANISM: Alkalilactibacillus ikkense

<400> SEQUENCE: 2

atggcaaaaa aattaaaaaa attcaactac ctcccaccaa aaaacgggta cccagagtgg	60
aataataatc cggaatttt tcaacttaat cgaagagagg cgcattgcaac attggtgcca	120
tattctaatt tggaattggc acttaaaggg gagcggacag catcatcatt ttatcaatct	180
ttaaattgta gttggcagtt tgcctttgcc caagagccaa ccaagcgagt gatagatttt	240

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tatcggaag attttgatca tcgcgattgg gattcgatta aagtaccaag tcattggcag	300
ttagaaggct atgactaccc gcaatacacc aacacaacgt acccatgggt agaaaaagaa	360
acgattaaac ctccatttgc accaacaat tataatccag tcggacaata tgttcgcacg	420
tttgaattac cgactgattg gaatggagct cccgtttatc tgaatttcca aggtgttgaa	480
tcagctttct acgtctggat aaatggtgat ttggtcggat acagtgagga cactttcaca	540
ccagctgaat ttgatataac tccctattta atagagggtg aaaataagct agcggtagaa	600
gtctatcggt ggagtgatgc gagctggctt gaagaccagg atttctggag gttaagcggg	660
atttttcgtg acgtctatct atatgcaaca ccagctcagc acattgatga tttctttgtc	720
acacacgaac ttgatgcaga ctatcgaaat gcaacgttga agattgatat gaaagtgcgc	780
gattatttgc agattggcga gcctgtcaca gttaatgcga tgctctttga tcttaatggg	840
aatccggttc tcaagcaacc gcttttatcg gcagtagatt tttcaggtaa agaagttgct	900
gatgtgagcg taataacaac aattgataat ccattgaaat ggagtgcgga agatcccaat	960
ctgtacactt tggttttaag tttagtgtat cagaatggca agttgcttga aacagaaagc	1020
tgctcgcgtt gatttctgaa atttgaacgc aaggacggat tgatgcaaat taatggaaag	1080
cggattgtct ttaaagggac aaatcgtcac gaattcgctt ctgataaagg tcgggcgata	1140
acgatagatg atatggttaa tgatattcag ctgatgaagc agcataacat taatgccgtt	1200
cgaacctcac attatccgaa tcatccgctt tgggtatgagt tgtgtgatac gtatgggtta	1260
tatgtgattg acgagacaaa cttagagacg cacgggacat gggtttatgg tcaaaaagga	1320
ttggctgaga caataccagg tagtctacca aagtggactg aaaacgtctt ggatcgttgt	1380
aattcaatgt tccaactgta taaaaaccac ccacgattc tggattggtc acttggtaat	1440
gaatcttttg gtggcgataa cttcttgaag atgcatgact tctttacgga acaagatcca	1500
gctcgtctgg tgcactatga ggggattttt cattatcgtg aatctgaacg ggcactctgat	1560
atggagagta ccattgtatat ttcgccagaa ggcataggg actatgcaa gaaagcgacc	1620
aaggagacga aaccatatat tttatgcgaa ttcagccatg cgatgggcaa ctgcctagga	1680
aacttttata agtataccga gctatttgat caatatccga tcttacaagg aggttcatt	1740
tgggattgga aggatcaatc gctgctaacg aagacagcag gaggcacacc gtatcttgct	1800
tatgggtggtg attttgggtga atcgccacac gacggcaact ttgctggtaa tggtttgatt	1860
tttgagatg gcaagggttag cccgaagatt tttgaagtga agcgttgtaa ccaaatggt	1920
gatttcaaag caatagactt agtgcacgga caaatcgaat tgaccaataa atacttggtc	1980
accaatctcg ctgactacca actaaattgg gttatcactc gaaacggtga tgcaatagag	2040
tcgggtgcta ctaacatcaa tgtcttacca ggtgaaaaa gagaggttat acttgactac	2100
acgttcccaa caggcgtttg catgacggat gaatatattt tgaccttcg ttttctgag	2160
aaaggatgac gcttatgggtg tgaagcggga catgaagttg catttaatca gtttgtttta	2220
ccaacaaaag ttacgaattt acgtgagaag acacaagata ccaagacgct ttcagtgtaa	2280
gtaatgcaag atcgacttgt tacatctggt gctggattta gcgtcggatt tgacactaaa	2340
tcgggtatgc ttgtttctta ccaagttgga ggtaatgaat tggtgaaaga ggcacttggtg	2400
ccaaacttct ggcgtgcaat gactgataat gatcgcgga acggactcga tcaacggagt	2460
cagatttggc gtgatgcaaa tgaggtaagt gaattggttt catttcagta tgaagtgttg	2520
accaatagag taagcatatc aacggttttc ttatatgaag acctcaacca ttcacgcgtt	2580
gaacttaact ttttgattac tggaaactggt gaaataaagg tggattatgt actgaaaccg	2640

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ggagaagatt taccagaaat accagagata ggtttgatgt taacgatgcc taagtcgttt 2700
gatcagttaa gttggtatgg aaaaggccca catgaatcgt attgggataa acaaaaaggc 2760
gcgaaaatag gtctttatca aggatttgtc gccgatcagt atgtgccgta tttgaaacca 2820
caagaatgtg gcaacaaagt aggagttcgt tcagcagaat tggttaatga tgttggtggt 2880
ggtttgatta taagtggact tccaacgctg gagttaaatg tcttaccata cacaccagt 2940
caactggaat cagctgatca tagctatcaa ttaccagaaa cagatcagac tgttggtgct 3000
attaatttag gacaaatggg agttggtggt gatgatagtt ggggacagcg aacacaccaa 3060
gactttacct tatttgcaaa taaaacctat cactatagct tcattgtgaa tagtttaaac 3120
aga 3123

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<210> SEQ ID NO 3
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic custom-made primer

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<400> SEQUENCE: 3

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ccgtcatcca taccacc 17

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<210> SEQ ID NO 4
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic custom-made primer

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<400> SEQUENCE: 4

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cctttgccca agagccaacc 20

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<210> SEQ ID NO 5
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic custom-made primer

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<400> SEQUENCE: 5

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gctattatca gacttggcac c 21

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<210> SEQ ID NO 6
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic custom-made primer

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<400> SEQUENCE: 6

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gtaattcaat gttccaacgt g 21

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<210> SEQ ID NO 7
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic custom-made primer

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<400> SEQUENCE: 7

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cgcttatggt gtgaag 16

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<210> SEQ ID NO 8
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic custom-made primer

<400> SEQUENCE: 8

gggctggcctt aactatgcgg                               20

<210> SEQ ID NO 9
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic custom-made primer

<400> SEQUENCE: 9

ctgaattcgc atatggcaaa aaaattaaaa aaattc           36

<210> SEQ ID NO 10
<211> LENGTH: 31
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic custom-made primer

<400> SEQUENCE: 10

ccaagcttat ctgtttaaac tattcaacat g                 31

<210> SEQ ID NO 11
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic custom-made primer

<400> SEQUENCE: 11

ggccatggat ccatggcaaa aaaattaaaa aaattc           36

<210> SEQ ID NO 12
<211> LENGTH: 37
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic custom-made primer

<400> SEQUENCE: 12

ggccatcccg gggtatctgt ttaactatt caacatg           37

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The invention claimed is:

1. A purified cold-active beta-galactosidase having the amino acid sequence as defined in SEQ ID NO. 1 or one having at least 90% homology to the amino acid sequence as defined in SEQ ID NO. 1, the amino acid sequence being selected so that the enzyme has a stable enzymatic activity at temperatures less than 8° C.

2. A beta-galactosidase according to claim 1, wherein the amino acid sequence has at least 95% homology to the amino acid sequence as defined in SEQ ID NO. 1.

3. A beta-galactosidase according to claim 1, wherein it is produced by a strain of an *Alkalilactibacillus*.

4. A beta-galactosidase according to claim 1, wherein it is produced by *Alkalilactibacillus ikkense*.

5. An isolated DNA sequence comprising a gene which encodes the beta-galactosidase according to claim 1.

6. An isolated DNA sequence, which a) encodes a protein with an amino acid sequence as given in SEQ ID NO. 2, or b) hybridizes to the sequence of a), at 6×SSC, 0.5% SDS and 50% formamide at 42° C., before being washed in a solution of 0.1% ×SSC, 0.5% SDS at 68° C., or c) is degenerative of the sequence of a) or b).

7. A DNA sequence according to claim 6, wherein the sequence is as given in SEQ ID NO. 2.

8. A recombinant vector comprising a DNA sequence of claim 5.

9. A vector of claim 8, wherein said vector is an expression vector.

10. A host cell transformed with a vector of claim 8.

11. A cell according to claim 10, wherein the cell is selected from the group consisting of *Escherichia*, *Bacillus*, *Bifidobacterium*, *Lactococcus*, *Lactobacillus*, *Streptomyces*, *Leu-*

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conostoc, *Streptomyces*, *Saccharomyces*, *Kluyveromyces*, *Candida*, *Torula*, *Torulopsis* and *Aspergillus*.

12. A cell of claim 11, wherein the cell is selected from the group consisting of *Bifidobacterium breve*, *Bifidobacterium longum*, *Bifidobacterium infantis*, *Bifidobacterium bifidum*, *Bifidobacterium animalis*, and *Lactococcus lactis*.

13. Use of a cell of claim 10 for producing a product selected from the group consisting of lactose-free milk, low-lactose milk, yoghurt, cheese, fermented milk products, dietary supplement and probiotic comestible product comprising adding the host cell of claim 10.

14. A method according to claim 13 for producing a dairy product with a lactose concentration at 1% w/v or lower.

15. A method according to claim 14, wherein the lactose concentration is 0.1% w/v or lower.

16. A method according to claim 15, wherein the lactose concentration is 0.01% w/v or lower.

17. A method of a beta-galactosidase according to claim 1 for producing a product selected from the group consisting of lactose-free milk, low-lactose milk, yoghurt, cheese, fer-

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mented milk products, dietary supplement and probiotic comestible product comprising adding the beta-galactosidase of claim 1.

18. A method according to claim 17 for producing a dairy product with a lactose concentration at 1% w/v or lower.

19. A method according to claim 18, wherein the lactose concentration is 0.1% w/v or lower.

20. A method according to claim 19, wherein the lactose concentration is 0.01% w/v or lower.

21. A process for producing an enzyme of claim 1, comprising culturing a cell of any one of claims 10 to 12 in a suitable culture medium under conditions permitting expression of said enzyme, and recovering the resulting enzyme from the culture.

22. A process according to claim 21, wherein the resulting enzyme is immobilized.

23. A psychrophilic bacterium *Alkalilactibacillus ikkense* BCCM Accession No LMG P-24866 and variants and mutants derived therefrom capable of producing a cold-active beta galactosidase defined by claim 1.

* * * * *