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(54) Titre : PRODUCTION DE MUTANTS INACTIFS OU FAIBLEMENT ACTIFS DE LA PHOSPHATASE ALCALINE ET
LEUR EXPRESSION DANS LA LEVURE

(54) Title: PRODUCTION OF WEAKLY ACTIVE OR INACTIVE MUTANTS OF ALKALINE PHOSPHATASE AND THEIR
EXPRESSION IN YEAST

(57) **Abrégé/Abstract:**

The invention concerns a method for the recombinant production or expression of eukaryotic alkaline phosphatase mutants in yeast cells wherein the specifically introduced mutations result in a reduction of the specific AP activity by at least a factor 1:100. The invention also concerns a method for inserting corresponding nucleic acid sequences into a vector for expression in methylotrophic yeast strains and it concerns corresponding vectors and host strains.

Abstract

The invention concerns a method for the recombinant production or expression of eukaryotic alkaline phosphatase mutants in yeast cells wherein the specifically introduced mutations result in a reduction of the specific AP activity by at least a factor 1:100. The invention also concerns a method for inserting corresponding nucleic acid sequences into a vector for expression in methylotrophic yeast strains and it concerns corresponding vectors and host strains.

Production of weakly active or inactive mutants of alkaline phosphatase and their expression in yeast

The invention concerns a method for the recombinant production and expression of mutants of a eukaryotic alkaline phosphatase which is weakly active or inactive. In addition the invention concerns codon-optimized DNAs based on the nucleic acid sequence which codes for a highly-active alkaline phosphatase and which has been modified by directed mutagenesis in such a manner that it codes for an alkaline phosphatase which has only a weak activity or is inactive. The invention also concerns a method for inserting the mutated DNA into a vector for expression in yeast cells and a method for expressing the alkaline phosphatase mutants in yeast.

Alkaline phosphatases (AP) are dimeric, zinc-containing, non-specific phosphomonoesterases which occur in prokaryotic and eukaryotic organisms e.g. in *E. coli* and mammals (McComb et al., 1979 *Alkaline Phosphatases Plenum Press, New York*). A comparison of the primary structure of various alkaline phosphatases showed that there is a high degree of homology (25 – 30 % homology between *E. coli* and mammalian AP; Millàn, 1988 *Anticancer Res.* 8, 995-1004; Harris, 1989 *Clin. Chim. Acta* 186, 133-150).

In humans and higher animals the AP family consists of four members which are coded in different gene loci (Millàn, 1988 *Anticancer Res.* 8, 995-1004; Harris 1989 *Clin. Chim. Acta* 186, 133-150). The family of alkaline phosphatases includes the tissue-specific APs (placental AP (PLAP), germ cell AP (GCAP) and intestinal AP (IAP)) and the non-tissue-specific APs (TnAP) which are mainly located in the liver, kidney and bones.

An important property of the previously known APs is the large variability in the catalytic activity of mammalian APs which have a 10-100-fold higher k_{cat} s value than *E. coli* AP. Among the mammalian APs the APs from the bovine intestine (bIAP)

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exhibit the highest specific activities. This property makes the bIAPs attractive for biochemical applications such as e.g. the use of corresponding enzyme conjugates as a diagnostic reagent or for dephosphorylating DNA. The existence of various alkaline phosphatases from the bovine intestine which have different levels of specific activity is described in EP 0955 369 and Manes et al. (1998), *J. Biol. Chem.* 273 No. 36, 23353-23360. Up to now recombinant expression of eukaryotic alkaline phosphatases of low activity (up to 3000 U/mg) has been described in various eukaryotic cell lines such as CHO cells (bIAP I/WO 93/18139; Weissig et al. 1993, *Biochem. J.* 260, 503-508), COS cells (human placental AP/Berger et al. 1987 *Biochemistry* 84, 4885-4889) or baculovirus expression system (human placental AP/Davis et al. 1992, *Biotechnology* 10, 1148-1150). The expression of APs having a higher activity (spec. activity > 3000 U/mg) from the bovine intestine in CHO cells has also been described (bIAP II, III and IV/Manes et al. 1998, *J. Biol. Chem.* 273 No. 36, 23353-23360). However, a disadvantage of expressing alkaline phosphatases in these expression systems is the low expression rate which makes it uneconomical to produce eukaryotic alkaline phosphatase recombinantly.

Although in principle it is possible to express eukaryotic alkaline phosphatases in prokaryotic expression hosts such as *E. coli* (human placental AP/Beck and Burtcher, 1994 *Protein Expression and Purification* 5, 192-197), the alkaline phosphatases expressed in prokaryotes have no glycosylation which is essential especially for the preparation of enzyme conjugates depending on the conjugate method.

Alkaline phosphatase is often used as an enzyme conjugate in the form of a complex with an antibody. In this case the alkaline phosphatase is conjugated with an antibody which is directed against a particular antigen. This antigen is firstly bound in a first reaction by an antibody immobilized on a vessel wall which recognizes a different epitope on the target antigen than does the antibody-AP conjugate. This antibody-antigen complex is then detected in a second reaction by the binding of the antibody-AP conjugate. False-positive results occur repeatedly in such tests and are caused by an unspecific binding of the antibody-AP conjugate to the vessel wall or to the first antibody. These interferences can be prevented by adding an excess of a conjugate

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containing an inactive or weakly active AP mutant as an interference-eliminating protein. However, in order to act very specifically as an interference-eliminating protein, the AP mutant must, in addition to having a low activity or no activity, also have essentially the same tertiary and quaternary structure.

Hence the object of the present invention is to use directed mutagenesis to produce mutants of alkaline phosphatase as an interference-eliminating protein which are only very weakly-active or completely inactive but whose amino acid sequence is only slightly modified and have a tertiary and quaternary structure that is changed as little as possible. Another object of the invention is to develop a robust and stable expression method for producing glycosylated eukaryotic alkaline phosphatase mutants which also enables an economical production of a corresponding alkaline phosphatase mutant due to the high expression rate.

The present invention concerns mutants of eukaryotic alkaline phosphatase, wherein

- the sequence to be mutated is at least 77 % homologous to SEQ ID NO.:2 and
- the mutant has an activity which is reduced by at least 100-fold compared to the wild-type and
- the mutant has one or more of the following mutations and the position of the mutation is defined relative to the position in SEQ ID NO.:2:

Asp42: for Asn, Val, Ala or Ser

Ser92: for Ala, Gly, Val or Leu

Ser155: for Ala, Gly, Val or Leu

Glu311: for Gln, Asn, Leu, Ile or Met

Asp316: for Asn, Val, Ala or Ser

His320: for Asn, Phe, Asp or Tyr,

Gly322: for any amino acid larger than Asp such as Phe, Trp, Arg, Lys,
Glu, Gln, His, Tyr or Ile

Asp357: for Asn, Val, Ala or Ser

His358: for Asn, Phe, Asp or Tyr

His432: for Asn, Phe, Asp or Tyr

A mutation of the amino acid sequence is understood as an exchange of the naturally occurring amino acid at the desired position for any other amino acid which does not

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hinder folding into the correct tertiary and quarternary structure, but however, are not functional.

The sequence to be mutated (wild type) can for example be a human intestinal AP or a human placental AP. In addition an AP of low activity or high activity from bovine intestine also come into consideration as the wild-type AP according to the invention. All these enzymes are at least 77 % homologous to SEQ ID NO.:2. The homology was determined with the software "Open VMS Vax Version V6.2"; (copyright) (c) 1982-2001, Genetics Computer Group, Inc.; A wholly owned subsidiary of Oxford Molecular Group, Inc. All rights reserved. Published research assisted by this software should cite: Wisconsin Package Version 10.2, Genetics Computer Group (GCG), Madison, Wisc.).

The stated position of the amino acid to be mutated relates to the amino acid sequence of native alkaline phosphatase according to SEQ ID NO.:2, without a signal sequence. However, the stated amino acid positions are also transferable to other bovine alkaline phosphatases or alkaline phosphatases from other organisms; the exchanges affect amino acids with highly conserved functions within the protein and hence it is only necessary to adapt the position after the respective amino acid sequence.

Directed mutagenesis of the DNA sequence means that one or more codons are changed by means of PCR mutagenesis. In this process only as few changes as necessary are changed in the base triplet of the codon-optimized gene according to SEQ ID NO.:3 and in the most favourable case only one base is changed.

Mutants of the eukaryotic alkaline phosphatase according to claim 1 are preferred according to the invention in which the mutant has one or more of the following mutations and the position of the mutation is defined relative to the position in SEQ ID NO.:2.

Asp42:	for Val or Asn
Ser92:	for Ala or Gly
Ser155:	for Ala or Gly
Glu311:	for Gln or Leu

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Asp316: for Val or Asn
His320: for Asn or Phe
Gly322: for Phe or Lys
Asp357: for Val or Asn
His358: for Asn or Phe
His432: for Asn or Phe

The above-mentioned mutants of the eukaryotic alkaline phosphatase are preferred according to the invention in which the enzyme having the wild-type sequence has a specific activity of more than 7000 U/mg. In addition a DNA sequence is preferred as a gene sequence which is based on the gene which codes for a eukaryotic alkaline phosphatase mutant having a specific activity of more than 7000 U/mg and has been specifically mutated at a few positions such that the resulting DNA sequence codes for an amino acid sequence of the eukaryotic alkaline phosphatase mutant which is modified at one or a few positions, wherein the mutation results in a substantial to total reduction of the specific activity.

The mutants according to the invention of eukaryotic alkaline phosphatase are particularly preferred in which the mutant has an at least 1000-fold reduced AP activity compared to the wild-type enzyme. Furthermore mutants of the eukaryotic alkaline phosphatase according to the invention are preferred in which the mutant has an at least 1000-fold reduced activity compared to the corresponding wild-type enzyme. Those mutants are especially preferred according to the invention in which the reduction of the specific activity is below the detection limit (determined according to the activity test described in example 4).

The following amino acid positions have proven to be suitable according to the invention: Asp316/His320/His432 (binding partners of zinc atom 1), Asp42/Asp357/His358 (binding partners of zinc atom 2), Ser155/Glu311 (binding partners of the magnesium atom), Ser92 (hydroxyl group is deprotonated for the nucleophilic attack on the substrate) (Ma and Kantrowitz (1994), J. Biol. Chem. 16 pp. 31614-31619; Ma et al. (1995), Protein Science, 4, pp. 1498-1506; Kimura and Kikuta (2000) JBIC, 5, pp. 139-155; Stec et al. (2000), JMB 299 pp. 1303-1311) and Gly322 (important for the specific activity; EP 0 955 369). According to the invention the positions

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described above come into consideration as single mutants or also in all possible combinations of the above-mentioned positions as double, triple or multiple mutants. The mutated amino acid sequences according to SEQ ID NO's: 4-7, are particularly preferred in which SEQ ID NO.:4 represents a single mutant at position 92 (Ser92Ala), SEQ ID NO.:5 represents a single mutant at position 322 (Gly322Phe), SEQ ID NO.:6 represents a double mutant at positions 320 and 322 (His320Asn/Gly322Phe) and SEQ ID NO.:7 represents a triple mutant at positions 92, 320 and 322 (Ser92Ala/His320Asn/Gly322Phe). The respective DNA sequences are shown in SEQ ID NO.: 8 – 11.

The present invention also concerns a DNA which codes for the mutant according to the invention described above. Furthermore the present invention concerns vectors which contain the nucleic acid sequence according to the invention. In particular these are vectors containing a nucleic acid sequence, wherein the nucleic acid sequence is selected from the SEQ ID NO's: 4 – 7. Suitable vectors are known to a person skilled in the art such as pPICZ α A, B, C; pPICZ, pPICZ-E, pPICZ α -E; pPIC6, pPIC6 α A, B, C; pGAPZ, pGAPZ α A, B, C; pPIC9; pPIC9K, pPIC3.5, pPIC3.5K, pAO815, pMET, pMET α A, B, C; pYES-Dest52, pYES2.1/V5-His-TOPO, pYC2-E, pYES2.1-E; Yes vectors, pTEF1/Zeo, pTEF1/Bsd, pNMT-TOPO (e.g. Invitrogen). The corresponding gene sequences are for example cloned into the vectors pPICZ α A or pPIC9K which are commercially available (Invitrogen) and which contain the gene sequences of SEQ ID NO's: 8 – 11 according to the invention which are under the control of the AOX1 promoter. The following are examples of vectors prepared according to the invention: vectors pNaAP31-1 (fig. 1) and pNaAP31-2 (fig. 2), which have the gene sequence according to SEQ ID NO.: 8 each cloned into pPICZ α A (pNaAP31-1) and pPIC9K (pNaAP31-2).

The vectors pNaAP31-1 and pNaAP31-1 are equally relevant for the vectors prepared according to the invention since the final production clone can contain copies of both vectors.

An expression vector obtained according to the invention is preferably transformed into various strains of yeast such as *Pichia pastoris* and stably integrated into the

genome. An advantage of the stable integration into the yeast genome is in particular that no selection pressure is necessary when for example the weakly-active or inactive alkaline phosphatase mutants are subsequently produced in large volume fermenters. Stable integration into the genome means that the expression vector is incorporated into the genome of for example *Pichia pastoris* by means of homologous recombination and is thus transmitted from generation to generation as a permanent component of the yeast genome (Cregg, J.M. et al., Mol. Cell. Biol. 5 (1985), 3376-3385).

Another subject matter of the invention is a yeast strain transformed with one of the vectors according to the invention. Methylophilic yeasts such as the yeast *Pichia pastoris*, *Hansenula polymorpha*, *Saccharomyces cerevisiae*, *Yarrowia lipolytica* or *Schizosaccharomyces pombe* are particularly suitable as the yeast host. *Pichia pastoris* is particularly preferably used as the host strain. The *Pichia pastoris* X-33 strain is particularly preferably transformed with one of the described vectors.

The invention also concerns a method for producing the mutant of the eukaryotic alkaline phosphatase according to the invention in yeast cells comprising the steps: a) cloning a gene sequence according to the invention into different vectors, b) transforming the yeast, c) expression and d) purifying the alkaline phosphatase characterized in that

- a first vector has a resistance gene to a first selection marker
 - transformants which have integrated the resistance gene and the desired gene sequence into the genome are selected by growth on nutrient medium containing a low concentration of a first selection marker,
 - the gene copy number is increased by multiple transformation whereby multiple transformants are selected by growth on nutrient medium with increased selection pressure,
 - a second vector which has a resistance gene to a second selection marker is added,
 - the gene copy number is increased by multiple transformation whereby multiple transformants are selected by growth on nutrient medium with increased selection pressure, and
- those clones are selected which have stably integrated several copies of the

gene sequence and of the selection marker resistance genes into the genome.

Methylotrophic yeast cells are preferably used in the method according to the invention. *Pichia pastoris* is particularly preferably used as the yeast cell.

Furthermore it is preferred that a vector is used for the method according to the invention which essentially corresponds to a vector which is selected from the following vectors: pPICZ α A, B, C; pIZCZ, pPICZ-E, pPICZ α -E, pPIC6, pPIC6 α A, B, C; pGAPZ, pGAPZ α A, B, C; pPIC9; pPIC9K, pPIC3.5, pPIC3.5 K, pAO815, (Invitrogen).

The copy number of the mutated gene sequence in the methylotrophic yeast was increased by multiple transformation while simultaneously increasing the selection pressure with a suitable selection marker e.g. an antibiotic such as Zeocin® or Geneticin (G418), after which only those clones are viable which have stably integrated several copies of the expression vector into the genome. In order to be resistant to high concentrations of the antibiotic used as the selection marker, it is necessary that the clones produce increased amounts of resistance proteins. This can for example be achieved by a multiple integration of the expression vector which, in addition to the expression cassette for the respective AP mutant e.g. the alkaline phosphatase mutant Ser92Ala, also contains the resistance gene for the antibiotic used as the selection marker.

The object of producing alkaline phosphatase mutants in a robust and stable expression method having a high expression rate and at the same time in economical yields was achieved by the method described in the following.

The directed mutagenesis for producing the mutants according to the invention was carried out as follows: based on the gene which codes for a bovine alkaline phosphatase mutant and which was prepared synthetically, oligonucleotides which were complementary to one another or which overlapped were designed in which one or several base positions were changed compared to SEQ ID NO.:3. One of these primers was subsequently used in a PCR reaction as a partner of the 5' or 3' primer

described in the following and thus the AP gene was amplified in two sections containing the desired base exchange(s).

The two sections were subsequently analysed by means of agarose gel electrophoresis, the products having the expected length were isolated from the gel by means of the QIAquick gel extraction kit (QIAGEN) and synthesized in a further PCR reaction to form the complete gene product. The first five cycles of the PCR reaction were carried out without adding the primer at the 5' end and at the 3' end of the whole gene so that at first only a few fragments of the gene product of the expected length are formed from the two sections. The annealing temperature depends on the melting temperature of the overlapping region. Subsequently the terminal primers were added and the annealing temperature was increased in accordance with the annealing temperature of the primer with the lowest melting temperature. Afterwards the gene fragment of the expected length was amplified in a further 25 cycles.

The PCR mixture was analysed by means of agarose gel electrophoresis and the gene fragment having the expected size was isolated (QIAquick gel extraction kit/Qiagen).

The cloning of a corresponding PCR fragment, the transformation in *Pichia pastoris* and the expression of the corresponding AP mutant are described in example 2.

The recombinant alkaline phosphatase mutants can be isolated from the biomass by extraction methods which are in principle known to a person skilled in the art e.g. by "protein purification", Springer Publishers, Editor Robert Scopes (1982). A pure band product is achieved by suitable chromatographic methods such as in particular by using hydrophobic column materials and a cation exchanger.

Hence the present invention describes for the first time a method which allows an economical production of recombinant alkaline phosphatase mutants from mammals e.g. bovine intestine, in yeast which have a very greatly reduced AP activity or no longer have an AP activity but otherwise have properties which correspond to those of recombinant alkaline phosphatase mutants from the bovine intestine. These mutants can be used especially as interference-eliminating proteins in immunological test procedures in which AP is used as a label such as MTP-ELISA.

Figures

Figure 1

Plasmid map of the expression vector pNaAP31-1 combining the mutated gene sequence according to SEQ ID NO.: 8 in pICZαA (Invitrogen).

Figure 2

Plasmid map of the expression vector pNaAP31-1 combining the mutated gene sequence according to SEQ ID NO.: 8 in pIC9K (Invitrogen).

Legends for the sequence protocols SEQ ID NO's 1-21

SEQ ID NO.:1	native DNA sequence coding for highly active bovine AP without a signal sequence
SEQ ID NO.:2	amino acid sequence of the highly active bovine AP
SEQ ID NO.:3	DNA sequence of the synthetic gene coding for a highly active AP, the restriction cleavage site EcoRI is located upstream of the coding sequence and the restriction cleavage site Asp718 is located downstream thereof
SEQ ID NO.:4	amino acid sequence of the AP single mutant Ser92Ala (wild-type: highly active bovine AP)
SEQ ID NO.:5	amino acid sequence of the AP single mutant Gly322Phe (wild-type: highly active bovine AP)
SEQ ID NO.: 6	amino acid sequence of the AP double mutant His320/Gly322Phe (wild-type: highly active bovine AP)
SEQ ID NO.:7	amino acid sequence of the AP triple mutant Ser92Ala/His320/Gly322Phe (wild-type: highly active bovine AP)
SEQ ID NO.:8	DNA sequence of the synthetic gene coding for the AP single mutant Ser92Ala with the cleavage sites EcoRI and Asp718 located upstream and downstream respectively of the coding sequence
SEQ ID NO.:9	DNA sequence of the synthetic gene coding for the AP single mutant Gly322Phe with the cleavage sites EcoRI and Asp718 located upstream and downstream respectively of the coding sequence
SEQ ID NO.:10	DNA sequence of the synthetic gene coding for the AP double

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mutant His320Asn/Gly322Phe with the cleavage sites EcoRI and Asp718 located upstream and downstream respectively of the coding sequence

SEQ ID NO.:11 DNA sequence of the synthetic gene coding for the AP triple mutant Ser92Ala/His320Asn/Gly322Phe with the cleavage sites EcoRI and Asp718 located upstream and downstream respectively of the coding sequence

SEQ ID NO's:12-21 DNA sequences which were used as primers

Abbreviations

YPD: yeast peptone dextrose
YPDS: yeast peptone dextrose sorbitol
BMGY: buffered glycerol-complex medium
BMMY: buffered methanol-complex medium
MTP: microtitre plates

Example 1:Mutagenesis of the synthetic DNA sequence which codes for the bovine alkaline phosphatase mutants.

For the mutagenesis of the desired base triplet(s) by means of the PCR reaction, oligonucleotides were designed which have a correspondingly modified base sequence and are complementary to one another or are partially overlapping and complementary. These oligonucleotides were subsequently used as corresponding partners for the 5' primer 5'-hAP according to SEQ ID NO.: 12 or for the 3' primer 3'-hAP according to SEQ ID NO.:13 which each hybridize with the 5' end or with the 3' end respectively of the gene which codes for the bovine alkaline phosphatase mutants. In this manner the mutated gene sequence was amplified in two segments in a first reaction, the first segment carrying a mutation at the 3' end and the second segment carrying a mutation at the 5' end and a short base sequence at the 3' end of the first segment being identical to a short base sequence at the 5' end of the second segment.

These two segments were then fused in a second PCR reaction to form the full length product. For this the PCR reaction was firstly started without the 5'-hAP and 3'-hAP primers according to SEQ ID NO.: 12 and 13 and 5 cycles were carried out. A few molecules of the full length product are formed in this process; the annealing temperature in these 5 cycles depends on the melting temperature of the overlapping region of the two segments. Subsequently the 5' and 3' primer according to SEQ ID NO.: 12 and 13 are added, the annealing temperature is adapted to the melting temperature of the primer with the lower melting temperature and the full length product is amplified in a further 25 cycles.

Mutagenesis to generate the single mutant Ser92Ala:

In order to generate the single mutant Ser92Ala the base triplet at position 274-276, with reference to the base triplet TTG according to SEQ ID NO.:3, which codes for the first amino acid of the highly-active bovine alkaline phosphatase was mutated from TCT into GCT. The primers 5'-S92A according to SEQ ID NO.:14 and 3'-S92A according to SEQ ID NO.:15 which are partially complementary to one another were

designed for this purpose. The first PCR reaction was subsequently started with the primer pairs 5'-hAP and 3'-S92A as well as 5'-S92A and 3'-hAP separate from one another using the gene sequence according to SEQ ID NO.:3 as the template such that the mutated gene sequence was firstly amplified in two segments. The segments were analysed by an agarose gel and isolated from the agarose gel (QIAquick gel extraction kit/Qiagen) and subsequently used in the second PCR reaction. In this second PCR reaction the two segments were fused as described above to form the full length product. The mutated gene sequence formed in this manner was cloned using PCR cloning vectors (PCR cloning kit – blunt end/Roche Diagnostics) and examined by means of restriction analysis and sequencing.

Mutagenesis to generate the single mutant Gly322Phe

In order to generate the single mutant Gly322Phe the base triplet at position 964-966, with reference to the base triplet TTG according to SEQ ID NO.:3, which codes for the first amino acid of the highly-active bovine alkaline phosphatase was mutated from GGT into TTT. The primers 5'-G322F according to SEQ ID NO.:16 and 3'-G322F according to SEQ ID NO.:17 which are partially complementary to one another were designed for this purpose. The first PCR reaction was subsequently started with the primer pairs 5'-hAP and 3'-G322F as well as 5'-G322F and 3'-hAP separate from one another using the gene sequence according to SEQ ID NO.:3 as the template such that the mutated gene sequence was firstly amplified in two segments. The segments were analysed by an agarose gel and isolated from the agarose gel (QIAquick gel extraction kit/Qiagen) and subsequently used in the second PCR reaction. In this second PCR reaction the two segments were fused as described above to form the full length product. The mutated gene sequence formed in this manner was cloned using PCR cloning vectors (PCR cloning kit – blunt end/Roche Diagnostics) and examined by means of restriction analysis and sequencing.

Mutagenesis to generate the double mutant His320Asn/Gly322Phe

In order to generate the double mutant His320Asn/Gly322Phe, the base triplets at positions 958-960 and 964-966, with reference to the first base triplet TTG according to SEQ ID NO.:3, which codes for the first amino acid of the highly-active bovine alkaline phosphatase was mutated from CAT into AAT and GGT into TTT. The

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primers 5'-H320N/G322F according to SEQ ID NO.:18 and 3'-H320N/G322F according to SEQ ID NO.:19 which are partially complementary to one another were designed for this purpose. The first PCR reaction was subsequently started with the primer pairs 5'-hAP and 3'-H320N/G322F as well as 5'-H320N/G322F and 3'-hAP separate from one another using the gene sequence according to SEQ ID NO.:3 as the template such that the mutated gene sequence was firstly amplified in two segments. The segments were analysed by an agarose gel and isolated from the agarose gel (QIAquick gel extraction kit/Qiagen) and subsequently used in the second PCR reaction. In this second PCR reaction the two segments were fused as described above to form the full length product. The mutated gene sequence formed in this manner was cloned using PCR cloning vectors (PCR cloning kit – blunt end/Roche Diagnostics) and examined by means of restriction analysis and sequencing.

Generation of the triple mutant Ser92Ala/His320Asn/Gly322Phe

The triple mutant Ser92Ala/His320Asn/Gly322Phe was generated by combining the single mutant Ser92Ala and the double mutant His320Asn/Gly322Phe. For this the two mutated gene sequences which were each cloned into PCR cloning vectors (PCR cloning kit – blunt end/Roche Diagnostics) were cleaved separately from one another with the restriction endonucleases MunI and Asp718, and the restriction mixture was separated by means of agarose gel electrophoresis. MunI cleaves between the positions of the triplets of Ser92 and His320. A ca. 3700 bp long vector fragment was isolated from the single mutant Ser92Ala and a ca. 900 bp long fragment of the 3' region of the mutated gene sequence of the double mutant His320Asn/Gly322Phe was isolated from the agarose gel and these two fragments were ligated together in the next step. The resulting gene sequence was checked by sequencing.

Example 2:

Cloning of the mutated gene sequences into the expression vector pPICZαA for *Pichia pastoris*

The verified mutated gene sequences were cleaved from the PCR cloning vectors by restriction with the restriction endonucleases EcoRI and Asp718, the restriction mixture was separated by means of agarose gel electrophoresis and the ca. 1480 bp

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long fragments were isolated from the agarose gel (QIAquick gel extraction kit/Qiagen). Subsequently the mutated gene sequences were ligated with the vector fragment from the expression vector pPICZ α A which was also linearized with EcoRI and Asp718. The restriction endonuclease cleavage sites required for EcoRI and Asp718 were incorporated into the mutated gene sequences by the primers 5'-hAP and 3'-hAP which have recognition sequences for the restriction endonuclease EcoRI and Asp718 upstream and downstream respectively of the coding sequence. The resulting expression vectors for alkaline phosphatase mutants were designated as follows: pNaAP31-1 (Ser92Ala), pNaAP43-1 (Gly322Phe), pNaAP51-1 (His320Asn/Gly322Phe) and pNaAP6-1 (Ser92Ala/His320Asn/Gly322Phe). In this vector the mutated gene sequences are under the control of the AOX 1 promoter (promoter for alcohol oxidase 1 from *Pichia pastoris*) which can be induced with methanol and is cloned in the correct reading frame behind the signal peptide of the α factor from *Saccharomyces cerevisiae*. The gene fragment inserted in this manner was then examined by means of restriction analysis and sequencing for an error-free base sequence. The resulting expression vectors which each encode one of the mutated gene sequences according to SEQ ID NO's.: 8-11, code for eukaryotic alkaline phosphatase mutants are shown with pNaAP31-1 as an example (see fig. 1).

Transformation of the expression vectors containing the mutated gene sequences in *Pichia pastoris*

In order to transform the expression vectors containing mutated gene sequences in *Pichia pastoris* X-33 with subsequent integration into the genome, the vectors were firstly linearized with SacI (Roche Diagnostics GmbH). The transformation was carried out by means of electroporation using a Gene Pulser II (Biorad).

For this a colony of *Pichia pastoris* wild type strain was inoculated in 5 ml YPD medium (Invitrogen) and incubated at 30°C overnight while shaking. The overnight culture was subsequently inoculated 1:2000 in 200 ml fresh YPD medium (Invitrogen) and incubated overnight at 30°C while shaking until an OD₆₀₀ of 1.3 – 1.5 was reached. The cells were centrifuged (1500 x g / 5 minutes) and the pellet was suspended in 200 ml ice-cold sterile water (0°C). The cells were again centrifuged (1500 x g / 5 minutes) and resuspended in 100 ml ice-cold, sterile water. The cells

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were again centrifuged and resuspended in 10 ml ice-cold (0°C) 1 M sorbitol (ICN). The cells were again centrifuged and resuspended in 0.5 ml ice-cold (0°C) 1 M sorbitol (ICN). The cells obtained in this manner were kept on ice and used immediately for the transformation.

About 1 µg linearized expression vector DNA was added to 80 µl of the cells and the entire mixture was transferred into an ice-cold (0°C) electroporation cuvette and incubated for a further 5 minutes on ice. The cuvette was subsequently transferred to a Gene Pulser II (Biorad) and the transformation was carried out at 1 kV, 1 kΩ and 25 µF. After the electroporation, 1 ml 1 M sorbitol (ICN) was added to the mixture and subsequently 100 to 150 µl was plated out on a YPDS agar plate (Invitrogen) containing 100 µg/ml Zeocin® (Invitrogen). The plates were subsequently incubated for 2-4 days at 30°C.

The clones were inoculated onto raster MD (= minimal dextrose) plates and analysed further. Grown clones were picked, resuspended in 20 µl sterile water, lysed (1 hour, 37°C) with 17.5 U lyticase (Roche Diagnostics GmbH) and directly examined by means of PCR for the correct integration of the expression cassette containing an appropriately mutated gene sequence.

Clones which had integrated the complete expression cassette into the genome in the transformation were then used in expression experiments.

Example 3:

Expression of the alkaline phosphatase mutants

Positive clones were inoculated in 3 ml BMGY medium (Invitrogen) and incubated overnight at 30°C while shaking. Subsequently the OD at 600 nm was determined and the inoculation in 10 ml BMMY medium (Invitrogen) was carried out in such a manner that it resulted in an OD₆₀₀ of 1. The BMMY medium (Invitrogen) contains methanol (Mallinckrodt Baker B.V.) which induces the expression of the alkaline phosphatase mutants via the AOX 1 promoter.

The shaking flasks were incubated at 30°C while shaking, samples were removed every 24 hours, the OD₆₀₀ was determined, an activity test was carried out for the

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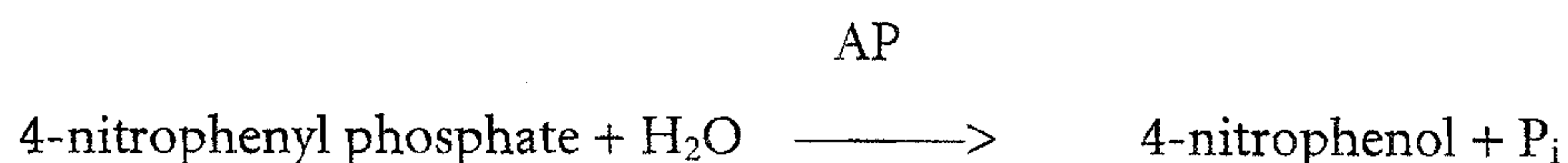
expression of the alkaline phosphatase mutants and each time 0.5 % methanol (Mallinckrodt Baker B.V.) was added for further induction. The expression experiments were carried out for 96 hours.

Example 4:

Test for the activity of alkaline phosphatase mutants

500 µl aliquots of the expression culture of example 3 were removed, the OD₆₀₀ was determined and the cells were centrifuged. The supernatant was stored and the cell pellet was resuspended in a quantity of Y-PER™ (50 to 300 µl/Pierce) according to the OD₆₀₀ for lysis and shaken for 1 hour at room temperature. Subsequently the lysate was centrifuged in order to separate the cell debris (15000 x g/5 minutes) and the supernatant was transferred to fresh reaction vessels. 5 µl of the lysate was then used in the activity test.

The activity test functions according to the following principle:



The absorption increase at 405 nm is measured.

50 µl 4-nitrophenyl phosphate solution (0.67 mol/l 4-nitrophenyl phosphate, Na salt (Roche Diagnostics GmbH) is added to 3 ml diethanolamine buffer (1 mol/l diethanolamine (Merck) pH 9.8, 0.5 mmol/l MgCl₂ (Riedel de Haen)) and the mixture was incubated at 37°C. Subsequently the reaction was started by adding 5 µl lysate and the change in absorbance at 37°C was determined for 3 minutes and the ΔA/min was calculated from this.

The activity was then calculated according to the following formula:

$$\text{activity} = \frac{3.10}{\epsilon \times 0.005 \times 1} \times \Delta A / \text{min} \times \frac{1}{\text{factor} \times} [\text{U/ml sample solution}]$$

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$$\varepsilon = 18.2 [1 \times \text{mmol}^{-1} \times \text{cm}^{-1}]$$

factor x = concentration factor after cell lysis

The activity of the medium supernatant of the expression cultures was determined in a similar manner. In this case the reaction was also started with 50 μl supernatant but 0.5 mM ZnCl_2 was additionally added. The activity was then calculated without using factor x. Supernatants of clones which express highly-active alkaline phosphatase according to SEQ ID NO.: 3 were used as a positive control and clones which were transformed with the initial vector pPICZ α A without a target gene were used as a negative control.

The residual activity of the mutants was determined with this activity test as follows:

- single mutant Ser92Ala: reduction of the specific activity by ca. 5000-fold
- single mutant Gly322Phe: reduction of the specific activity by ca. 2500-fold
- double mutant His320Asn/Gly322Phe: reduction of the specific activity by ca. 10000-fold (near to the detection limit)
- triple mutant Ser92Ala/His320Asn/Gly322Phe: reduction of the specific activity by ca. 10000-fold (near to the detection limit).

Example 5:

Detection of the expression of the AP mutants by Western-blot:

10 μl unconcentrated supernatant or crude extract after cell lysis was applied to a 10 % SDS gel (Novex Pre-Cast gel/Invitrogen) and the proteins that were present were separated according to size by applying an electrical field. The proteins separated in this manner were blotted onto a nitrocellulose membrane (Novex® Western Transfer Apparatus XCell II™ Blot Module/Invitrogen). After the blotting the membrane was washed twice with 20 ml high-purity water for 5 minutes and subsequently shaken for 30 minutes in 10 ml blocking solution (Invitrogen). The membrane was then again washed twice for 5 minutes with 20 ml high-purity water, and subsequently incubated for 1 hour in 10 ml blocking solution (Invitrogen) which this time contained antibody 1 (anti-AP-rabbit/Rockland Inc. diluted from a 10 mg/ml stock solution 1:5000). It was then washed four times for 5 minutes each

time with 20 ml of an antibody wash solution (Invitrogen) and subsequently the membrane was incubated for 30 min with 10 ml of a secondary antibody solution (contains the anti-rabbit antibody/Invitrogen). This was followed by a four-fold wash for 5 minutes each time with 20 ml of an antibody wash solution (Invitrogen) and a three-fold wash with 20 ml high-purity water for 2 minutes each time. The membrane was then incubated for 1 – 60 minutes with a dye solution (chromogenic substrate/Invitrogen) for the staining. The incubation period depends on the quality of the stain. After optimal staining, the membrane is washed three times with 20 ml high-purity water for 2 minutes each time and subsequently the membrane is dried at room temperature. All solutions with the exception of the high-purity water were derived from the Western Breeze chromogenic immunodetection kit from Invitrogen, all incubation steps were carried out at room temperature. The procedure was according to the instructions of the manufacturer.

Example 6:

Increasing the expression rate by multiple transformation

The best clones from the expression experiments were in turn prepared for electroporation as described in example 2 and again transformed with 1 µg linearized expression vector vector DNA and the transformation mixture was plated out on YPDS agar plates (Invitrogen) containing 1000 to 2000 µg/ml Zeocin® (Invitrogen). In this manner the selection pressure is increased to such an extent that only those clones can grow which have integrated several copies of the expression vector and thus also integrated several copies of the respective resistance gene (in this case Zeocin®) into the genome. The Zeocin® resistance protein is the product of the bleomycin gene of *Streptoalloteichus hindustanus* (Chalmers, T. et al., Curr. Genet. 20 (1991), 309-314; Drocourt, D. et al., Nucleic Acid Research 18 (1990), 4009), which binds Zeocin® in a stoichiometric concentration ratio and thus makes the cell resistant to Zeocin®. The higher the concentration of Zeocin® in the YPDS agar plates, the more resistance protein the cell has to generate in order to quantitatively bind the Zeocin® and thus enable growth. This is possible when for example multiple copies of the resistance gene are integrated into the genome. Clones were inoculated on raster MD plates as described above and again examined as described

in example 2 by means of PCR analysis for the correct integration of the respective expression cassette. Subsequently these clones were again tested as described in examples 4 and 5 for AP activity or by Western blot analysis.

Example 7:

Increasing the expression rate by using a second selection pressure

Increasing the Zeocin® concentration above 2000 µg/ml does not lead to an improved expression rate of the alkaline phosphatase mutants. The gene copy number of the genes according to SEQ ID NO's: 8-11 which code for the alkaline phosphatase mutants and are codon-optimized for expression in yeast was further increased in the expression clones by integrating additional expression vectors into the genome of the expression clone from example 6 which had the highest expression rate which were selected by means of a second selection pressure, preferably G418 (Roche Diagnostics GmbH). For this purpose the entire expression cassette from pNaAP31-1 consisting of AOX 1 promoter signal peptide of the α factor from *Saccharomyces cerevisiae*, codon-optimized gene for the alkaline phosphatase mutants according to SEQ ID NO's: 8-11 and AOX 1 transcription termination region, was isolated by PCR using appropriately selected primers and, as described below, integrated into the vector pPIC9K whose integration into the genome of *Pichia pastoris* was selected by means of G418 (Roche Diagnostics GmbH). The primers used in this case, 5' expr and 3' expr, have the sequences SEQ ID NO.:20 and SEQ ID NO.:21.

The PCR preparation was analysed by means of agarose gel electrophoresis, the gene fragment having the expected size was isolated (QIAquick gel extraction kit/Qiagen), recleaved with SacI and NotI (Roche Diagnostics GmbH), subsequently isolated again from the agarose gel (QIAquick gel extraction kit/Qiagen) and ligated into a vector fragment isolated from pPIC9K which had also been linearized with SacI/NotI (Roche Diagnostics GmbH). This ensures that the entire expression cassette from the respective expression vectors was present in an identical form in pPIC9K. The inserted fragment was examined by means of restriction analysis and sequencing with the flanking regions. The resulting expression vectors for alkaline phosphatase mutants

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were designated pNaAP31-2(Ser92Ala), pNaAP43-2 (Gly322Phe), pNaAP51-2 (His320Asn/Gly322Phe) and pNaAP6-2(Ser92Ala/His320Asn/Gly322Phe).

The clones with the highest AP mutant expression rate from the multiple transformation using Zeocin® as the selection marker were prepared for electroporation as described in example 2 and transformed with 1 µg vector fragment pNaAP31-2 and derivatives linearized with SacI (Roche Diagnostics GmbH) as described in example 2. The transformation preparation was subsequently stored for 1 to 3 days at 4°C in 1 M sorbitol (ICN) (to develop the G418 resistance) and then 100 to 200 µl was plated out on YPD plates (Invitrogen) containing 1, 2 or 4 mg/ml G418 (Roche Diagnostics GmbH) and incubated for 3 to 5 days at 30°C. The resulting clones were again examined as described above with the activity test for an increased expression of the eukaryotic alkaline phosphatase mutants.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Roche Diagnostics GmbH
- (B) STREET: Grenzacherstrasse 124
- (C) CITY: CH 4070 Basel
- (D) STATE/PROVINCE:
- (E) COUNTRY: Switzerland
- (F) POSTAL CODE/ZIP:
- (G) TELEPHONE:
- (I) TELEFAX:

(ii) TITLE OF INVENTION: Production of weakly active or inactive mutants of alkaline phosphatase and their expression in yeast

(iii) NUMBER OF SEQUENCES: 21

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Borden Ladner Gervais LLP
- (B) STREET: 1100-100 Queen Street
- (C) CITY: Ottawa
- (D) PROVINCE: Ontario
- (E) COUNTRY: CANADA
- (F) POSTAL CODE: K1P 1J9

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Ver. 2.1

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: PAT 54150-1
- (B) FILING DATE: 25-Mar-2003

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: DE 102 13 201.1
- (B) FILING DATE: 25-Mar-2002

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Fritz, Joachim
- (B) REGISTRATION NUMBER: 4173
- (C) REFERENCE/DOCKET NUMBER: PAT 54150-1

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (613) 237-5160
- (B) TELEFAX: (613) 787-3558

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ctc atc cca gct gag gag gaa aac ccc gcc ttc tgg aac cgc cag gca 48
Leu Ile Pro Ala Glu Glu Glu Asn Pro Ala Phe Trp Asn Arg Gln Ala
1 5 10 15

gcc cag gcc ctt gat gta gcc aag aag ttg cag ccg atc cag aca gct 96
Ala Gln Ala Leu Asp Val Ala Lys Lys Leu Gln Pro Ile Gln Thr Ala
20 25 30

gcc aag aat gtc atc ctc ttc ttg ggg gat ggg atg ggg gtg cct acg 144
Ala Lys Asn Val Ile Leu Phe Leu Gly Asp Gly Met Gly Val Pro Thr
35 40 45

gtg aca gcc act cgg atc cta aag ggg cag atg aat ggc aaa ctg gga 192
Val Thr Ala Thr Arg Ile Leu Lys Gly Gln Met Asn Gly Lys Leu Gly
50 55 60

cct gag aca ccc ctg gcc atg gac cag ttc cca tac gtg gct ctg tcc 240
Pro Glu Thr Pro Leu Ala Met Asp Gln Phe Pro Tyr Val Ala Leu Ser
65 70 75 80

aag aca tac aac gtg gac aga cag gtg cca gac agc gca ggc act gcc 288
Lys Thr Tyr Asn Val Asp Arg Gln Val Pro Asp Ser Ala Gly Thr Ala
85 90 95

act gcc tac ctg tgt ggg gtc aag ggc aac tac aga acc atc ggt gta 336
Thr Ala Tyr Leu Cys Gly Val Lys Gly Asn Tyr Arg Thr Ile Gly Val
100 105 110

agt gca gcc gcc cgc tac aat cag tgc aac acg aca cgt ggg aat gag 384
 Ser Ala Ala Ala Arg Tyr Asn Gln Cys Asn Thr Thr Arg Gly Asn Glu
 115 120 125

```
gtc acg tct gtg atc aac cgg gcc aag aaa gca ggg aag gcc gtg gga      432
Val Thr Ser Val Ile Asn Arg Ala Lys Lys Ala Gly Lys Ala Val Gly
      130                      135                      140
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gtg gtg acc acc acc agg gtg cag cat gcc tcc cca gcc ggg gcc tac 480
Val Val Thr Thr Thr Arg Val Gln His Ala Ser Pro Ala Gly Ala Tyr

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145		150		155		160	
gcg cac acg gtg aac cga aac tgg tac tca gac gcc gac ctg cct gct	528						
Ala His Thr Val Asn Arg Asn Trp Tyr Ser Asp Ala Asp Leu Pro Ala							
		165		170		175	
gat gca cag aag aat ggc tgc cag gac atc gcc gca cag ctg gtc tac	576						
Asp Ala Gln Lys Asn Gly Cys Gln Asp Ile Ala Ala Gln Leu Val Tyr							
		180		185		190	
aac atg gat att gac gtg atc ctg ggt gga ggc cga atg tac atg ttt	624						
Asn Met Asp Ile Asp Val Ile Leu Gly Gly Gly Arg Met Tyr Met Phe							
		195		200		205	
cct gag ggg acc cca gac cct gaa tac cca gat gat gcc agt gtg aat	672						
Pro Glu Gly Thr Pro Asp Pro Glu Tyr Pro Asp Asp Ala Ser Val Asn							
		210		215		220	
gga gtc cgg aag gac aag cag aac ctg gtg cag gaa tgg cag gcc aag	720						
Gly Val Arg Lys Asp Lys Gln Asn Leu Val Gln Glu Trp Gln Ala Lys							
		225		230		235	
cac cag gga gcc cag tat gtg tgg aac cgc act gcg ctc ctt cag gcg	768						
His Gln Gly Ala Gln Tyr Val Trp Asn Arg Thr Ala Leu Leu Gln Ala							
		245		250		255	
gcc gat gac tcc agt gta aca cac ctc atg ggc ctc ttt gag ccg gca	816						
Ala Asp Asp Ser Ser Val Thr His Leu Met Gly Leu Phe Glu Pro Ala							
		260		265		270	
gac atg aag tat aat gtt cag caa gac cac acc aag gac ccg acc ctg	864						
Asp Met Lys Tyr Asn Val Gln Gln Asp His Thr Lys Asp Pro Thr Leu							
		275		280		285	
gcg gag atg acg gag gcg gcc ctg caa gtg ctg agc agg aac ccc cgg	912						
Ala Glu Met Thr Glu Ala Ala Leu Gln Val Leu Ser Arg Asn Pro Arg							
		290		295		300	
ggc ttc tac ctc ttc gtg gag gga ggc cgc att gac cac ggt cac cat	960						
Gly Phe Tyr Leu Phe Val Glu Gly Gly Arg Ile Asp His Gly His His							
		305		310		315	
gac ggc aaa gct tat atg gca ctg act gag gcg atc atg ttt gac aat	1008						
Asp Gly Lys Ala Tyr Met Ala Leu Thr Glu Ala Ile Met Phe Asp Asn							
		325		330		335	
gcc atc gcc aag gct aac gag ctc act agc gaa ctg gac acg ctg atc	1056						
Ala Ile Ala Lys Ala Asn Glu Leu Thr Ser Glu Leu Asp Thr Leu Ile							
		340		345		350	
ctt gtc act gca gac cac tcc cat gtc ttc tct ttt ggt ggc tac aca	1104						
Leu Val Thr Ala Asp His Ser His Val Phe Ser Phe Gly Gly Tyr Thr							
		355		360		365	
ctg cgt ggg acc tcc att ttc ggt ctg gcc ccc ggc aag gcc tta gac	1152						
Leu Arg Gly Thr Ser Ile Phe Gly Leu Ala Pro Gly Lys Ala Leu Asp							
		370		375		380	

(2) INFORMATION FOR SEQ ID NO:2:

(A) LENGTH: 487 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Leu	Ile	Pro	Ala	Glu	Glu	Glu	Asn	Pro	Ala	Phe	Trp	Asn	Arg	Gln	Ala
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Ala	Gln	Ala	Leu	Asp	Val	Ala	Lys	Lys	Leu	Gln	Pro	Ile	Gln	Thr	Ala
			20					25					30		
Ala	Lys	Asn	Val	Ile	Leu	Phe	Leu	Gly	Asp	Gly	Met	Gly	Val	Pro	Thr
			35				40					45			
Val	Thr	Ala	Thr	Arg	Ile	Leu	Lys	Gly	Gln	Met	Asn	Gly	Lys	Leu	Gly
	50					55					60				

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Pro	Glu	Thr	Pro	Leu	Ala	Met	Asp	Gln	Phe	Pro	Tyr	Val	Ala	Leu	Ser	65	70	75	80
Lys	Thr	Tyr	Asn	Val	Asp	Arg	Gln	Val	Pro	Asp	Ser	Ala	Gly	Thr	Ala	85	90	95	
Thr	Ala	Tyr	Leu	Cys	Gly	Val	Lys	Gly	Asn	Tyr	Arg	Thr	Ile	Gly	Val	100	105	110	
Ser	Ala	Ala	Ala	Arg	Tyr	Asn	Gln	Cys	Asn	Thr	Thr	Arg	Gly	Asn	Glu	115	120	125	
Val	Thr	Ser	Val	Ile	Asn	Arg	Ala	Lys	Lys	Ala	Gly	Lys	Ala	Val	Gly	130	135	140	
Val	Val	Thr	Thr	Thr	Arg	Val	Gln	His	Ala	Ser	Pro	Ala	Gly	Ala	Tyr	145	150	155	160
Ala	His	Thr	Val	Asn	Arg	Asn	Trp	Tyr	Ser	Asp	Ala	Asp	Leu	Pro	Ala	165	170	175	
Asp	Ala	Gln	Lys	Asn	Gly	Cys	Gln	Asp	Ile	Ala	Ala	Gln	Leu	Val	Tyr	180	185	190	
Asn	Met	Asp	Ile	Asp	Val	Ile	Leu	Gly	Gly	Gly	Arg	Met	Tyr	Met	Phe	195	200	205	
Pro	Glu	Gly	Thr	Pro	Asp	Pro	Glu	Tyr	Pro	Asp	Asp	Ala	Ser	Val	Asn	210	215	220	
Gly	Val	Arg	Lys	Asp	Lys	Gln	Asn	Leu	Val	Gln	Glu	Trp	Gln	Ala	Lys	225	230	235	240
His	Gln	Gly	Ala	Gln	Tyr	Val	Trp	Asn	Arg	Thr	Ala	Leu	Leu	Gln	Ala	245	250	255	
Ala	Asp	Asp	Ser	Ser	Val	Thr	His	Leu	Met	Gly	Leu	Phe	Glu	Pro	Ala	260	265	270	
Asp	Met	Lys	Tyr	Asn	Val	Gln	Gln	Asp	His	Thr	Lys	Asp	Pro	Thr	Leu	275	280	285	
Ala	Glu	Met	Thr	Glu	Ala	Ala	Leu	Gln	Val	Leu	Ser	Arg	Asn	Pro	Arg	290	295	300	
Gly	Phe	Tyr	Leu	Phe	Val	Glu	Gly	Gly	Arg	Ile	Asp	His	Gly	His	His	305	310	315	320
Asp	Gly	Lys	Ala	Tyr	Met	Ala	Leu	Thr	Glu	Ala	Ile	Met	Phe	Asp	Asn	325	330	335	
Ala	Ile	Ala	Lys	Ala	Asn	Glu	Leu	Thr	Ser	Glu	Leu	Asp	Thr	Leu	Ile	340	345	350	
Leu	Val	Thr	Ala	Asp	His	Ser	His	Val	Phe	Ser	Phe	Gly	Gly	Tyr	Thr	355	360	365	

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Leu Arg Gly Thr Ser Ile Phe Gly Leu Ala Pro Gly Lys Ala Leu Asp
 370 375 380
 Ser Lys Ser Tyr Thr Ser Ile Leu Tyr Gly Asn Gly Pro Gly Tyr Ala
 385 390 395 400
 Leu Gly Gly Gly Ser Arg Pro Asp Val Asn Gly Ser Thr Ser Glu Glu
 405 410 415
 Pro Ser Tyr Arg Gln Gln Ala Ala Val Pro Leu Ala Ser Glu Thr His
 420 425 430
 Gly Gly Glu Asp Val Ala Val Phe Ala Arg Gly Pro Gln Ala His Leu
 435 440 445
 Val His Gly Val Gln Glu Glu Thr Phe Val Ala His Ile Met Ala Phe
 450 455 460
 Ala Gly Cys Val Glu Pro Tyr Thr Asp Cys Asn Leu Pro Ala Pro Ala
 465 470 475 480
 Thr Ala Thr Ser Ile Pro Asp
 485

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1476 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

gaattcttga ttccagctga agaagaaaat ccagcttttt ggaatagaca agctgctcaa 60
 gctttggatg ttgctaagaa gttgcaacca attcaaactg ctgctaagaa tgttattttg 120
 tttttgggtg atggtatggg tgttccaact gttactgcta ctagaatttt gaagggtcaa 180
 atgaatggta agttgggtcc agaaactcca ttggctatgg atcaatttcc atacgttgct 240
 ttgtctaaga cttacaatgt tgatagacaa gttccagatt ctgctgggtac tgctactgct 300
 tacttggtg gtgttaaggg taattacaga actattgggtg tttctgctgc tgctagatac 360

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aatcaatgta atactactag aggtaatgaa gttacttctg ttattaatag agctaagaag 420
gctggtaagg ctggttggtgt tgttactact actagagttc aacatgcttc tccagctggt 480
gcttacgctc atactgttaa tagaaattgg tactctgatg ctgatttgcc agctgatgct 540
caaaagaatg gttgtcaaga tattgctgct caattgggtt acaatatgga tattgatggt 600
atthttgggtg gtggtagaat gtacatgttt ccagaaggta ctccagatcc agaataccca 660
gatgatgctt ctgttaatgg tgtagaaaag gataagcaaa atthgggttca agaatggcaa 720
gctaagcatc aagggtgctca atatgttttg aatagaactg ctttggttga agctgctgat 780
gattctagtg ttactcattt gatgggtttg tttgaaccag ctgatatgaa gtataatggt 840
caacaagatc atactaagga tccaactttg gctgaaatga ctgaagctgc tttgcaagtt 900
ttgtctagaa atccaagagg tttttacttg tttgttgaag gtggtagaat tgatcatggt 960
catcatgatg gtaaggctta tatggctttg actgaagcta ttatgtttga taatgctatt 1020
gctaaggcta atgaattgac ttctgaattg gatactttga ttttggttac tgctgatcat 1080
agtcatgttt tttcttttgg tggttacact ttgagaggta cttctattht tggthttggct 1140
ccaggtaagg cthttgatag taagtcttac acttctattht tgtatggtaa tggthccagg 1200
tatgctthtg gtgggtggttc tagaccagat gthaatggta gtactagtga agaaccatct 1260
tacagacaac aagctgctgt tccattggct agtgaaactc atgggtggtga agatgthtgc 1320
gtthtttgcta gaggtccaca agctcatttg gthcatggtg thcaagaaga aactthttgt 1380
gctcatatta tggctthttgc tggthtggtt gaaccataca ctgattgtha tthgccagct 1440
ccagctactg ctactagtat tccagattaa ggtacc 1476

```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein - Bovine/mutated

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu Ile Pro Ala Glu Glu Glu Asn Pro Ala Phe Trp Asn Arg Gln Ala

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1		5		10		15										
Ala	Gln	Ala	Leu	Asp	Val	Ala	Lys	Lys	Leu	Gln	Pro	Ile	Gln	Thr	Ala	
			20					25					30			
Ala	Lys	Asn	Val	Ile	Leu	Phe	Leu	Gly	Asp	Gly	Met	Gly	Val	Pro	Thr	
		35					40					45				
Val	Thr	Ala	Thr	Arg	Ile	Leu	Lys	Gly	Gln	Met	Asn	Gly	Lys	Leu	Gly	
	50					55					60					
Pro	Glu	Thr	Pro	Leu	Ala	Met	Asp	Gln	Phe	Pro	Tyr	Val	Ala	Leu	Ser	
65					70					75					80	
Lys	Thr	Tyr	Asn	Val	Asp	Arg	Gln	Val	Pro	Asp	Ala	Ala	Gly	Thr	Ala	
			85						90					95		
Thr	Ala	Tyr	Leu	Cys	Gly	Val	Lys	Gly	Asn	Tyr	Arg	Thr	Ile	Gly	Val	
			100					105					110			
Ser	Ala	Ala	Ala	Arg	Tyr	Asn	Gln	Cys	Asn	Thr	Thr	Arg	Gly	Asn	Glu	
		115					120					125				
Val	Thr	Ser	Val	Ile	Asn	Arg	Ala	Lys	Lys	Ala	Gly	Lys	Ala	Val	Gly	
	130					135					140					
Val	Val	Thr	Thr	Thr	Arg	Val	Gln	His	Ala	Ser	Pro	Ala	Gly	Ala	Tyr	
145					150					155					160	
Ala	His	Thr	Val	Asn	Arg	Asn	Trp	Tyr	Ser	Asp	Ala	Asp	Leu	Pro	Ala	
				165					170					175		
Asp	Ala	Gln	Lys	Asn	Gly	Cys	Gln	Asp	Ile	Ala	Ala	Gln	Leu	Val	Tyr	
			180					185					190			
Asn	Met	Asp	Ile	Asp	Val	Ile	Leu	Gly	Gly	Gly	Arg	Met	Tyr	Met	Phe	
		195					200					205				
Pro	Glu	Gly	Thr	Pro	Asp	Pro	Glu	Tyr	Pro	Asp	Asp	Ala	Ser	Val	Asn	
	210					215					220					
Gly	Val	Arg	Lys	Asp	Lys	Gln	Asn	Leu	Val	Gln	Glu	Trp	Gln	Ala	Lys	
225					230					235					240	
His	Gln	Gly	Ala	Gln	Tyr	Val	Trp	Asn	Arg	Thr	Ala	Leu	Leu	Gln	Ala	
				245					250					255		
Ala	Asp	Asp	Ser	Ser	Val	Thr	His	Leu	Met	Gly	Leu	Phe	Glu	Pro	Ala	
			260					265					270			
Asp	Met	Lys	Tyr	Asn	Val	Gln	Gln	Asp	His	Thr	Lys	Asp	Pro	Thr	Leu	
		275					280					285				
Ala	Glu	Met	Thr	Glu	Ala	Ala	Leu	Gln	Val	Leu	Ser	Arg	Asn	Pro	Arg	
	290					295					300					
Gly	Phe	Tyr	Leu	Phe	Val	Glu	Gly	Gly	Arg	Ile	Asp	His	Gly	His	His	

(2) INFORMATION FOR SEQ ID NO:5:

(A) LENGTH: 487 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Leu Ile Pro Ala Glu Glu Glu Asn Pro Ala Phe Trp Asn Arg Gln Ala
1 5 10 15

Gly Phe Tyr Leu Phe Val Glu Gly Gly Arg Ile Asp His Gly His His
305 310 315 320

- 32 -

Asp Phe Lys Ala Tyr Met Ala Leu Thr Glu Ala Ile Met Phe Asp Asn
 325 330 335
 Ala Ile Ala Lys Ala Asn Glu Leu Thr Ser Glu Leu Asp Thr Leu Ile
 340 345 350
 Leu Val Thr Ala Asp His Ser His Val Phe Ser Phe Gly Gly Tyr Thr
 355 360 365
 Leu Arg Gly Thr Ser Ile Phe Gly Leu Ala Pro Gly Lys Ala Leu Asp
 370 375 380
 Ser Lys Ser Tyr Thr Ser Ile Leu Tyr Gly Asn Gly Pro Gly Tyr Ala
 385 390 395 400
 Leu Gly Gly Gly Ser Arg Pro Asp Val Asn Gly Ser Thr Ser Glu Glu
 405 410 415
 Pro Ser Tyr Arg Gln Gln Ala Ala Val Pro Leu Ala Ser Glu Thr His
 420 425 430
 Gly Gly Glu Asp Val Ala Val Phe Ala Arg Gly Pro Gln Ala His Leu
 435 440 445
 Val His Gly Val Gln Glu Glu Thr Phe Val Ala His Ile Met Ala Phe
 450 455 460
 Ala Gly Cys Val Glu Pro Tyr Thr Asp Cys Asn Leu Pro Ala Pro Ala
 465 470 475 480
 Thr Ala Thr Ser Ile Pro Asp
 485

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein - Bovine/mutated

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu Ile Pro Ala Glu Glu Glu Asn Pro Ala Phe Trp Asn Arg Gln Ala
 1 5 10 15
 Ala Gln Ala Leu Asp Val Ala Lys Lys Leu Gln Pro Ile Gln Thr Ala
 20 25 30

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Ala	Lys	Asn	Val	Ile	Leu	Phe	Leu	Gly	Asp	Gly	Met	Gly	Val	Pro	Thr	35	40	45	
Val	Thr	Ala	Thr	Arg	Ile	Leu	Lys	Gly	Gln	Met	Asn	Gly	Lys	Leu	Gly	50	55	60	
Pro	Glu	Thr	Pro	Leu	Ala	Met	Asp	Gln	Phe	Pro	Tyr	Val	Ala	Leu	Ser	65	70	75	80
Lys	Thr	Tyr	Asn	Val	Asp	Arg	Gln	Val	Pro	Asp	Ser	Ala	Gly	Thr	Ala	85	90	95	
Thr	Ala	Tyr	Leu	Cys	Gly	Val	Lys	Gly	Asn	Tyr	Arg	Thr	Ile	Gly	Val	100	105	110	
Ser	Ala	Ala	Ala	Arg	Tyr	Asn	Gln	Cys	Asn	Thr	Thr	Arg	Gly	Asn	Glu	115	120	125	
Val	Thr	Ser	Val	Ile	Asn	Arg	Ala	Lys	Lys	Ala	Gly	Lys	Ala	Val	Gly	130	135	140	
Val	Val	Thr	Thr	Thr	Arg	Val	Gln	His	Ala	Ser	Pro	Ala	Gly	Ala	Tyr	145	150	155	160
Ala	His	Thr	Val	Asn	Arg	Asn	Trp	Tyr	Ser	Asp	Ala	Asp	Leu	Pro	Ala	165	170	175	
Asp	Ala	Gln	Lys	Asn	Gly	Cys	Gln	Asp	Ile	Ala	Ala	Gln	Leu	Val	Tyr	180	185	190	
Asn	Met	Asp	Ile	Asp	Val	Ile	Leu	Gly	Gly	Gly	Arg	Met	Tyr	Met	Phe	195	200	205	
Pro	Glu	Gly	Thr	Pro	Asp	Pro	Glu	Tyr	Pro	Asp	Asp	Ala	Ser	Val	Asn	210	215	220	
Gly	Val	Arg	Lys	Asp	Lys	Gln	Asn	Leu	Val	Gln	Glu	Trp	Gln	Ala	Lys	225	230	235	240
His	Gln	Gly	Ala	Gln	Tyr	Val	Trp	Asn	Arg	Thr	Ala	Leu	Leu	Gln	Ala	245	250	255	
Ala	Asp	Asp	Ser	Ser	Val	Thr	His	Leu	Met	Gly	Leu	Phe	Glu	Pro	Ala	260	265	270	
Asp	Met	Lys	Tyr	Asn	Val	Gln	Gln	Asp	His	Thr	Lys	Asp	Pro	Thr	Leu	275	280	285	
Ala	Glu	Met	Thr	Glu	Ala	Ala	Leu	Gln	Val	Leu	Ser	Arg	Asn	Pro	Arg	290	295	300	
Gly	Phe	Tyr	Leu	Phe	Val	Glu	Gly	Gly	Arg	Ile	Asp	His	Gly	His	Asn	305	310	315	320
Asp	Phe	Lys	Ala	Tyr	Met	Ala	Leu	Thr	Glu	Ala	Ile	Met	Phe	Asp	Asn	325	330	335	

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Ala Ile Ala Lys Ala Asn Glu Leu Thr Ser Glu Leu Asp Thr Leu Ile
340 345 350

Leu Val Thr Ala Asp His Ser His Val Phe Ser Phe Gly Gly Tyr Thr
355 360 365

Leu Arg Gly Thr Ser Ile Phe Gly Leu Ala Pro Gly Lys Ala Leu Asp
370 375 380

Ser Lys Ser Tyr Thr Ser Ile Leu Tyr Gly Asn Gly Pro Gly Tyr Ala
385 390 395 400

Leu Gly Gly Gly Ser Arg Pro Asp Val Asn Gly Ser Thr Ser Glu Glu
405 410 415

Pro Ser Tyr Arg Gln Gln Ala Ala Val Pro Leu Ala Ser Glu Thr His
420 425 430

Gly Gly Glu Asp Val Ala Val Phe Ala Arg Gly Pro Gln Ala His Leu
435 440 445

Val His Gly Val Gln Glu Glu Thr Phe Val Ala His Ile Met Ala Phe
450 455 460

Ala Gly Cys Val Glu Pro Tyr Thr Asp Cys Asn Leu Pro Ala Pro Ala
465 470 475 480

Thr Ala Thr Ser Ile Pro Asp
485

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein - Bovine/mutated

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:

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

Leu Ile Pro Ala Glu Glu Glu Asn Pro Ala Phe Trp Asn Arg Gln Ala
1 5 10 15

Ala Gln Ala Leu Asp Val Ala Lys Lys Leu Gln Pro Ile Gln Thr Ala
20 25 30

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Ala	Lys	Asn	Val	Ile	Leu	Phe	Leu	Gly	Asp	Gly	Met	Gly	Val	Pro	Thr	35	40	45	
Val	Thr	Ala	Thr	Arg	Ile	Leu	Lys	Gly	Gln	Met	Asn	Gly	Lys	Leu	Gly	50	55	60	
Pro	Glu	Thr	Pro	Leu	Ala	Met	Asp	Gln	Phe	Pro	Tyr	Val	Ala	Leu	Ser	65	70	75	80
Lys	Thr	Tyr	Asn	Val	Asp	Arg	Gln	Val	Pro	Asp	Ala	Ala	Gly	Thr	Ala	85	90	95	
Thr	Ala	Tyr	Leu	Cys	Gly	Val	Lys	Gly	Asn	Tyr	Arg	Thr	Ile	Gly	Val	100	105	110	
Ser	Ala	Ala	Ala	Arg	Tyr	Asn	Gln	Cys	Asn	Thr	Thr	Arg	Gly	Asn	Glu	115	120	125	
Val	Thr	Ser	Val	Ile	Asn	Arg	Ala	Lys	Lys	Ala	Gly	Lys	Ala	Val	Gly	130	135	140	
Val	Val	Thr	Thr	Thr	Arg	Val	Gln	His	Ala	Ser	Pro	Ala	Gly	Ala	Tyr	145	150	155	160
Ala	His	Thr	Val	Asn	Arg	Asn	Trp	Tyr	Ser	Asp	Ala	Asp	Leu	Pro	Ala	165	170	175	
Asp	Ala	Gln	Lys	Asn	Gly	Cys	Gln	Asp	Ile	Ala	Ala	Gln	Leu	Val	Tyr	180	185	190	
Asn	Met	Asp	Ile	Asp	Val	Ile	Leu	Gly	Gly	Gly	Arg	Met	Tyr	Met	Phe	195	200	205	
Pro	Glu	Gly	Thr	Pro	Asp	Pro	Glu	Tyr	Pro	Asp	Asp	Ala	Ser	Val	Asn	210	215	220	
Gly	Val	Arg	Lys	Asp	Lys	Gln	Asn	Leu	Val	Gln	Glu	Trp	Gln	Ala	Lys	225	230	235	240
His	Gln	Gly	Ala	Gln	Tyr	Val	Trp	Asn	Arg	Thr	Ala	Leu	Leu	Gln	Ala	245	250	255	
Ala	Asp	Asp	Ser	Ser	Val	Thr	His	Leu	Met	Gly	Leu	Phe	Glu	Pro	Ala	260	265	270	
Asp	Met	Lys	Tyr	Asn	Val	Gln	Gln	Asp	His	Thr	Lys	Asp	Pro	Thr	Leu	275	280	285	
Ala	Glu	Met	Thr	Glu	Ala	Ala	Leu	Gln	Val	Leu	Ser	Arg	Asn	Pro	Arg	290	295	300	
Gly	Phe	Tyr	Leu	Phe	Val	Glu	Gly	Gly	Arg	Ile	Asp	His	Gly	His	Asn	305	310	315	320
Asp	Phe	Lys	Ala	Tyr	Met	Ala	Leu	Thr	Glu	Ala	Ile	Met	Phe	Asp	Asn	325	330	335	

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Ala Ile Ala Lys Ala Asn Glu Leu Thr Ser Glu Leu Asp Thr Leu Ile
 340 345 350

Leu Val Thr Ala Asp His Ser His Val Phe Ser Phe Gly Gly Tyr Thr
 355 360 365

Leu Arg Gly Thr Ser Ile Phe Gly Leu Ala Pro Gly Lys Ala Leu Asp
 370 375 380

Ser Lys Ser Tyr Thr Ser Ile Leu Tyr Gly Asn Gly Pro Gly Tyr Ala
 385 390 395 400

Leu Gly Gly Gly Ser Arg Pro Asp Val Asn Gly Ser Thr Ser Glu Glu
 405 410 415

Pro Ser Tyr Arg Gln Gln Ala Ala Val Pro Leu Ala Ser Glu Thr His
 420 425 430

Gly Gly Glu Asp Val Ala Val Phe Ala Arg Gly Pro Gln Ala His Leu
 435 440 445

Val His Gly Val Gln Glu Glu Thr Phe Val Ala His Ile Met Ala Phe
 450 455 460

Ala Gly Cys Val Glu Pro Tyr Thr Asp Cys Asn Leu Pro Ala Pro Ala
 465 470 475 480

Thr Ala Thr Ser Ile Pro Asp
 485

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1476 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:

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

gaattcttga ttccagctga agaagaaaat ccagcttttt ggaatagaca agctgctcaa 60

gctttggatg ttgctaagaa gttgcaacca attcaaactg ctgctaagaa tgttattttg 120

tttttgggtg atggtatggg tgttccaact gttactgcta ctagaatttt gaagggtcaa 180

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atgaatggta agttgggtcc agaaactcca ttggctatgg atcaatttcc atacgttgct 240
ttgtctaaga cttacaatgt tgatagacaa gttccagatg ctgctgggtac tgctactgct 300
tacttgtgtg gtgttaaggg taattacaga actattgggtg tttctgctgc tgctagatac 360
aatcaatgta atactactag aggtaatgaa gttacttctg ttattaatag agctaagaag 420
gctggtaagg ctgttggtgt tgttactact actagagttc aacatgcttc tccagctggt 480
gcttacgctc atactgttaa tagaaattgg tactctgatg ctgatttgcc agctgatgct 540
caaaagaatg gttgtcaaga tattgctgct caattggttt acaatatgga tattgatggt 600
atthttgggtg gtggtagaat gtacatgttt ccagaaggta ctccagatcc agaataccca 660
gatgatgctt ctgttaatgg tgttagaaag gataagcaaa atttggttca agaatggcaa 720
gctaagcatc aagggtgctca atatgtttgg aatagaactg ctttgttgca agctgctgat 780
gattctagtg ttactcattt gatgggtttg tttgaaccag ctgatatgaa gtataatggt 840
caacaagatc atactaagga tccaactttg gctgaaatga ctgaagctgc tttgcaagtt 900
ttgtctagaa atccaagagg tttttacttg tttggtgaag gtggtagaat tgatcatggt 960
catcatgatg gtaaggctta tatggctttg actgaagcta ttatgtttga taatgctatt 1020
gctaaggcta atgaattgac ttctgaattg gatactttga ttttggttac tgctgatcat 1080
agtcatgttt tttctttttg tggttacact ttgagaggta cttctattht tggtttggct 1140
ccaggtaagg ctttggatag taagtcttac acttctattht tgtatggtaa tgggccaggt 1200
tatgcttttg gtggtgggtc tagaccagat gttaatggta gtactagtga agaaccatct 1260
tacagacaac aagctgctgt tccattggct agtgaaactc atgggtgggtga agatggtgct 1320
gtttttgcta gaggtccaca agctcatttg gttcatgggtg ttcaagaaga aacttttggt 1380
gctcatatta tggctttttg tggttgtggt gaaccataca ctgattgtaa tttgccagct 1440
ccagctactg ctactagtat tccagattaa ggtacc 1476

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(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1476 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

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(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

gaattcttga ttccagctga agaagaaaat ccagcttttt ggaatagaca agctgctcaa	60
gctttggatg ttgctaagaa gttgcaacca attcaaactg ctgctaagaa tgttattttg	120
tttttgggtg atggtatggg tgttccaact gttactgcta ctagaatttt gaagggtcaa	180
atgaatggta agttgggtcc agaaactcca ttggctatgg atcaatttcc atacgttgct	240
ttgtctaaga cttacaatgt tgatagacaa gttccagatt ctgctgggtac tgctactgct	300
tacttggtg gtgttaaggg taattacaga actattgggtg tttctgctgc tgctagatac	360
aatcaatgta atactactag aggtaatgaa gttacttctg ttattaatag agctaagaag	420
gctggtaagg ctggttggtg tgttactact actagagttc aacatgcttc tccagctggg	480
gcttacgctc atactgttaa tagaaattgg tactctgatg ctgatttgcc agctgatgct	540
caaaagaatg gttgtcaaga tattgctgct caattggttt acaatatgga tattgatggt	600
attttgggtg gtggtagaat gtacatgttt ccagaaggta ctccagatcc agaataccca	660
gatgatgctt ctgttaatgg tgtagaaaag gataagcaaa atttggttca agaatggcaa	720
gctaagcatc aagggtgctc atatgttttg aatagaactg ctttgttgca agctgctgat	780
gattctagtg ttactcattt gatggggttg tttgaaccag ctgatatgaa gtataatggt	840
caacaagatc atactaagga tccaactttg gctgaaatga ctgaagctgc tttgcaagtt	900
ttgtctagaa atccaagagg tttttacttg tttgttgaag gtggtagaat tgatcatggg	960
catcatgatt ttaaggctta tatggctttg actgaagcta ttatgtttga taatgctatt	1020
gctaaggcta atgaattgac ttctgaattg gatactttga ttttggttac tgctgatcat	1080
agtcatgttt tttcttttgg tggttacact ttgagaggta cttctatttt tggtttggt	1140
ccaggtaagg ctttggatag taagtcttac acttctattt tgtatggtaa tgggtccagg	1200
tatgcttttg gtggtgggtc tagaccagat gttaatggta gtactagtga agaaccatct	1260
tacagacaac aagctgctgt tccattggct agtgaaactc atggtgggtga agatgttgct	1320
gtttttgcta gaggtccaca agctcatttg gttcatgggtg ttcaagaaga aacttttggt	1380
gctcatatta tggcttttgc tggttgtggt gaaccataca ctgattgtaa tttgccagct	1440
ccagctactg ctactagtat tccagattaa ggtacc	1476

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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1476 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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gaattcttga ttccagctga agaagaaaat ccagcttttt ggaatagaca agctgctcaa      60
gctttggatg ttgctaagaa gttgcaacca attcaaactg ctgctaagaa tgttattttg      120
tttttgggtg atgggtatggg tgttccaact gttactgcta ctagaatttt gaagggtcaa      180
atgaatggta agttgggtcc agaaactcca ttggctatgg atcaatttcc atacgttgct      240
ttgtctaaga cttacaatgt tgatagacaa gttccagatt ctgctggtag tgctactgct      300
tacttggtg gtgttaaggg taattacaga actattgggtg tttctgctgc tgctagatac      360
aatcaatgta atactactag aggtaatgaa gttacttctg ttattaatag agctaagaag      420
gctggtaagg ctgttggtgt tggttactact actagagttc aacatgcttc tccagctggc      480
gcttacgctc atactgttaa tagaaattgg tactctgatg ctgatttgcc agctgatgct      540
caaaagaatg gttgtcaaga tattgctgct caattggttt acaatatgga tattgatggt      600
attttgggtg gtggtagaat gtacatgttt ccagaaggta ctccagatcc agaataccca      660
gatgatgctt ctgttaatgg tgtagaaag gataagcaaa atttggttca agaatggcaa      720
gctaagcatc aagggtgctc atatgtttgg aatagaactg ctttggttgc agctgctgat      780
gattctagtg ttactcattt gatggggttg tttgaaccag ctgatatgaa gtataatggt      840
caacaagatc atactaagga tccaactttg gctgaaatga ctgaagctgc tttgcaagtt      900
ttgtctagaa atccaagagg tttttacttg tttggtgaag gtggtagaat tgatcatggc      960
cataatgatt ttaaggctta tatggctttg actgaagcta ttatgtttga taatgctatt     1020
gctaaggcta atgaattgac ttctgaattg gatactttga ttttggttac tgctgatcat     1080
agtcatgttt tttcttttgg tggttacact ttgagaggta cttctatttt tggtttggct     1140

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ccaggtaagg ctttggatag taagtcttac acttctatatt tgatatggtaa tgggccaggt 1200
tatgcttttg gtggtgggtc tagaccagat gttaatggta gtactagtga agaaccatct 1260
tacagacaac aagctgctgt tccattggct agtgaaactc atggtgggtga agatggtgct 1320
gtttttgcta gaggtccaca agctcatttg gttcatgggtg ttcaagaaga aacttttggt 1380
gctcatatta tggcttttgc tggttgtgtt gaaccataca ctgattgtaa tttgccagct 1440
ccagctactg ctactagtat tccagattaa ggtacc 1476

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(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1476 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

gaattcttga ttccagctga agaagaaaat ccagcttttt ggaatagaca agctgctcaa 60
gctttggatg ttgctaagaa gttgcaacca attcaaactg ctgctaagaa tggtattttg 120
tttttgggtg atggtatggg tgttccaact gttactgcta ctagaatttt gaagggtcaa 180
atgaatggta agttgggtcc agaaactcca ttggctatgg atcaatttcc atacggtgct 240
ttgtctaaga cttacaatgt tgatagacaa gttccagatg ctgctgggtac tgctactgct 300
tacttggtg gtggttaagg taattacaga actattgggtg tttctgctgc tgctagatac 360
aatcaatgta atactactag aggtaatgaa gttacttctg ttattaatag agctaagaag 420
gctggtaagg ctggtgggtg tgttactact actagagttc aacatgcttc tccagctggt 480
gcttacgctc atactgttaa tagaaattgg tactctgatg ctgatttgcc agctgatgct 540
caaaagaatg gttgtcaaga tattgctgct caattggttt acaatatgga tattgatgtt 600
attttgggtg gtggtagaat gtacatgttt ccagaaggta ctccagatcc agaataccca 660
gatgatgctt ctgttaatgg tgttagaaag gataagcaaa atttgggttca agaatggcaa 720
gctaagcatc aaggtgctca atatgttttg aatagaactg ctttgttgca agctgctgat 780

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gattctagtg ttactcattt gatggggtttg tttgaaccag ctgatatgaa gtataatggt 840
caacaagatc atactaagga tccaactttg gctgaaatga ctgaagctgc tttgcaagtt 900
ttgtctagaa atccaagagg tttttacttg tttggtgaag gtggtagaat tgatcatggt 960
cataatgatt ttaaggctta tatggccttg actgaagcta ttatgtttga taatgctatt 1020
gctaaggcta atgaattgac ttctgaattg gatactttga ttttggttac tgctgatcat 1080
agtcatgttt tttctttttg tggttacact ttgagaggta cttctatattt tggtttggt 1140
ccaggtaagg ctttgatag taagtcttac acttctatattt tgtatggtaa tgggtccagg 1200
tatgctttgg gtggtggttc tagaccagat gttaatggta gtactagtga agaaccatct 1260
tacagacaac aagctgctgt tccattggct agtgaaactc atgggtggtga agatgttgct 1320
gtttttgcta gaggtccaca agctcatttg gttcatggtg ttcaagaaga aacttttggt 1380
gctcatatta tggcttttgc tggttgtgtt gaaccataca ctgattgtaa tttgccagct 1440
ccagctactg ctactagtat tccagattaa ggtacc 1476

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(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA - Primer 5'-hAP

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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gcgcgaattc ttgattccag ctgaagaaga aaatccagct ttttgg 46

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA - Primer 3'-hAP

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(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

gcgcggtacc ttaatctgga atactagtag cagtagctgg agctggc

47

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA - Primer 5'-S92A

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ccagatgctg ctggtactgc tactgc

26

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA - Primer 3'-S92A

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

gcagtagcag taccagcagc atctggaact tgtc

34

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA - Primer 5'-G322H

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

gatcatggtc atcatgattt taaggcttat atggc

35

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA - Primer 3'-G322H

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

gccatataag ccttaaaatc atgatgacca tgatc

35

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA - 5'-H32ON/G322H

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

gatcatggtc ataatgattt taaggcttat atggc

35

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA - Primer 5'H32ON/G322F

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

gccatataag ccttaaaatc attatgacca tgate

35

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA - Primer 5'-Expr

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

gcgcgcctag gagatctaac atccaaagac g

31

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA - Primer 3'-Expr

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

cgcgcgctag cggatccgca caaacgaag

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CLAIMS:

1. A mutant of eukaryotic alkaline phosphatase, wherein
 - an enzyme sequence to be mutated is a wild-type sequence which is at least 77 % identical to SEQ ID NO.: 2,
 - the mutant has an activity which is reduced by at least 100-fold compared to the wild-type, andthe mutant has one or more of the following mutations, the position of the mutation being defined relative to the position in SEQ ID NO.: 2:
 - Ser92: for Ala, Gly, Val or Leu
 - His320: for Asn, Phe, Asp or Tyr, or
 - Gly322: for any amino acid larger than Asp.
2. The mutant of eukaryotic alkaline phosphatase as claimed in claim 1 wherein the mutant has one or more of the following mutations and the position of the mutation is defined relative to the position in SEQ ID NO.: 2:
 - Ser92: for Ala or Gly
 - His320: for Asn or Phe, or
 - Gly322: for Phe or Lys.
3. The mutant of eukaryotic alkaline phosphatase as claimed in claim 1 or 2, wherein the enzyme with the wild type sequence has a specific activity of more than 7000 U/mg.
4. The mutant of eukaryotic alkaline phosphatase as claimed in any one of claims 1 to 3, wherein the mutant has an activity which is reduced by at least 1000-fold compared to the wild type.
5. The mutant of eukaryotic alkaline phosphatase as claimed in any one of claims 1 to 4, wherein the mutant has an activity which is reduced by at least 10000-fold compared to the wild type.

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6. The mutant of eukaryotic alkaline phosphatase as claimed in any one of claims 1 to 5, wherein the mutant has an amino acid sequence which is SEQ ID NO.: 4, SEQ ID NO.: 5, SEQ ID NO.: 6 or SEQ ID NO.: 7.
7. Recombinant DNA coding for the mutant of eukaryotic alkaline phosphatase as claimed in any one of claims 1 to 6.
8. Recombinant DNA coding for a mutant of eukaryotic alkaline phosphatase, wherein the mutant has a nucleic acid sequence which is SEQ ID NO.: 8, SEQ ID NO.: 9, SEQ ID NO.: 10 or SEQ ID NO.: 11.
9. Vector containing a nucleic acid sequence which is SEQ ID NO.: 8, SEQ ID NO.: 9, SEQ ID NO.: 10 or SEQ ID NO.: 11.
10. Vector as claimed in claim 9, which corresponds to a vector which is pPICZ α ATM, BTM, CTM; pPICZTM, pPICZ-ETM, pPICZ α -ETM; pPIC6TM, pPIC6 α ATM, BTM, CTM; pGAPZTM, pGAPZ α ATM, BTM, CTM; pPIC9TM; pPIC9KTM, pPIC3.5TM, pPIC3.5KTM, pAO815TM, pMETTM, pMET α ATM, BTM, CTM; pYES-Dest52TM, pYES2.1/V5-His-TOPOTM, pYC2-ETM, pYES2.1-ETM; Yes-vectorsTM, pTEF1/ZeoTM, pTEF1/BsdTM or pNMT-TOPOTM.
11. Host strain transformed with the vector as claimed in claim 9 or 10.
12. Host strain as claimed in claim 11, wherein *Pichia pastoris* is used as the host strain.
13. Method for producing the mutant of eukaryotic alkaline phosphatase (AP) as claimed in any one of claims 1 to 6 in yeast cells comprising the steps:
 - a) cloning the DNA as claimed in claim 7 or 8 into a first vector and a second vector,

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b) transforming the yeast with the first vector which has a resistance gene to a first selection marker and the second vector which has a resistance gene to a second selection marker, such that transformants which have integrated the resistance gene and the DNA into the genome are selected by growth on nutrient medium containing a low concentration of the first selection marker,

c) expressing the AP mutant such that the gene copy number is increased by multiple transformation whereby multiple transformants are selected by growth on nutrient medium with increased selection pressure, and the gene copy number is increased by multiple transformation with the second vector whereby multiple transformants are selected by growth on nutrient medium with increased selection pressure, and those clones are selected which have stably integrated several copies of the DNA and of the selection marker resistance genes into the genome, and

d) purifying the alkaline phosphatase.

14. The method as claimed in claim 13, wherein methylotrophic yeast cells are used.
15. The method as claimed in claim 14, wherein *Pichia pastoris* is used as the yeast cell.
16. The method as claimed in any one of claims 13 to 15, wherein the first vector which is used corresponds to a vector which is pPICZ α ATM, BTM, CTM; pPICZTM, pPICZ-ETM, pPICZ α -ETM; pPIC6TM, pPIC6 α ATM, BTM, CTM; pGAPZTM, pGAPZ α ATM, BTM, CTM; pPIC9TM; pPIC9KTM, pPIC3.5TM, pPIC3.5KTM or pAO815TM.

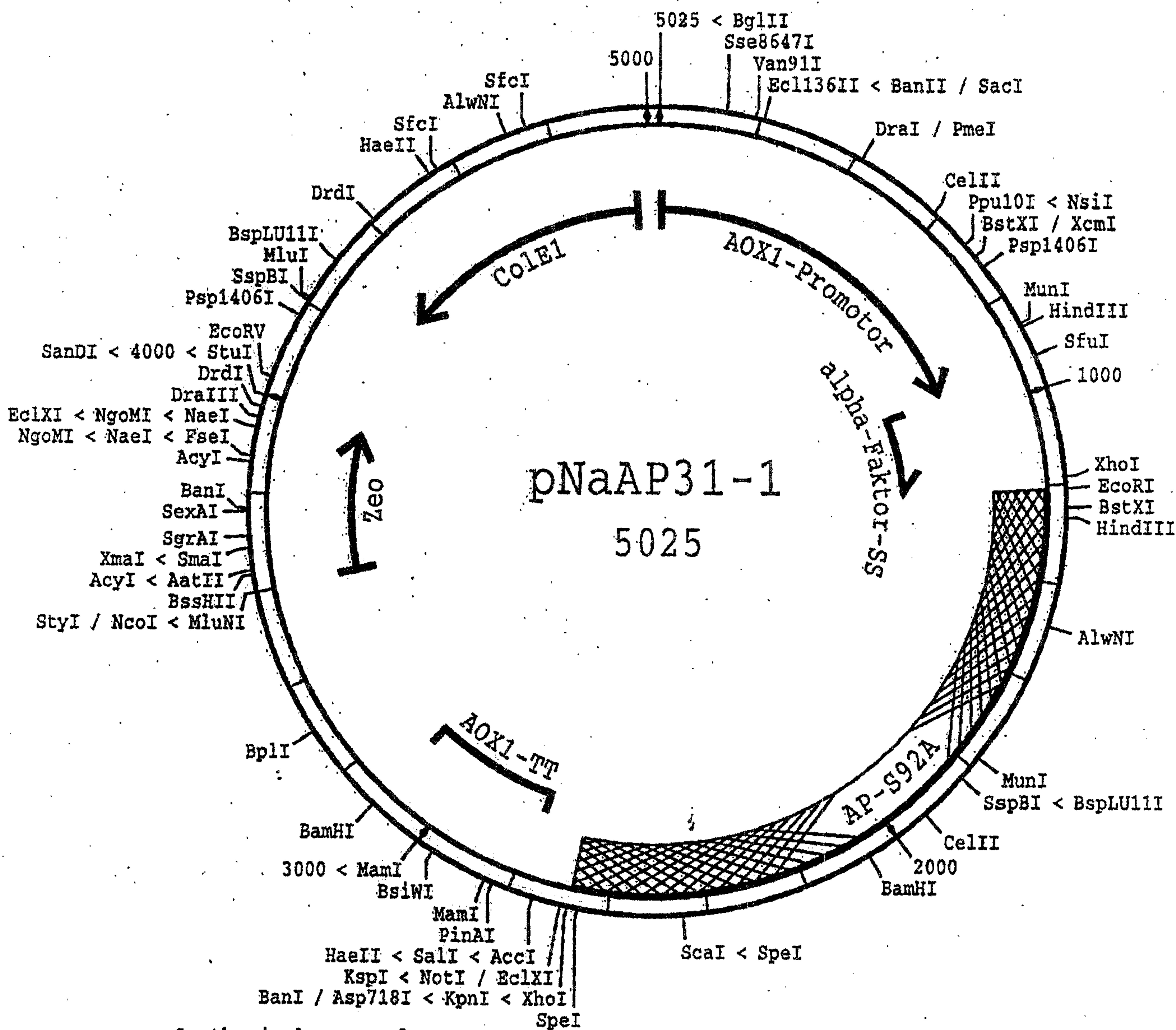


Fig. 1 Plasmid map of the expression vector pNaAP31-1 which contains the gene for the alkaline phosphatase single mutant Ser92Ala. pNaAP31-1 is shown as an example of the other expression vectors pNaAP43-1, pNaAP51-1 and pNaAP6-1.

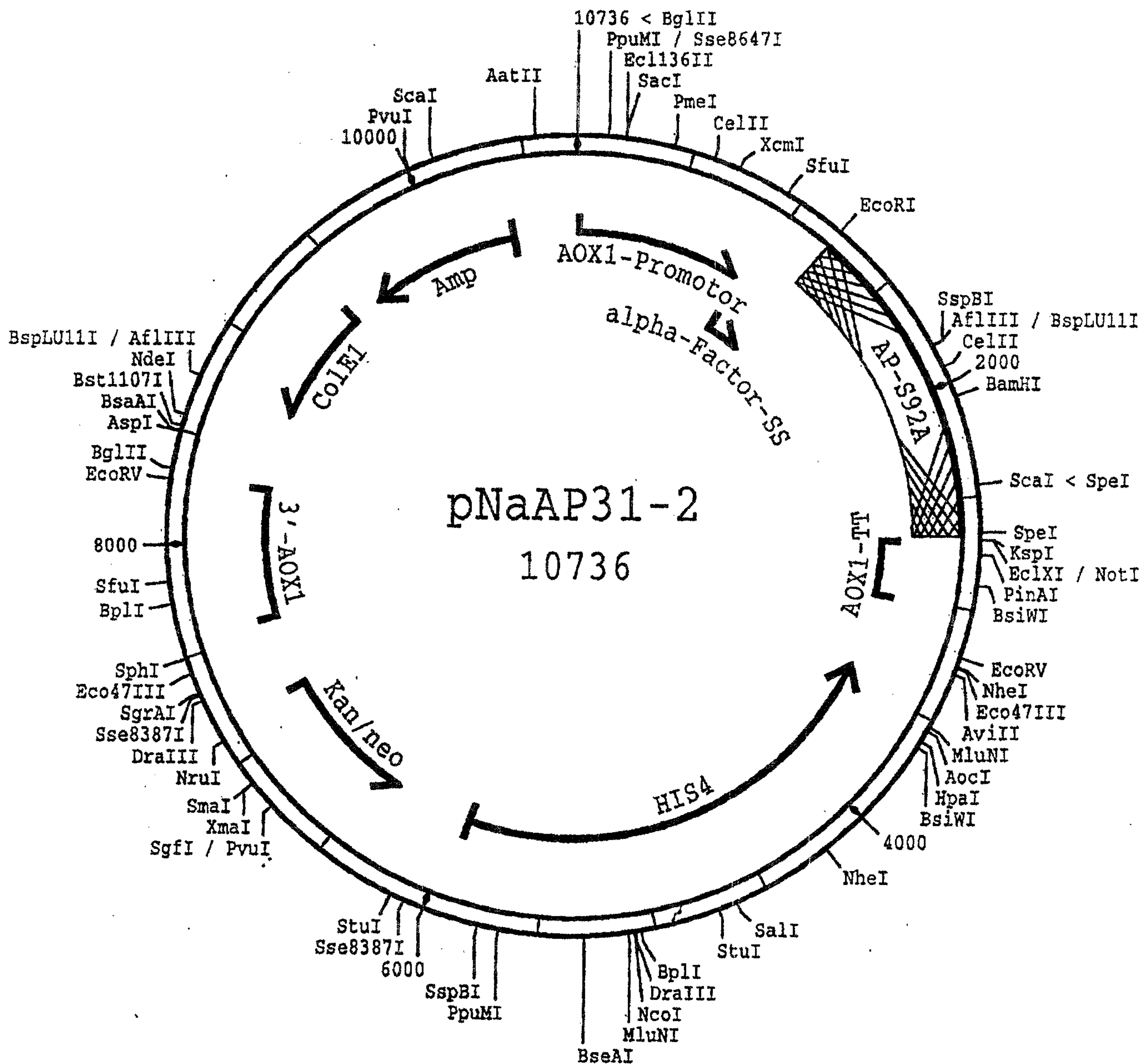


Fig. 2 Plasmid map of the expression vector pNaAP31-2 which contains the gene for the alkaline phosphatase single mutant Ser92Ala. pNaA31-1 is shown as an example of the other expression vectors pNaAP43-2, pNaAP51-2 and pNaAP6-2.