

***Candida tropicalis* cells and use thereof**

Field of the invention

The invention relates to genetically engineered *Candida tropicalis* cells, use thereof and a method of production of ω -hydroxycarboxylic acids and ω -hydroxycarboxylic acid esters.

Prior art

Owing to its ability to form dicarboxylic acids from alkanes, *Candida tropicalis* is a well-characterized ascomycete.

WO91/006660 describes *Candida tropicalis* cells that are completely inhibited in β -oxidation through interruption of the POX4 and/or POX5 genes, and achieve increased yields of α,ω -dicarboxylic acids.

WO00/020566 describes cytochrome P450 monooxygenases and NADPH cytochrome P450 oxidoreductases from *Candida tropicalis* and use thereof for influencing ω -hydroxylation, the first step in ω -oxidation.

WO03/089610 describes enzymes from *Candida tropicalis* which catalyse the second step of ω -oxidation, the conversion of a fatty alcohol to an aldehyde, and use thereof for improved production of dicarboxylic acids.

The cells and methods described so far are not suitable for the production of ω -hydroxycarboxylic acids or their esters, as the ω -hydroxycarboxylic acids are always only present as a short-lived intermediate and are immediately metabolized further.

ω -Hydroxycarboxylic acids and their esters are economically important compounds as precursors of polymers, and this forms the basis of the commercial usability of the present invention.

The task of the invention was to find a way of preparing ω -hydroxycarboxylic acids or ω -hydroxycarboxylic acid esters by fermentation in sufficient amounts, in particular in the medium surrounding the cells.

Description of the invention

It was found, surprisingly, that the cells described hereunder make a contribution to solution of this task.

The object of the present invention is therefore a cell as described in claim 1.

Another object of the invention is the use of the cell according to the invention and a method of production of ω -hydroxycarboxylic acids and ω -hydroxycarboxylic acid esters using the cells according to the invention.

Advantages of the invention are the gentle conversion of the educt used to the ω -hydroxycarboxylic acids and corresponding esters and a high specificity of the method and an associated high yield based on the educt used.

One object of the present invention is a *Candida tropicalis* cell, in particular one from the strain ATCC 20336, which is characterized in that the cell has, compared with its wild type, a reduced activity of at least one of the enzymes that are encoded by the intron-free nucleic acid sequences selected from the two group comprising

A) Seq ID No. 1, Seq ID No. 3, Seq ID No. 5, Seq ID No. 7, Seq ID No. 9, Seq ID No. 11, Seq ID No. 13, Seq ID No. 15, Seq ID No. 17, Seq ID No. 19, Seq ID No. 21, Seq ID No. 23, Seq ID No. 25, Seq ID No. 27, Seq ID No. 29, Seq ID No. 31, Seq ID No. 33, Seq ID No. 35, Seq ID No. 37, Seq ID No. 39, Seq ID No. 41, Seq ID No. 43, Seq ID No. 45, Seq ID No. 47, Seq ID No. 49, Seq ID No. 51, Seq ID No. 53, Seq ID No. 55, Seq ID No. 57, Seq ID No. 59, Seq ID No. 61, Seq ID No. 63, Seq ID No. 65 and Seq ID No. 67; in particular Seq ID No. 1, Seq ID No. 3, Seq ID No. 5, Seq ID No. 7, Seq ID No. 9, Seq ID No. 11, Seq ID No. 13, Seq ID No. 15, Seq ID No. 17, Seq ID No. 19, Seq ID No. 21, Seq ID No. 23, Seq ID No. 25, Seq ID No. 27, Seq ID No. 29, Seq ID No. 31, Seq ID No. 33, Seq ID No. 35, Seq ID No. 37, Seq ID No. 39, Seq ID No. 41, Seq ID No. 43, Seq ID No. 45, Seq ID No. 47, Seq ID No. 49 and Seq ID No. 51; quite especially Seq ID No. 1, Seq ID No. 3, Seq ID No. 5, Seq ID No. 7, Seq ID No. 9, Seq ID No. 11, Seq ID No. 13, Seq ID No. 15, Seq ID No. 17, Seq ID No. 19, Seq ID No. 21, Seq ID No. 23, Seq ID No. 25 and Seq ID No. 27,

B) a sequence that is identical to at least 80%, especially preferably to at least 90%, even more preferably to at least 95% and most preferably to at least 99% to one of the sequences Seq ID No. 1, Seq ID No. 3, Seq ID No. 5, Seq ID No. 7, Seq ID No. 9, Seq ID No. 11, Seq ID No. 13, Seq ID No. 15, Seq ID No. 17, Seq ID No. 19, Seq ID No. 21, Seq ID No. 23, Seq ID No. 25, Seq ID No. 27, Seq ID No. 29, Seq ID No. 31, Seq ID No. 33, Seq ID No. 35, Seq ID No. 37, Seq ID No. 39, Seq ID No. 41, Seq ID No. 43, Seq ID No. 45, Seq ID No. 47, Seq ID No. 49, Seq ID No. 51, Seq ID No. 53, Seq ID No. 55, Seq ID No. 57, Seq ID No. 59, Seq ID No. 61, Seq ID No. 63, Seq ID No. 65 and Seq ID No. 67; in particular to Seq ID No. 1, Seq ID No. 3, Seq ID No. 5, Seq ID No. 7, Seq ID No. 9, Seq ID No. 11, Seq ID No. 13, Seq ID No. 15, Seq ID No. 17, Seq ID No. 19, Seq ID No. 21, Seq ID No. 23, Seq ID

No. 25, Seq ID No. 27, Seq ID No. 29, Seq ID No. 31, Seq ID No. 33, Seq ID No. 35, Seq ID No. 37, Seq ID No. 39, Seq ID No. 41, Seq ID No. 43, Seq ID No. 45, Seq ID No. 47, Seq ID No. 49 and Seq ID No. 51; quite especially to Seq ID No. 1, Seq ID No. 3, Seq ID No. 5, Seq ID No. 7, Seq ID No. 9, Seq ID No. 11, Seq ID No. 13, Seq ID No. 15, Seq ID No. 17, Seq ID No. 19, Seq ID No. 21, Seq ID No. 23, Seq ID No. 25 and Seq ID No. 27.

In this connection, the nucleic acid sequence group that is preferred according to the invention is group A).

A "wild type" of a cell preferably means, in connection with the present invention, the starting strain from which the cell according to the invention was derived by manipulation of the elements (for example the genes comprising the aforesaid nucleic acid sequences coding for a corresponding enzyme or the promoters contained in the corresponding gene, which are linked functionally with the aforesaid nucleic acid sequences), which influence the activities of the enzymes encoded by the stated nucleic acid Seq ID No. If for example the activity of the enzyme encoded by Seq ID No. 1 in the strain ATCC 20336 is reduced by interruption of the corresponding gene, then the strain ATCC 20336 that is unchanged and was used for the corresponding manipulation is to be regarded as the "wild type".

The term "gene" means, in connection with the present invention, not only the encoding DNA region or that transcribed to mRNA, the "structural gene", but in addition promoter, possible intron, enhancer and other regulatory sequence, and terminator, regions.

The term "activity of an enzyme" always means, in connection with the invention, the enzymatic activity that catalyses the reactions of 12-hydroxydodecanoic acid to

1,12-dodecane diacid by the entire cell. This activity is preferably determined by the following method:

Starting from a single colony, a 100-ml Erlenmeyer flask with 10 ml of YM medium (0.3% yeast extract, 0.3% malt extract, 0.5% peptone and 1.0% (w/w) glucose) is cultivated at 30°C and 90 rpm for 24 h. Then, starting from this culture, 10 ml is inoculated into a 1-litre Erlenmeyer flask with 100 ml of production medium (for 1 litre: 25 g glucose, 7.6 g NH_4Cl , 1.5 g Na_2SO_4 , 300 ml of a 1 mM potassium phosphate buffer (pH 7.0), 20 mg $\text{ZnSO}_4 \times 7 \text{H}_2\text{O}$, 20 mg $\text{MnSO}_4 \times 4 \text{H}_2\text{O}$, 20 mg nicotinic acid, 20 mg pyridoxine, 8 mg thiamine and 6 mg pantothenate). It is cultivated for 24 h at 30°C.

After 24 h, 12-hydroxydodecanoic acid is added to the cell suspension, so that the concentration is not greater than 0.5 g/l. Glucose or glycerol is also added as co-substrate, so that the concentration of the co-substrate does not drop below 0.2 g/l. After 0h, 0.5 h, 1h, and then hourly up to a cultivation time of 24 h, samples (1 ml) are taken for measurement of 12-hydroxydodecanoic acid, 12-oxo-dodecanoic acid and 1,12-dodecane diacid and the corresponding methyl esters, and for checking the cell count. After each measurement, the pH is kept between 5.0 and 6.5 with 6N NaOH or 4N H_2SO_4 . During cultivation, cell growth is verified by checking the "colony forming units" (CFU). The decrease of 12-hydroxydodecanoic acid and the production of 1,12-dodecane diacid or the corresponding methyl esters are verified by LC-MS. For this, 500 μl of culture broth is adjusted to pH 1 and then extracted with the same volume of diethyl ether or ethyl acetate and analysed by LC-MS.

The measuring system consists of an HP1100 HPLC (Agilent Technologies, Waldbronn, Germany) with degasser, autosampler and column furnace, coupled to a mass-

selective quadrupole detector MSD (Agilent Technologies, Waldbronn, Germany). Chromatographic separation is achieved on a reversed phase e.g. 125x2 mm Luna C18(2) column (Phenomenex, Aschaffenburg, Germany) at 40°C. Gradient elution is performed at a flow of 0.3 ml/min (A: 0.02% formic acid in water and B: 0.02% formic acid in acetonitrile). Alternatively, the organic extracts are analysed by GC-FID (Perkin Elmer, Rodgau-Jügesheim, Germany). Chromatographic separation is performed on a methylpolysiloxane (5% phenyl) phase e.g. Elite 5, 30 m, 0.25 mm ID, 0.25 µm FD (Perkin Elmer, Rodgau-Jügesheim, Germany). Before measurement, a methylation reagent e.g. trimethylsulphonium hydroxide "TMSH" (Macherey-Nagel GmbH & Co. KG, Düren, Germany) is added to free acids and on injection they are converted to the corresponding methyl esters.

By calculating the measured concentration of 1,12-dodecane diacid and the cell number at the time of sampling, it is possible to determine the specific production rate of 1,12-dodecane diacid from 12-hydroxydodecanoic acid and therefore the "activity of an enzyme" in a cell as defined above. The formulation "reduced activity compared with its wild type" means an activity relative to the wild-type activity preferably reduced by at least 50%, especially preferably by at least 90%, more preferably by at least 99.9%, even more preferably by at least 99.99% and most preferably by at least 99.999%.

The decrease in activity of the cell according to the invention compared with its wild type is determined by the method described above for determining activity using cell numbers/concentrations as identical as possible, the cells having been grown under the same conditions, for example medium, gassing, agitation.

"Nucleotide identity" relative to the stated sequences can be determined using known methods. Generally, special computer programs are used with algorithms taking special requirements into account. Preferred methods for determining identity first produce the greatest agreement between the sequences to be compared. Computer programs for determining identity comprise, but are not restricted to, the GCG software package, including

- GAP (Deveroy, J. et al., Nucleic Acid Research 12 (1984), page 387, Genetics Computer Group University of Wisconsin, Medicine (Wi), and

- BLASTP, BLASTN and FASTA (Altschul, S. et al., Journal of Molecular Biology 215 (1990), pages 403-410. The BLAST program can be obtained from the National Center for Biotechnology Information (NCBI) and from other sources (BLAST Manual, Altschul S. et al., NCBI NLM NIH Bethesda ND 22894; Altschul S. et al., above).

The known Smith-Waterman algorithm can also be used for determining nucleotide identity.

Preferred parameters for the determination of "nucleotide identity" are, when using the BLASTN program (Altschul, S. et al., Journal of Molecular Biology 215 (1990), pages 403-410):

Expect Threshold:	10
Word size:	28
Match score:	1
Mismatch score:	-2
Gap costs:	linear

The above parameters are the default parameters in nucleotide sequence comparison.

The GAP program is also suitable for use with the above parameters.

An identity of 80% according to the above algorithm means, in connection with the present invention, 80% identity. The same applies to higher identities.

The term "that are encoded by the intron-free nucleic acid sequences" makes clear that in a sequence comparison with the sequences given here, the nucleic acid sequences to be compared must be purified of any introns beforehand.

All stated percentages (%) are percentages by weight unless stated otherwise.

Methods of lowering enzymatic activities in microorganisms are known by a person skilled in the art.

In particular, techniques in molecular biology can be used for this. A person skilled in the art can find instructions on modification and decrease of protein expression and the associated decrease in enzyme activity especially for *Candida tropicalis*, in particular for interrupting specified genes, in WO91/006660; WO03/100013; Picataggio et al. Mol Cell Biol. 1991 Sep; 11(9):4333-9; Rohrer et al. Appl Microbiol Biotechnol. 1992 Feb; 36(5):650-4; Picataggio et al. Biotechnology (N Y). 1992 Aug; 10(8):894-8; Ueda et al. Biochim Biophys Acta. 2003 Mar 17; 1631(2):160-8; Ko et al. Appl Environ Microbiol. 2006 Jun; 72(6):4207-13; Hara et al. Arch Microbiol. 2001 Nov; 176(5):364-9; Kanayama et al. J Bacteriol. 1998 Feb; 180(3): 690-8.

Cells preferred according to the invention are characterized in that the decrease in enzymatic activity is achieved by modification of at least one gene comprising one of the sequences selected from the

previously stated nucleic acid sequence groups A) and B), the modification being selected from the group comprising, preferably consisting of, insertion of foreign DNA into the gene, deletion at least of parts of the gene, point mutations in the gene sequence and subjecting the gene to the influence of RNA interference or exchange of parts of the gene with foreign DNA, in particular of the promoter region.

Foreign DNA means, in this context, any DNA sequence that is "foreign" to the gene (and not to the organism), i.e. even *Candida tropicalis* endogenous DNA sequences can, in this context, function as "foreign DNA".

In this context, it is in particular preferable for the gene to be interrupted by insertion of a selection marker gene, therefore the foreign DNA is a selection marker gene, the insertion preferably having been effected by homologous recombination into the gene locus.

In this context, it may be advantageous if the selection marker gene is expanded with further functionalities, which in their turn make subsequent removal from the gene possible, this can be achieved for example with a Cre/loxP system, with *Flippase Recognition Targets* (FRT) or by homologous recombination.

Cells preferred according to the invention are characterized in that they are blocked in their β -oxidation at least partially, preferably completely, as this prevents outflow of substrate and therefore higher titres become possible.

Examples of *Candida tropicalis* cells partially blocked in their β -oxidation are described in EP0499622 as strains H41, H41B, H51, H45, H43, H53, H534, H534B and H435, from which a *Candida tropicalis* cell preferred according to the invention is derived.

Other *Candida tropicalis* cells blocked for β -oxidation are described for example in W003/100013.

In this context, cells are preferred for which the β -oxidation is caused by an induced malfunction of at least one of the genes POX2, POX4 or POX5.

Therefore, in this context, cells are preferred that are characterized in that a *Candida tropicalis* cell preferred according to the invention is derived from strains selected from the group comprising ATCC 20962 and the *Candida tropicalis* HDC100 described in US2004/0014198.

The use of the cells according to the invention for the production of ω -hydroxycarboxylic acids or ω -hydroxycarboxylic acid esters also contributes to solution of the task facing the invention.

In particular, the use of the cells according to the invention for the production of ω -hydroxycarboxylic acids or ω -hydroxycarboxylic acid esters with a chain length of the carboxylic acid from 6 to 24, preferably 8 to 18 and especially preferably 10 to 16 carbon atoms, which are preferably linear, saturated and unsubstituted, and a chain length of the alcohol component of the ester from 1 to 4, in particular 1 or 2 carbon atoms, is advantageous. In this context, it is preferable for the ω -hydroxycarboxylic acids to be 12-hydroxydodecanoic acid and for the ω -hydroxycarboxylic acid ester to be 12-hydroxydodecanoic acid methyl ester.

A preferred use is characterized according to the invention in that preferred cells according to the invention as described above are used.

Another contribution to solving the task facing the invention is made by a method of production of the *C. tropicalis* cell according to the invention described above comprising the steps:

I) Preparation of a *C. tropicalis* cell, preferably a cell that is blocked in its β -oxidation at least partially, preferably completely

II) Modification of at least one gene comprising one of the intron-free nucleic acid sequences selected from the previously stated nucleic acid sequence groups A) and B) by insertion of foreign DNA, in particular of DNA coding for a selection marker gene, into the gene, deletion of at least parts of the gene, point mutations in the gene sequence and subjecting the gene to the influence of RNA interference or exchange of parts of the gene with foreign DNA, in particular of the promoter region.

Another contribution to solving the task facing the invention is made by a method of production of ω -hydroxycarboxylic acids or ω -hydroxycarboxylic acid esters, in particular of ω -hydroxycarboxylic acids or ω -hydroxycarboxylic acid esters with a chain length of the carboxylic acid from 6 to 24, preferably 8 to 18 and especially preferably 10 to 16 carbon atoms, which are preferably linear, saturated and unsubstituted, and a chain length of the alcohol component of the ester from 1 to 4, in particular of 1 or 2 carbon atoms, in particular of 12-hydroxydodecanoic acid or 12-hydroxydodecanoic acid methyl ester comprising the steps

A) contacting a previously described cell according to the invention with a medium comprising a carboxylic acid or a carboxylic acid ester, in particular a carboxylic acid or a carboxylic acid ester with a chain length of the carboxylic acid from 6 to 24, preferably 8 to 18 and

especially preferably 10 to 16 carbon atoms, which are preferably linear, saturated and unsubstituted, and a chain length of the alcohol component of the ester from 1 to 4 carbon atoms, in particular dodecanoic acid or dodecanoic acid methyl ester,

B) cultivating the cell under conditions that enable the cell to form the corresponding ω -hydroxycarboxylic acid or ω -hydroxycarboxylic acid esters from the carboxylic acid or the carboxylic acid ester and

C) optionally isolating the ω -hydroxycarboxylic acid or ω -hydroxycarboxylic acid esters that formed.

Preferred methods according to the invention use cells stated above as being preferred according to the invention.

Therefore, for example a method of production of 12-hydroxydodecanoic acid or 12-hydroxydodecanoic acid methyl ester comprising the steps

a) contacting a *Candida tropicalis* cell of the strain ATTC 20336 at least partially blocked in its β -oxidation, which has, compared with its wild type, a reduced activity of at least one of the enzymes, which are encoded by the intron-free nucleic acid sequences selected from the previously stated nucleic acid sequence groups A) and B), the decrease in enzymatic activity being achieved by modification of a gene comprising one of the nucleic acid sequences selected from the previously stated nucleic acid sequence groups A) and B), wherein the modification consists of insertion of a selection marker gene into the gene, with a medium comprising dodecanoic acid or dodecanoic acid methyl ester,

b) cultivating the cell under conditions that enable the cell to form the corresponding ω -hydroxycarboxylic acid or ω -hydroxycarboxylic acid esters from the carboxylic acid or the carboxylic acid ester and

c) optionally isolating the ω -hydroxycarboxylic acid or ω -hydroxycarboxylic acid esters that formed

is quite especially preferred.

Suitable cultivation conditions for *Candida tropicalis* are known by a person skilled in the art. In particular, suitable conditions for step b) are those that are known by a person skilled in the art from bioconversion methods of production of dicarboxylic acids with *Candida tropicalis*.

These cultivation conditions are described for example in WO00/017380 and WO00/015828.

Methods for isolating the ω -hydroxycarboxylic acid or ω -hydroxycarboxylic acid esters that formed are known by a person skilled in the art. These are standard methods for isolating long-chain carboxylic acids from aqueous solution, for example distillation or extraction, and can for example also be found in WO2009/077461.

It is advantageous to use the ω -hydroxycarboxylic acids or ω -hydroxycarboxylic acid esters obtained by the method according to the invention for the production of polymers, in particular polyesters. Moreover, lactones can also be produced from the ω -hydroxy carboxylic acids, and can then for example be used in their turn for the production of polyesters.

Another advantageous use is to convert the ω -hydroxycarboxylic acids or ω -hydroxycarboxylic acid esters

to ω -aminocarboxylic acids or ω -aminocarboxylic acid esters, in order to obtain polyamides as polymers. The ω -aminocarboxylic acids or ω -aminocarboxylic acid esters can also be converted first to the corresponding lactams, which can then in their turn be converted using anionic, or also acid catalysis to a polyamide.

It is quite especially advantageous, in a first reaction step, to convert the ω -hydroxycarboxylic acids or corresponding esters into the ω -oxo-carboxylic acids or the corresponding esters and then to carry out amination of the oxo-group, e.g. in the course of reductive amination.

In this context, the use of 12-hydroxy dodecanoic acid or 12-hydroxydodecanoic acid methyl ester for the production of polymers, in particular of polyamide 12, is especially preferred.

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Ile Ile Lys Val Lys Gly Asn Gly Arg Leu Ala Arg Phe Trp
Pro Ile

65

70

75

80

Lys Thr Phe Asp Asp Tyr Pro Asn His Thr Phe Tyr Met Ser
Ile Ile

85

90

95

Gly Ala Leu Lys Ile Val Leu Thr Val Ile Gln Glu Asn Ile
Lys Ala

100

105

110

Val Leu Ala Thr Gln Phe Thr Asp Phe Ser Leu Gly Thr Arg
His Ala

115

120

125

His Phe Tyr Pro Leu Leu Gly Asp Gly Ile Phe Thr Leu Asp
Gly Glu

130

135

140

Gly Trp Lys His Ser Arg Ala Met Leu Arg Pro Gln Phe Ala
Arg Asp

145

150

155

160

Gln Ile Gly His Val Lys Ala Leu Glu Pro His Ile Gln Ile
Leu Ala

165

170

175

Lys Gln Ile Lys Leu Asn Lys Gly Lys Thr Phe Asp Ile Gln
Glu Leu
180 185 190

Phe Phe Arg Phe Thr Val Asp Thr Ala Thr Glu Phe Leu Phe
Gly Glu
195 200 205

Ser Val His Ser Leu Tyr Asp Glu Lys Leu Gly Ile Pro Thr
Pro Asn
210 215 220

Glu Ile Pro Gly Arg Asp Asn Phe Ala Thr Ala Phe Asn Thr
Ser Gln
225 230 235
240

His Tyr Leu Ala Thr Arg Thr Tyr Ser Gln Thr Phe Tyr Phe
Leu Thr
245 250
255

Asn Pro Lys Glu Phe Arg Asp Cys Asn Ala Lys Val His Tyr
Leu Ala
260 265 270

Lys Tyr Phe Val Asn Lys Ala Leu Asn Phe Thr Pro Glu Glu
Ile Glu
275 280 285

Glu Lys Ser Lys Ser Gly Tyr Val Phe Leu Tyr Glu Leu Val
Lys Gln
290 295 300

Thr Arg Asp Pro Lys Val Leu Gln Asp Gln Leu Leu Asn Ile
Met Val
305 310 315
320

Ala Gly Arg Asp Thr Thr Ala Gly Leu Leu Ser Phe Ala Met

Phe Glu

325

330

335

Leu Ala Arg His Pro Glu Ile Trp Ser Lys Leu Arg Glu Glu
Ile Glu

340

345

350

Val Asn Phe Gly Val Gly Glu Glu Ser Arg Val Glu Glu Ile
Thr Phe

355

360

365

Glu Ser Leu Lys Arg Cys Glu Tyr Leu Lys Ala Ile Leu Asn
Glu Thr

370

375

380

Leu Arg Met Tyr Pro Ser Val Pro Val Asn Ser Arg Thr Ala
Thr Arg

385

390

395

400

Asp Thr Thr Leu Pro Arg Gly Gly Gly Pro Asn Gly Thr Asp
Pro Ile

405

410

415

Phe Ile Pro Lys Gly Ser Thr Val Ala Tyr Ile Val Tyr Lys
Thr His

420

425

430

Arg Leu Glu Glu Tyr Tyr Gly Lys Asp Ala Asp Asp Phe Arg
Pro Glu

435

440

445

Arg Trp Phe Glu Pro Ser Thr Lys Lys Leu Gly Trp Ala Tyr
Val Pro

450

455

460

Phe Asn Gly Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe Ala
Leu Thr

465

470

475

480

Glu Ala Ser Tyr Val Ile Thr Arg Leu Val Gln Met Phe Glu
Thr Val

485

490

495

Ser Ser Pro Pro Asp Val Glu Tyr Pro Pro Pro Lys Cys Ile
His Leu

500

505

510

Thr Met Ser His Asp Asp Gly Val Phe Val Lys Met
515 520

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<213> Candida tropicalis

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acc aaa 48

Met Ala Thr Gln Glu Ile Ile Asp Ser Val Leu Pro Tyr Leu
Thr Lys

1 5

10

15

tgg tac act gtg att act gca gca gta tta gtc ttc ctt atc
tcc aca 96

Trp Tyr Thr Val Ile Thr Ala Ala Val Leu Val Phe Leu Ile
Ser Thr

20

25

30

aac atc aag aac tac gtc aag gca aag aaa ttg aaa tgt gtc
gat cca 144

Asn Ile Lys Asn Tyr Val Lys Ala Lys Lys Leu Lys Cys Val
Asp Pro

35

40

45

cca tac ttg aag gat gcc ggt ctc act ggt att ctg tct ttg
atc gcc 192

[illegible]

cag atc aag ttg aac cag gga aag act ttc gat atc caa gaa
ttg ttc 576
Gln Ile Lys Leu Asn Gln Gly Lys Thr Phe Asp Ile Gln Glu
Leu Phe
180 185 190

ttt aga ttt acc gtc gac acc gct act gag ttc ttg ttt ggt
gaa tcc 624
Phe Arg Phe Thr Val Asp Thr Ala Thr Glu Phe Leu Phe Gly
Glu Ser
195 200 205

gtt cac tcc ttg tac gat gaa aaa ttg ggc atc cca act cca
aac gaa 672
Val His Ser Leu Tyr Asp Glu Lys Leu Gly Ile Pro Thr Pro
Asn Glu
210 215 220

atc cca gga aga gaa aac ttt gcc gct gct ttc aac gtt tcc
caa cac 720
Ile Pro Gly Arg Glu Asn Phe Ala Ala Ala Phe Asn Val Ser
Gln His
225 230 235
240

tac ttg gcc acc aga agt tac tcc cag act ttt tac ttt ttg
acc aac 768
Tyr Leu Ala Thr Arg Ser Tyr Ser Gln Thr Phe Tyr Phe Leu
Thr Asn
245 250
255

cct aag gaa ttc aga gac tgt aac gcc aag gtc cac cac ttg
gcc aag 816
Pro Lys Glu Phe Arg Asp Cys Asn Ala Lys Val His His Leu
Ala Lys
260 265 270

tac ttt gtc aac aag gcc ttg aac ttt act cct gaa gaa ctc
gaa gag 864
Tyr Phe Val Asn Lys Ala Leu Asn Phe Thr Pro Glu Glu Leu
Glu Glu
275 280 285

aaa tcc aag tcc ggt tac gtt ttc ttg tac gaa ttg gtt aag
caa acc 912
Lys Ser Lys Ser Gly Tyr Val Phe Leu Tyr Glu Leu Val Lys
Gln Thr
290 295 300

aga gat cca aag gtc ttg caa gat caa ttg ttg aac att atg
ggt gcc 960
Arg Asp Pro Lys Val Leu Gln Asp Gln Leu Leu Asn Ile Met
Val Ala
305 310 315
320

gga aga gac acc act gcc ggt ttg ttg tcc ttt gct ttg ttt
gaa ttg 1008
Gly Arg Asp Thr Thr Ala Gly Leu Leu Ser Phe Ala Leu Phe
Glu Leu
325 330
335

gct aga cac cca gag atg tgg tcc aag ttg aga gaa gaa atc
gaa gtt 1056
Ala Arg His Pro Glu Met Trp Ser Lys Leu Arg Glu Glu Ile
Glu Val
340 345 350

aac ttt ggt gtt ggt gaa gac tcc cgc gtt gaa gaa att acc
ttc gaa 1104
Asn Phe Gly Val Gly Glu Asp Ser Arg Val Glu Glu Ile Thr
Phe Glu
355 360 365

gcc ttg aag aga tgt gaa tac ttg aag gct atc ctt aac gaa
acc ttg 1152
Ala Leu Lys Arg Cys Glu Tyr Leu Lys Ala Ile Leu Asn Glu
Thr Leu
370 375 380

cgt atg tac cca tct gtt cct gtc aac ttt aga acc gcc acc
aga gac 1200
Arg Met Tyr Pro Ser Val Pro Val Asn Phe Arg Thr Ala Thr
Arg Asp
385 390 395
400

acc act ttg cca aga ggt ggt ggt gct aac ggt acc gac cca
atc tac 1248
Thr Thr Leu Pro Arg Gly Gly Gly Ala Asn Gly Thr Asp Pro
Ile Tyr
405 410
415

att cct aaa ggc tcc act gtt gct tac gtt gtc tac aag acc
cac cgt 1296
Ile Pro Lys Gly Ser Thr Val Ala Tyr Val Val Tyr Lys Thr
His Arg

			420				425				430			
ttg	gaa	gaa	tac	tac	ggt	aag	gac	gct	aac	gac	ttc	aga	cca	
gaa	aga		1344											
Leu	Glu	Glu	Tyr	Tyr	Gly	Lys	Asp	Ala	Asn	Asp	Phe	Arg	Pro	
Glu	Arg		435				440				445			
tggt	ttt	gaa	cca	tct	act	aag	aag	ttg	ggc	tggt	gct	tat	gtt	
cca	ttc		1392											
Trp	Phe	Glu	Pro	Ser	Thr	Lys	Lys	Leu	Gly	Trp	Ala	Tyr	Val	
Pro	Phe		450				455				460			
aac	ggt	ggt	cca	aga	gtc	tgc	ttg	ggt	caa	caa	ttc	gcc	ttg	
act	gaa		1440											
Asn	Gly	Gly	Pro	Arg	Val	Cys	Leu	Gly	Gln	Gln	Phe	Ala	Leu	
Thr	Glu		465				470				475			
480														
gct	tct	tat	gtg	atc	act	aga	ttg	gcc	cag	atg	ttt	gaa	act	
gtc	tca		1488											
Ala	Ser	Tyr	Val	Ile	Thr	Arg	Leu	Ala	Gln	Met	Phe	Glu	Thr	
Val	Ser		485				490							
495														
tct	gat	cca	ggt	ctc	gaa	tac	cct	cca	cca	aag	tgt	att	cac	
ttg	acc		1536											
Ser	Asp	Pro	Gly	Leu	Glu	Tyr	Pro	Pro	Pro	Lys	Cys	Ile	His	
Leu	Thr		500				505				510			
atg	agt	cac	aac	gat	ggt	gtc	ttt	gtc	aag	atg	taa			
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Met	Ser	His	Asn	Asp	Gly	Val	Phe	Val	Lys	Met				
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Thr Lys
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Trp Lys His Ser Arg Ala Met Leu Arg Pro Gln Phe Ala Arg
 Asp Gln
 145 150 155
 160

Ile Gly His Val Lys Ala Leu Glu Pro His Ile Gln Ile Met
Ala Lys
165 170
175

Gln Ile Lys Leu Asn Gln Gly Lys Thr Phe Asp Ile Gln Glu
Leu Phe
180 185 190

Phe Arg Phe Thr Val Asp Thr Ala Thr Glu Phe Leu Phe Gly
Glu Ser
195 200 205

Val His Ser Leu Tyr Asp Glu Lys Leu Gly Ile Pro Thr Pro
Asn Glu
210 215 220

Ile Pro Gly Arg Glu Asn Phe Ala Ala Ala Phe Asn Val Ser
Gln His
225 230 235
240

Tyr Leu Ala Thr Arg Ser Tyr Ser Gln Thr Phe Tyr Phe Leu
Thr Asn
245 250
255

Pro Lys Glu Phe Arg Asp Cys Asn Ala Lys Val His His Leu
Ala Lys
260 265 270

Tyr Phe Val Asn Lys Ala Leu Asn Phe Thr Pro Glu Glu Leu
Glu Glu
275 280 285

Lys Ser Lys Ser Gly Tyr Val Phe Leu Tyr Glu Leu Val Lys
Gln Thr
290 295 300

Arg Asp Pro Lys Val Leu Gln Asp Gln Leu Leu Asn Ile Met

Val Ala
305
320

310

315

Gly Arg Asp Thr Thr Ala Gly Leu Leu Ser Phe Ala Leu Phe
Glu Leu
325 330
335

Ala Arg His Pro Glu Met Trp Ser Lys Leu Arg Glu Glu Ile
Glu Val
340 345 350

Asn Phe Gly Val Gly Glu Asp Ser Arg Val Glu Glu Ile Thr
Phe Glu
355 360 365

Ala Leu Lys Arg Cys Glu Tyr Leu Lys Ala Ile Leu Asn Glu
Thr Leu
370 375 380

Arg Met Tyr Pro Ser Val Pro Val Asn Phe Arg Thr Ala Thr
Arg Asp
385 390 395
400

Thr Thr Leu Pro Arg Gly Gly Gly Ala Asn Gly Thr Asp Pro
Ile Tyr
405 410
415

Ile Pro Lys Gly Ser Thr Val Ala Tyr Val Val Tyr Lys Thr
His Arg
420 425 430

Leu Glu Glu Tyr Tyr Gly Lys Asp Ala Asn Asp Phe Arg Pro
Glu Arg
435 440 445

Trp Phe Glu Pro Ser Thr Lys Lys Leu Gly Trp Ala Tyr Val
Pro Phe

450

455

460

Asn Gly Gly Pro Arg Val Cys Leu Gly Gln Gln Phe Ala Leu
Thr Glu

465

470

475

480

Ala Ser Tyr Val Ile Thr Arg Leu Ala Gln Met Phe Glu Thr
Val Ser

485

490

495

Ser Asp Pro Gly Leu Glu Tyr Pro Pro Pro Lys Cys Ile His
Leu Thr

500

505

510

Met Ser His Asn Asp Gly Val Phe Val Lys Met

515

520

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<213> Candida tropicalis

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<222> (1)..(1569)

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tac gtg 48

Met Thr Val His Asp Ile Ile Ala Thr Tyr Phe Thr Lys Trp

Tyr Val

1

5

10

15

ata gta cca ctc gct ttg att gct tat aga gtc ctc gac tac

ttc tat 96

Ile Val Pro Leu Ala Leu Ile Ala Tyr Arg Val Leu Asp Tyr

Phe Tyr

20

25

30

ggc aga tac ttg atg tac aag ctt ggt gct aaa cca ttt ttc

cag aaa 144

Gly	Arg	Tyr	Leu	Met	Tyr	Lys	Leu	Gly	Ala	Lys	Pro	Phe	Phe
Gln	Lys												
		35					40					45	
cag	aca	gac	ggc	tgt	ttc	gga	ttc	aaa	gct	ccg	ctt	gaa	ttg
ttg	aag		192										
Gln	Thr	Asp	Gly	Cys	Phe	Gly	Phe	Lys	Ala	Pro	Leu	Glu	Leu
Leu	Lys												
	50					55					60		
aag	aag	agc	gac	ggc	acc	ctc	ata	gac	ttc	aca	ctc	cag	cgt
atc	cac		240										
Lys	Lys	Ser	Asp	Gly	Thr	Leu	Ile	Asp	Phe	Thr	Leu	Gln	Arg
Ile	His												
65					70					75			
80													
gat	ctc	gat	cgt	ccc	gat	atc	cca	act	ttc	aca	ttc	ccg	gtc
ttt	tcc		288										
Asp	Leu	Asp	Arg	Pro	Asp	Ile	Pro	Thr	Phe	Thr	Phe	Pro	Val
Phe	Ser												
			85						90				
95													
atc	aac	ctt	gtc	aat	acc	ctt	gag	ccg	gag	aac	atc	aag	gcc
atc	ttg		336										
Ile	Asn	Leu	Val	Asn	Thr	Leu	Glu	Pro	Glu	Asn	Ile	Lys	Ala
Ile	Leu												
			100				105					110	
gcc	act	cag	ttc	aac	gat	ttc	tcc	ttg	ggc	acc	aga	cac	tcg
cac	ttt		384										
Ala	Thr	Gln	Phe	Asn	Asp	Phe	Ser	Leu	Gly	Thr	Arg	His	Ser
His	Phe												
		115					120				125		
gct	cct	ttg	ttg	ggc	gat	ggc	atc	ttt	acg	ttg	gat	ggc	gcc
ggc	tgg		432										
Ala	Pro	Leu	Leu	Gly	Asp	Gly	Ile	Phe	Thr	Leu	Asp	Gly	Ala
Gly	Trp												
	130					135					140		
aag	cac	agc	aga	tct	atg	ttg	aga	cca	cag	ttt	gcc	aga	gaa
cag	att		480										
Lys	His	Ser	Arg	Ser	Met	Leu	Arg	Pro	Gln	Phe	Ala	Arg	Glu
Gln	Ile												
145					150					155			
160													
tcc	cac	gtc	aag	ttg	ttg	gag	cca	cac	gtt	cag	gtg	ttc	ttc

aaa cac 528
Ser His Val Lys Leu Leu Glu Pro His Val Gln Val Phe Phe
Lys His
165 170
175
gtc aga aag gca cag ggc aag act ttt gac atc cag gaa ttg
ttt ttc 576
Val Arg Lys Ala Gln Gly Lys Thr Phe Asp Ile Gln Glu Leu
Phe Phe
180 185 190
aga ttg acc gtc gac tcc gcc acc gag ttt ttg ttt ggt gaa
tcc gtt 624
Arg Leu Thr Val Asp Ser Ala Thr Glu Phe Leu Phe Gly Glu
Ser Val
195 200 205
gag tcc ttg aga gat gaa tct atc ggc atg tcc atc aat gcg
ctt gac 672
Glu Ser Leu Arg Asp Glu Ser Ile Gly Met Ser Ile Asn Ala
Leu Asp
210 215 220
ttt gac ggc aag gct ggc ttt gct gat gct ttt aac tat tcg
cag aat 720
Phe Asp Gly Lys Ala Gly Phe Ala Asp Ala Phe Asn Tyr Ser
Gln Asn
225 230 235
240
tat ttg gct tcg aga gcg gtt atg caa caa ttg tac tgg gtg
ttg aac 768
Tyr Leu Ala Ser Arg Ala Val Met Gln Gln Leu Tyr Trp Val
Leu Asn
245 250
255
ggg aaa aag ttt aag gag tgc aac gct aaa gtg cac aag ttt
gct gac 816
Gly Lys Lys Phe Lys Glu Cys Asn Ala Lys Val His Lys Phe
Ala Asp
260 265 270
tac tac gtc aac aag gct ttg gac ttg acg cct gaa caa ttg
gaa aag 864
Tyr Tyr Val Asn Lys Ala Leu Asp Leu Thr Pro Glu Gln Leu
Glu Lys
275 280 285

cag	gat	ggt	tat	gtg	ttt	ttg	tac	gaa	ttg	gtc	aag	caa	acc
aga	gac				912								
Gln	Asp	Gly	Tyr	Val	Phe	Leu	Tyr	Glu	Leu	Val	Lys	Gln	Thr
Arg	Asp												
	290					295					300		

aag	caa	gtg	ttg	aga	gac	caa	ttg	ttg	aac	atc	atg	gtt	gct
ggt	aga			960									
Lys	Gln	Val	Leu	Arg	Asp	Gln	Leu	Leu	Asn	Ile	Met	Val	Ala
Gly	Arg												
305						310					315		
320													

gac	acc	acc	gcc	ggt	ttg	ttg	tcg	ttt	gtt	ttc	ttt	gaa	ttg
gcc	aga			1008									
Asp	Thr	Thr	Ala	Gly	Leu	Leu	Ser	Phe	Val	Phe	Phe	Glu	Leu
Ala	Arg												
				325						330			
335													

aac	cca	gaa	gtt	acc	aac	aag	ttg	aga	gaa	gaa	att	gag	gac
aag	ttt			1056									
Asn	Pro	Glu	Val	Thr	Asn	Lys	Leu	Arg	Glu	Glu	Ile	Glu	Asp
Lys	Phe												
			340					345				350	

gga	ctc	ggt	gag	aat	gct	agt	ggt	gaa	gac	att	tcc	ttt	gag
tcg	ttg			1104									
Gly	Leu	Gly	Glu	Asn	Ala	Ser	Val	Glu	Asp	Ile	Ser	Phe	Glu
Ser	Leu												
		355					360					365	

aag	tcc	tgt	gaa	tac	ttg	aag	gct	ggt	ctc	aac	gaa	acc	ttg
aga	ttg			1152									
Lys	Ser	Cys	Glu	Tyr	Leu	Lys	Ala	Val	Leu	Asn	Glu	Thr	Leu
Arg	Leu												
	370					375					380		

tac	cca	tcc	gtg	cca	cag	aat	ttc	aga	ggt	gcc	acc	aag	aac
act	acc			1200									
Tyr	Pro	Ser	Val	Pro	Gln	Asn	Phe	Arg	Val	Ala	Thr	Lys	Asn
Thr	Thr												
385					390					395			
400													

ctc	cca	aga	ggt	ggt	ggt	aag	gac	ggg	ttg	tct	cct	gtt	ttg
gtg	aga			1248									
Leu	Pro	Arg	Gly	Gly	Gly	Lys	Asp	Gly	Leu	Ser	Pro	Val	Leu
Val	Arg												
				405					410				

415

aag ggt cag acc gtt att tac ggt gtc tac gca gcc cac aga
aac cca 1296
Lys Gly Gln Thr Val Ile Tyr Gly Val Tyr Ala Ala His Arg
Asn Pro

420

425

430

gct gtt tac ggt aag gac gct ctt gag ttt aga cca gag aga
tgg ttt 1344
Ala Val Tyr Gly Lys Asp Ala Leu Glu Phe Arg Pro Glu Arg
Trp Phe

435

440

445

gag cca gag aca aag aag ctt ggc tgg gcc ttc ctc cca ttc
aac ggt 1392
Glu Pro Glu Thr Lys Lys Leu Gly Trp Ala Phe Leu Pro Phe
Asn Gly

450

455

460

ggt cca aga atc tgt ttg gga cag cag ttt gcc ttg aca gaa
gct tcg 1440
Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe Ala Leu Thr Glu
Ala Ser

465

470

475

480

tat gtc act gtc agg ttg ctc cag gag ttt gca cac ttg tct
atg gac 1488
Tyr Val Thr Val Arg Leu Leu Gln Glu Phe Ala His Leu Ser
Met Asp

485

490

495

cca gac acc gaa tat cca cct aag aaa atg tcg cat ttg acc
atg tcg 1536
Pro Asp Thr Glu Tyr Pro Pro Lys Lys Met Ser His Leu Thr
Met Ser

500

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510

ctt ttc gac ggt gcc aat att gag atg tat tag
1569

Leu Phe Asp Gly Ala Asn Ile Glu Met Tyr

515

520

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<211> 522

<212> PRT

<213> Candida tropicalis

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Met Thr Val His Asp Ile Ile Ala Thr Tyr Phe Thr Lys Trp
Tyr Val

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Ile Val Pro Leu Ala Leu Ile Ala Tyr Arg Val Leu Asp Tyr
Phe Tyr

20 25 30

Gly Arg Tyr Leu Met Tyr Lys Leu Gly Ala Lys Pro Phe Phe
Gln Lys

35 40 45

Gln Thr Asp Gly Cys Phe Gly Phe Lys Ala Pro Leu Glu Leu
Leu Lys

50 55 60

Lys Lys Ser Asp Gly Thr Leu Ile Asp Phe Thr Leu Gln Arg
Ile His

65 70 75
80

Asp Leu Asp Arg Pro Asp Ile Pro Thr Phe Thr Phe Pro Val
Phe Ser

85 90
95

Ile Asn Leu Val Asn Thr Leu Glu Pro Glu Asn Ile Lys Ala
Ile Leu

100 105 110

Ala Thr Gln Phe Asn Asp Phe Ser Leu Gly Thr Arg His Ser
His Phe

115 120 125

Ala Pro Leu Leu Gly Asp Gly Ile Phe Thr Leu Asp Gly Ala
Gly Trp

130 135 140

Lys His Ser Arg Ser Met Leu Arg Pro Gln Phe Ala Arg Glu
Gln Ile
145 150 155
160

Ser His Val Lys Leu Leu Glu Pro His Val Gln Val Phe Phe
Lys His
165 170
175

Val Arg Lys Ala Gln Gly Lys Thr Phe Asp Ile Gln Glu Leu
Phe Phe
180 185 190

Arg Leu Thr Val Asp Ser Ala Thr Glu Phe Leu Phe Gly Glu
Ser Val
195 200 205

Glu Ser Leu Arg Asp Glu Ser Ile Gly Met Ser Ile Asn Ala
Leu Asp
210 215 220

Phe Asp Gly Lys Ala Gly Phe Ala Asp Ala Phe Asn Tyr Ser
Gln Asn
225 230 235
240

Tyr Leu Ala Ser Arg Ala Val Met Gln Gln Leu Tyr Trp Val
Leu Asn
245 250
255

Gly Lys Lys Phe Lys Glu Cys Asn Ala Lys Val His Lys Phe
Ala Asp
260 265 270

Tyr Tyr Val Asn Lys Ala Leu Asp Leu Thr Pro Glu Gln Leu
Glu Lys
275 280 285

- 24/269 -

Gln Asp Gly Tyr Val Phe Leu Tyr Glu Leu Val Lys Gln Thr
Arg Asp
290 295 300

Lys Gln Val Leu Arg Asp Gln Leu Leu Asn Ile Met Val Ala
Gly Arg
305 310 315
320

Asp Thr Thr Ala Gly Leu Leu Ser Phe Val Phe Phe Glu Leu
Ala Arg
325 330
335

Asn Pro Glu Val Thr Asn Lys Leu Arg Glu Glu Ile Glu Asp
Lys Phe
340 345 350

Gly Leu Gly Glu Asn Ala Ser Val Glu Asp Ile Ser Phe Glu
Ser Leu
355 360 365

Lys Ser Cys Glu Tyr Leu Lys Ala Val Leu Asn Glu Thr Leu
Arg Leu
370 375 380

Tyr Pro Ser Val Pro Gln Asn Phe Arg Val Ala Thr Lys Asn
Thr Thr
385 390 395
400

Leu Pro Arg Gly Gly Gly Lys Asp Gly Leu Ser Pro Val Leu
Val Arg
405 410
415

Lys Gly Gln Thr Val Ile Tyr Gly Val Tyr Ala Ala His Arg
Asn Pro
420 425 430

Ala Val Tyr Gly Lys Asp Ala Leu Glu Phe Arg Pro Glu Arg

Trp Phe
435 440 445

Glu Pro Glu Thr Lys Lys Leu Gly Trp Ala Phe Leu Pro Phe
Asn Gly
450 455 460

Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe Ala Leu Thr Glu
Ala Ser
465 470 475
480

Tyr Val Thr Val Arg Leu Leu Gln Glu Phe Ala His Leu Ser
Met Asp
485 490
495

Pro Asp Thr Glu Tyr Pro Pro Lys Lys Met Ser His Leu Thr
Met Ser
500 505 510

Leu Phe Asp Gly Ala Asn Ile Glu Met Tyr
515 520

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<222> (1)..(1569)

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tac gtg 48
Met Thr Ala Gln Asp Ile Ile Ala Thr Tyr Ile Thr Lys Trp
Tyr Val
1 5 10
15
ata gta cca ctc gct ttg att gct tat agg gtc ctc gac tac
ttt tac 96

Ile Phe	Val Tyr	Pro	Leu	Ala	Leu	Ile	Ala	Tyr	Arg	Val	Leu	Asp	Tyr
			20			25			30				
ggc cag	aga aaa	tac	ttg	atg	tac	aag	ctt	ggt	gct	aaa	ccg	ttt	ttc
Gly Gln	Arg Lys	Tyr	Leu	Met	Tyr	Lys	Leu	Gly	Ala	Lys	Pro	Phe	Phe
35						40			45				
caa tta	aca aaa	gac	ggg	tat	ttc	gga	ttc	aaa	gct	cca	ctt	gaa	ttg
Gln Leu	Thr Lys	Asp	Gly	Tyr	Phe	Gly	Phe	Lys	Ala	Pro	Leu	Glu	Leu
50						55			60				
aag atc	aag caa	agt	gac	ggg	acc	ctc	ata	gac	ttc	act	ctc	gag	cgt
Lys Ile	Lys Gln	Ser	Asp	Gly	Thr	Leu	Ile	Asp	Phe	Thr	Leu	Glu	Arg
65			70						75				
80													
gcg ttt	ctc tcc	aat	cgt	cca	gat	atc	cca	act	ttt	aca	ttc	cca	atc
Ala Phe	Leu Ser	Asn	Arg	Pro	Asp	Ile	Pro	Thr	Phe	Thr	Phe	Pro	Ile
95			85						90				
atc atc	aac ttg	ctt	atc	agc	acc	ctt	gag	ccg	gag	aac	atc	aag	gct
Ile Ile	Asn Leu	Leu	Ile	Ser	Thr	Leu	Glu	Pro	Glu	Asn	Ile	Lys	Ala
			100						105				
gcc cac	acc ttt	cag	ttc	aac	gat	ttc	tcc	ttg	ggc	acc	aga	cac	tcg
Ala His	Thr Phe	Gln	Phe	Asn	Asp	Phe	Ser	Leu	Gly	Thr	Arg	His	Ser
115						120			125				
gct ggc	cct tgg	ttg	ttg	ggc	gat	ggg	atc	ttt	acc	ttg	gac	ggg	gcc
Ala Gly	Pro Trp	Leu	Leu	Gly	Asp	Gly	Ile	Phe	Thr	Leu	Asp	Gly	Ala
130						135			140				
aag cag	cac att	agc	aga	tct	atg	ttg	aga	cca	cag	ttt	gcc	aga	gaa
			480										

Lys His Ser Arg Ser Met Leu Arg Pro Gln Phe Ala Arg Glu
Gln Ile
145 150 155
160

tcc cac gtc aag ttg ttg gag cca cac atg cag gtg ttc ttc
aag cac 528
Ser His Val Lys Leu Leu Glu Pro His Met Gln Val Phe Phe
Lys His
165 170
175

gtc aga aag gca cag ggc aag act ttt gac atc caa gaa ttg
ttt ttc 576
Val Arg Lys Ala Gln Gly Lys Thr Phe Asp Ile Gln Glu Leu
Phe Phe
180 185 190

aga ttg acc gtc gac tcc gcc act gag ttt ttg ttt ggt gaa
tcc gtt 624
Arg Leu Thr Val Asp Ser Ala Thr Glu Phe Leu Phe Gly Glu
Ser Val
195 200 205

gag tcc ttg aga gat gaa tct att ggg atg tcc atc aat gca
ctt gac 672
Glu Ser Leu Arg Asp Glu Ser Ile Gly Met Ser Ile Asn Ala
Leu Asp
210 215 220

ttt gac ggc aag gct ggc ttt gct gat gct ttt aac tac tcg
cag aac 720
Phe Asp Gly Lys Ala Gly Phe Ala Asp Ala Phe Asn Tyr Ser
Gln Asn
225 230 235
240

tat ttg gct tcg aga gcg gtt atg caa caa ttg tac tgg gtg
ttg aac 768
Tyr Leu Ala Ser Arg Ala Val Met Gln Gln Leu Tyr Trp Val
Leu Asn
245 250
255

ggg aaa aag ttt aag gag tgc aac gct aaa gtg cac aag ttt
gct gac 816
Gly Lys Lys Phe Lys Glu Cys Asn Ala Lys Val His Lys Phe
Ala Asp
260 265 270

tat tac gtc agc aag gct ttg gac ttg aca cct gaa caa ttg
gaa aag 864
Tyr Tyr Val Ser Lys Ala Leu Asp Leu Thr Pro Glu Gln Leu
Glu Lys
275 280 285

cag gat ggt tat gtg ttc ttg tac gag ttg gtc aag caa acc
aga gac 912
Gln Asp Gly Tyr Val Phe Leu Tyr Glu Leu Val Lys Gln Thr
Arg Asp
290 295 300

agg caa gtg ttg aga gac cag ttg ttg aac atc atg gtt gcc
ggt aga 960
Arg Gln Val Leu Arg Asp Gln Leu Leu Asn Ile Met Val Ala
Gly Arg
305 310 315
320

gac acc acc gcc ggt ttg ttg tcg ttt gtt ttc ttt gaa ttg
gcc aga 1008
Asp Thr Thr Ala Gly Leu Leu Ser Phe Val Phe Phe Glu Leu
Ala Arg
325 330
335

aac cca gag gtg acc aac aag ttg aga gaa gaa atc gag gac
aag ttt 1056
Asn Pro Glu Val Thr Asn Lys Leu Arg Glu Glu Ile Glu Asp
Lys Phe
340 345 350

ggt ctt ggt gag aat gct cgt gtt gaa gac att tcc ttt gag
tcg ttg 1104
Gly Leu Gly Glu Asn Ala Arg Val Glu Asp Ile Ser Phe Glu
Ser Leu
355 360 365

aag tca tgt gaa tac ttg aag gct gtt ctc aac gaa act ttg
aga ttg 1152
Lys Ser Cys Glu Tyr Leu Lys Ala Val Leu Asn Glu Thr Leu
Arg Leu
370 375 380

tac cca tcc gtg cca cag aat ttc aga gtt gcc acc aaa aac
act acc 1200
Tyr Pro Ser Val Pro Gln Asn Phe Arg Val Ala Thr Lys Asn
Thr Thr
385 390 395
400

ctt cca agg gga ggt ggt aag gac ggg tta tct cct gtt ttg
gtc aga 1248
Leu Pro Arg Gly Gly Gly Lys Asp Gly Leu Ser Pro Val Leu
Val Arg

405

410

415

aag ggt caa acc gtt atg tac ggt gtc tac gct gcc cac aga
aac cca 1296
Lys Gly Gln Thr Val Met Tyr Gly Val Tyr Ala Ala His Arg
Asn Pro

420

425

430

gct gtc tac ggt aag gac gcc ctt gag ttt aga cca gag agg
tgg ttt 1344
Ala Val Tyr Gly Lys Asp Ala Leu Glu Phe Arg Pro Glu Arg
Trp Phe

435

440

445

gag cca gag aca aag aag ctt ggc tgg gcc ttc ctt cca ttc
aac ggt 1392
Glu Pro Glu Thr Lys Lys Leu Gly Trp Ala Phe Leu Pro Phe
Asn Gly

450

455

460

ggt cca aga att tgc ttg gga cag cag ttt gcc ttg aca gaa
gct tcg 1440
Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe Ala Leu Thr Glu
Ala Ser

465

470

475

480

tat gtc act gtc aga ttg ctc caa gag ttt gga cac ttg tct
atg gac 1488
Tyr Val Thr Val Arg Leu Leu Gln Glu Phe Gly His Leu Ser
Met Asp

485

490

495

ccc aac acc gaa tat cca cct agg aaa atg tcg cat ttg acc
atg tcc 1536
Pro Asn Thr Glu Tyr Pro Pro Arg Lys Met Ser His Leu Thr
Met Ser

500

505

510

ctt ttc gac ggt gcc aac att gag atg tat tag
1569

Leu Phe Asp Gly Ala Asn Ile Glu Met Tyr
515 520

<210> 8
 <211> 522
 <212> PRT
 <213> Candida tropicalis

<400> 8

Met Thr Ala Gln Asp Ile Ile Ala Thr Tyr Ile Thr Lys Trp
 Tyr Val
 1 5 10
 15

Ile Val Pro Leu Ala Leu Ile Ala Tyr Arg Val Leu Asp Tyr
 Phe Tyr
 20 25 30

Gly Arg Tyr Leu Met Tyr Lys Leu Gly Ala Lys Pro Phe Phe
 Gln Lys
 35 40 45

Gln Thr Asp Gly Tyr Phe Gly Phe Lys Ala Pro Leu Glu Leu
 Leu Lys
 50 55 60

Lys Lys Ser Asp Gly Thr Leu Ile Asp Phe Thr Leu Glu Arg
 Ile Gln
 65 70 75
 80

Ala Leu Asn Arg Pro Asp Ile Pro Thr Phe Thr Phe Pro Ile
 Phe Ser
 85 90
 95

Ile Asn Leu Ile Ser Thr Leu Glu Pro Glu Asn Ile Lys Ala
 Ile Leu
 100 105 110

Ala Thr Gln Phe Asn Asp Phe Ser Leu Gly Thr Arg His Ser
 His Phe
 115 120 125

Ala Pro Leu Leu Gly Asp Gly Ile Phe Thr Leu Asp Gly Ala
Gly Trp
130 135 140

Lys His Ser Arg Ser Met Leu Arg Pro Gln Phe Ala Arg Glu
Gln Ile
145 150 155
160

Ser His Val Lys Leu Leu Glu Pro His Met Gln Val Phe Phe
Lys His
165 170
175

Val Arg Lys Ala Gln Gly Lys Thr Phe Asp Ile Gln Glu Leu
Phe Phe
180 185 190

Arg Leu Thr Val Asp Ser Ala Thr Glu Phe Leu Phe Gly Glu
Ser Val
195 200 205

Glu Ser Leu Arg Asp Glu Ser Ile Gly Met Ser Ile Asn Ala
Leu Asp
210 215 220

Phe Asp Gly Lys Ala Gly Phe Ala Asp Ala Phe Asn Tyr Ser
Gln Asn
225 230 235
240

Tyr Leu Ala Ser Arg Ala Val Met Gln Gln Leu Tyr Trp Val
Leu Asn
245 250
255

Gly Lys Lys Phe Lys Glu Cys Asn Ala Lys Val His Lys Phe
Ala Asp
260 265 270

Tyr Tyr Val Ser Lys Ala Leu Asp Leu Thr Pro Glu Gln Leu
Glu Lys
275 280 285

Gln Asp Gly Tyr Val Phe Leu Tyr Glu Leu Val Lys Gln Thr
Arg Asp
290 295 300

Arg Gln Val Leu Arg Asp Gln Leu Leu Asn Ile Met Val Ala
Gly Arg
305 310 315
320

Asp Thr Thr Ala Gly Leu Leu Ser Phe Val Phe Phe Glu Leu
Ala Arg
325 330
335

Asn Pro Glu Val Thr Asn Lys Leu Arg Glu Glu Ile Glu Asp
Lys Phe
340 345 350

Gly Leu Gly Glu Asn Ala Arg Val Glu Asp Ile Ser Phe Glu
Ser Leu
355 360 365

Lys Ser Cys Glu Tyr Leu Lys Ala Val Leu Asn Glu Thr Leu
Arg Leu
370 375 380

Tyr Pro Ser Val Pro Gln Asn Phe Arg Val Ala Thr Lys Asn
Thr Thr
385 390 395
400

Leu Pro Arg Gly Gly Gly Lys Asp Gly Leu Ser Pro Val Leu
Val Arg
405 410
415

- 33/269 -

Lys Gly Gln Thr Val Met Tyr Gly Val Tyr Ala Ala His Arg
Asn Pro
420 425 430

Ala Val Tyr Gly Lys Asp Ala Leu Glu Phe Arg Pro Glu Arg
Trp Phe
435 440 445

Glu Pro Glu Thr Lys Lys Leu Gly Trp Ala Phe Leu Pro Phe
Asn Gly
450 455 460

Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe Ala Leu Thr Glu
Ala Ser
465 470 475
480

Tyr Val Thr Val Arg Leu Leu Gln Glu Phe Gly His Leu Ser
Met Asp
485 490
495

Pro Asn Thr Glu Tyr Pro Pro Arg Lys Met Ser His Leu Thr
Met Ser
500 505 510

Leu Phe Asp Gly Ala Asn Ile Glu Met Tyr
515 520

<210> 9
<211> 1623
<212> DNA
<213> Candida tropicalis

<220>
<221> CDS
<222> (1)..(1623)

<400> 9
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act agt 48
Met Ser Ser Ser Pro Ser Phe Ala Gln Glu Val Leu Ala Thr

Thr 1 15	Ser												
		5					10						
cct tac Pro Tyr	tac ttc Tyr Phe	atc Ile	gag Glu	tac Tyr	ttt Phe	ctt Leu	gac Asp	aac Asn	tac Tyr	acc Thr	aga Arg	tgg Trp	tac Tyr
		20					25					30	
ata cac Ile His	cct aca Pro Thr	ttg Leu	gtg Val	ctt Leu	ctt Leu	tcg Ser	ttg Leu	aac Asn	ttt Phe	ata Ile	agt Ser	ttg Leu	ctc Leu
		35					40					45	
agg ttt Arg Phe	tac gtc Tyr Val	ttg Leu	gaa Glu	cgc Arg	agg Arg	ttc Phe	cac His	gcc Ala	aag Lys	cca Pro	ctc Leu	ggt Gly	aac Asn
		50					55					60	
agg tac Arg Tyr 65 80	gac ttg Asp Leu	cct Pro	acg Thr	ttt Phe	ggt Gly	atc Ile	gct Ala	act Thr	ccg Pro	ttg Leu	ctt Leu	ttg Leu	atc Ile
		70					75						
aag aac Lys Asn	tcg aac Ser Asn	aaa Lys	ggt Gly	acg Thr	gtc Val	atg Met	aag Lys	ttt Phe	gct Ala	tgg Trp	ggc Gly	ctc Leu	tgg Trp
		85					90						
aag agg Lys Arg	tac att Tyr Ile	atc Ile	gtc Val	aga Arg	gac Asp	cca Pro	aag Lys	tac Tyr	aag Lys	aca Thr	act Thr	ggg Gly	ctc Leu
		100					105					110	
gtt aag Val Lys	ggc gct Gly Ala	ctc Leu	cca Pro	ttg Leu	att Ile	gaa Glu	acc Thr	atg Met	gac Asp	cca Pro	gag Glu	aac Asn	atc Ile
		115					120					125	
gtt cac	ttg gat	gct	act 432	cag	ttc	aat	gat	ttc	tct	ttg	gga	acc	aga

Val His	Leu Asp 130	Ala	Thr	Gln	Phe	Asn	Asp	Phe	Ser	Leu	Gly	Thr	Arg
135						140							
ttc ggg Phe Gly 145 160	ttg gct Leu Ala	tac Tyr	tcc Ser	ttg Leu	ttg Leu	ggg Gly	gac Asp	ggg Gly	att Ile	ttc Phe	acc Thr	ttg Leu	gac Asp
150						155							
ggc aga Gly Arg 175	tgg gaa Trp Glu	aaa Lys	cat His	agt Ser	aga Arg	act Thr	atg Met	ttg Leu	aga Arg	cca Pro	cag Gln	ttt Phe	gct Ala
165						170							
cag ttc Gln Phe	gtt ttc Val Phe	tct Ser	cac His	gtc Val	aag Lys	ttg Leu	ttg Leu	gag Glu	cca Pro	cac His	gtt Val	cag Gln	gtg Val
180						185						190	
aag gaa Lys Glu	cac ttg His Leu	gtt Val	aga Arg	aag Lys	cac His	cgc Arg	ggg Gly	caa Gln	acg Thr	ttc Phe	gac Asp	atc Ile	caa Gln
195				200				205					
ttc ggg Phe Gly 210	ttc gag Phe Glu	agg Arg	ttg Leu	acc Thr	gtc Val	gac Asp	tcc Ser	gcc Ala	acc Thr	gag Glu	ttc Phe	ttg Leu	ttt Phe
215						220							
tct acc Ser Thr 225 240	gct acc Ala Thr	gaa Glu	tcc Ser	ttg Leu	agg Arg	gac Asp	gaa Glu	tct Ser	att Ile	gga Gly	ttg Leu	acc Thr	cca Pro
230						235							
aag tat Lys Tyr 255	gat tcg Asp Ser	ttc Phe	gat Asp	ggc Gly	aga Arg	aga Arg	gat Asp	ttc Phe	gct Ala	gac Asp	gct Ala	ttc Phe	aac Asn
245						250							

cag act tac cag gcc tac aga ttt ttg ttg caa caa atg tac
tgg atc 816
Gln Thr Tyr Gln Ala Tyr Arg Phe Leu Leu Gln Gln Met Tyr
Trp Ile

260

265

270

ttg aat ggc tcg gaa ttc aga aag tcg att gct gtc gtg cac
aag ttt 864
Leu Asn Gly Ser Glu Phe Arg Lys Ser Ile Ala Val Val His
Lys Phe

275

280

285

gct gac cac tat gtg caa aag gct ttg gag ttg acc gac gat
gac ttg 912
Ala Asp His Tyr Val Gln Lys Ala Leu Glu Leu Thr Asp Asp
Asp Leu

290

295

300

cag aaa caa gac ggc tat gtg ttc ttg tac gag ttg gct aag
caa acc 960
Gln Lys Gln Asp Gly Tyr Val Phe Leu Tyr Glu Leu Ala Lys
Gln Thr

305

310

315

320

aga gac cca aag gtc ttg aga gac cag tta ttg aac att ttg
gtt gcc 1008
Arg Asp Pro Lys Val Leu Arg Asp Gln Leu Leu Asn Ile Leu
Val Ala

325

330

335

ggt aga gac acg acc gcc ggt ttg ttg tca ttt gtt ttc tac
gag ttg 1056
Gly Arg Asp Thr Thr Ala Gly Leu Leu Ser Phe Val Phe Tyr
Glu Leu

340

345

350

tca aga aac cct gag gtg ttt gct aag ttg aga gag gag gtg
gaa aac 1104
Ser Arg Asn Pro Glu Val Phe Ala Lys Leu Arg Glu Glu Val
Glu Asn

355

360

365

aga ttt gga ctc ggt gaa gaa gct cgt gtt gaa gag atc tcg
ttt gag 1152
Arg Phe Gly Leu Gly Glu Glu Ala Arg Val Glu Glu Ile Ser
Phe Glu

370

375

380

tcc ttg aag tct tgt gag tac ttg aag gct gtc atc aat gaa
acc ttg 1200
Ser Leu Lys Ser Cys Glu Tyr Leu Lys Ala Val Ile Asn Glu
Thr Leu
385 390 395
400

aga ttg tac cca tcg gtt cca cac aac ttt aga gtt gct acc
aga aac 1248
Arg Leu Tyr Pro Ser Val Pro His Asn Phe Arg Val Ala Thr
Arg Asn
405 410
415

act acc ctc cca aga ggt ggt ggt gaa gat gga tac tcg cca
att gtc 1296
Thr Thr Leu Pro Arg Gly Gly Gly Glu Asp Gly Tyr Ser Pro
Ile Val
420 425 430

gtc aag aag ggt caa gtt gtc atg tac act gtt att gct acc
cac aga 1344
Val Lys Lys Gly Gln Val Val Met Tyr Thr Val Ile Ala Thr
His Arg
435 440 445

gac cca agt atc tac ggt gcc gac gct gac gtc ttc aga cca
gaa aga 1392
Asp Pro Ser Ile Tyr Gly Ala Asp Ala Asp Val Phe Arg Pro
Glu Arg
450 455 460

tgg ttt gaa cca gaa act aga aag ttg ggc tgg gca tac gtt
cca ttc 1440
Trp Phe Glu Pro Glu Thr Arg Lys Leu Gly Trp Ala Tyr Val
Pro Phe
465 470 475
480

aat ggt ggt cca aga atc tgt ttg ggt caa cag ttt gcc ttg
acc gaa 1488
Asn Gly Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe Ala Leu
Thr Glu
485 490
495

gct tca tac gtc act gtc aga ttg ctc cag gag ttt gca cac
ttg tct 1536
Ala Ser Tyr Val Thr Val Arg Leu Leu Gln Glu Phe Ala His
Leu Ser

500							505					510		
atg	gac	cca	gac	acc	gaa	tat	cca	cca	aaa	ttg	cag	aac	acc	
ttg	acc	1584												
Met	Asp	Pro	Asp	Thr	Glu	Tyr	Pro	Pro	Lys	Leu	Gln	Asn	Thr	
Leu	Thr													
515							520					525		
ttg	tcg	ctc	ttt	gat	ggt	gct	gat	ggt	aga	atg	tac	taa		
1623														
Leu	Ser	Leu	Phe	Asp	Gly	Ala	Asp	Val	Arg	Met	Tyr			
530							535					540		

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<212> PRT
<213> Candida tropicalis
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<400> 10

Met Ser Ser Ser Pro Ser Phe Ala Gln Glu Val Leu Ala Thr
Thr Ser

1 5 10 15

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

Ile Pro Leu Val Leu Leu Ser Leu Asn Phe Ile Ser Leu Leu
His Thr

35 40 45

Arg Tyr Leu Glu Arg Arg Phe His Ala Lys Pro Leu Gly Asn
Phe Val
50 55 60

Arg Asp Pro Thr Phe Gly Ile Ala Thr Pro Leu Leu Leu Ile
Tyr Leu
65 70 75
80

Lys Ser Lys Gly Thr Val Met Lys Phe Ala Trp Gly Leu Trp
Asn Asn

Lys Asp Phe Asp Gly Arg Arg Asp Phe Ala Asp Ala Phe Asn
Tyr Ser

245

250

255

Gln Thr Tyr Gln Ala Tyr Arg Phe Leu Leu Gln Gln Met Tyr
Trp Ile

260

265

270

Leu Asn Gly Ser Glu Phe Arg Lys Ser Ile Ala Val Val His
Lys Phe

275

280

285

Ala Asp His Tyr Val Gln Lys Ala Leu Glu Leu Thr Asp Asp
Asp Leu

290

295

300

Gln Lys Gln Asp Gly Tyr Val Phe Leu Tyr Glu Leu Ala Lys
Gln Thr

305

310

315

320

Arg Asp Pro Lys Val Leu Arg Asp Gln Leu Leu Asn Ile Leu
Val Ala

325

330

335

Gly Arg Asp Thr Thr Ala Gly Leu Leu Ser Phe Val Phe Tyr
Glu Leu

340

345

350

Ser Arg Asn Pro Glu Val Phe Ala Lys Leu Arg Glu Glu Val
Glu Asn

355

360

365

Arg Phe Gly Leu Gly Glu Glu Ala Arg Val Glu Glu Ile Ser
Phe Glu

370

375

380

Ser Leu Lys Ser Cys Glu Tyr Leu Lys Ala Val Ile Asn Glu
Thr Leu
385 390 395
400

Arg Leu Tyr Pro Ser Val Pro His Asn Phe Arg Val Ala Thr
Arg Asn
405 410
415

Thr Thr Leu Pro Arg Gly Gly Gly Glu Asp Gly Tyr Ser Pro
Ile Val
420 425 430

Val Lys Lys Gly Gln Val Val Met Tyr Thr Val Ile Ala Thr
His Arg
435 440 445

Asp Pro Ser Ile Tyr Gly Ala Asp Ala Asp Val Phe Arg Pro
Glu Arg
450 455 460

Trp Phe Glu Pro Glu Thr Arg Lys Leu Gly Trp Ala Tyr Val
Pro Phe
465 470 475
480

Asn Gly Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe Ala Leu
Thr Glu
485 490
495

Ala Ser Tyr Val Thr Val Arg Leu Leu Gln Glu Phe Ala His
Leu Ser
500 505 510

Met Asp Pro Asp Thr Glu Tyr Pro Pro Lys Leu Gln Asn Thr
Leu Thr
515 520 525

Leu Ser Leu Phe Asp Gly Ala Asp Val Arg Met Tyr

530

535

540

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<222> (1)..(1623)

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act agt 48
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Thr Ser
1 5 10
15

cct tac atc gag tac ttt ctt gac aac tac acc aga tgg tac
tac ttc 96
Pro Tyr Ile Glu Tyr Phe Leu Asp Asn Tyr Thr Arg Trp Tyr
Tyr Phe
20 25 30

atc cct ttg gtg ctt ctt tcg ttg aac ttc atc agc ttg ctc
cac aca 144
Ile Pro Leu Val Leu Leu Ser Leu Asn Phe Ile Ser Leu Leu
His Thr
35 40 45

aag tac ttg gaa cgc agg ttc cac gcc aag ccg ctc ggt aac
gtc gtg 192
Lys Tyr Leu Glu Arg Arg Phe His Ala Lys Pro Leu Gly Asn
Val Val
50 55 60

ttg gat cct acg ttt ggt atc gct act ccg ttg atc ttg atc
tac tta 240
Leu Asp Pro Thr Phe Gly Ile Ala Thr Pro Leu Ile Leu Ile
Tyr Leu
65 70 75
80

aag tcg aaa ggt aca gtc atg aag ttt gcc tgg agc ttc tgg
aac aac 288
Lys Ser Lys Gly Thr Val Met Lys Phe Ala Trp Ser Phe Trp
Asn Asn

	85	90
95		
aag tac att gtc aaa gac cca aag tac aag acc act ggc ctt		
aga att 336		
Lys Tyr Ile Val Lys Asp Pro Lys Tyr Lys Thr Thr Gly Leu		
Arg Ile		
	100	105 110
gtc ggc ctc cca ttg att gaa acc ata gac cca gag aac atc		
aaa gct 384		
Val Gly Leu Pro Leu Ile Glu Thr Ile Asp Pro Glu Asn Ile		
Lys Ala		
	115	120 125
gtg ttg gct act cag ttc aac gat ttc tcc ttg gga act aga		
cac gat 432		
Val Leu Ala Thr Gln Phe Asn Asp Phe Ser Leu Gly Thr Arg		
His Asp		
	130	135 140
ttc ttg tac tcc ttg ttg ggc gat ggt att ttt acc ttg gac		
ggt gct 480		
Phe Leu Tyr Ser Leu Leu Gly Asp Gly Ile Phe Thr Leu Asp		
Gly Ala		
145	150	155
160		
ggc tgg aaa cac agt aga act atg ttg aga cca cag ttt gct		
aga gaa 528		
Gly Trp Lys His Ser Arg Thr Met Leu Arg Pro Gln Phe Ala		
Arg Glu		
	165	170
175		
cag gtt tcc cac gtc aag ttg ttg gaa cca cac gtt cag gtg		
ttc ttc 576		
Gln Val Ser His Val Lys Leu Leu Glu Pro His Val Gln Val		
Phe Phe		
	180	185 190
aag cac gtt aga aaa cac cgc ggt cag act ttt gac atc caa		
gaa ttg 624		
Lys His Val Arg Lys His Arg Gly Gln Thr Phe Asp Ile Gln		
Glu Leu		
	195	200 205
ttc ttc aga ttg acc gtc gac tcc gcc acc gag ttc ttg ttt		
ggt gag 672		
Phe Phe Arg Leu Thr Val Asp Ser Ala Thr Glu Phe Leu Phe		

Gly Glu
210 215 220

tct gct gaa tcc ttg aga gac gac tct gtt ggt ttg acc cca
acc acc 720
Ser Ala Glu Ser Leu Arg Asp Asp Ser Val Gly Leu Thr Pro
Thr Thr
225 230 235
240

aag gat ttc gaa ggc aga gga gat ttc gct gac gct ttc aac
tac tcg 768
Lys Asp Phe Glu Gly Arg Gly Asp Phe Ala Asp Ala Phe Asn
Tyr Ser
245 250
255

cag act tac cag gcc tac aga ttt ttg ttg caa caa atg tac
tgg att 816
Gln Thr Tyr Gln Ala Tyr Arg Phe Leu Leu Gln Gln Met Tyr
Trp Ile
260 265 270

ttg aat ggc gcg gaa ttc aga aag tcg att gcc atc gtg cac
aag ttt 864
Leu Asn Gly Ala Glu Phe Arg Lys Ser Ile Ala Ile Val His
Lys Phe
275 280 285

gct gac cac tat gtg caa aag gct ttg gag ttg acc gac gat
gac ttg 912
Ala Asp His Tyr Val Gln Lys Ala Leu Glu Leu Thr Asp Asp
Asp Leu
290 295 300

cag aaa caa gac ggc tat gtg ttc ttg tac gag ttg gct aag
caa act 960
Gln Lys Gln Asp Gly Tyr Val Phe Leu Tyr Glu Leu Ala Lys
Gln Thr
305 310 315
320

aga gac cca aag gtc ttg aga gac cag ttg ttg aac att ttg
gtt gcc 1008
Arg Asp Pro Lys Val Leu Arg Asp Gln Leu Leu Asn Ile Leu
Val Ala
325 330
335

ggc aga gac acg acc gcc ggt ttg ttg tcg ttt gtg ttc tac

gag ttg 1056													
Gly	Arg	Asp	Thr	Thr	Ala	Gly	Leu	Leu	Ser	Phe	Val	Phe	Tyr
Glu	Leu												
340				345				350					
tcg aga aac cct gaa gtg ttt gcc aag ttg aga gag gag gtg													
gaa aac 1104													
Ser	Arg	Asn	Pro	Glu	Val	Phe	Ala	Lys	Leu	Arg	Glu	Glu	Val
Glu	Asn												
355				360				365					
aga ttt gga ctc ggc gaa gag gct cgt gtt gaa gag atc tct													
ttt gag 1152													
Arg	Phe	Gly	Leu	Gly	Glu	Glu	Ala	Arg	Val	Glu	Glu	Ile	Ser
Phe	Glu												
370				375				380					
tcc ttg aag tcc tgt gag tac ttg aag gct gtc atc aat gaa													
gcc ttg 1200													
Ser	Leu	Lys	Ser	Cys	Glu	Tyr	Leu	Lys	Ala	Val	Ile	Asn	Glu
Ala	Leu												
385				390				395					
400													
aga ttg tac cca tct gtt cca cac aac ttc aga gtt gcc acc													
aga aac 1248													
Arg	Leu	Tyr	Pro	Ser	Val	Pro	His	Asn	Phe	Arg	Val	Ala	Thr
Arg	Asn												
405				410									
415													
act acc ctt cca aga ggc ggt ggt aaa gac gga tgc tcg cca													
att gtt 1296													
Thr	Thr	Leu	Pro	Arg	Gly	Gly	Gly	Lys	Asp	Gly	Cys	Ser	Pro
Ile	Val												
420				425				430					
gtc aag aag ggt caa gtt gtc atg tac act gtc att ggt acc													
cac aga 1344													
Val	Lys	Lys	Gly	Gln	Val	Val	Met	Tyr	Thr	Val	Ile	Gly	Thr
His	Arg												
435				440				445					
gac cca agt atc tac ggt gcc gac gcc gac gtc ttc aga cca													
gaa aga 1392													
Asp	Pro	Ser	Ile	Tyr	Gly	Ala	Asp	Ala	Asp	Val	Phe	Arg	Pro
Glu	Arg												
450				455				460					
tgg ttc gag cca gaa act aga aag ttg ggc tgg gca tat gtt													

cca ttc 1440
Trp Phe Glu Pro Glu Thr Arg Lys Leu Gly Trp Ala Tyr Val
Pro Phe
465 470 475
480

aat ggt ggt cca aga atc tgt ttg ggt cag cag ttt gcc ttg
act gaa 1488
Asn Gly Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe Ala Leu
Thr Glu
485 490
495

gct tca tac gtc act gtc aga ttg ctc caa gag ttt gga aac
ttg tcc 1536
Ala Ser Tyr Val Thr Val Arg Leu Leu Gln Glu Phe Gly Asn
Leu Ser
500 505 510

ctg gat cca aac gct gag tac cca cca aaa ttg cag aac acc
ttg acc 1584
Leu Asp Pro Asn Ala Glu Tyr Pro Pro Lys Leu Gln Asn Thr
Leu Thr
515 520 525

ttg tca ctc ttt gat ggt gct gac gtt aga atg ttc taa
1623
Leu Ser Leu Phe Asp Gly Ala Asp Val Arg Met Phe
530 535 540

<210> 12
<211> 540
<212> PRT
<213> Candida tropicalis

<400> 12

Met Ser Ser Ser Pro Ser Phe Ala Gln Glu Val Leu Ala Thr
Thr Ser
1 5 10
15

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

Ile Pro Leu Val Leu Leu Ser Leu Asn Phe Ile Ser Leu Leu

- 48/269 -

	180		185		190
Lys His Val Arg Lys His Arg Gly Gln Thr Phe Asp Ile Gln Glu Leu					
	195		200		205
Phe Phe Arg Leu Thr Val Asp Ser Ala Thr Glu Phe Leu Phe Gly Glu					
	210		215		220
Ser Ala Glu Ser Leu Arg Asp Asp Ser Val Gly Leu Thr Pro Thr Thr					
225		230		235	
240					
Lys Asp Phe Glu Gly Arg Gly Asp Phe Ala Asp Ala Phe Asn Tyr Ser					
		245		250	
255					
Gln Thr Tyr Gln Ala Tyr Arg Phe Leu Leu Gln Gln Met Tyr Trp Ile					
	260		265		270
Leu Asn Gly Ala Glu Phe Arg Lys Ser Ile Ala Ile Val His Lys Phe					
	275		280		285
Ala Asp His Tyr Val Gln Lys Ala Leu Glu Leu Thr Asp Asp Asp Leu					
	290		295		300
Gln Lys Gln Asp Gly Tyr Val Phe Leu Tyr Glu Leu Ala Lys Gln Thr					
305		310		315	
320					
Arg Asp Pro Lys Val Leu Arg Asp Gln Leu Leu Asn Ile Leu Val Ala					
		325		330	
335					

Gly Arg Asp Thr Thr Ala Gly Leu Leu Ser Phe Val Phe Tyr
Glu Leu
340 345 350

Ser Arg Asn Pro Glu Val Phe Ala Lys Leu Arg Glu Glu Val
Glu Asn
355 360 365

Arg Phe Gly Leu Gly Glu Glu Ala Arg Val Glu Glu Ile Ser
Phe Glu
370 375 380

Ser Leu Lys Ser Cys Glu Tyr Leu Lys Ala Val Ile Asn Glu
Ala Leu
385 390 395
400

Arg Leu Tyr Pro Ser Val Pro His Asn Phe Arg Val Ala Thr
Arg Asn
405 410
415

Thr Thr Leu Pro Arg Gly Gly Gly Lys Asp Gly Cys Ser Pro
Ile Val
420 425 430

Val Lys Lys Gly Gln Val Val Met Tyr Thr Val Ile Gly Thr
His Arg
435 440 445

Asp Pro Ser Ile Tyr Gly Ala Asp Ala Asp Val Phe Arg Pro
Glu Arg
450 455 460

Trp Phe Glu Pro Glu Thr Arg Lys Leu Gly Trp Ala Tyr Val
Pro Phe
465 470 475
480

Asn Gly Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe Ala Leu
Thr Glu

485

490

495

Ala Ser Tyr Val Thr Val Arg Leu Leu Gln Glu Phe Gly Asn
Leu Ser

500

505

510

Leu Asp Pro Asn Ala Glu Tyr Pro Pro Lys Leu Gln Asn Thr
Leu Thr

515

520

525

Leu Ser Leu Phe Asp Gly Ala Asp Val Arg Met Phe
530 535 540

<210> 13

<211> 1554

<212> DNA

<213> Candida tropicalis

<220>

<221> CDS

<222> (1)..(1554)

<400> 13

atg att gaa caa ctc cta gaa tat tgg tat gtc gtt gtg cca
gtg ttg 48

Met Ile Glu Gln Leu Leu Glu Tyr Trp Tyr Val Val Val Pro
Val Leu

1 5

10

15

tac atc atc aaa caa ctc ctt gca tac aca aag act cgc gtc
ttg atg 96

Tyr Ile Ile Lys Gln Leu Leu Ala Tyr Thr Lys Thr Arg Val
Leu Met

20

25

30

aaa aag ttg ggt gct gct cca gtc aca aac aag ttg tac gac
aac gct 144

Lys Lys Leu Gly Ala Ala Pro Val Thr Asn Lys Leu Tyr Asp
Asn Ala

35

40

45

ttc ggt atc gtc aat gga tgg aag gct ctc cag ttc aag aaa
gag ggc 192
Phe Gly Ile Val Asn Gly Trp Lys Ala Leu Gln Phe Lys Lys
Glu Gly
50 55 60

agg gct caa gag tac aac gat tac aag ttt gac cac tcc aag
aac cca 240
Arg Ala Gln Glu Tyr Asn Asp Tyr Lys Phe Asp His Ser Lys
Asn Pro
65 70 75
80

agc gtg ggc acc tac gtc agt att ctt ttc ggc acc agg atc
gtc gtg 288
Ser Val Gly Thr Tyr Val Ser Ile Leu Phe Gly Thr Arg Ile
Val Val
85 90
95

acc aaa gat cca gag aat atc aaa gct att ttg gca acc cag
ttt ggt 336
Thr Lys Asp Pro Glu Asn Ile Lys Ala Ile Leu Ala Thr Gln
Phe Gly
100 105 110

gat ttt tct ttg ggc aag agg cac act ctt ttt aag cct ttg
tta ggt 384
Asp Phe Ser Leu Gly Lys Arg His Thr Leu Phe Lys Pro Leu
Leu Gly
115 120 125

gat ggg atc ttc aca ttg gac ggc gaa ggc tgg aag cac agc
aga gcc 432
Asp Gly Ile Phe Thr Leu Asp Gly Glu Gly Trp Lys His Ser
Arg Ala
130 135 140

atg ttg aga cca cag ttt gcc aga gaa caa gtt gct cat gtg
acg tcg 480
Met Leu Arg Pro Gln Phe Ala Arg Glu Gln Val Ala His Val
Thr Ser
145 150 155
160

ttg gaa cca cac ttc cag ttg ttg aag aag cat att ctt aag
cac aag 528
Leu Glu Pro His Phe Gln Leu Leu Lys Lys His Ile Leu Lys
His Lys
165 170

175

ggt gaa tac ttt gat atc cag gaa ttg ttc ttt aga ttt acc
ggt gat 576
Gly Glu Tyr Phe Asp Ile Gln Glu Leu Phe Phe Arg Phe Thr
Val Asp

180

185

190

tcg gcc acg gag ttc tta ttt ggt gag tcc gtg cac tcc tta
aag gac 624
Ser Ala Thr Glu Phe Leu Phe Gly Glu Ser Val His Ser Leu
Lys Asp

195

200

205

gaa tct att ggt atc aac caa gac gat ata gat ttt gct ggt
aga aag 672
Glu Ser Ile Gly Ile Asn Gln Asp Asp Ile Asp Phe Ala Gly
Arg Lys

210

215

220

gac ttt gct gag tcg ttc aac aaa gcc cag gaa tac ttg gct
att aga 720
Asp Phe Ala Glu Ser Phe Asn Lys Ala Gln Glu Tyr Leu Ala
Ile Arg

225

230

235

240

acc ttg gtg cag acg ttc tac tgg ttg gtc aac aac aag gag
ttt aga 768
Thr Leu Val Gln Thr Phe Tyr Trp Leu Val Asn Asn Lys Glu
Phe Arg

245

250

255

gac tgt acc aag ctg gtg cac aag ttc acc aac tac tat gtt
cag aaa 816
Asp Cys Thr Lys Leu Val His Lys Phe Thr Asn Tyr Tyr Val
Gln Lys

260

265

270

gct ttg gat gct agc cca gaa gag ctt gaa aag caa agt ggg
tat gtg 864
Ala Leu Asp Ala Ser Pro Glu Glu Leu Glu Lys Gln Ser Gly
Tyr Val

275

280

285

ttc ttg tac gag ctt gtc aag cag aca aga gac ccc aat gtg
ttg cgt 912
Phe Leu Tyr Glu Leu Val Lys Gln Thr Arg Asp Pro Asn Val
Leu Arg

290	295	300
gac cag tct ttg aac atc ttg ttg gcc gga aga gac acc act		
gct ggg 960		
Asp Gln Ser Leu Asn Ile Leu Leu Ala Gly Arg Asp Thr Thr		
Ala Gly		
305 310 315		
320		
ttg ttg tcg ttt gct gtc ttt gag ttg gcc aga cac cca gag		
atc tgg 1008		
Leu Leu Ser Phe Ala Val Phe Glu Leu Ala Arg His Pro Glu		
Ile Trp		
325 330		
335		
gcc aag ttg aga gag gaa att gaa caa cag ttt ggt ctt gga		
gaa gac 1056		
Ala Lys Leu Arg Glu Glu Ile Glu Gln Gln Phe Gly Leu Gly		
Glu Asp		
340 345 350		
tct cgt gtt gaa gag att acc ttt gag agc ttg aag aga tgt		
gag tac 1104		
Ser Arg Val Glu Glu Ile Thr Phe Glu Ser Leu Lys Arg Cys		
Glu Tyr		
355 360 365		
ttg aaa gcg ttc ctt aat gaa acc ttg cgt att tac cca agt		
gtc cca 1152		
Leu Lys Ala Phe Leu Asn Glu Thr Leu Arg Ile Tyr Pro Ser		
Val Pro		
370 375 380		
aga aac ttc aga atc gcc acc aag aac acg aca ttg cca agg		
ggc ggt 1200		
Arg Asn Phe Arg Ile Ala Thr Lys Asn Thr Thr Leu Pro Arg		
Gly Gly		
385 390 395		
400		
ggt tca gac ggt acc tcg cca atc ttg atc caa aag gga gaa		
gct gtg 1248		
Gly Ser Asp Gly Thr Ser Pro Ile Leu Ile Gln Lys Gly Glu		
Ala Val		
405 410		
415		
tcg tat ggt atc aac tct act cat ttg gac cct gtc tat tac		
ggc cct 1296		

Ser Tyr Gly Ile Asn Ser Thr His Leu Asp Pro Val Tyr Tyr
Gly Pro

420

425

430

gat gct gct gag ttc aga cca gag aga tgg ttt gag cca tca
acc aaa 1344

Asp Ala Ala Glu Phe Arg Pro Glu Arg Trp Phe Glu Pro Ser
Thr Lys

435

440

445

aag ctc ggc tgg gct tac ttg cca ttc aac ggt ggt cca aga
atc tgt 1392

Lys Leu Gly Trp Ala Tyr Leu Pro Phe Asn Gly Gly Pro Arg
Ile Cys

450

455

460

ttg ggt cag cag ttt gcc ttg acg gaa gct ggc tat gtg ttg
gtt aga 1440

Leu Gly Gln Gln Phe Ala Leu Thr Glu Ala Gly Tyr Val Leu
Val Arg

465

470

475

480

ttg gtg caa gag ttc tcc cac gtt agg ctg gac cca gac gag
gtg tac 1488

Leu Val Gln Glu Phe Ser His Val Arg Leu Asp Pro Asp Glu
Val Tyr

485

490

495

ccg cca aag agg ttg acc aac ttg acc atg tgt ttg cag gat
ggt gct 1536

Pro Pro Lys Arg Leu Thr Asn Leu Thr Met Cys Leu Gln Asp
Gly Ala

500

505

510

att gtc aag ttt gac tag
1554

Ile Val Lys Phe Asp
515

<210> 14

<211> 517

<212> PRT

<213> Candida tropicalis

<400> 14

Met Ile Glu Gln Leu Leu Glu Tyr Trp Tyr Val Val Val Pro

Val Leu
1
15

5

10

Tyr Ile Ile Lys Gln Leu Leu Ala Tyr Thr Lys Thr Arg Val
Leu Met
20 25 30

Lys Lys Leu Gly Ala Ala Pro Val Thr Asn Lys Leu Tyr Asp
Asn Ala
35 40 45

Phe Gly Ile Val Asn Gly Trp Lys Ala Leu Gln Phe Lys Lys
Glu Gly
50 55 60

Arg Ala Gln Glu Tyr Asn Asp Tyr Lys Phe Asp His Ser Lys
Asn Pro
65 70 75
80

Ser Val Gly Thr Tyr Val Ser Ile Leu Phe Gly Thr Arg Ile
Val Val
85 90
95

Thr Lys Asp Pro Glu Asn Ile Lys Ala Ile Leu Ala Thr Gln
Phe Gly
100 105 110

Asp Phe Ser Leu Gly Lys Arg His Thr Leu Phe Lys Pro Leu
Leu Gly
115 120 125

Asp Gly Ile Phe Thr Leu Asp Gly Glu Gly Trp Lys His Ser
Arg Ala
130 135 140

Met Leu Arg Pro Gln Phe Ala Arg Glu Gln Val Ala His Val
Thr Ser
145 150 155

160

Leu Glu Pro His Phe Gln Leu Leu Lys Lys His Ile Leu Lys
His Lys

165

170

175

Gly Glu Tyr Phe Asp Ile Gln Glu Leu Phe Phe Arg Phe Thr
Val Asp

180

185

190

Ser Ala Thr Glu Phe Leu Phe Gly Glu Ser Val His Ser Leu
Lys Asp

195

200

205

Glu Ser Ile Gly Ile Asn Gln Asp Asp Ile Asp Phe Ala Gly
Arg Lys

210

215

220

Asp Phe Ala Glu Ser Phe Asn Lys Ala Gln Glu Tyr Leu Ala
Ile Arg

225

230

235

240

Thr Leu Val Gln Thr Phe Tyr Trp Leu Val Asn Asn Lys Glu
Phe Arg

245

250

255

Asp Cys Thr Lys Leu Val His Lys Phe Thr Asn Tyr Tyr Val
Gln Lys

260

265

270

Ala Leu Asp Ala Ser Pro Glu Glu Leu Glu Lys Gln Ser Gly
Tyr Val

275

280

285

Phe Leu Tyr Glu Leu Val Lys Gln Thr Arg Asp Pro Asn Val
Leu Arg

290

295

300

Asp Gln Ser Leu Asn Ile Leu Leu Ala Gly Arg Asp Thr Thr
Ala Gly
305 310 315
320

Leu Leu Ser Phe Ala Val Phe Glu Leu Ala Arg His Pro Glu
Ile Trp
325 330
335

Ala Lys Leu Arg Glu Glu Ile Glu Gln Gln Phe Gly Leu Gly
Glu Asp
340 345 350

Ser Arg Val Glu Glu Ile Thr Phe Glu Ser Leu Lys Arg Cys
Glu Tyr
355 360 365

Leu Lys Ala Phe Leu Asn Glu Thr Leu Arg Ile Tyr Pro Ser
Val Pro
370 375 380

Arg Asn Phe Arg Ile Ala Thr Lys Asn Thr Thr Leu Pro Arg
Gly Gly
385 390 395
400

Gly Ser Asp Gly Thr Ser Pro Ile Leu Ile Gln Lys Gly Glu
Ala Val
405 410
415

Ser Tyr Gly Ile Asn Ser Thr His Leu Asp Pro Val Tyr Tyr
Gly Pro
420 425 430

Asp Ala Ala Glu Phe Arg Pro Glu Arg Trp Phe Glu Pro Ser
Thr Lys
435 440 445

- 58/269 -

Lys Leu Gly Trp Ala Tyr Leu Pro Phe Asn Gly Gly Pro Arg
Ile Cys
450 455 460

Leu Gly Gln Gln Phe Ala Leu Thr Glu Ala Gly Tyr Val Leu
Val Arg
465 470 475
480

Leu Val Gln Glu Phe Ser His Val Arg Leu Asp Pro Asp Glu
Val Tyr
485 490
495

Pro Pro Lys Arg Leu Thr Asn Leu Thr Met Cys Leu Gln Asp
Gly Ala
500 505 510

Ile Val Lys Phe Asp
515

<210> 15
<211> 1554
<212> DNA
<213> Candida tropicalis

<220>
<221> CDS
<222> (1)..(1554)

<400> 15
atg att gaa caa atc cta gaa tat tgg tat att gtt gtg cct
gtg ttg 48
Met Ile Glu Gln Ile Leu Glu Tyr Trp Tyr Ile Val Val Pro
Val Leu
1 5 10
15

tac atc atc aaa caa ctc att gcc tac agc aag act cgc gtc
ttg atg 96
Tyr Ile Ile Lys Gln Leu Ile Ala Tyr Ser Lys Thr Arg Val
Leu Met
20 25 30

aaa cag ttg ggt gct gct cca atc aca aac cag ttg tac gac
aac gtt 144
Lys Gln Leu Gly Ala Ala Pro Ile Thr Asn Gln Leu Tyr Asp
Asn Val

35

40

45

ttc ggt atc gtc aac gga tgg aag gct ctc cag ttc aag aaa
gag ggc 192
Phe Gly Ile Val Asn Gly Trp Lys Ala Leu Gln Phe Lys Lys
Glu Gly

50

55

60

aga gct caa gag tac aac gat cac aag ttt gac agc tcc aag
aac cca 240
Arg Ala Gln Glu Tyr Asn Asp His Lys Phe Asp Ser Ser Lys
Asn Pro

65

70

75

80

agc gtc ggc acc tat gtc agt att ctt ttt ggc acc aag att
gtc gtg 288
Ser Val Gly Thr Tyr Val Ser Ile Leu Phe Gly Thr Lys Ile
Val Val

85

90

95

acc aag gat cca gag aat atc aaa gct att ttg gca acc cag
ttt ggc 336
Thr Lys Asp Pro Glu Asn Ile Lys Ala Ile Leu Ala Thr Gln
Phe Gly

100

105

110

gat ttt tct ttg ggc aag aga cac gct ctt ttt aaa cct ttg
tta ggt 384
Asp Phe Ser Leu Gly Lys Arg His Ala Leu Phe Lys Pro Leu
Leu Gly

115

120

125

gat ggg atc ttc acc ttg gac ggc gaa ggc tgg aag cat agc
aga tcc 432
Asp Gly Ile Phe Thr Leu Asp Gly Glu Gly Trp Lys His Ser
Arg Ser

130

135

140

atg tta aga cca cag ttt gcc aga gaa caa gtt gct cat gtg
acg tcg 480
Met Leu Arg Pro Gln Phe Ala Arg Glu Gln Val Ala His Val
Thr Ser

145

150

155

160

ttg gaa cca cac ttc cag ttg ttg aag aag cat atc ctt aaa
cac aag 528
Leu Glu Pro His Phe Gln Leu Leu Lys Lys His Ile Leu Lys
His Lys

165

170

175

ggt gag tac ttt gat atc cag gaa ttg ttc ttt aga ttt act
gtc gac 576
Gly Glu Tyr Phe Asp Ile Gln Glu Leu Phe Phe Arg Phe Thr
Val Asp

180

185

190

tcg gcc acg gag ttc tta ttt ggt gag tcc gtg cac tcc tta
aag gac 624
Ser Ala Thr Glu Phe Leu Phe Gly Glu Ser Val His Ser Leu
Lys Asp

195

200

205

gaa act atc ggt atc aac caa gac gat ata gat ttt gct ggt
aga aag 672
Glu Thr Ile Gly Ile Asn Gln Asp Asp Ile Asp Phe Ala Gly
Arg Lys

210

215

220

gac ttt gct gag tcg ttc aac aaa gcc cag gag tat ttg tct
att aga 720
Asp Phe Ala Glu Ser Phe Asn Lys Ala Gln Glu Tyr Leu Ser
Ile Arg

225

230

235

240

att ttg gtg cag acc ttc tac tgg ttg atc aac aac aag gag
ttt aga 768
Ile Leu Val Gln Thr Phe Tyr Trp Leu Ile Asn Asn Lys Glu
Phe Arg

245

250

255

gac tgt acc aag ctg gtg cac aag ttt acc aac tac tat gtt
cag aaa 816
Asp Cys Thr Lys Leu Val His Lys Phe Thr Asn Tyr Tyr Val
Gln Lys

260

265

270

gct ttg gat gct acc cca gag gaa ctt gaa aag caa ggc ggg
tat gtg 864
Ala Leu Asp Ala Thr Pro Glu Glu Leu Glu Lys Gln Gly Gly
Tyr Val

275				280				285					
ttc	ttg	tat	gag	ctt	gtc	aag	cag	acg	aga	gac	ccc	aag	gtg
ttg	cgt		912										
Phe	Leu	Tyr	Glu	Leu	Val	Lys	Gln	Thr	Arg	Asp	Pro	Lys	Val
Leu	Arg												
	290				295						300		
gac	cag	tct	ttg	aac	atc	ttg	ttg	gca	gga	aga	gac	acc	act
gct	ggg		960										
Asp	Gln	Ser	Leu	Asn	Ile	Leu	Leu	Ala	Gly	Arg	Asp	Thr	Thr
Ala	Gly												
305					310						315		
320													
ttg	ttg	tcc	ttt	gct	gtg	ttt	gag	ttg	gcc	aga	aac	cca	cac
atc	tgg		1008										
Leu	Leu	Ser	Phe	Ala	Val	Phe	Glu	Leu	Ala	Arg	Asn	Pro	His
Ile	Trp												
					325						330		
335													
gcc	aag	ttg	aga	gag	gaa	att	gaa	cag	cag	ttt	ggt	ctt	gga
gaa	gac		1056										
Ala	Lys	Leu	Arg	Glu	Glu	Ile	Glu	Gln	Gln	Phe	Gly	Leu	Gly
Glu	Asp												
					340				345				350
tct	cgt	gtt	gaa	gag	att	acc	ttt	gag	agc	ttg	aag	aga	tgt
gag	tac		1104										
Ser	Arg	Val	Glu	Glu	Ile	Thr	Phe	Glu	Ser	Leu	Lys	Arg	Cys
Glu	Tyr												
					355				360				365
ttg	aaa	gcg	ttc	ctt	aac	gaa	acc	ttg	cgt	gtt	tac	cca	agt
gtc	cca		1152										
Leu	Lys	Ala	Phe	Leu	Asn	Glu	Thr	Leu	Arg	Val	Tyr	Pro	Ser
Val	Pro												
					370				375				380
aga	aac	ttc	aga	atc	gcc	acc	aag	aat	aca	aca	ttg	cca	agg
ggt	ggt		1200										
Arg	Asn	Phe	Arg	Ile	Ala	Thr	Lys	Asn	Thr	Thr	Leu	Pro	Arg
Gly	Gly												
385					390						395		
400													
ggt	cca	gac	ggt	acc	cag	cca	atc	ttg	atc	caa	aag	gga	gaa
ggt	gtg		1248										
Gly	Pro	Asp	Gly	Thr	Gln	Pro	Ile	Leu	Ile	Gln	Lys	Gly	Glu

Gly Val

405

410

415

tcg tat ggt atc aac tct acc cac tta gat cct gtc tat tat
ggc cct 1296
Ser Tyr Gly Ile Asn Ser Thr His Leu Asp Pro Val Tyr Tyr
Gly Pro

420

425

430

gat gct gct gag ttc aga cca gag aga tgg ttt gag cca tca
acc aga 1344
Asp Ala Ala Glu Phe Arg Pro Glu Arg Trp Phe Glu Pro Ser
Thr Arg

435

440

445

aag ctc ggc tgg gct tac ttg cca ttc aac ggt ggg cca cga
atc tgt 1392
Lys Leu Gly Trp Ala Tyr Leu Pro Phe Asn Gly Gly Pro Arg
Ile Cys
450

455

460

ttg ggt cag cag ttt gcc ttg acc gaa gct ggt tac gtt ttg
gtc aga 1440
Leu Gly Gln Gln Phe Ala Leu Thr Glu Ala Gly Tyr Val Leu
Val Arg
465 470 475
480

ttg gtg caa gag ttc tcc cac att agg ctg gac cca gat gaa
gtg tat 1488
Leu Val Gln Glu Phe Ser His Ile Arg Leu Asp Pro Asp Glu
Val Tyr

485

490

495

cca cca aag agg ttg acc aac ttg acc atg tgt ttg cag gat
ggt gct 1536
Pro Pro Lys Arg Leu Thr Asn Leu Thr Met Cys Leu Gln Asp
Gly Ala

500

505

510

att gtc aag ttt gac tag
1554
Ile Val Lys Phe Asp
515

<210> 16

<211> 517

<212> PRT

<213> Candida tropicalis

<400> 16

Met Ile Glu Gln Ile Leu Glu Tyr Trp Tyr Ile Val Val Pro
Val Leu
1 5 10
15

Tyr Ile Ile Lys Gln Leu Ile Ala Tyr Ser Lys Thr Arg Val
Leu Met
20 25 30

Lys Gln Leu Gly Ala Ala Pro Ile Thr Asn Gln Leu Tyr Asp
Asn Val
35 40 45

Phe Gly Ile Val Asn Gly Trp Lys Ala Leu Gln Phe Lys Lys
Glu Gly
50 55 60

Arg Ala Gln Glu Tyr Asn Asp His Lys Phe Asp Ser Ser Lys
Asn Pro
65 70 75
80

Ser Val Gly Thr Tyr Val Ser Ile Leu Phe Gly Thr Lys Ile
Val Val
85 90
95

Thr Lys Asp Pro Glu Asn Ile Lys Ala Ile Leu Ala Thr Gln
Phe Gly
100 105 110

Asp Phe Ser Leu Gly Lys Arg His Ala Leu Phe Lys Pro Leu
Leu Gly
115 120 125

Asp Gly Ile Phe Thr Leu Asp Gly Glu Gly Trp Lys His Ser
Arg Ser

130	135	140
Met Leu Arg Pro Gln Phe Ala Arg Glu Gln Val Ala His Val		
Thr Ser		
145	150	155
160		
Leu Glu Pro His Phe Gln Leu Leu Lys Lys His Ile Leu Lys		
His Lys		
	165	170
175		
Gly Glu Tyr Phe Asp Ile Gln Glu Leu Phe Phe Arg Phe Thr		
Val Asp		
	180	185
		190
Ser Ala Thr Glu Phe Leu Phe Gly Glu Ser Val His Ser Leu		
Lys Asp		
	195	200
		205
Glu Thr Ile Gly Ile Asn Gln Asp Asp Ile Asp Phe Ala Gly		
Arg Lys		
	210	215
		220
Asp Phe Ala Glu Ser Phe Asn Lys Ala Gln Glu Tyr Leu Ser		
Ile Arg		
225	230	235
240		
Ile Leu Val Gln Thr Phe Tyr Trp Leu Ile Asn Asn Lys Glu		
Phe Arg		
	245	250
255		
Asp Cys Thr Lys Leu Val His Lys Phe Thr Asn Tyr Tyr Val		
Gln Lys		
	260	265
		270
Ala Leu Asp Ala Thr Pro Glu Glu Leu Glu Lys Gln Gly Gly		
Tyr Val		
	275	280
		285

Phe Leu Tyr Glu Leu Val Lys Gln Thr Arg Asp Pro Lys Val
Leu Arg
290 295 300

Asp Gln Ser Leu Asn Ile Leu Leu Ala Gly Arg Asp Thr Thr
Ala Gly
305 310 315
320

Leu Leu Ser Phe Ala Val Phe Glu Leu Ala Arg Asn Pro His
Ile Trp
325 330
335

Ala Lys Leu Arg Glu Glu Ile Glu Gln Gln Phe Gly Leu Gly
Glu Asp
340 345 350

Ser Arg Val Glu Glu Ile Thr Phe Glu Ser Leu Lys Arg Cys
Glu Tyr
355 360 365

Leu Lys Ala Phe Leu Asn Glu Thr Leu Arg Val Tyr Pro Ser
Val Pro
370 375 380

Arg Asn Phe Arg Ile Ala Thr Lys Asn Thr Thr Leu Pro Arg
Gly Gly
385 390 395
400

Gly Pro Asp Gly Thr Gln Pro Ile Leu Ile Gln Lys Gly Glu
Gly Val
405 410
415

Ser Tyr Gly Ile Asn Ser Thr His Leu Asp Pro Val Tyr Tyr
Gly Pro
420 425 430

Asp Ala Ala Glu Phe Arg Pro Glu Arg Trp Phe Glu Pro Ser
Thr Arg
435 440 445

Lys Leu Gly Trp Ala Tyr Leu Pro Phe Asn Gly Gly Pro Arg
Ile Cys
450 455 460

Leu Gly Gln Gln Phe Ala Leu Thr Glu Ala Gly Tyr Val Leu
Val Arg
465 470 475
480

Leu Val Gln Glu Phe Ser His Ile Arg Leu Asp Pro Asp Glu
Val Tyr
485 490
495

Pro Pro Lys Arg Leu Thr Asn Leu Thr Met Cys Leu Gln Asp
Gly Ala
500 505 510

Ile Val Lys Phe Asp
515

<210> 17
<211> 1539
<212> DNA
<213> Candida tropicalis

<220>
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<222> (1)..(1539)

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ttg ttg 48
Met Leu Asp Gln Ile Leu His Tyr Trp Tyr Ile Val Leu Pro
Leu Leu
1 5 10
15

gcc att atc aac cag atc gtg gct cat gtc agg acc aat tat			
ttg atg	96		
Ala Ile Ile Asn Gln Ile Val Ala His Val Arg Thr Asn Tyr			
Leu Met			
	20	25	30
aag aaa ttg ggt gct aag cca ttc aca cac gtc caa cgt gac			
ggg tgg	144		
Lys Lys Leu Gly Ala Lys Pro Phe Thr His Val Gln Arg Asp			
Gly Trp			
	35	40	45
ttg ggc ttc aaa ttc ggc cgt gaa ttc ctc aaa gca aaa agt			
gct ggg	192		
Leu Gly Phe Lys Phe Gly Arg Glu Phe Leu Lys Ala Lys Ser			
Ala Gly			
	50	55	60
aga ctg gtt gat tta atc atc tcc cgt ttc cac gat aat gag			
gac act	240		
Arg Leu Val Asp Leu Ile Ile Ser Arg Phe His Asp Asn Glu			
Asp Thr			
	65	70	75
	80		
ttc tcc agc tat gct ttt ggc aac cat gtg gtg ttc acc agg			
gac ccc	288		
Phe Ser Ser Tyr Ala Phe Gly Asn His Val Val Phe Thr Arg			
Asp Pro			
	85	90	
	95		
gag aat atc aag gcg ctt ttg gca acc cag ttt ggt gat ttt			
tca ttg	336		
Glu Asn Ile Lys Ala Leu Leu Ala Thr Gln Phe Gly Asp Phe			
Ser Leu			
	100	105	110
ggc agc agg gtc aag ttc ttc aaa cca tta ttg ggg tac ggt			
atc ttc	384		
Gly Ser Arg Val Lys Phe Phe Lys Pro Leu Leu Gly Tyr Gly			
Ile Phe			
	115	120	125
aca ttg gac gcc gaa ggc tgg aag cac agc aga gcc atg ttg			
aga cca	432		
Thr Leu Asp Ala Glu Gly Trp Lys His Ser Arg Ala Met Leu			
Arg Pro			
	130	135	140

cag ttt gcc aga gaa caa gtt gct cat gtg acg tcg ttg gaa
cca cac 480
Gln Phe Ala Arg Glu Gln Val Ala His Val Thr Ser Leu Glu
Pro His
145 150 155
160

ttc cag ttg ttg aag aag cat atc ctt aaa cac aag ggt gag
tac ttt 528
Phe Gln Leu Leu Lys Lys His Ile Leu Lys His Lys Gly Glu
Tyr Phe
165 170
175

gat atc cag gaa ttg ttc ttt aga ttt act gtc gac tcg gcc
acg gag 576
Asp Ile Gln Glu Leu Phe Phe Arg Phe Thr Val Asp Ser Ala
Thr Glu
180 185 190

ttc tta ttt ggt gag tcc gtg cac tcc tta aag gac gag gaa
att ggc 624
Phe Leu Phe Gly Glu Ser Val His Ser Leu Lys Asp Glu Glu
Ile Gly
195 200 205

tac gac acg aaa gac atg tct gaa gaa aga cgc aga ttt gcc
gac gcg 672
Tyr Asp Thr Lys Asp Met Ser Glu Glu Arg Arg Arg Phe Ala
Asp Ala
210 215 220

ttc aac aag tcg caa gtc tac gtg gcc acc aga gtt gct tta
cag aac 720
Phe Asn Lys Ser Gln Val Tyr Val Ala Thr Arg Val Ala Leu
Gln Asn
225 230 235
240

ttg tac tgg ttg gtc aac aac aaa gag ttc aag gag tgc aat
gac att 768
Leu Tyr Trp Leu Val Asn Asn Lys Glu Phe Lys Glu Cys Asn
Asp Ile
245 250
255

gtc cac aag ttt acc aac tac tat gtt cag aaa gcc ttg gat
gct acc 816
Val His Lys Phe Thr Asn Tyr Tyr Val Gln Lys Ala Leu Asp
Ala Thr

			260						265						270	
cca	gag	gaa	ctt	gaa	aag	caa	ggc	ggg	tat	gtg	ttc	ttg	tat			
gag	ctt		864													
Pro	Glu	Glu	Leu	Glu	Lys	Gln	Gly	Gly	Tyr	Val	Phe	Leu	Tyr			
Glu	Leu		275						280						285	
gtc	aag	cag	acg	aga	gac	ccc	aag	gtg	ttg	cgt	gac	cag	tct			
ttg	aac		912													
Val	Lys	Gln	Thr	Arg	Asp	Pro	Lys	Val	Leu	Arg	Asp	Gln	Ser			
Leu	Asn		290						295						300	
atc	ttg	ttg	gca	gga	aga	gac	acc	act	gct	ggg	ttg	ttg	tcc			
ttt	gct		960													
Ile	Leu	Leu	Ala	Gly	Arg	Asp	Thr	Thr	Ala	Gly	Leu	Leu	Ser			
Phe	Ala		305						310						315	
305																
320																
gtg	ttt	gag	ttg	gcc	aga	aac	cca	cac	atc	tgg	gcc	aag	ttg			
aga	gag		1008													
Val	Phe	Glu	Leu	Ala	Arg	Asn	Pro	His	Ile	Trp	Ala	Lys	Leu			
Arg	Glu		325						330							
335																
gaa	att	gaa	cag	cag	ttt	ggc	ctt	gga	gaa	gac	tct	cgt	gtt			
gaa	gag		1056													
Glu	Ile	Glu	Gln	Gln	Phe	Gly	Leu	Gly	Glu	Asp	Ser	Arg	Val			
Glu	Glu		340						345						350	
att	acc	ttt	gag	agc	ttg	aag	aga	tgt	gag	tac	ttg	aag	gcc			
gtg	ttg		1104													
Ile	Thr	Phe	Glu	Ser	Leu	Lys	Arg	Cys	Glu	Tyr	Leu	Lys	Ala			
Val	Leu		355						360						365	
aac	gaa	act	ttg	aga	tta	cac	cca	agt	gtc	cca	aga	aac	gca			
aga	ttt		1152													
Asn	Glu	Thr	Leu	Arg	Leu	His	Pro	Ser	Val	Pro	Arg	Asn	Ala			
Arg	Phe		370						375						380	
gcg	att	aaa	gac	acg	act	tta	cca	aga	ggc	ggc	ggc	ccc	aac			
ggc	aag		1200													
Ala	Ile	Lys	Asp	Thr	Thr	Leu	Pro	Arg	Gly	Gly	Gly	Pro	Asn			
Gly	Lys															

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385                                     390                                     395
400

gat cct atc ttg atc agg aag gat gag gtg gtg cag tac tcc
atc tcg      1248
Asp Pro Ile Leu Ile Arg Lys Asp Glu Val Val Gln Tyr Ser
Ile Ser

                                     405                                     410
415

gca act cag aca aat cct gct tat tat ggc gcc gat gct gct
gat ttt      1296
Ala Thr Gln Thr Asn Pro Ala Tyr Tyr Gly Ala Asp Ala Ala
Asp Phe

                                     420                                     425                                     430

aga ccg gaa aga tgg ttt gaa cca tca act aga aac ttg gga
tgg gct      1344
Arg Pro Glu Arg Trp Phe Glu Pro Ser Thr Arg Asn Leu Gly
Trp Ala

                                     435                                     440                                     445

ttc ttg cca ttc aac ggt ggt cca aga atc tgt ttg gga caa
cag ttt      1392
Phe Leu Pro Phe Asn Gly Gly Pro Arg Ile Cys Leu Gly Gln
Gln Phe

                                     450                                     455                                     460

gct ttg act gaa gcc ggt tac gtt ttg gtt aga ctt gtt cag
gag ttt      1440
Ala Leu Thr Glu Ala Gly Tyr Val Leu Val Arg Leu Val Gln
Glu Phe

465                                     470                                     475
480

cca aac ttg tca caa gac ccc gaa acc aag tac cca cca cct
aga ttg      1488
Pro Asn Leu Ser Gln Asp Pro Glu Thr Lys Tyr Pro Pro Pro
Arg Leu

                                     485                                     490
495

gca cac ttg acg atg tgc ttg ttt gac ggt gca cac gtc aag
atg tca      1536
Ala His Leu Thr Met Cys Leu Phe Asp Gly Ala His Val Lys
Met Ser

                                     500                                     505                                     510

tag
1539
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<211> 512
<212> PRT
<213> Candida tropicalis

<400> 18

Met Leu Asp Gln Ile Leu His Tyr Trp Tyr Ile Val Leu Pro
Leu Leu
1 5 10
15

Ala Ile Ile Asn Gln Ile Val Ala His Val Arg Thr Asn Tyr
Leu Met
20 25 30

Lys Lys Leu Gly Ala Lys Pro Phe Thr His Val Gln Arg Asp
Gly Trp
35 40 45

Leu Gly Phe Lys Phe Gly Arg Glu Phe Leu Lys Ala Lys Ser
Ala Gly
50 55 60

Arg Leu Val Asp Leu Ile Ile Ser Arg Phe His Asp Asn Glu
Asp Thr
65 70 75
80

Phe Ser Ser Tyr Ala Phe Gly Asn His Val Val Phe Thr Arg
Asp Pro
85 90
95

Glu Asn Ile Lys Ala Leu Leu Ala Thr Gln Phe Gly Asp Phe
Ser Leu
100 105 110

Gly Ser Arg Val Lys Phe Phe Lys Pro Leu Leu Gly Tyr Gly
Ile Phe
115 120 125

Thr Leu Asp Ala Glu Gly Trp Lys His Ser Arg Ala Met Leu
Arg Pro
130 135 140

Gln Phe Ala Arg Glu Gln Val Ala His Val Thr Ser Leu Glu
Pro His
145 150 155
160

Phe Gln Leu Leu Lys Lys His Ile Leu Lys His Lys Gly Glu
Tyr Phe
165 170
175

Asp Ile Gln Glu Leu Phe Phe Arg Phe Thr Val Asp Ser Ala
Thr Glu
180 185 190

Phe Leu Phe Gly Glu Ser Val His Ser Leu Lys Asp Glu Glu
Ile Gly
195 200 205

Tyr Asp Thr Lys Asp Met Ser Glu Glu Arg Arg Arg Phe Ala
Asp Ala
210 215 220

Phe Asn Lys Ser Gln Val Tyr Val Ala Thr Arg Val Ala Leu
Gln Asn
225 230 235
240

Leu Tyr Trp Leu Val Asn Asn Lys Glu Phe Lys Glu Cys Asn
Asp Ile
245 250
255

Val His Lys Phe Thr Asn Tyr Tyr Val Gln Lys Ala Leu Asp
Ala Thr
260 265 270

Pro Glu Glu Leu Glu Lys Gln Gly Gly Tyr Val Phe Leu Tyr
Glu Leu
275 280 285

Val Lys Gln Thr Arg Asp Pro Lys Val Leu Arg Asp Gln Ser
Leu Asn
290 295 300

Ile Leu Leu Ala Gly Arg Asp Thr Thr Ala Gly Leu Leu Ser
Phe Ala
305 310 315
320

Val Phe Glu Leu Ala Arg Asn Pro His Ile Trp Ala Lys Leu
Arg Glu
325 330
335

Glu Ile Glu Gln Gln Phe Gly Leu Gly Glu Asp Ser Arg Val
Glu Glu
340 345 350

Ile Thr Phe Glu Ser Leu Lys Arg Cys Glu Tyr Leu Lys Ala
Val Leu
355 360 365

Asn Glu Thr Leu Arg Leu His Pro Ser Val Pro Arg Asn Ala
Arg Phe
370 375 380

Ala Ile Lys Asp Thr Thr Leu Pro Arg Gly Gly Gly Pro Asn
Gly Lys
385 390 395
400

Asp Pro Ile Leu Ile Arg Lys Asp Glu Val Val Gln Tyr Ser
Ile Ser

415 405 410

- 74/269 -

Ala Thr Gln Thr Asn Pro Ala Tyr Tyr Gly Ala Asp Ala Ala
Asp Phe
420 425 430

Arg Pro Glu Arg Trp Phe Glu Pro Ser Thr Arg Asn Leu Gly
Trp Ala
435 440 445

Phe Leu Pro Phe Asn Gly Gly Pro Arg Ile Cys Leu Gly Gln
Gln Phe
450 455 460

Ala Leu Thr Glu Ala Gly Tyr Val Leu Val Arg Leu Val Gln
Glu Phe
465 470 475
480

Pro Asn Leu Ser Gln Asp Pro Glu Thr Lys Tyr Pro Pro Pro
Arg Leu
485 490
495

Ala His Leu Thr Met Cys Leu Phe Asp Gly Ala His Val Lys
Met Ser
500 505 510

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<220>
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<222> (1)..(1539)

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ttg ttg 48
Met Leu Asp Gln Ile Phe His Tyr Trp Tyr Ile Val Leu Pro
Leu Leu
1 5 10
15

gtc att atc aag cag atc gtg gct cat gcc agg acc aat tat
ttg atg 96
Val Ile Ile Lys Gln Ile Val Ala His Ala Arg Thr Asn Tyr
Leu Met
20 25 30

aag aag ttg ggc gct aag cca ttc aca cat gtc caa cta gac
ggg tgg 144
Lys Lys Leu Gly Ala Lys Pro Phe Thr His Val Gln Leu Asp
Gly Trp
35 40 45

ttt ggc ttc aaa ttt ggc cgt gaa ttc ctc aaa gct aaa agt
gct ggg 192
Phe Gly Phe Lys Phe Gly Arg Glu Phe Leu Lys Ala Lys Ser
Ala Gly
50 55 60

agg cag gtt gat tta atc atc tcc cgt ttc cac gat aat gag
gac act 240
Arg Gln Val Asp Leu Ile Ile Ser Arg Phe His Asp Asn Glu
Asp Thr
65 70 75
80

ttc tcc agc tat gct ttt ggc aac cat gtg gtg ttc acc agg
gac ccc 288
Phe Ser Ser Tyr Ala Phe Gly Asn His Val Val Phe Thr Arg
Asp Pro
85 90
95

gag aat atc aag gcg ctt ttg gca acc cag ttt ggt gat ttt
tca ttg 336
Glu Asn Ile Lys Ala Leu Leu Ala Thr Gln Phe Gly Asp Phe
Ser Leu
100 105 110

gga agc agg gtc aaa ttc ttc aaa cca ttg ttg ggg tac ggt
atc ttc 384
Gly Ser Arg Val Lys Phe Phe Lys Pro Leu Leu Gly Tyr Gly
Ile Phe
115 120 125

acc ttg gac ggc gaa ggc tgg aag cac agc aga gcc atg ttg
aga cca 432
Thr Leu Asp Gly Glu Gly Trp Lys His Ser Arg Ala Met Leu
Arg Pro
130 135 140

cag ttt gcc aga gag caa gtt gct cat gtg acg tcg ttg gaa
cca cat 480
Gln Phe Ala Arg Glu Gln Val Ala His Val Thr Ser Leu Glu
Pro His
145 150 155
160

ttc cag ttg ttg aag aag cat att ctt aag cac aag ggt gaa
tac ttt 528
Phe Gln Leu Leu Lys Lys His Ile Leu Lys His Lys Gly Glu
Tyr Phe
165 170
175

gat atc cag gaa ttg ttc ttt aga ttt acc gtt gat tca gcg
acg gag 576
Asp Ile Gln Glu Leu Phe Phe Arg Phe Thr Val Asp Ser Ala
Thr Glu
180 185 190

ttc tta ttt ggt gag tcc gtg cac tcc tta agg gac gag gaa
att ggc 624
Phe Leu Phe Gly Glu Ser Val His Ser Leu Arg Asp Glu Glu
Ile Gly
195 200 205

tac gat acg aag gac atg gct gaa gaa aga cgc aaa ttt gcc
gac gcg 672
Tyr Asp Thr Lys Asp Met Ala Glu Glu Arg Arg Lys Phe Ala
Asp Ala
210 215 220

ttc aac aag tcg caa gtc tat ttg tcc acc aga gtt gct tta
cag aca 720
Phe Asn Lys Ser Gln Val Tyr Leu Ser Thr Arg Val Ala Leu
Gln Thr
225 230 235
240

ttg tac tgg ttg gtc aac aac aaa gag ttc aag gag tgc aac
gac att 768
Leu Tyr Trp Leu Val Asn Asn Lys Glu Phe Lys Glu Cys Asn
Asp Ile
245 250
255

gtc cac aag ttc acc aac tac tat gtt cag aaa gcc ttg gat
gct acc 816
Val His Lys Phe Thr Asn Tyr Tyr Val Gln Lys Ala Leu Asp
Ala Thr

			260						265						270	
cca	gag	gaa	ctt	gaa	aaa	caa	ggc	ggg	tat	gtg	ttc	ttg	tac			
gag	ctt		864													
Pro	Glu	Glu	Leu	Glu	Lys	Gln	Gly	Gly	Tyr	Val	Phe	Leu	Tyr			
Glu	Leu								285							
		275						280								
gcc	aag	cag	acg	aaa	gac	ccc	aat	gtg	ttg	cgt	gac	cag	tct			
ttg	aac		912													
Ala	Lys	Gln	Thr	Lys	Asp	Pro	Asn	Val	Leu	Arg	Asp	Gln	Ser			
Leu	Asn								300							
		290						295								
atc	ttg	ttg	gct	gga	agg	gac	acc	act	gct	ggg	ttg	ttg	tcc			
ttt	gct		960													
Ile	Leu	Leu	Ala	Gly	Arg	Asp	Thr	Thr	Ala	Gly	Leu	Leu	Ser			
Phe	Ala								315							
305		310														
320																
gtg	ttt	gag	ttg	gcc	agg	aac	cca	cac	atc	tgg	gcc	aag	ttg			
aga	gag		1008													
Val	Phe	Glu	Leu	Ala	Arg	Asn	Pro	His	Ile	Trp	Ala	Lys	Leu			
Arg	Glu								330							
		325														
335																
gaa	att	gaa	tca	cac	ttt	ggg	ctg	ggt	gag	gac	tct	cgt	gtt			
gaa	gag		1056													
Glu	Ile	Glu	Ser	His	Phe	Gly	Leu	Gly	Glu	Asp	Ser	Arg	Val			
Glu	Glu								350							
		340						345								
att	acc	ttt	gag	agc	ttg	aag	aga	tgt	gag	tac	ttg	aaa	gcc			
gtg	ttg		1104													
Ile	Thr	Phe	Glu	Ser	Leu	Lys	Arg	Cys	Glu	Tyr	Leu	Lys	Ala			
Val	Leu								365							
		355						360								
aac	gaa	acg	ttg	aga	tta	cac	cca	agt	gtc	cca	aga	aac	gca			
aga	ttt		1152													
Asn	Glu	Thr	Leu	Arg	Leu	His	Pro	Ser	Val	Pro	Arg	Asn	Ala			
Arg	Phe								380							
		370						375								
gcg	att	aaa	gac	acg	act	tta	cca	aga	ggc	ggt	ggc	ccc	aac			
ggc	aag		1200													
Ala	Ile	Lys	Asp	Thr	Thr	Leu	Pro	Arg	Gly	Gly	Gly	Pro	Asn			
Gly	Lys															

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385                                     390                                     395
400

gat cct atc ttg atc aga aag aat gag gtg gtg caa tac tcc
atc tcg      1248
Asp Pro Ile Leu Ile Arg Lys Asn Glu Val Val Gln Tyr Ser
Ile Ser

                                     405                                     410
415

gca act cag aca aat cct gct tat tat ggc gcc gat gct gct
gat ttt      1296
Ala Thr Gln Thr Asn Pro Ala Tyr Tyr Gly Ala Asp Ala Ala
Asp Phe

                                     420                                     425                                     430

aga ccg gaa aga tgg ttt gag cca tca act aga aac ttg gga
tgg gct      1344
Arg Pro Glu Arg Trp Phe Glu Pro Ser Thr Arg Asn Leu Gly
Trp Ala

                                     435                                     440                                     445

tac ttg cca ttc aac ggt ggt cca aga atc tgc ttg gga caa
cag ttt      1392
Tyr Leu Pro Phe Asn Gly Gly Pro Arg Ile Cys Leu Gly Gln
Gln Phe

                                     450                                     455                                     460

gct ttg acc gaa gcc ggt tac gtt ttg gtt aga ctt gtt cag
gaa ttc      1440
Ala Leu Thr Glu Ala Gly Tyr Val Leu Val Arg Leu Val Gln
Glu Phe

465                                     470                                     475
480

cct agc ttg tca cag gac ccc gaa act gag tac cca cca cct
aga ttg      1488
Pro Ser Leu Ser Gln Asp Pro Glu Thr Glu Tyr Pro Pro Pro
Arg Leu

                                     485                                     490
495

gca cac ttg acg atg tgc ttg ttt gac ggg gca tac gtc aag
atg caa      1536
Ala His Leu Thr Met Cys Leu Phe Asp Gly Ala Tyr Val Lys
Met Gln

                                     500                                     505                                     510

tag
1539
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<210> 20
<211> 512
<212> PRT
<213> Candida tropicalis

<400> 20

Met Leu Asp Gln Ile Phe His Tyr Trp Tyr Ile Val Leu Pro
Leu Leu
1 5 10
15

Val Ile Ile Lys Gln Ile Val Ala His Ala Arg Thr Asn Tyr
Leu Met
20 25 30

Lys Lys Leu Gly Ala Lys Pro Phe Thr His Val Gln Leu Asp
Gly Trp
35 40 45

Phe Gly Phe Lys Phe Gly Arg Glu Phe Leu Lys Ala Lys Ser
Ala Gly
50 55 60

Arg Gln Val Asp Leu Ile Ile Ser Arg Phe His Asp Asn Glu
Asp Thr
65 70 75
80

Phe Ser Ser Tyr Ala Phe Gly Asn His Val Val Phe Thr Arg
Asp Pro
85 90
95

Glu Asn Ile Lys Ala Leu Leu Ala Thr Gln Phe Gly Asp Phe
Ser Leu
100 105 110

Gly Ser Arg Val Lys Phe Phe Lys Pro Leu Leu Gly Tyr Gly
Ile Phe
115 120 125

Thr Leu Asp Gly Glu Gly Trp Lys His Ser Arg Ala Met Leu
Arg Pro
130 135 140

Gln Phe Ala Arg Glu Gln Val Ala His Val Thr Ser Leu Glu
Pro His
145 150 155
160

Phe Gln Leu Leu Lys Lys His Ile Leu Lys His Lys Gly Glu
Tyr Phe
165 170
175

Asp Ile Gln Glu Leu Phe Phe Arg Phe Thr Val Asp Ser Ala
Thr Glu
180 185 190

Phe Leu Phe Gly Glu Ser Val His Ser Leu Arg Asp Glu Glu
Ile Gly
195 200 205

Tyr Asp Thr Lys Asp Met Ala Glu Glu Arg Arg Lys Phe Ala
Asp Ala
210 215 220

Phe Asn Lys Ser Gln Val Tyr Leu Ser Thr Arg Val Ala Leu
Gln Thr
225 230 235
240

Leu Tyr Trp Leu Val Asn Asn Lys Glu Phe Lys Glu Cys Asn
Asp Ile
245 250
255

Val His Lys Phe Thr Asn Tyr Tyr Val Gln Lys Ala Leu Asp
Ala Thr
260 265 270

Pro Glu Glu Leu Glu Lys Gln Gly Gly Tyr Val Phe Leu Tyr
Glu Leu
275 280 285

Ala Lys Gln Thr Lys Asp Pro Asn Val Leu Arg Asp Gln Ser
Leu Asn
290 295 300

Ile Leu Leu Ala Gly Arg Asp Thr Thr Ala Gly Leu Leu Ser
Phe Ala
305 310 315
320

Val Phe Glu Leu Ala Arg Asn Pro His Ile Trp Ala Lys Leu
Arg Glu
325 330
335

Glu Ile Glu Ser His Phe Gly Leu Gly Glu Asp Ser Arg Val
Glu Glu
340 345 350

Ile Thr Phe Glu Ser Leu Lys Arg Cys Glu Tyr Leu Lys Ala
Val Leu
355 360 365

Asn Glu Thr Leu Arg Leu His Pro Ser Val Pro Arg Asn Ala
Arg Phe
370 375 380

Ala Ile Lys Asp Thr Thr Leu Pro Arg Gly Gly Gly Pro Asn
Gly Lys
385 390 395
400

Asp Pro Ile Leu Ile Arg Lys Asn Glu Val Val Gln Tyr Ser
Ile Ser
405 410
415

- 82/269 -

Ala Thr Gln Thr Asn Pro Ala Tyr Tyr Gly Ala Asp Ala Ala
Asp Phe
420 425 430

Arg Pro Glu Arg Trp Phe Glu Pro Ser Thr Arg Asn Leu Gly
Trp Ala
435 440 445

Tyr Leu Pro Phe Asn Gly Gly Pro Arg Ile Cys Leu Gly Gln
Gln Phe
450 455 460

Ala Leu Thr Glu Ala Gly Tyr Val Leu Val Arg Leu Val Gln
Glu Phe
465 470 475
480

Pro Ser Leu Ser Gln Asp Pro Glu Thr Glu Tyr Pro Pro Pro
Arg Leu
485 490
495

Ala His Leu Thr Met Cys Leu Phe Asp Gly Ala Tyr Val Lys
Met Gln
500 505 510

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<212> DNA
<213> Candida tropicalis

<220>
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<222> (1)..(390)

<400> 21
atg acc gac aca gac acc acg acc acc atc tac acc cac gaa
gag gtt 48
Met Thr Asp Thr Asp Thr Thr Thr Thr Ile Tyr Thr His Glu
Glu Val
1 5 10
15

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gcc cag cac acc acc cac gac gac ttg tgg gtt att ctc aat
ggt aag          96
Ala Gln His Thr Thr His Asp Asp Leu Trp Val Ile Leu Asn
Gly Lys
          20          25          30

gtc tac aac atc tcc aac tat ata gac gag cac cca ggt ggt
gaa gaa          144
Val Tyr Asn Ile Ser Asn Tyr Ile Asp Glu His Pro Gly Gly
Glu Glu
          35          40          45

gtc att ctt gat tgc gcc ggc aca gac gcc act gaa gcc ttt
gac gac          192
Val Ile Leu Asp Cys Ala Gly Thr Asp Ala Thr Glu Ala Phe
Asp Asp
          50          55          60

att ggc cac tcc gac gag gcc cac gag atc ttg gaa aag ttg
tac att          240
Ile Gly His Ser Asp Glu Ala His Glu Ile Leu Glu Lys Leu
Tyr Ile
          65          70          75
80

ggt aac ttg aag ggc gct aag att gtt gag gcc aag cac gcg
cag tcg          288
Gly Asn Leu Lys Gly Ala Lys Ile Val Glu Ala Lys His Ala
Gln Ser
          85          90
95

ttc agc acg gaa gaa gac tcg ggt atc aac ttc cca ttg att
gct gtt          336
Phe Ser Thr Glu Glu Asp Ser Gly Ile Asn Phe Pro Leu Ile
Ala Val
          100          105          110

ggt gtg ttt ttg gct gct ttc ggt gtc tac tac tac aag acc
aac ttt          384
Gly Val Phe Leu Ala Ala Phe Gly Val Tyr Tyr Tyr Lys Thr
Asn Phe
          115          120          125

gcc taa
390
Ala

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<210> 22
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<212> PRT
<213> Candida tropicalis

<400> 22

Met Thr Asp Thr Asp Thr Thr Thr Thr Ile Tyr Thr His Glu
Glu Val
1 5 10
15

Ala Gln His Thr Thr His Asp Asp Leu Trp Val Ile Leu Asn
Gly Lys
20 25 30

Val Tyr Asn Ile Ser Asn Tyr Ile Asp Glu His Pro Gly Gly
Glu Glu
35 40 45

Val Ile Leu Asp Cys Ala Gly Thr Asp Ala Thr Glu Ala Phe
Asp Asp
50 55 60

Ile Gly His Ser Asp Glu Ala His Glu Ile Leu Glu Lys Leu
Tyr Ile
65 70 75
80

Gly Asn Leu Lys Gly Ala Lys Ile Val Glu Ala Lys His Ala
Gln Ser
85 90
95

Phe Ser Thr Glu Glu Asp Ser Gly Ile Asn Phe Pro Leu Ile
Ala Val
100 105 110

Gly Val Phe Leu Ala Ala Phe Gly Val Tyr Tyr Tyr Lys Thr
Asn Phe
115 120 125

Ala

<210> 23
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<212> DNA
<213> *Candida tropicalis*

<220>
<221> CDS
<222> (1)..(2115)

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gac acc 48
Met Ala Pro Phe Leu Pro Asp Gln Val Asp Tyr Lys His Val
Asp Thr
1 5 10
15

ctt atg tta tta tgt gac ggg atc atc cac gaa acc acc gtg
gac gaa 96
Leu Met Leu Leu Cys Asp Gly Ile Ile His Glu Thr Thr Val
Asp Glu
20 25 30

atc aaa gac gtc att gcc cct gac ttc ccc gcc gac aaa tac
gag gag 144
Ile Lys Asp Val Ile Ala Pro Asp Phe Pro Ala Asp Lys Tyr
Glu Glu
35 40 45

tac gtc agg aca ttc acc aaa ccc tcc gaa acc cca ggg ttc
agg gaa 192
Tyr Val Arg Thr Phe Thr Lys Pro Ser Glu Thr Pro Gly Phe
Arg Glu
50 55 60

acc gtc tac aac acc gtc aac gca aac acc atg gat gca atc
cac cag 240
Thr Val Tyr Asn Thr Val Asn Ala Asn Thr Met Asp Ala Ile
His Gln
65 70 75
80

ttc att atc ttg acc aat gtt ttg gga tca agg gtc ttg gca
cca gct 288
Phe Ile Ile Leu Thr Asn Val Leu Gly Ser Arg Val Leu Ala

Pro Ala

85

90

95

ttg acc aac tcg ttg act cct atc aag gac atg agc ttg gaa
gac cgt 336
Leu Thr Asn Ser Leu Thr Pro Ile Lys Asp Met Ser Leu Glu
Asp Arg

100

105

110

gaa aag ttg tta gcc tcg tgg cgt gac tcc cct att gct gct
aaa agg 384
Glu Lys Leu Leu Ala Ser Trp Arg Asp Ser Pro Ile Ala Ala
Lys Arg

115

120

125

aag ttg ttc agg ttg gtt tct acg ctt acc ttg gtc acg ttc
acg aga 432
Lys Leu Phe Arg Leu Val Ser Thr Leu Thr Leu Val Thr Phe
Thr Arg

130

135

140

ttg gcc aat gag ttg cat ttg aaa gcc att cat tat cca gga
aga gaa 480
Leu Ala Asn Glu Leu His Leu Lys Ala Ile His Tyr Pro Gly
Arg Glu

145

150

155

160

gac cgt gaa aag gct tat gaa acc cag gag att gac cct ttt
aag tac 528
Asp Arg Glu Lys Ala Tyr Glu Thr Gln Glu Ile Asp Pro Phe
Lys Tyr

165

170

175

cag ttt ttg gaa aaa ccg aag ttt tac ggc gct gag ttg tac
ttg cca 576
Gln Phe Leu Glu Lys Pro Lys Phe Tyr Gly Ala Glu Leu Tyr
Leu Pro

180

185

190

gat att gat gtg atc att att gga tct ggg gcc ggt gct ggt
gtc gtg 624
Asp Ile Asp Val Ile Ile Ile Gly Ser Gly Ala Gly Ala Gly
Val Val

195

200

205

gcc cac act ttg acc aac gac ggc ttc aag agt ttg gtt ttg
gaa aag 672

Ala Glu	His Lys 210	Thr	Leu	Thr	Asn	Asp	Gly	Phe	Lys	Ser	Leu	Val	Leu
215220													
ggc gac Gly Asp 225 240	aga ggg Arg Gly	tac Tyr	ttt Phe	agc Ser	aac Asn	tcc Ser	gag Glu	ttg Leu	aac Asn	ttt Phe	gat Asp	gac Asp	aag Lys
230235													
ggt aac Val Asn 255	caa cag Gln Gln	gaa Glu	tta Leu	tac Tyr	caa Gln	agt Ser	gga Gly	ggt Gly	act Thr	ttg Leu	acc Thr	acc Thr	gtc Val
245250													
cag act Gln Thr	ttg gtc Leu Val	ttt Phe	ggt Val	ctt Leu	gct Ala	ggg Gly	tcc Ser	act Thr	ttt Phe	ggg Gly	ggg Gly	ggg Gly	acc Thr
260265270													
aat gaa Asn Glu	tgg tgg Trp Trp	tcg Ser	gcc Ala	tgt Cys	ctt Leu	aaa Lys	acg Thr	cca Pro	ttc Phe	aag Lys	gtg Val	cgt Arg	aag Lys
275280285													
tat gac Tyr Asp	gat aaa Asp Lys 290	gag Glu	ttt Phe	ggc Gly	gtt Val	gac Asp	ttt Phe	gct Ala	gcc Ala	gat Asp	gaa Glu	gcc Ala	tac Tyr
295300													
gca ggc Ala Gly 305 320	cag atc Gln Ile	gat Asp	tat Tyr	gtt Val	tgg Trp	cag Gln	caa Gln	atg Met	gga Gly	gct Ala	tct Ser	acc Thr	gaa Glu
310315													
acc aaa Thr Lys 335	cac tta His Leu	tct Ser	ttg Leu	gct Ala	aac Asn	gag Glu	att Ile	att Ile	att Ile	gaa Glu	ggg Gly	ggc Gly	aag Lys
325330													

ggt tac aag gcc aag gta tta gac caa aac agc ggt ggt cat
cct cat 1056
Gly Tyr Lys Ala Lys Val Leu Asp Gln Asn Ser Gly Gly His
Pro His
340 345 350

cac aga tgc ggt ttc tgt tat ttg ggt tgt aag cac ggt atc
aag cag 1104
His Arg Cys Gly Phe Cys Tyr Leu Gly Cys Lys His Gly Ile
Lys Gln
355 360 365

ggc tct gtt aat aac tgg ttt aga gac gca gct gcc cac ggt
tct cag 1152
Gly Ser Val Asn Asn Trp Phe Arg Asp Ala Ala Ala His Gly
Ser Gln
370 375 380

ttc atg caa cag gtt aga gtt ttg caa atc ctt aac aag aag
ggc atc 1200
Phe Met Gln Gln Val Arg Val Leu Gln Ile Leu Asn Lys Lys
Gly Ile
385 390 395
400

gct tat ggt atc ttg tgt gag gat gtt gta acc ggt gcc aag
ttc acc 1248
Ala Tyr Gly Ile Leu Cys Glu Asp Val Val Thr Gly Ala Lys
Phe Thr
405 410
415

att act ggc ccc aaa aag ttt gtt gtt gcc gcc ggc gcc tta
aac act 1296
Ile Thr Gly Pro Lys Lys Phe Val Val Ala Ala Gly Ala Leu
Asn Thr
420 425 430

cca tct gtg ttg gtc aac tcc gga ttc aag aac aag aac atc
ggt aag 1344
Pro Ser Val Leu Val Asn Ser Gly Phe Lys Asn Lys Asn Ile
Gly Lys
435 440 445

aac tta act ttg cat cca gtt tct gtc gtg ttt ggt gat ttt
ggc aaa 1392
Asn Leu Thr Leu His Pro Val Ser Val Val Phe Gly Asp Phe
Gly Lys
450 455 460

gac gtt caa gca gat cac ttc cac aac tcc atc atg act gct
 ctt tgt 1440
 Asp Val Gln Ala Asp His Phe His Asn Ser Ile Met Thr Ala
 Leu Cys
 465 470 475
 480

tca gaa gcc gct gat tta gac ggc aag ggt cat gga tgc aga
 att gaa 1488
 Ser Glu Ala Ala Asp Leu Asp Gly Lys Gly His Gly Cys Arg
 Ile Glu
 485 490
 495

acc atc ttg aac gct cca ttc atc cag gct tca ttc tta cca
 tgg aga 1536
 Thr Ile Leu Asn Ala Pro Phe Ile Gln Ala Ser Phe Leu Pro
 Trp Arg
 500 505 510

ggt agt aac gag gct aga cga gac ttg ttg cgt tac aac aac
 atg gtg 1584
 Gly Ser Asn Glu Ala Arg Arg Asp Leu Leu Arg Tyr Asn Asn
 Met Val
 515 520 525

gcc atg tta ctt ctt agt cgt gat acc acc agt ggt tcc gtt
 tcg tcc 1632
 Ala Met Leu Leu Leu Ser Arg Asp Thr Thr Ser Gly Ser Val
 Ser Ser
 530 535 540

cat cca act aaa cct gaa gca tta gtt gtc gag tac gac gtg
 aac aag 1680
 His Pro Thr Lys Pro Glu Ala Leu Val Val Glu Tyr Asp Val
 Asn Lys
 545 550 555
 560

ttt gac aga aac tcc atc ttg cag gca ttg ttg gtc act gct
 gac ttg 1728
 Phe Asp Arg Asn Ser Ile Leu Gln Ala Leu Leu Val Thr Ala
 Asp Leu
 565 570
 575

ttg tac att caa ggt gcc aag aga atc ctt agt ccc caa cca
 tgg gtg 1776
 Leu Tyr Ile Gln Gly Ala Lys Arg Ile Leu Ser Pro Gln Pro
 Trp Val

	580		585		590
cca att ttt	gaa tcc gac	aag cca aag	gat aag aga	tca atc	
aag gac	1824				
Pro Ile Phe	Glu Ser Asp	Lys Pro Lys	Asp Lys Arg	Ser Ile	
Lys Asp					
	595		600		605
gag gac tat	gtc gaa tgg	aga gcc aag	gtt gcc aag	att cct	
ttt gac	1872				
Glu Asp Tyr	Val Glu Trp	Arg Ala Lys	Val Ala Lys	Ile Pro	
Phe Asp					
	610		615		620
acc tac ggc	tcg cct tat	ggc tcg gcg	cat caa atg	tct tct	
tgt cgt	1920				
Thr Tyr Gly	Ser Pro Tyr	Gly Ser Ala	His Gln Met	Ser Ser	
Cys Arg					
625		630		635	
640					
atg tca ggt	aag ggt cct	aaa tac ggt	gct gtt gat	acc gat	
ggc aga	1968				
Met Ser Gly	Lys Gly Pro	Lys Tyr Gly	Ala Val Asp	Thr Asp	
Gly Arg					
	645		650		
655					
ttg ttt gaa	tgt tcg aat	gtt tat gtt	gct gac gct	agt ctt	
ttg cca	2016				
Leu Phe Glu	Cys Ser Asn	Val Tyr Val	Ala Asp Ala	Ser Leu	
Leu Pro					
	660		665		670
act gct agc	ggc gct aat	cct atg gtc	acc acc atg	act ctt	
gca aga	2064				
Thr Ala Ser	Gly Ala Asn	Pro Met Val	Thr Thr Met	Thr Leu	
Ala Arg					
	675		680		685
cat gtt gcg	tta ggt ttg	gca gac tcc	ttg aag acc	aag gcc	
aag ttg	2112				
His Val Ala	Leu Gly Leu	Ala Asp Ser	Leu Lys Thr	Lys Ala	
Lys Leu					
	690		695		700
tag					
2115					

<210> 24
<211> 704
<212> PRT
<213> Candida tropicalis

<400> 24

Met Ala Pro Phe Leu Pro Asp Gln Val Asp Tyr Lys His Val
Asp Thr
1 5 10
15

Leu Met Leu Leu Cys Asp Gly Ile Ile His Glu Thr Thr Val
Asp Glu
20 25 30

Ile Lys Asp Val Ile Ala Pro Asp Phe Pro Ala Asp Lys Tyr
Glu Glu
35 40 45

Tyr Val Arg Thr Phe Thr Lys Pro Ser Glu Thr Pro Gly Phe
Arg Glu
50 55 60

Thr Val Tyr Asn Thr Val Asn Ala Asn Thr Met Asp Ala Ile
His Gln
65 70 75
80

Phe Ile Ile Leu Thr Asn Val Leu Gly Ser Arg Val Leu Ala
Pro Ala
85 90
95

Leu Thr Asn Ser Leu Thr Pro Ile Lys Asp Met Ser Leu Glu
Asp Arg
100 105 110

Glu Lys Leu Leu Ala Ser Trp Arg Asp Ser Pro Ile Ala Ala
Lys Arg
115 120 125

Lys Leu Phe Arg Leu Val Ser Thr Leu Thr Leu Val Thr Phe
Thr Arg
130 135 140

Leu Ala Asn Glu Leu His Leu Lys Ala Ile His Tyr Pro Gly
Arg Glu
145 150 155
160

Asp Arg Glu Lys Ala Tyr Glu Thr Gln Glu Ile Asp Pro Phe
Lys Tyr
165 170
175

Gln Phe Leu Glu Lys Pro Lys Phe Tyr Gly Ala Glu Leu Tyr
Leu Pro
180 185 190

Asp Ile Asp Val Ile Ile Ile Gly Ser Gly Ala Gly Ala Gly
Val Val
195 200 205

Ala His Thr Leu Thr Asn Asp Gly Phe Lys Ser Leu Val Leu
Glu Lys
210 215 220

Gly Arg Tyr Phe Ser Asn Ser Glu Leu Asn Phe Asp Asp Lys
Asp Gly
225 230 235
240

Val Gln Glu Leu Tyr Gln Ser Gly Gly Thr Leu Thr Thr Val
Asn Gln
245 250
255

Gln Leu Phe Val Leu Ala Gly Ser Thr Phe Gly Gly Gly Thr
Thr Val
260 265 270

Asn Trp Ser Ala Cys Leu Lys Thr Pro Phe Lys Val Arg Lys

Glu	Trp	275					280					285			
Tyr	Asp	Glu	Phe	Gly	Val	Asp	Phe	Ala	Ala	Asp	Glu	Ala	Tyr		
Asp	Lys	290					295					300			
Ala	Gln	Asp	Tyr	Val	Trp	Gln	Gln	Met	Gly	Ala	Ser	Thr	Glu		
Gly	Ile	305					310					315			
320															
Thr	His	Ser	Leu	Ala	Asn	Glu	Ile	Ile	Ile	Glu	Gly	Gly	Lys		
Lys	Leu	325					330								
335															
Gly	Tyr	Lys	Ala	Lys	Val	Leu	Asp	Gln	Asn	Ser	Gly	Gly	His		
Pro	His	340					345					350			
His	Arg	Cys	Gly	Phe	Cys	Tyr	Leu	Gly	Cys	Lys	His	Gly	Ile		
Lys	Gln	355					360					365			
Gly	Ser	Val	Asn	Asn	Trp	Phe	Arg	Asp	Ala	Ala	Ala	His	Gly		
Ser	Gln	370					375					380			
Phe	Met	Gln	Gln	Val	Arg	Val	Leu	Gln	Ile	Leu	Asn	Lys	Lys		
Gly	Ile	385					390					395			
400															
Ala	Tyr	Gly	Ile	Leu	Cys	Glu	Asp	Val	Val	Thr	Gly	Ala	Lys		
Phe	Thr	405					410								
415															
Ile	Thr	Gly	Pro	Lys	Lys	Phe	Val	Val	Ala	Ala	Gly	Ala	Leu		
Asn	Thr														

	420		425		430
Pro Ser Val Leu Val Asn Ser Gly Phe Lys Asn Lys Asn Ile					
Gly Lys					
	435		440		445
Asn Leu Thr Leu His Pro Val Ser Val Val Phe Gly Asp Phe					
Gly Lys					
	450		455		460
Asp Val Gln Ala Asp His Phe His Asn Ser Ile Met Thr Ala					
Leu Cys					
465		470		475	
480					
Ser Glu Ala Ala Asp Leu Asp Gly Lys Gly His Gly Cys Arg					
Ile Glu					
	485		490		
495					
Thr Ile Leu Asn Ala Pro Phe Ile Gln Ala Ser Phe Leu Pro					
Trp Arg					
	500		505		510
Gly Ser Asn Glu Ala Arg Arg Asp Leu Leu Arg Tyr Asn Asn					
Met Val					
	515		520		525
Ala Met Leu Leu Leu Ser Arg Asp Thr Thr Ser Gly Ser Val					
Ser Ser					
	530		535		540
His Pro Thr Lys Pro Glu Ala Leu Val Val Glu Tyr Asp Val					
Asn Lys					
545		550		555	
560					
Phe Asp Arg Asn Ser Ile Leu Gln Ala Leu Leu Val Thr Ala					
Asp Leu					
	565		570		
575					

Leu	Tyr	Ile	Gln	Gly	Ala	Lys	Arg	Ile	Leu	Ser	Pro	Gln	Pro
Trp	Val												
			580					585					590

Pro	Ile	Phe	Glu	Ser	Asp	Lys	Pro	Lys	Asp	Lys	Arg	Ser	Ile
Lys	Asp												
		595					600					605	

Glu	Asp	Tyr	Val	Glu	Trp	Arg	Ala	Lys	Val	Ala	Lys	Ile	Pro
Phe	Asp												
		610				615					620		

Thr	Tyr	Gly	Ser	Pro	Tyr	Gly	Ser	Ala	His	Gln	Met	Ser	Ser
Cys	Arg												
625					630						635		
640													

Met	Ser	Gly	Lys	Gly	Pro	Lys	Tyr	Gly	Ala	Val	Asp	Thr	Asp
Gly	Arg												
			645						650				
655													

Leu	Phe	Glu	Cys	Ser	Asn	Val	Tyr	Val	Ala	Asp	Ala	Ser	Leu
Leu	Pro												
			660					665					670

Thr	Ala	Ser	Gly	Ala	Asn	Pro	Met	Val	Thr	Thr	Met	Thr	Leu
Ala	Arg												
		675					680					685	

His	Val	Ala	Leu	Gly	Leu	Ala	Asp	Ser	Leu	Lys	Thr	Lys	Ala
Lys	Leu												
		690				695					700		

<210> 25
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Lys Arg
115 120 125

aga ttg ttc aga ttg att tcc tcg ctt acc ttg acg acg ttt
acg aga 432
Arg Leu Phe Arg Leu Ile Ser Ser Leu Thr Leu Thr Thr Phe
Thr Arg
130 135 140

ttg gcc agc gaa ttg cac ttg aaa gcc atc cac tac cct ggc
aga gac 480
Leu Ala Ser Glu Leu His Leu Lys Ala Ile His Tyr Pro Gly
Arg Asp
145 150 155
160

ttg cgt gaa aag gcg tat gaa acc cag gtg gtt gac cct ttc
agg tac 528
Leu Arg Glu Lys Ala Tyr Glu Thr Gln Val Val Asp Pro Phe
Arg Tyr
165 170
175

ctg ttt atg gag aaa cca aag ttt gac ggc gcc gaa ttg tac
ttg cca 576
Leu Phe Met Glu Lys Pro Lys Phe Asp Gly Ala Glu Leu Tyr
Leu Pro
180 185 190

gat atc gac gtc atc atc att gga tca ggc gcc ggt gct ggt
gtc atg 624
Asp Ile Asp Val Ile Ile Ile Gly Ser Gly Ala Gly Ala Gly
Val Met
195 200 205

gcc cac act ctc gcc aac gac ggg ttc aag acc ttg gtt ttg
gaa aag 672
Ala His Thr Leu Ala Asn Asp Gly Phe Lys Thr Leu Val Leu
Glu Lys
210 215 220

gga aag tat ttc agc aac tcc gag ttg aac ttt aat gac gct
gat ggc 720
Gly Lys Tyr Phe Ser Asn Ser Glu Leu Asn Phe Asn Asp Ala
Asp Gly
225 230 235
240

gtg aaa gag ttg tac caa ggt aaa ggt gct ttg gcc acc acc
aat cag 768
Val Lys Glu Leu Tyr Gln Gly Lys Gly Ala Leu Ala Thr Thr
Asn Gln

245 250

255

cag atg ttt att ctt gcc ggt tcc act ttg ggc ggt ggt acc
act gtc 816
Gln Met Phe Ile Leu Ala Gly Ser Thr Leu Gly Gly Gly Thr
Thr Val

260 265 270

aac tgg tct gct tgc ctt aaa aca cca ttt aaa gtg cgt aag
gag tgg 864
Asn Trp Ser Ala Cys Leu Lys Thr Pro Phe Lys Val Arg Lys
Glu Trp

275 280 285

tac gac gag ttt ggt ctt gaa ttt gct gcc gat gaa gcc tac
gac aaa 912
Tyr Asp Glu Phe Gly Leu Glu Phe Ala Ala Asp Glu Ala Tyr
Asp Lys

290 295 300

gcg cag gat tat gtt tgg aaa caa atg ggt gct tca aca gat
gga atc 960
Ala Gln Asp Tyr Val Trp Lys Gln Met Gly Ala Ser Thr Asp
Gly Ile

305 310 315

320

act cac tcc ttg gcc aac gaa gtt gtg gtt gaa gga ggt aag
aag ttg 1008
Thr His Ser Leu Ala Asn Glu Val Val Val Glu Gly Gly Lys
Lys Leu

325 330

335

ggc tac aag agc aag gaa att gag cag aac aac ggt ggc cac
cct gac 1056
Gly Tyr Lys Ser Lys Glu Ile Glu Gln Asn Asn Gly Gly His
Pro Asp

340 345 350

cac cca tgt ggt ttc tgt tac ttg ggc tgt aag tac ggt att
 aaa cag 1104
 His Pro Cys Gly Phe Cys Tyr Leu Gly Cys Lys Tyr Gly Ile
 Lys Gln

355				360				365					
ggt	tct	gtg	aat	aac	tgg	ttt	aga	gac	gca	gct	gcc	cac	ggg
tcc	aag		1152										
Gly	Ser	Val	Asn	Asn	Trp	Phe	Arg	Asp	Ala	Ala	Ala	His	Gly
Ser	Lys												
		370			375						380		
ttc	atg	caa	caa	gtc	aga	gtt	gtg	caa	atc	ctc	aac	aag	aat
ggc	gtc		1200										
Phe	Met	Gln	Gln	Val	Arg	Val	Val	Gln	Ile	Leu	Asn	Lys	Asn
Gly	Val												
385					390						395		
400													
gct	tat	ggg	atc	ttg	tgt	gag	gat	gtc	gaa	acc	gga	gtc	agg
ttc	act		1248										
Ala	Tyr	Gly	Ile	Leu	Cys	Glu	Asp	Val	Glu	Thr	Gly	Val	Arg
Phe	Thr												
			405								410		
415													
att	agt	ggc	ccc	aaa	aag	ttt	gtt	gtt	tct	gct	ggg	tct	ttg
aac	acg		1296										
Ile	Ser	Gly	Pro	Lys	Lys	Phe	Val	Val	Ser	Ala	Gly	Ser	Leu
Asn	Thr												
			420						425				430
cca	act	gtg	ttg	acc	aac	tcc	gga	ttc	aag	aac	aag	cac	att
ggg	aag		1344										
Pro	Thr	Val	Leu	Thr	Asn	Ser	Gly	Phe	Lys	Asn	Lys	His	Ile
Gly	Lys												
		435					440					445	
aac	ttg	acg	ttg	cac	cca	gtt	tcc	acc	gtg	ttt	ggg	gac	ttt
ggc	aga		1392										
Asn	Leu	Thr	Leu	His	Pro	Val	Ser	Thr	Val	Phe	Gly	Asp	Phe
Gly	Arg												
		450					455					460	
gac	gtg	caa	gcc	gac	cat	ttc	cac	aaa	tct	att	atg	act	tcg
ctt	tgt		1440										
Asp	Val	Gln	Ala	Asp	His	Phe	His	Lys	Ser	Ile	Met	Thr	Ser
Leu	Cys												
465					470						475		
480													
tac	gag	gtt	gct	gac	ttg	gac	ggc	aag	ggc	cac	gga	tgc	aga
atc	gaa		1488										
Tyr	Glu	Val	Ala	Asp	Leu	Asp	Gly	Lys	Gly	His	Gly	Cys	Arg

Ile Glu

485

490

495

acc atc ttg aac gct cca ttc atc caa gct tct ttg ttg cca
tgg aga 1536
Thr Ile Leu Asn Ala Pro Phe Ile Gln Ala Ser Leu Leu Pro
Trp Arg

500

505

510

gga agt gac gag gtc aga aga gac ttg ttg cgt tac aac aac
atg gtg 1584
Gly Ser Asp Glu Val Arg Arg Asp Leu Leu Arg Tyr Asn Asn
Met Val

515

520

525

gcc atg ttg ctt atc acg cgt gat acc acc agt ggt tca gtt
tct gct 1632
Ala Met Leu Leu Ile Thr Arg Asp Thr Thr Ser Gly Ser Val
Ser Ala
530

535

540

gac cca aag aag ccc gac gct ttg att gtc gac tat gag att
aac aag 1680
Asp Pro Lys Lys Pro Asp Ala Leu Ile Val Asp Tyr Glu Ile
Asn Lys
545 550 555
560

ttt gac aag aat gcc atc ttg caa gct ttc ttg atc act tcc
gac atg 1728
Phe Asp Lys Asn Ala Ile Leu Gln Ala Phe Leu Ile Thr Ser
Asp Met

565

570

575

ttg tac att gaa ggt gcc aag aga atc ctc agt cca cag cca
tgg gtg 1776
Leu Tyr Ile Glu Gly Ala Lys Arg Ile Leu Ser Pro Gln Pro
Trp Val

580

585

590

cca atc ttt gag tcg aac aag cca aag gag caa aga acg atc
aag gac 1824
Pro Ile Phe Glu Ser Asn Lys Pro Lys Glu Gln Arg Thr Ile
Lys Asp

595

600

605

aag gac tat gtt gag tgg aga gcc aag gct gct aag ata cct
ttc gac 1872

- 101/269 -

Lys Asp Tyr Val Glu Trp Arg Ala Lys Ala Ala Lys Ile Pro
Phe Asp
610 615 620

acc tac ggt tct gca tat ggg tcc gca cat caa atg tcc acc
tgt cgt 1920
Thr Tyr Gly Ser Ala Tyr Gly Ser Ala His Gln Met Ser Thr
Cys Arg
625 630 635
640

atg tcc gga aag ggt cct aaa tac ggt gct gtt gat act gat
ggg aga 1968
Met Ser Gly Lys Gly Pro Lys Tyr Gly Ala Val Asp Thr Asp
Gly Arg
645 650
655

ttg ttt gaa tgt tcg aat gtc tat gtt gct gat gct agt gtt
ttg cct 2016
Leu Phe Glu Cys Ser Asn Val Tyr Val Ala Asp Ala Ser Val
Leu Pro
660 665 670

act gcc agc ggt gcc aac cca atg ata tcc acc atg acc ttt
gct aga 2064
Thr Ala Ser Gly Ala Asn Pro Met Ile Ser Thr Met Thr Phe
Ala Arg
675 680 685

cag att gcg tta ggt ttg gct gac tcc ttg aag acc aaa ccc
aag ttg 2112
Gln Ile Ala Leu Gly Leu Ala Asp Ser Leu Lys Thr Lys Pro
Lys Leu
690 695 700

tag
2115

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<213> Candida tropicalis

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Met Asn Thr Phe Leu Pro Asp Val Leu Glu Tyr Lys His Val
Asp Thr
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References

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9

100

105

110

$$= y \circ \tau \circ y$$

115

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125

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130

135

140

145

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155

160

Leu Arg Glu Lys Ala Tyr Glu Thr Gln Val Val Asp Pro Phe
 Arg Tyr
 165 170
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Leu Phe Met Glu Lys Pro Lys Phe Asp Gly Ala Glu Leu Tyr
 Leu Pro
 180 185 190

Asp Ile Asp Val Ile Ile Ile Gly Ser Gly Ala Gly Ala Gly
 Val Met
 195 200 205

Ala His Thr Leu Ala Asn Asp Gly Phe Lys Thr Leu Val Leu
 Glu Lys
 210 215 220

Gly Lys Tyr Phe Ser Asn Ser Glu Leu Asn Phe Asn Asp Ala
 Asp Gly
 225 230 235
 240

Val Lys Glu Leu Tyr Gln Gly Lys Gly Ala Leu Ala Thr Thr
 Asn Gln
 245 250
 255

Gln Met Phe Ile Leu Ala Gly Ser Thr Leu Gly Gly Gly Thr
 Thr Val
 260 265 270

Asn Trp Ser Ala Cys Leu Lys Thr Pro Phe Lys Val Arg Lys
 Glu Trp
 275 280 285

Tyr Asp Glu Phe Gly Leu Glu Phe Ala Ala Asp Glu Ala Tyr
 Asp Lys
 290 295 300

Ala Gln Asp Tyr Val Trp Lys Gln Met Gly Ala Ser Thr Asp

Gly Ile
305
320

310

315

Thr His Ser Leu Ala Asn Glu Val Val Val Glu Gly Gly Lys
Lys Leu
325 330
335

Gly Tyr Lys Ser Lys Glu Ile Glu Gln Asn Asn Gly Gly His
Pro Asp
340 345 350

His Pro Cys Gly Phe Cys Tyr Leu Gly Cys Lys Tyr Gly Ile
Lys Gln
355 360 365

Gly Ser Val Asn Asn Trp Phe Arg Asp Ala Ala Ala His Gly
Ser Lys
370 375 380

Phe Met Gln Gln Val Arg Val Val Gln Ile Leu Asn Lys Asn
Gly Val
385 390 395
400

Ala Tyr Gly Ile Leu Cys Glu Asp Val Glu Thr Gly Val Arg
Phe Thr
405 410
415

Ile Ser Gly Pro Lys Lys Phe Val Val Ser Ala Gly Ser Leu
Asn Thr
420 425 430

Pro Thr Val Leu Thr Asn Ser Gly Phe Lys Asn Lys His Ile
Gly Lys
435 440 445

Asn Leu Thr Leu His Pro Val Ser Thr Val Phe Gly Asp Phe
Gly Arg

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Asp	Val	Gln	Ala	Asp	His	Phe	His	Lys	Ser	Ile	Met	Thr	Ser
Leu	Cys												
465						470					475		
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Tyr	Glu	Val	Ala	Asp	Leu	Asp	Gly	Lys	Gly	His	Gly	Cys	Arg
Ile	Glu												
					485					490			
495													
Thr	Ile	Leu	Asn	Ala	Pro	Phe	Ile	Gln	Ala	Ser	Leu	Leu	Pro
Trp	Arg												
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Gly	Ser	Asp	Glu	Val	Arg	Arg	Asp	Leu	Leu	Arg	Tyr	Asn	Asn
Met	Val												
		515					520					525	
Ala	Met	Leu	Leu	Ile	Thr	Arg	Asp	Thr	Thr	Ser	Gly	Ser	Val
Ser	Ala												
	530					535					540		
Asp	Pro	Lys	Lys	Pro	Asp	Ala	Leu	Ile	Val	Asp	Tyr	Glu	Ile
Asn	Lys												
545					550					555			
560													
Phe	Asp	Lys	Asn	Ala	Ile	Leu	Gln	Ala	Phe	Leu	Ile	Thr	Ser
Asp	Met												
				565					570				
575													
Leu	Tyr	Ile	Glu	Gly	Ala	Lys	Arg	Ile	Leu	Ser	Pro	Gln	Pro
Trp	Val												
			580					585				590	
Pro	Ile	Phe	Glu	Ser	Asn	Lys	Pro	Lys	Glu	Gln	Arg	Thr	Ile
Lys	Asp												
		595				600					605		

Lys Asp Tyr Val Glu Trp Arg Ala Lys Ala Ala Lys Ile Pro
Phe Asp
610 615 620

Thr Tyr Gly Ser Ala Tyr Gly Ser Ala His Gln Met Ser Thr
Cys Arg
625 630 635
640

Met Ser Gly Lys Gly Pro Lys Tyr Gly Ala Val Asp Thr Asp
Gly Arg
645 650
655

Leu Phe Glu Cys Ser Asn Val Tyr Val Ala Asp Ala Ser Val
Leu Pro
660 665 670

Thr Ala Ser Gly Ala Asn Pro Met Ile Ser Thr Met Thr Phe
Ala Arg
675 680 685

Gln Ile Ala Leu Gly Leu Ala Asp Ser Leu Lys Thr Lys Pro
Lys Leu
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gat acc 48
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Asp Thr
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15

ctt ttg tta tta tgt gac ggg atc atc cac gaa acc aca gtc
gac cag 96
Leu Leu Leu Leu Cys Asp Gly Ile Ile His Glu Thr Thr Val
Asp Gln

20

25

30

atc agg gac gcc att gct ccc gac ttc cct gaa gac cag tac
gag gag 144
Ile Arg Asp Ala Ile Ala Pro Asp Phe Pro Glu Asp Gln Tyr
Glu Glu

35

40

45

tat ctc aag acc ttc acc aag cca tct gag acc cct ggg ttc
aga gaa 192
Tyr Leu Lys Thr Phe Thr Lys Pro Ser Glu Thr Pro Gly Phe
Arg Glu

50

55

60

gcc gtc tac gac acg atc aac agc acc cca acc gag gct gtg
cac atg 240
Ala Val Tyr Asp Thr Ile Asn Ser Thr Pro Thr Glu Ala Val
His Met

65

70

75

80

tgt att gta ttg acc acc gca ttg gac tcg aga atc ttg gcc
ccc acg 288
Cys Ile Val Leu Thr Thr Ala Leu Asp Ser Arg Ile Leu Ala
Pro Thr

85

90

95

ttg acc aac tcg ttg acg cct atc aag gat atg acc ttg aaa
gag cgt 336
Leu Thr Asn Ser Leu Thr Pro Ile Lys Asp Met Thr Leu Lys
Glu Arg

100

105

110

gaa caa ttg ttg gct gcc tgg cgt gat tcc ccg atc gcg gcc
aag aga 384
Glu Gln Leu Leu Ala Ala Trp Arg Asp Ser Pro Ile Ala Ala
Lys Arg

115

120

125

aga ttg ttc aga ttg att tcc tca ctt acc ttg acg acc ttt
acg aga 432
Arg Leu Phe Arg Leu Ile Ser Ser Leu Thr Leu Thr Thr Phe
Thr Arg

130	135	140
ttg gcc agc gac ttg cac ttg aga gcc atc cac tac cct ggc		
aga gac 480		
Leu Ala Ser Asp Leu His Leu Arg Ala Ile His Tyr Pro Gly		
Arg Asp		
145	150	155
160		
ttg cgt gaa aag gca tat gaa acc cag gtg gtt gac cct ttc		
agg tac 528		
Leu Arg Glu Lys Ala Tyr Glu Thr Gln Val Val Asp Pro Phe		
Arg Tyr		
	165	170
175		
ctg ttt atg gaa aaa cca aag ttt gac ggc acc gag ttg tac		
ttg cca 576		
Leu Phe Met Glu Lys Pro Lys Phe Asp Gly Thr Glu Leu Tyr		
Leu Pro		
	180	185
		190
gat atc gac gtc atc atc att gga tcc ggt gcc ggt gct ggt		
gtc atg 624		
Asp Ile Asp Val Ile Ile Ile Gly Ser Gly Ala Gly Ala Gly		
Val Met		
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gcc cac act tta gcc aac gac ggg tac aag acc ttg gtt ttg		
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Ala His Thr Leu Ala Asn Asp Gly Tyr Lys Thr Leu Val Leu		
Glu Lys		
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gga aag tat ttc agc aac tcc gag ttg aac ttt aat gat gcc		
gat ggt 720		
Gly Lys Tyr Phe Ser Asn Ser Glu Leu Asn Phe Asn Asp Ala		
Asp Gly		
225	230	235
240		
atg aaa gag ttg tac caa ggt aaa tgt gcg ttg acc acc acg		
aac cag 768		
Met Lys Glu Leu Tyr Gln Gly Lys Cys Ala Leu Thr Thr Thr		
Asn Gln		
	245	250
255		
cag atg ttt att ctt gcc ggt tcc act ttg ggc ggt ggt acc		
act gtt 816		

Gln Thr	Met Val	Phe	Ile	Leu	Ala	Gly	Ser	Thr	Leu	Gly	Gly	Gly	Thr
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aac gag	tgg tgg	tct	gct	tgt	ctt	aaa	aca	cca	ttt	aaa	gtg	cgt	aag
Asn Glu	Trp Trp	Ser	Ala	Cys	Leu	Lys	Thr	Pro	Phe	Lys	Val	Arg	Lys
			275			280						285	
tac gac	gac aaa	gag	ttt	ggc	ctt	gaa	ttt	gct	gcc	gac	gaa	gcc	tac
Tyr Asp	Asp Lys	Glu	Phe	Gly	Leu	Glu	Phe	Ala	Ala	Asp	Glu	Ala	Tyr
			290			295						300	
gca gga	caa atc	gac	tat	gtt	tgg	aaa	caa	atg	ggc	gct	tct	acc	gaa
Ala Gly	Gln Ile	Asp	Tyr	Val	Trp	Lys	Gln	Met	Gly	Ala	Ser	Thr	Glu
			305			310						315	
			320										
act aag	cac ttg	tct	ttg	gcg	aac	gcg	gtt	gtg	gtt	gaa	gga	ggc	aag
Thr Lys	His Leu	Ser	Leu	Ala	Asn	Ala	Val	Val	Val	Glu	Gly	Gly	Lys
			325			330							
			335										
ggc cct	tac gac	aag	agc	aag	gaa	atc	gag	cag	aac	aat	ggc	ggc	cat
Gly Pro	Tyr Asp	Lys	Ser	Lys	Glu	Ile	Glu	Gln	Asn	Asn	Gly	Gly	His
			340			345						350	
cac aag	ccc cag	tgt	ggc	ttc	tgt	tac	ttg	ggc	tgt	aag	tac	ggc	att
His Lys	Pro Gln	Cys	Gly	Phe	Cys	Tyr	Leu	Gly	Cys	Lys	Tyr	Gly	Ile
			355			360						365	
ggc tcc	tct aag	gtg	aat	aac	tgg	ttt	aga	gac	gca	gct	gcc	cac	ggc
Gly Ser	Ser Lys	Val	Asn	Asn	Trp	Phe	Arg	Asp	Ala	Ala	Ala	His	Gly
			370			375						380	
ttc ggc	atg gtc	caa	caa	gtc	aga	gtt	gtg	caa	atc	ctc	cac	aat	aaa
			1200										

Phe Met Gln Gln Val Arg Val Val Gln Ile Leu His Asn Lys
Gly Val
385 390 395
400

gct tat ggc atc ttg tgt gag gat gtc gag acc gga gtc aaa
ttc act 1248
Ala Tyr Gly Ile Leu Cys Glu Asp Val Glu Thr Gly Val Lys
Phe Thr
405 410
415

atc agt ggc ccc aaa aag ttt gtt gtt tct gca ggt tct ttg
aac acg 1296
Ile Ser Gly Pro Lys Lys Phe Val Val Ser Ala Gly Ser Leu
Asn Thr
420 425 430

cca acg gtg ttg acc aac tcc gga ttc aag aac aaa cac atc
ggt aag 1344
Pro Thr Val Leu Thr Asn Ser Gly Phe Lys Asn Lys His Ile
Gly Lys
435 440 445

aac ttg acg ttg cac cca gtt tcg acc gtg ttt ggt gac ttt
ggc aga 1392
Asn Leu Thr Leu His Pro Val Ser Thr Val Phe Gly Asp Phe
Gly Arg
450 455 460

gac gtg caa gcc gac cat ttc cac aaa tct att atg act tcg
ctc tgt 1440
Asp Val Gln Ala Asp His Phe His Lys Ser Ile Met Thr Ser
Leu Cys
465 470 475
480

tac gaa gtc gct gac ttg gac ggc aag ggc cac gga tgc aga
atc gag 1488
Tyr Glu Val Ala Asp Leu Asp Gly Lys Gly His Gly Cys Arg
Ile Glu
485 490
495

acc atc ttg aac gct cca ttc atc caa gct tct ttg ttg cca
tgg aga 1536
Thr Ile Leu Asn Ala Pro Phe Ile Gln Ala Ser Leu Leu Pro
Trp Arg
500 505 510

gga atg Gly Met	agc gtg Ser Val	gac Asp	gag 1584 Glu	gtc Val	aga Arg	aga Arg	gac Asp	ttg Leu	ttg Leu	cgt Arg	tac Tyr	aac Asn	aac Asn
515						520						525	
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530						535						540	
gac aac Asp Asn 545 560	cca aag Pro Lys	aag Lys	aag 1680 Lys	ccc Pro	gac Asp	gct Ala	ttg Leu	att Ile	gtc Val	gac Asp	tat Tyr	gac Asp	atc Ile
			550						555				
ttt gac Phe Asp 575	gac atg Asp Met	aag Lys	aat 1728 Asn	gcc Ala	atc Ile	ttg Leu	caa Gln	gct Ala	ttc Phe	ttg Leu	atc Ile	acc Thr	tcc Ser
			565						570				
ttg tgg Leu Trp	tac gtg Tyr Val	atc Ile	gaa 1776 Glu	ggc Gly	gcc Ala	aag Lys	aga Arg	atc Ile	ctc Leu	agt Ser	cca Pro	cag Gln	gca Ala
			580						585			590	
cca aag Pro Lys	atc gac Ile Asp	ttt Phe	gag 1824 Glu	tcg Ser	aac Asn	aag Lys	cca Pro	aag Lys	gag Glu	caa Gln	aga Arg	aca Thr	atc Ile
595						600						605	
aag ttc Lys Phe	gac gac Asp Asp	tat Tyr	gtc 1872 Val	gaa Glu	tgg Trp	aga Arg	gcc Ala	aag Lys	gct Ala	gcc Ala	aag Lys	ata Ile	cct Pro
610						615						620	
acc tgt Thr Cys 625 640	tac cgt Tyr Arg	ggt Gly	tct 1920 Ser	gcc Ala	tat Tyr	ggg Gly	tcc Ser	gca Ala	cat His	caa Gln	atg Met	tcc Ser	acc Thr
			630						635				

atg tcc gga aag ggt cct aaa tac ggc gcc gtt gat acc gat
 ggt aga 1968
 Met Ser Gly Lys Gly Pro Lys Tyr Gly Ala Val Asp Thr Asp
 Gly Arg

645

650

655

ttg ttt gaa tgt tcg aat gtc tat gtt gct gat gct agt gtt
 ttg cct 2016
 Leu Phe Glu Cys Ser Asn Val Tyr Val Ala Asp Ala Ser Val
 Leu Pro

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665

670

act gcc agc ggt gcc aac cca atg atc tcc acc atg acg ttt
 gct aga 2064
 Thr Ala Ser Gly Ala Asn Pro Met Ile Ser Thr Met Thr Phe
 Ala Arg

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680

685

cag att gcg tta ggt ttg gct gac tct ttg aag acc aaa ccc
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 Lys Leu

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tag
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 <213> Candida tropicalis

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 Asp Thr
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 Asp Gln
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Ile Arg Asp Ala Ile Ala Pro Asp Phe Pro Glu Asp Gln Tyr
 Glu Glu

- 113/269 -

35

40

45

Tyr Leu Lys Thr Phe Thr Lys Pro Ser Glu Thr Pro Gly Phe
Arg Glu
50 55 60

Ala Val Tyr Asp Thr Ile Asn Ser Thr Pro Thr Glu Ala Val
His Met
65 70 75
80

Cys Ile Val Leu Thr Thr Ala Leu Asp Ser Arg Ile Leu Ala
Pro Thr
85 90
95

Leu Thr Asn Ser Leu Thr Pro Ile Lys Asp Met Thr Leu Lys
Glu Arg
100 105 110

Glu Gln Leu Leu Ala Ala Trp Arg Asp Ser Pro Ile Ala Ala
Lys Arg
115 120 125

Arg Leu Phe Arg Leu Ile Ser Ser Leu Thr Leu Thr Thr Phe
Thr Arg
130 135 140

Leu Ala Ser Asp Leu His Leu Arg Ala Ile His Tyr Pro Gly
Arg Asp
145 150 155
160

Leu Arg Glu Lys Ala Tyr Glu Thr Gln Val Val Asp Pro Phe
Arg Tyr
165 170
175

Leu Phe Met Glu Lys Pro Lys Phe Asp Gly Thr Glu Leu Tyr
Leu Pro
180 185 190

Asp Ile Asp Val Ile Ile Ile Gly Ser Gly Ala Gly Ala Gly
Val Met
195 200 205

Ala His Thr Leu Ala Asn Asp Gly Tyr Lys Thr Leu Val Leu
Glu Lys
210 215 220

Gly Lys Tyr Phe Ser Asn Ser Glu Leu Asn Phe Asn Asp Ala
Asp Gly
225 230 235
240

Met Lys Glu Leu Tyr Gln Gly Lys Cys Ala Leu Thr Thr Thr
Asn Gln
245 250
255

Gln Met Phe Ile Leu Ala Gly Ser Thr Leu Gly Gly Gly Thr
Thr Val
260 265 270

Asn Trp Ser Ala Cys Leu Lys Thr Pro Phe Lys Val Arg Lys
Glu Trp
275 280 285

Tyr Asp Glu Phe Gly Leu Glu Phe Ala Ala Asp Glu Ala Tyr
Asp Lys
290 295 300

Ala Gln Asp Tyr Val Trp Lys Gln Met Gly Ala Ser Thr Glu
Gly Ile
305 310 315
320

Thr His Ser Leu Ala Asn Ala Val Val Val Glu Gly Gly Lys
Lys Leu
325 330
335

Gly Tyr Lys Ser Lys Glu Ile Glu Gln Asn Asn Gly Gly His
Pro Asp
340 345 350

His Pro Cys Gly Phe Cys Tyr Leu Gly Cys Lys Tyr Gly Ile
Lys Gln
355 360 365

Gly Ser Val Asn Asn Trp Phe Arg Asp Ala Ala Ala His Gly
Ser Lys
370 375 380

Phe Met Gln Gln Val Arg Val Val Gln Ile Leu His Asn Lys
Gly Val
385 390 395
400

Ala Tyr Gly Ile Leu Cys Glu Asp Val Glu Thr Gly Val Lys
Phe Thr
405 410
415

Ile Ser Gly Pro Lys Lys Phe Val Val Ser Ala Gly Ser Leu
Asn Thr
420 425 430

Pro Thr Val Leu Thr Asn Ser Gly Phe Lys Asn Lys His Ile
Gly Lys
435 440 445

Asn Leu Thr Leu His Pro Val Ser Thr Val Phe Gly Asp Phe
Gly Arg
450 455 460

Asp Val Gln Ala Asp His Phe His Lys Ser Ile Met Thr Ser
Leu Cys
465 470 475
480

Tyr Glu Val Ala Asp Leu Asp Gly Lys Gly His Gly Cys Arg

Ile	Glu													
				485						490				
495														
Thr	Ile	Leu	Asn	Ala	Pro	Phe	Ile	Gln	Ala	Ser	Leu	Leu	Pro	
Trp	Arg													
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Gly	Ser	Asp	Glu	Val	Arg	Arg	Asp	Leu	Leu	Arg	Tyr	Asn	Asn	
Met	Val													
		515					520					525		
Ala	Met	Leu	Leu	Ile	Thr	Arg	Asp	Thr	Thr	Ser	Gly	Ser	Val	
Ser	Ala													
	530					535					540			
Asp	Pro	Lys	Lys	Pro	Asp	Ala	Leu	Ile	Val	Asp	Tyr	Asp	Ile	
Asn	Lys													
545					550					555				
560														
Phe	Asp	Lys	Asn	Ala	Ile	Leu	Gln	Ala	Phe	Leu	Ile	Thr	Ser	
Asp	Met													
				565					570					
575														
Leu	Tyr	Ile	Glu	Gly	Ala	Lys	Arg	Ile	Leu	Ser	Pro	Gln	Ala	
Trp	Val													
			580					585					590	
Pro	Ile	Phe	Glu	Ser	Asn	Lys	Pro	Lys	Glu	Gln	Arg	Thr	Ile	
Lys	Asp													
		595					600					605		
Lys	Asp	Tyr	Val	Glu	Trp	Arg	Ala	Lys	Ala	Ala	Lys	Ile	Pro	
Phe	Asp													
	610					615					620			
Thr	Tyr	Gly	Ser	Ala	Tyr	Gly	Ser	Ala	His	Gln	Met	Ser	Thr	
Cys	Arg													
625					630					635				

640

Met Ser Gly Lys Gly Pro Lys Tyr Gly Ala Val Asp Thr Asp
Gly Arg

645

650

655

Leu Phe Glu Cys Ser Asn Val Tyr Val Ala Asp Ala Ser Val
Leu Pro

660

665

670

Thr Ala Ser Gly Ala Asn Pro Met Ile Ser Thr Met Thr Phe
Ala Arg

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Gln Ile Ala Leu Gly Leu Ala Asp Ser Leu Lys Thr Lys Pro
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690

695

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Phe Ser

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10

15

tat ttg cta tat gta att ctc gat ata gta cta cca cca ttc
aat ttt 96

Tyr Leu Leu Tyr Val Ile Leu Asp Ile Val Leu Pro Pro Phe
Asn Phe

20

25

30

ccc aaa aat atc cca aca atc cca ttc tat gtt tcc ttc tta
ggg gct 144

Pro	Lys	Asn	Ile	Pro	Thr	Ile	Pro	Phe	Tyr	Val	Ser	Phe	Leu
Gly	Ala												
		35				40						45	

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aga	gag		192										
Tyr	Thr	Asn	Leu	Asp	Gln	Arg	Asp	Ile	Tyr	Asn	Leu	Tyr	Leu
Arg	Glu					55					60		
		50											

aag	ttg	gaa	aag	tac	ggg	gca	gta	aag	ata	tat	ttt	gct	tca
aga	tgg		240										
Lys	Leu	Glu	Lys	Tyr	Gly	Ala	Val	Lys	Ile	Tyr	Phe	Ala	Ser
Arg	Trp					70				75			
65													
80													

aac	ata	ctc	att	act	agg	cca	gaa	tat	ctt	ctt	gaa	atg	ttt
aga	aat		288										
Asn	Ile	Leu	Ile	Thr	Arg	Pro	Glu	Tyr	Leu	Leu	Glu	Met	Phe
Arg	Asn												
			85						90				
95													

gaa	gat	gtg	tac	tca	aaa	cgg	gga	aac	cac	cta	aaa	atc	cct
ggt	tca		336										
Glu	Asp	Val	Tyr	Ser	Lys	Arg	Gly	Asn	His	Leu	Lys	Ile	Pro
Gly	Ser												
			100					105				110	

gtg	atg	gct	aca	tac	act	ggt	gat	aat	atc	att	agt	gct	cat
gga	gaa		384										
Val	Met	Ala	Thr	Tyr	Thr	Gly	Asp	Asn	Ile	Ile	Ser	Ala	His
Gly	Glu												
		115				120					125		

tta	tgg	aaa	tta	tat	cga	gaa	ggt	att	gcc	aaa	agt	att	caa
ttt	ccc		432										
Leu	Trp	Lys	Leu	Tyr	Arg	Glu	Val	Ile	Ala	Lys	Ser	Ile	Gln
Phe	Pro												
		130				135					140		

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att	att		480										
Asp	Phe	Glu	Pro	Ile	Thr	Lys	Asn	Thr	Lys	Ser	Leu	Leu	Glu
Ile	Ile												
145					150					155			
160													

gat	ggt	atg	att	gac	agt	gat	aaa	aat	cat	gca	att	att	cca
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

atc	aca			528									
Asp	Gly	Met	Ile	Asp	Ser	Asp	Lys	Asn	His	Ala	Ile	Ile	Pro
Ile	Thr												
				165					170				
175													
gat	tta	ttt	caa	aaa	tat	tca	tta	gca	aac	gtt	aca	gaa	tct
ata	ctt		576										
Asp	Leu	Phe	Gln	Lys	Tyr	Ser	Leu	Ala	Asn	Val	Thr	Glu	Ser
Ile	Leu												
			180					185					190
gga	gta	aat	ttt	aag	gtt	ctt	gaa	ggc	gat	caa	tca	atc	atg
cat	caa		624										
Gly	Val	Asn	Phe	Lys	Val	Leu	Glu	Gly	Asp	Gln	Ser	Ile	Met
His	Gln												
		195					200					205	
aaa	ata	aag	tac	gtc	aag	ctg	caa	ata	ttc	aaa	cct	ttt	ttc
ttg	aac		672										
Lys	Ile	Lys	Tyr	Val	Lys	Leu	Gln	Ile	Phe	Lys	Pro	Phe	Phe
Leu	Asn												
	210					215					220		
ttt	cct	tat	ttt	gat	agc	ttt	cct	att	cca	agt	agg	tta	caa
gca	aga		720										
Phe	Pro	Tyr	Phe	Asp	Ser	Phe	Pro	Ile	Pro	Ser	Arg	Leu	Gln
Ala	Arg												
225					230					235			
240													
aag	gaa	gtt	att	aat	ttt	agg	aat	tgg	tat	ggt	caa	agt	att
att	gac		768										
Lys	Glu	Val	Ile	Asn	Phe	Arg	Asn	Trp	Tyr	Gly	Gln	Ser	Ile
Ile	Asp												
			245							250			
255													
aag	cat	gat	cca	caa	ctt	cct	aat	agt	gca	gct	aca	aaa	tta
gtt	gat		816										
Lys	His	Asp	Pro	Gln	Leu	Pro	Asn	Ser	Ala	Ala	Thr	Lys	Leu
Val	Asp												
			260					265					270
ggc	ttg	atg	caa	gaa	aaa	ctc	act	gaa	aaa	caa	ttt	ttg	gat
aat	gcc		864										
Gly	Leu	Met	Gln	Glu	Lys	Leu	Thr	Glu	Lys	Gln	Phe	Leu	Asp
Asn	Ala												
		275					280					285	

- 120/269 -

att att gtg atg att gct gga cat gaa aat cca ctt ttg tta
atg tta 912
Ile Ile Val Met Ile Ala Gly His Glu Asn Pro Leu Leu Leu
Met Leu
290 295 300

tcg ttg atg ttt gtt gct gca aaa tat cca aaa gtt cag gag
gcc ata 960
Ser Leu Met Phe Val Ala Ala Lys Tyr Pro Lys Val Gln Glu
Ala Ile
305 310 315
320

cgt tca gaa ata gat cca aca aaa cct tat cta cac tct gtt
att tat 1008
Arg Ser Glu Ile Asp Pro Thr Lys Pro Tyr Leu His Ser Val
Ile Tyr
325 330
335

gaa act tta aga atg tat cca cca ttg gga tta atc att aat
cgt tat 1056
Glu Thr Leu Arg Met Tyr Pro Pro Leu Gly Leu Ile Ile Asn
Arg Tyr
340 345 350

acc acc aga cct act aaa cta ggc aac ata gta att ccc aaa
ggg gtt 1104
Thr Thr Arg Pro Thr Lys Leu Gly Asn Ile Val Ile Pro Lys
Gly Val
355 360 365

tac tgt ggc tat aat aat ttt ggt acg ggt aga gac aga aat
gtt tgg 1152
Tyr Cys Gly Tyr Asn Asn Phe Gly Thr Gly Arg Asp Arg Asn
Val Trp
370 375 380

gga cca gac tcg gat gag ttt aaa cca gag aga tgg gga agg
gat aat 1200
Gly Pro Asp Ser Asp Glu Phe Lys Pro Glu Arg Trp Gly Arg
Asp Asn
385 390 395
400

att gaa gaa ata aat cgc aat tat gct aat gcc aaa aga tca
gct gaa 1248
Ile Glu Glu Ile Asn Arg Asn Tyr Ala Asn Ala Lys Arg Ser
Ala Glu
405 410

415

tta cct gcg ttt cat ggc aga aag aga gct tgt tta gga gaa
aag tat 1296
Leu Pro Ala Phe His Gly Arg Lys Arg Ala Cys Leu Gly Glu
Lys Tyr

420

425

430

gcc tta tat gaa gtt aaa gaa ttg cta act agt att tta gga
cat tac 1344
Ala Leu Tyr Glu Val Lys Glu Leu Leu Thr Ser Ile Leu Gly
His Tyr

435

440

445

aaa gtt act tta gat gca agt tgg aaa gag aaa ata acc cct
gct gga 1392
Lys Val Thr Leu Asp Ala Ser Trp Lys Glu Lys Ile Thr Pro
Ala Gly

450

455

460

cct att agt cca ttt ggt ttg aag gtg aaa ttt gaa aag ctt
att gtt 1440
Pro Ile Ser Pro Phe Gly Leu Lys Val Lys Phe Glu Lys Leu
Ile Val

465

470

475

480

gca taa
1446
Ala

<210> 30
<211> 481
<212> PRT
<213> Candida tropicalis

<400> 30

Met Ile Met Phe Asp Ile Val Lys Tyr Thr Leu Ile Gly Leu
Phe Ser

1

5

10

15

Tyr Leu Leu Tyr Val Ile Leu Asp Ile Val Leu Pro Pro Phe
Asn Phe

20

25

30

- 122/269 -

Pro Lys Asn Ile Pro Thr Ile Pro Phe Tyr Val Ser Phe Leu
Gly Ala
35 40 45

Tyr Thr Asn Leu Asp Gln Arg Asp Ile Tyr Asn Leu Tyr Leu
Arg Glu
50 55 60

Lys Leu Glu Lys Tyr Gly Ala Val Lys Ile Tyr Phe Ala Ser
Arg Trp
65 70 75
80

Asn Ile Leu Ile Thr Arg Pro Glu Tyr Leu Leu Glu Met Phe
Arg Asn
85 90
95

Glu Asp Val Tyr Ser Lys Arg Gly Asn His Leu Lys Ile Pro
Gly Ser
100 105 110

Val Met Ala Thr Tyr Thr Gly Asp Asn Ile Ile Ser Ala His
Gly Glu
115 120 125

Leu Trp Lys Leu Tyr Arg Glu Val Ile Ala Lys Ser Ile Gln
Phe Pro
130 135 140

Asp Phe Glu Pro Ile Thr Lys Asn Thr Lys Ser Leu Leu Glu
Ile Ile
145 150 155
160

Asp Gly Met Ile Asp Ser Asp Lys Asn His Ala Ile Ile Pro
Ile Thr
165 170
175

- 123/269 -

Asp Leu Phe Gln Lys Tyr Ser Leu Ala Asn Val Thr Glu Ser
Ile Leu
180 185 190

Gly Val Asn Phe Lys Val Leu Glu Gly Asp Gln Ser Ile Met
His Gln
195 200 205

Lys Ile Lys Tyr Val Lys Leu Gln Ile Phe Lys Pro Phe Phe
Leu Asn
210 215 220

Phe Pro Tyr Phe Asp Ser Phe Pro Ile Pro Ser Arg Leu Gln
Ala Arg
225 230 235
240

Lys Glu Val Ile Asn Phe Arg Asn Trp Tyr Gly Gln Ser Ile
Ile Asp
245 250
255

Lys His Asp Pro Gln Leu Pro Asn Ser Ala Ala Thr Lys Leu
Val Asp
260 265 270

Gly Leu Met Gln Glu Lys Leu Thr Glu Lys Gln Phe Leu Asp
Asn Ala
275 280 285

Ile Ile Val Met Ile Ala Gly His Glu Asn Pro Leu Leu Leu
Met Leu
290 295 300

Ser Leu Met Phe Val Ala Ala Lys Tyr Pro Lys Val Gln Glu
Ala Ile
305 310 315
320

Arg Ser Glu Ile Asp Pro Thr Lys Pro Tyr Leu His Ser Val
Ile Tyr

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

Ala

<210> 31
<211> 1623
<212> DNA
<213> *Candida tropicalis*

<220>
<221> CDS
<222> (1)..(1623)

<400> 31
atg tcg tcg tct cca tct att gct caa gaa ttt ctc gca acc
att act 48
Met Ser Ser Ser Pro Ser Ile Ala Gln Glu Phe Leu Ala Thr
Ile Thr
1 5 10
15

cca tat gtt gag tat tgt caa gag aat tat acc aaa tgg tac
tac ttc 96
Pro Tyr Val Glu Tyr Cys Gln Glu Asn Tyr Thr Lys Trp Tyr
Tyr Phe
20 25 30

att cca ttg gtg att ctt tcg ttg aat ctt atc tcc atg ctt
cat aca 144
Ile Pro Leu Val Ile Leu Ser Leu Asn Leu Ile Ser Met Leu
His Thr
35 40 45

aag tat ttg gaa cgt aaa ttt aag gct aaa ccg ctt gct gtc
tat gtt 192
Lys Tyr Leu Glu Arg Lys Phe Lys Ala Lys Pro Leu Ala Val
Tyr Val
50 55 60

caa gat tat acc ttt ggt ctt att act cca ctt gtt ttg atc
tac tac 240
Gln Asp Tyr Thr Phe Gly Leu Ile Thr Pro Leu Val Leu Ile
Tyr Tyr
65 70 75
80

aag tct aaa ggt acc gtg atg caa ttt gcc tgt gat tta tgg

gac aag 288
Lys Ser Lys Gly Thr Val Met Gln Phe Ala Cys Asp Leu Trp
Asp Lys
85 90
95
aaa ctc att gtc agt gat cca aag gca aag act att ggt ctt
aag att 336
Lys Leu Ile Val Ser Asp Pro Lys Ala Lys Thr Ile Gly Leu
Lys Ile
100 105 110
tta ggt att cca ttg att gaa act aaa gac cca gag aat gtc
aag gct 384
Leu Gly Ile Pro Leu Ile Glu Thr Lys Asp Pro Glu Asn Val
Lys Ala
115 120 125
att tta gcc acc cag ttt aat gat ttt tct ttg gga act aga
cat gat 432
Ile Leu Ala Thr Gln Phe Asn Asp Phe Ser Leu Gly Thr Arg
His Asp
130 135 140
ttc ttg tat tca ttg tta gga gat ggt att ttc act tta gat
ggt gct 480
Phe Leu Tyr Ser Leu Leu Gly Asp Gly Ile Phe Thr Leu Asp
Gly Ala
145 150 155
160
ggc tgg aaa cac agc aga acc atg ttg aga cca caa ttc gct
aga gag 528
Gly Trp Lys His Ser Arg Thr Met Leu Arg Pro Gln Phe Ala
Arg Glu
165 170
175
caa gtt tcg cat gta aag ttg ttg gaa ccc cat atg caa gtt
tta ttt 576
Gln Val Ser His Val Lys Leu Leu Glu Pro His Met Gln Val
Leu Phe
180 185 190
aaa cac att aga aaa cat cat ggc caa act ttt gat atc caa
gaa ttg 624
Lys His Ile Arg Lys His His Gly Gln Thr Phe Asp Ile Gln
Glu Leu
195 200 205

- 127/269 -

ttt ttc aga tta act gtt gat tcg gct act gag ttt ttg ttt
ggt gaa 672
Phe Phe Arg Leu Thr Val Asp Ser Ala Thr Glu Phe Leu Phe
Gly Glu
210 215 220

tct gct gaa tct tta aga gac gag tct gtc ggt tta act cca
aca acc 720
Ser Ala Glu Ser Leu Arg Asp Glu Ser Val Gly Leu Thr Pro
Thr Thr
225 230 235
240

aaa gat ttt gat ggt aga aat gag ttt gcc gat gcg ttc aac
tat tct 768
Lys Asp Phe Asp Gly Arg Asn Glu Phe Ala Asp Ala Phe Asn
Tyr Ser
245 250
255

caa act tac caa gcg tac aga ttc ttg ttg caa caa atg tat
tgg att 816
Gln Thr Tyr Gln Ala Tyr Arg Phe Leu Leu Gln Gln Met Tyr
Trp Ile
260 265 270

ttg aat ggt tct gaa ttt aga aaa tct att gct att gtc cac
aag ttt 864
Leu Asn Gly Ser Glu Phe Arg Lys Ser Ile Ala Ile Val His
Lys Phe
275 280 285

gct gac cac tat gtt caa aag gca ttg gaa tta act gat gaa
gat ttg 912
Ala Asp His Tyr Val Gln Lys Ala Leu Glu Leu Thr Asp Glu
Asp Leu
290 295 300

gaa aag aaa gaa ggc tat gta ttt tta ttc gag tta gcc aaa
caa acc 960
Glu Lys Lys Glu Gly Tyr Val Phe Leu Phe Glu Leu Ala Lys
Gln Thr
305 310 315
320

aga gat cca aag gtt ttg aga gat caa ttg tta aat atc ttg
gtt gct 1008
Arg Asp Pro Lys Val Leu Arg Asp Gln Leu Leu Asn Ile Leu
Val Ala
325 330

335

ggt aga gat acc aca gct ggc ttg ttg tcg ttt ctt ttc ttt
gaa ttg 1056
Gly Arg Asp Thr Thr Ala Gly Leu Leu Ser Phe Leu Phe Phe
Glu Leu

340

345

350

tct aga aac cca gaa ata ttt gca aaa ttg aga gaa gaa atc
gaa aac 1104
Ser Arg Asn Pro Glu Ile Phe Ala Lys Leu Arg Glu Glu Ile
Glu Asn

355

360

365

aag ttt ggt ctt gga caa gat gct cgt gtt gaa gag att tct
ttt gaa 1152
Lys Phe Gly Leu Gly Gln Asp Ala Arg Val Glu Glu Ile Ser
Phe Glu

370

375

380

aca ttg aaa tct tgt gaa tac ttg aag gct gtt atc aat gaa
act ttg 1200
Thr Leu Lys Ser Cys Glu Tyr Leu Lys Ala Val Ile Asn Glu
Thr Leu

385

390

395

400

aga att tat cct tcc gtc cca cat aat ttt aga gtt gct act
aga aac 1248
Arg Ile Tyr Pro Ser Val Pro His Asn Phe Arg Val Ala Thr
Arg Asn

405

410

415

aca act tta cca aga ggt ggt ggt gaa ggt ggt tta tcc cca
att gct 1296
Thr Thr Leu Pro Arg Gly Gly Gly Glu Gly Gly Leu Ser Pro
Ile Ala

420

425

430

att aag aag ggc caa gtt gtt atg tac acg att ctt gct act
cac aga 1344
Ile Lys Lys Gly Gln Val Val Met Tyr Thr Ile Leu Ala Thr
His Arg

435

440

445

gat aaa gac att tat ggt gaa gat gct tat gtt ttc agg cca
gaa aga 1392
Asp Lys Asp Ile Tyr Gly Glu Asp Ala Tyr Val Phe Arg Pro
Glu Arg

- 129/269 -

450	455	460
tgg ttt gaa cct gaa acc aga aaa ttg ggc tgg gca tat gtt		
cca ttc	1440	
Trp Phe Glu Pro Glu Thr Arg Lys Leu Gly Trp Ala Tyr Val		
Pro Phe		
465	470	475
480		
aat ggc ggt cca aga att tgt ttg ggt caa cag ttt gct tta		
act gaa	1488	
Asn Gly Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe Ala Leu		
Thr Glu		
	485	490
495		
gca tca tat gtc act gtt aga ttg ctt caa gaa ttt ggt aac		
ttg aaa	1536	
Ala Ser Tyr Val Thr Val Arg Leu Leu Gln Glu Phe Gly Asn		
Leu Lys		
	500	505
		510
caa gat cca aat act gaa tat cca cca aaa tta caa aac aca		
ttg act	1584	
Gln Asp Pro Asn Thr Glu Tyr Pro Pro Lys Leu Gln Asn Thr		
Leu Thr		
	515	520
		525
ttg tct ctt ttt gaa ggt gct gaa gta caa atg tat taa		
1623		
Leu Ser Leu Phe Glu Gly Ala Glu Val Gln Met Tyr		
530	535	540

<210> 32
<211> 540
<212> PRT
<213> Candida tropicalis

<400> 32

Met Ser Ser Ser Pro Ser Ile Ala Gln Glu Phe Leu Ala Thr		
Ile Thr		
1	5	10
15		

Pro Tyr Val Glu Tyr Cys Gln Glu Asn Tyr Thr Lys Trp Tyr		
Tyr Phe		
	20	25
		30

Ile Pro Leu Val Ile Leu Ser Leu Asn Leu Ile Ser Met Leu
His Thr
35 40 45

Lys Tyr Leu Glu Arg Lys Phe Lys Ala Lys Pro Leu Ala Val
Tyr Val
50 55 60

Gln Asp Tyr Thr Phe Gly Leu Ile Thr Pro Leu Val Leu Ile
Tyr Tyr
65 70 75
80

Lys Ser Lys Gly Thr Val Met Gln Phe Ala Cys Asp Leu Trp
Asp Lys
85 90
95

Lys Leu Ile Val Ser Asp Pro Lys Ala Lys Thr Ile Gly Leu
Lys Ile
100 105 110

Leu Gly Ile Pro Leu Ile Glu Thr Lys Asp Pro Glu Asn Val
Lys Ala
115 120 125

Ile Leu Ala Thr Gln Phe Asn Asp Phe Ser Leu Gly Thr Arg
His Asp
130 135 140

Phe Leu Tyr Ser Leu Leu Gly Asp Gly Ile Phe Thr Leu Asp
Gly Ala
145 150 155
160

Gly Trp Lys His Ser Arg Thr Met Leu Arg Pro Gln Phe Ala
Arg Glu
165 170
175

- 131/269 -

Gln	Val	Ser	His	Val	Lys	Leu	Leu	Glu	Pro	His	Met	Gln	Val
Leu	Phe												
			180					185					190

Lys	His	Ile	Arg	Lys	His	His	Gly	Gln	Thr	Phe	Asp	Ile	Gln
Glu	Leu												
		195					200					205	

Phe	Phe	Arg	Leu	Thr	Val	Asp	Ser	Ala	Thr	Glu	Phe	Leu	Phe
Gly	Glu												
	210					215					220		

Ser	Ala	Glu	Ser	Leu	Arg	Asp	Glu	Ser	Val	Gly	Leu	Thr	Pro
Thr	Thr												
225					230					235			
240													

Lys	Asp	Phe	Asp	Gly	Arg	Asn	Glu	Phe	Ala	Asp	Ala	Phe	Asn
Tyr	Ser												
				245					250				
255													

Gln	Thr	Tyr	Gln	Ala	Tyr	Arg	Phe	Leu	Leu	Gln	Gln	Met	Tyr
Trp	Ile												
			260					265					270

Leu	Asn	Gly	Ser	Glu	Phe	Arg	Lys	Ser	Ile	Ala	Ile	Val	His
Lys	Phe												
		275					280					285	

Ala	Asp	His	Tyr	Val	Gln	Lys	Ala	Leu	Glu	Leu	Thr	Asp	Glu
Asp	Leu												
	290					295					300		

Glu	Lys	Lys	Glu	Gly	Tyr	Val	Phe	Leu	Phe	Glu	Leu	Ala	Lys
Gln	Thr												
305					310					315			
320													

Arg	Asp	Pro	Lys	Val	Leu	Arg	Asp	Gln	Leu	Leu	Asn	Ile	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- 132/269 -

Val Ala

325

330

335

Gly Arg Asp Thr Thr Ala Gly Leu Leu Ser Phe Leu Phe Phe
Glu Leu

340

345

350

Ser Arg Asn Pro Glu Ile Phe Ala Lys Leu Arg Glu Glu Ile
Glu Asn

355

360

365

Lys Phe Gly Leu Gly Gln Asp Ala Arg Val Glu Glu Ile Ser
Phe Glu

370

375

380

Thr Leu Lys Ser Cys Glu Tyr Leu Lys Ala Val Ile Asn Glu
Thr Leu

385

390

395

400

Arg Ile Tyr Pro Ser Val Pro His Asn Phe Arg Val Ala Thr
Arg Asn

405

410

415

Thr Thr Leu Pro Arg Gly Gly Gly Glu Gly Gly Leu Ser Pro
Ile Ala

420

425

430

Ile Lys Lys Gly Gln Val Val Met Tyr Thr Ile Leu Ala Thr
His Arg

435

440

445

Asp Lys Asp Ile Tyr Gly Glu Asp Ala Tyr Val Phe Arg Pro
Glu Arg

450

455

460

Trp Phe Glu Pro Glu Thr Arg Lys Leu Gly Trp Ala Tyr Val
Pro Phe

465

470

475

480

Asn Gly Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe Ala Leu
Thr Glu

485

490

495

Ala Ser Tyr Val Thr Val Arg Leu Leu Gln Glu Phe Gly Asn
Leu Lys

500

505

510

Gln Asp Pro Asn Thr Glu Tyr Pro Pro Lys Leu Gln Asn Thr
Leu Thr

515

520

525

Leu Ser Leu Phe Glu Gly Ala Glu Val Gln Met Tyr
530 535 540

<210> 33
<211> 1569
<212> DNA
<213> Candida tropicalis

<220>
<221> CDS
<222> (1)..(1569)

<400> 33
atg agt att caa gat att gtt gaa act tac agt acc aaa tgg
tac gtt 48
Met Ser Ile Gln Asp Ile Val Glu Thr Tyr Ser Thr Lys Trp
Tyr Val
1 5 10
15

gtt gta ctg gtt gct ttg att gta tac aag gtt ttt gat ttc
ttt tat 96
Val Val Leu Val Ala Leu Ile Val Tyr Lys Val Phe Asp Phe
Phe Tyr
20 25 30

gct aga tat ttg atg tat aag ctt ggt gct aag cca ttc ctt
caa agt 144
Ala Arg Tyr Leu Met Tyr Lys Leu Gly Ala Lys Pro Phe Leu

Ser	His	Val	Lys	Leu	Leu	Glu	Pro	His	Met	Gln	Val	Phe	Phe
Lys	His												
				165					170				
175													
att	aga	aaa	cat	cat	ggc	caa	acc	ttt	gat	ata	caa	gaa	ttg
ttt	ttc		576										
Ile	Arg	Lys	His	His	Gly	Gln	Thr	Phe	Asp	Ile	Gln	Glu	Leu
Phe	Phe												
			180					185					190
aga	tta	act	gtt	gat	tct	gcc	act	gag	ttt	ttg	ttt	ggt	gaa
tct	ggt		624										
Arg	Leu	Thr	Val	Asp	Ser	Ala	Thr	Glu	Phe	Leu	Phe	Gly	Glu
Ser	Val												
		195					200					205	
gag	tct	tta	aga	gac	gag	tcc	atc	ggt	atg	tta	aac	gat	gct
ctt	gat		672										
Glu	Ser	Leu	Arg	Asp	Glu	Ser	Ile	Gly	Met	Leu	Asn	Asp	Ala
Leu	Asp												
		210				215					220		
ttt	gat	ggt	aag	gct	gga	ttt	gct	gat	gcc	ttt	aac	tat	tct
caa	aac		720										
Phe	Asp	Gly	Lys	Ala	Gly	Phe	Ala	Asp	Ala	Phe	Asn	Tyr	Ser
Gln	Asn												
225					230					235			
240													
tat	ttg	gct	tct	cga	gct	ctt	atg	caa	caa	atg	tac	tgg	att
ttg	aac		768										
Tyr	Leu	Ala	Ser	Arg	Ala	Leu	Met	Gln	Gln	Met	Tyr	Trp	Ile
Leu	Asn												
			245					250					
255													
gga	aaa	aag	ttt	aaa	gaa	tgt	aat	gcc	aag	ggt	cac	aag	ttt
gct	gat		816										
Gly	Lys	Lys	Phe	Lys	Glu	Cys	Asn	Ala	Lys	Val	His	Lys	Phe
Ala	Asp												
			260					265				270	
tat	tat	ggt	gaa	aaa	gca	ttg	gaa	tta	act	ccg	gac	caa	ttg
gaa	aaa		864										
Tyr	Tyr	Val	Glu	Lys	Ala	Leu	Glu	Leu	Thr	Pro	Asp	Gln	Leu
Glu	Lys												
		275				280					285		
caa	gat	ggg	tat	ggt	ttc	ttg	tat	gaa	ttg	gta	aaa	caa	acc

aga gac 912
Gln Asp Gly Tyr Val Phe Leu Tyr Glu Leu Val Lys Gln Thr
Arg Asp
290 295 300

aga caa gtc ttg aga gat cag tta ttg aat ata tta gtt gct
ggt aga 960
Arg Gln Val Leu Arg Asp Gln Leu Leu Asn Ile Leu Val Ala
Gly Arg
305 310 315
320

gat acc act gct ggt tta tta tca ttt gtg ttt ttt gaa ttg
gca aga 1008
Asp Thr Thr Ala Gly Leu Leu Ser Phe Val Phe Phe Glu Leu
Ala Arg
325 330
335

act cca aga gta gca aat aaa tta aga gaa gaa atc gaa gac
aaa ttt 1056
Thr Pro Arg Val Ala Asn Lys Leu Arg Glu Glu Ile Glu Asp
Lys Phe
340 345 350

ggc ctt gga caa gat gct cgt gtt gaa gaa att tcc ttt gaa
tct tta 1104
Gly Leu Gly Gln Asp Ala Arg Val Glu Glu Ile Ser Phe Glu
Ser Leu
355 360 365

aaa tca tgt gaa tat ttg aag gca gtg ctt aat gaa tgt tta
aga tta 1152
Lys Ser Cys Glu Tyr Leu Lys Ala Val Leu Asn Glu Cys Leu
Arg Leu
370 375 380

tac cca tct gtt cca caa aac ttt aga gtt gct acc aga aat
acc aca 1200
Tyr Pro Ser Val Pro Gln Asn Phe Arg Val Ala Thr Arg Asn
Thr Thr
385 390 395
400

tta cca aga ggt ggt ggc aag gat ggt tta tca cca gta tta
gtt aga 1248
Leu Pro Arg Gly Gly Gly Lys Asp Gly Leu Ser Pro Val Leu
Val Arg
405 410
415

aag ggt caa act gtg atg tac agt gtg tat gct gcc cat aga
 aac aaa 1296
 Lys Gly Gln Thr Val Met Tyr Ser Val Tyr Ala Ala His Arg
 Asn Lys

420 425 430

caa att tat ggt gaa gac gca ctt gaa ttc agg cca gaa aga
 tgg ttt 1344
 Gln Ile Tyr Gly Glu Asp Ala Leu Glu Phe Arg Pro Glu Arg
 Trp Phe

435 440 445

gaa cca gag aca aag aaa ttg ggc tgg gcc ttc tta cct ttt
 aat ggt 1392
 Glu Pro Glu Thr Lys Lys Leu Gly Trp Ala Phe Leu Pro Phe
 Asn Gly

450 455 460

ggt cca aga att tgt ttg ggt caa caa ttt gct ttg act gaa
 gct tct 1440
 Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe Ala Leu Thr Glu
 Ala Ser

465 470 475
 480

tat gtt act gtt aga tta ctt caa gag ttt agc cac ttg aca
 atg gat 1488
 Tyr Val Thr Val Arg Leu Leu Gln Glu Phe Ser His Leu Thr
 Met Asp

485 490
 495

cca aac act gaa tac ccg cca aag aaa atg tcc cat ttg aca
 atg tct 1536
 Pro Asn Thr Glu Tyr Pro Pro Lys Lys Met Ser His Leu Thr
 Met Ser

500 505 510

cta ttt gat ggt gcc aac att caa atg tat tag
 1569

Leu Phe Asp Gly Ala Asn Ile Gln Met Tyr
 515 520

<210> 34
 <211> 522
 <212> PRT
 <213> Candida tropicalis

<400> 34

Met Ser Ile Gln Asp Ile Val Glu Thr Tyr Ser Thr Lys Trp
Tyr Val
1 5 10
15

Val Val Leu Val Ala Leu Ile Val Tyr Lys Val Phe Asp Phe
Phe Tyr
20 25 30

Ala Arg Tyr Leu Met Tyr Lys Leu Gly Ala Lys Pro Phe Leu
Gln Ser
35 40 45

Gln Thr Asp Gly Tyr Leu Gly Phe Arg Val Pro Phe Glu Leu
Met Gly
50 55 60

Lys Lys Ser Glu Gly Thr Leu Ile Asp Phe Thr Tyr Gln Arg
Thr Leu
65 70 75
80

Glu Leu Asp Asn Pro Asp Ile Pro Thr Phe Thr Phe Pro Ile
Phe Ser
85 90
95

Val Leu Ile Ile Ser Thr Leu Glu Pro Asp Asn Ile Lys Ala
Ile Leu
100 105 110

Ala Thr Gln Phe Asn Asp Phe Ser Leu Gly Thr Arg His Ser
His Phe
115 120 125

Ala Pro Leu Leu Gly Asp Gly Ile Phe Thr Leu Asp Gly Ala
Gly Trp
130 135 140

- 139/269 -

Lys His Ser Arg Ser Met Leu Arg Pro Gln Phe Ala Arg Glu
Gln Val
145 150 155
160

Ser His Val Lys Leu Leu Glu Pro His Met Gln Val Phe Phe
Lys His
165 170
175

Ile Arg Lys His His Gly Gln Thr Phe Asp Ile Gln Glu Leu
Phe Phe
180 185 190

Arg Leu Thr Val Asp Ser Ala Thr Glu Phe Leu Phe Gly Glu
Ser Val
195 200 205

Glu Ser Leu Arg Asp Glu Ser Ile Gly Met Leu Asn Asp Ala
Leu Asp
210 215 220

Phe Asp Gly Lys Ala Gly Phe Ala Asp Ala Phe Asn Tyr Ser
Gln Asn
225 230 235
240

Tyr Leu Ala Ser Arg Ala Leu Met Gln Gln Met Tyr Trp Ile
Leu Asn
245 250
255

Gly Lys Lys Phe Lys Glu Cys Asn Ala Lys Val His Lys Phe
Ala Asp
260 265 270

Tyr Tyr Val Glu Lys Ala Leu Glu Leu Thr Pro Asp Gln Leu
Glu Lys
275 280 285

Gln Asp Gly Tyr Val Phe Leu Tyr Glu Leu Val Lys Gln Thr

[illegible]

- 141/269 -

435

440

445

Glu Pro Glu Thr Lys Lys Leu Gly Trp Ala Phe Leu Pro Phe
Asn Gly
450 455 460

Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe Ala Leu Thr Glu
Ala Ser
465 470 475
480

Tyr Val Thr Val Arg Leu Leu Gln Glu Phe Ser His Leu Thr
Met Asp
485 490
495

Pro Asn Thr Glu Tyr Pro Pro Lys Lys Met Ser His Leu Thr
Met Ser
500 505 510

Leu Phe Asp Gly Ala Asn Ile Gln Met Tyr
515 520

<210> 35
<211> 1572
<212> DNA
<213> Candida tropicalis

<220>
<221> CDS
<222> (1)..(1572)

<400> 35
atg gcc aca caa gaa att att gat tct gca ctt ccg tac ttg
aca aag 48
Met Ala Thr Gln Glu Ile Ile Asp Ser Ala Leu Pro Tyr Leu
Thr Lys
1 5 10
15

tgg tat act gtt atc act tta gca gct ttg gtt ttc tta att
tca tct 96
Trp Tyr Thr Val Ile Thr Leu Ala Ala Leu Val Phe Leu Ile

Ser	Ser													
			20					25					30	
aat	att	aaa	aat	tac	gtc	aag	gct	aag	aag	ttg	aaa	tgc	aga	
gat	cct		144											
Asn	Ile	Lys	Asn	Tyr	Val	Lys	Ala	Lys	Lys	Leu	Lys	Cys	Arg	
Asp	Pro		35				40					45		
cca	tat	ttc	aaa	gga	gcc	ggt	tgg	aca	ggt	att	agt	cca	tta	
att	gaa		192											
Pro	Tyr	Phe	Lys	Gly	Ala	Gly	Trp	Thr	Gly	Ile	Ser	Pro	Leu	
Ile	Glu		50				55				60			
att	att	aaa	gtt	aaa	ggt	aat	ggt	aga	ttg	gca	gat	ttt	gcc	
gat	aaa		240											
Ile	Ile	Lys	Val	Lys	Gly	Asn	Gly	Arg	Leu	Ala	Asp	Phe	Ala	
Asp	Lys						70				75			
65														
80														
aca	ttc	gac	gac	tat	cca	aac	cat	act	ttt	tac	atg	tct	att	
att	ggt		288											
Thr	Phe	Asp	Asp	Tyr	Pro	Asn	His	Thr	Phe	Tyr	Met	Ser	Ile	
Ile	Gly						85				90			
95														
gct	ttg	aaa	atc	gtc	ttg	act	ggt	gat	cca	gaa	aat	att	aaa	
gct	ggt		336											
Ala	Leu	Lys	Ile	Val	Leu	Thr	Val	Asp	Pro	Glu	Asn	Ile	Lys	
Ala	Val		100						105				110	
ttg	gct	act	caa	ttt	act	gat	ttc	tcc	tta	ggt	acc	aga	cat	
gct	cat		384											
Leu	Ala	Thr	Gln	Phe	Thr	Asp	Phe	Ser	Leu	Gly	Thr	Arg	His	
Ala	His		115						120			125		
ttc	tat	cca	tta	tta	ggt	gat	ggt	att	ttt	act	ttg	gat	ggt	
gaa	ggt		432											
Phe	Tyr	Pro	Leu	Leu	Gly	Asp	Gly	Ile	Phe	Thr	Leu	Asp	Gly	
Glu	Gly		130						135			140		
tgg	aaa	cat	agt	aga	gct	atg	ttg	aga	cca	caa	ttt	gct	aga	
gat	caa		480											
Trp	Lys	His	Ser	Arg	Ala	Met	Leu	Arg	Pro	Gln	Phe	Ala	Arg	

Asp Gln
145 150 155
160

att ggt cat gtt aaa gct ttg gaa cca cat att caa atc ttg
gcc aaa 528
Ile Gly His Val Lys Ala Leu Glu Pro His Ile Gln Ile Leu
Ala Lys
165 170
175

caa att aaa ttg aat aaa ggt aaa act ttt gat att caa gaa
ttg ttt 576
Gln Ile Lys Leu Asn Lys Gly Lys Thr Phe Asp Ile Gln Glu
Leu Phe
180 185 190

ttc aga ttt act gtt gat act gct act gaa ttc ttg ttt ggt
gaa tct 624
Phe Arg Phe Thr Val Asp Thr Ala Thr Glu Phe Leu Phe Gly
Glu Ser
195 200 205

gtt cac tct ttg tat gat gaa aaa tta ggt att cct act cca
aat gaa 672
Val His Ser Leu Tyr Asp Glu Lys Leu Gly Ile Pro Thr Pro
Asn Glu
210 215 220

att cca ggt aga gat aat ttt gca act gct ttt aac act tct
caa cat 720
Ile Pro Gly Arg Asp Asn Phe Ala Thr Ala Phe Asn Thr Ser
Gln His
225 230 235
240

tat ttg gct acc aga aca tac tcc caa act ttc tac ttt tta
act aac 768
Tyr Leu Ala Thr Arg Thr Tyr Ser Gln Thr Phe Tyr Phe Leu
Thr Asn
245 250
255

cct aag gaa ttt aga gac tgt aat gct aaa gtt cat tac ttg
gct aaa 816
Pro Lys Glu Phe Arg Asp Cys Asn Ala Lys Val His Tyr Leu
Ala Lys
260 265 270

tat ttt gtc aat aaa gct ttg aat ttc act ccg gaa gaa att

gaa gaa 864													
Tyr	Phe	Val	Asn	Lys	Ala	Leu	Asn	Phe	Thr	Pro	Glu	Glu	Ile
Glu	Glu												
275				280				285					
aag tcc aaa tct ggt tat gtt ttc ttg tat gaa ttg gtt aaa													
caa acc 912													
Lys	Ser	Lys	Ser	Gly	Tyr	Val	Phe	Leu	Tyr	Glu	Leu	Val	Lys
Gln	Thr												
290				295				300					
aga gat cca aaa gtt tta caa gat caa tta ttg aac att atg													
gtt gcc 960													
Arg	Asp	Pro	Lys	Val	Leu	Gln	Asp	Gln	Leu	Leu	Asn	Ile	Met
Val	Ala												
305				310				315					
320													
ggt aga gat acc act gct ggt tta tta tca ttt gca atg ttt													
gaa tta 1008													
Gly	Arg	Asp	Thr	Thr	Ala	Gly	Leu	Leu	Ser	Phe	Ala	Met	Phe
Glu	Leu												
325				330									
335													
gct aga cat cca gaa att tgg tct aaa tta aga gaa gaa att													
gaa gtt 1056													
Ala	Arg	His	Pro	Glu	Ile	Trp	Ser	Lys	Leu	Arg	Glu	Glu	Ile
Glu	Val												
340				345				350					
aac ttt ggt gtt ggt gaa gaa tct cgt gtt gaa gaa att act													
ttt gaa 1104													
Asn	Phe	Gly	Val	Gly	Glu	Glu	Ser	Arg	Val	Glu	Glu	Ile	Thr
Phe	Glu												
355				360				365					
tct ttg aag aga tgt gaa tac ttg aaa gct att ctt aat gaa													
act ttg 1152													
Ser	Leu	Lys	Arg	Cys	Glu	Tyr	Leu	Lys	Ala	Ile	Leu	Asn	Glu
Thr	Leu												
370				375				380					
cgt atg tat cct tct gtt cca gtc aat tcc aga aca gcc act													
aga gat 1200													
Arg	Met	Tyr	Pro	Ser	Val	Pro	Val	Asn	Ser	Arg	Thr	Ala	Thr
Arg	Asp												
385				390				395					
400													

acc aca tta cca aga ggt ggt ggt cca aat ggt act gat cca
att ttt 1248
Thr Thr Leu Pro Arg Gly Gly Gly Pro Asn Gly Thr Asp Pro
Ile Phe

405

410

415

att cca aag ggt tcc act gtt gct tat att gtt tac aaa act
cat cgt 1296
Ile Pro Lys Gly Ser Thr Val Ala Tyr Ile Val Tyr Lys Thr
His Arg

420

425

430

tta gaa gaa tat tat ggt aaa gat gct gat gat ttc aga cca
gaa aga 1344
Leu Glu Glu Tyr Tyr Gly Lys Asp Ala Asp Asp Phe Arg Pro
Glu Arg

435

440

445

tgg ttt gaa cca tca act aaa aag tta ggt tgg gct tat gtt
cca ttt 1392
Trp Phe Glu Pro Ser Thr Lys Lys Leu Gly Trp Ala Tyr Val
Pro Phe

450

455

460

aat ggt ggt cca aga att tgt tta ggc caa caa ttt gct tta
act gaa 1440
Asn Gly Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe Ala Leu
Thr Glu

465

470

475

480

gct tct tat gtt att acc aga ttg gta caa atg ttt gaa act
gtt tct 1488
Ala Ser Tyr Val Ile Thr Arg Leu Val Gln Met Phe Glu Thr
Val Ser

485

490

495

tct tcc cca gat gtt gaa tac cct cca cca aaa tgt att cat
ttg act 1536
Ser Ser Pro Asp Val Glu Tyr Pro Pro Pro Lys Cys Ile His
Leu Thr

500

505

510

atg agt cat gat gat ggt gtt ttc gtt aaa atg taa
1572

Met Ser His Asp Asp Gly Val Phe Val Lys Met
515 520

<210> 36
<211> 523
<212> PRT
<213> Candida tropicalis

<400> 36

Met Ala Thr Gln Glu Ile Ile Asp Ser Ala Leu Pro Tyr Leu
Thr Lys
1 5 10
15

Trp Tyr Thr Val Ile Thr Leu Ala Ala Leu Val Phe Leu Ile
Ser Ser
20 25 30

Asn Ile Lys Asn Tyr Val Lys Ala Lys Lys Leu Lys Cys Arg
Asp Pro
35 40 45

Pro Tyr Phe Lys Gly Ala Gly Trp Thr Gly Ile Ser Pro Leu
Ile Glu
50 55 60

Ile Ile Lys Val Lys Gly Asn Gly Arg Leu Ala Asp Phe Ala
Asp Lys
65 70 75
80

Thr Phe Asp Asp Tyr Pro Asn His Thr Phe Tyr Met Ser Ile
Ile Gly
85 90
95

Ala Leu Lys Ile Val Leu Thr Val Asp Pro Glu Asn Ile Lys
Ala Val
100 105 110

Leu Ala Thr Gln Phe Thr Asp Phe Ser Leu Gly Thr Arg His
Ala His
115 120 125

Phe Tyr Pro Leu Leu Gly Asp Gly Ile Phe Thr Leu Asp Gly
Glu Gly
130 135 140

Trp Lys His Ser Arg Ala Met Leu Arg Pro Gln Phe Ala Arg
Asp Gln
145 150 155
160

Ile Gly His Val Lys Ala Leu Glu Pro His Ile Gln Ile Leu
Ala Lys
165 170
175

Gln Ile Lys Leu Asn Lys Gly Lys Thr Phe Asp Ile Gln Glu
Leu Phe
180 185 190

Phe Arg Phe Thr Val Asp Thr Ala Thr Glu Phe Leu Phe Gly
Glu Ser
195 200 205

Val His Ser Leu Tyr Asp Glu Lys Leu Gly Ile Pro Thr Pro
Asn Glu
210 215 220

Ile Pro Gly Arg Asp Asn Phe Ala Thr Ala Phe Asn Thr Ser
Gln His
225 230 235
240

Tyr Leu Ala Thr Arg Thr Tyr Ser Gln Thr Phe Tyr Phe Leu
Thr Asn
245 250
255

Pro Lys Glu Phe Arg Asp Cys Asn Ala Lys Val His Tyr Leu
Ala Lys
260 265 270

- 148/269 -

Tyr	Phe	Val	Asn	Lys	Ala	Leu	Asn	Phe	Thr	Pro	Glu	Glu	Ile
Glu	Glu												
		275					280					285	

Lys	Ser	Lys	Ser	Gly	Tyr	Val	Phe	Leu	Tyr	Glu	Leu	Val	Lys
Gln	Thr												
	290					295					300		

Arg	Asp	Pro	Lys	Val	Leu	Gln	Asp	Gln	Leu	Leu	Asn	Ile	Met
Val	Ala												
305					310					315			
320													

Gly	Arg	Asp	Thr	Thr	Ala	Gly	Leu	Leu	Ser	Phe	Ala	Met	Phe
Glu	Leu												
				325					330				
335													

Ala	Arg	His	Pro	Glu	Ile	Trp	Ser	Lys	Leu	Arg	Glu	Glu	Ile
Glu	Val												
			340					345					350

Asn	Phe	Gly	Val	Gly	Glu	Glu	Ser	Arg	Val	Glu	Glu	Ile	Thr
Phe	Glu												
		355					360					365	

Ser	Leu	Lys	Arg	Cys	Glu	Tyr	Leu	Lys	Ala	Ile	Leu	Asn	Glu
Thr	Leu												
	370					375					380		

Arg	Met	Tyr	Pro	Ser	Val	Pro	Val	Asn	Ser	Arg	Thr	Ala	Thr
Arg	Asp												
385					390					395			
400													

Thr	Thr	Leu	Pro	Arg	Gly	Gly	Gly	Pro	Asn	Gly	Thr	Asp	Pro
Ile	Phe												
				405					410				
415													

Ile	Pro	Lys	Gly	Ser	Thr	Val	Ala	Tyr	Ile	Val	Tyr	Lys	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- 149/269 -

His Arg
420 425 430

Leu Glu Glu Tyr Tyr Gly Lys Asp Ala Asp Asp Phe Arg Pro
Glu Arg
435 440 445

Trp Phe Glu Pro Ser Thr Lys Lys Leu Gly Trp Ala Tyr Val
Pro Phe
450 455 460

Asn Gly Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe Ala Leu
Thr Glu
465 470 475
480

Ala Ser Tyr Val Ile Thr Arg Leu Val Gln Met Phe Glu Thr
Val Ser
485 490
495

Ser Ser Pro Asp Val Glu Tyr Pro Pro Pro Lys Cys Ile His
Leu Thr
500 505 510

Met Ser His Asp Asp Gly Val Phe Val Lys Met
515 520

<210> 37
<211> 1512
<212> DNA
<213> Candida tropicalis

<220>
<221> CDS
<222> (1)..(1512)

<400> 37
atg tca tta aca gaa aca act gct acg ttt att tac aat tat
tgg tac 48
Met Ser Leu Thr Glu Thr Thr Ala Thr Phe Ile Tyr Asn Tyr
Trp Tyr

1		5		10									
15													
atc	ata	ttc	att	ata	ttc	tac	aca	acc	agc	aaa	atc	atc	aag
tat	cat				96								
Ile	Ile	Phe	Ile	Ile	Phe	Tyr	Thr	Thr	Ser	Lys	Ile	Ile	Lys
Tyr	His												
		20				25						30	
cac	acg	aca	tat	ctt	atg	ata	aag	ttc	aaa	gct	tct	ccg	cct
ttg	aat				144								
His	Thr	Thr	Tyr	Leu	Met	Ile	Lys	Phe	Lys	Ala	Ser	Pro	Pro
Leu	Asn												
		35				40						45	
tac	ata	aat	aaa	ggt	ttt	ttt	gga	att	cag	gcg	acg	ttc	acg
gaa	ttg				192								
Tyr	Ile	Asn	Lys	Gly	Phe	Phe	Gly	Ile	Gln	Ala	Thr	Phe	Thr
Glu	Leu												
	50					55						60	
aaa	cat	ctt	ata	tgt	cac	aca	tcg	att	gat	tac	gcc	atc	gat
caa	ttc				240								
Lys	His	Leu	Ile	Cys	His	Thr	Ser	Ile	Asp	Tyr	Ala	Ile	Asp
Gln	Phe												
65					70					75			
80													
aat	aac	gtc	cca	ttc	cca	cat	ggt	cat	act	ttt	gta	acc	aaa
ggt	ctt				288								
Asn	Asn	Val	Pro	Phe	Pro	His	Val	His	Thr	Phe	Val	Thr	Lys
Val	Leu												
			85							90			
95													
ggt	aat	gag	tta	atc	atg	aca	aaa	gat	cct	gaa	aat	att	aaa
ggt	tta												
Gly	Asn	Glu	Leu	Ile	Met	Thr	Lys	Asp	Pro	Glu	Asn	Ile	Lys
Val	Leu												
			100						105				110
ttg	agt	tcc	agt	ttt	gat	aag	ttt	gat	tat	gga	aca	cgt	tca
agt	gcc												
Leu	Ser	Ser	Ser	Phe	Asp	Lys	Phe	Asp	Tyr	Gly	Thr	Arg	Ser
Ser	Ala												
		115					120					125	
gtg	caa	cca	tct	tta	gga	atg	ggg	ata	ttc	act	ctt	gaa	gga
gaa	aat												
Val	Gln	Pro	Ser	Leu	Gly	Met	Gly	Ile	Phe	Thr	Leu	Glu	Gly

Glu	Asn													
130						135						140		
tgg	aaa	gca	aca	aga	agt	ggt	tta	agg	aac	atg	ttt	gat	aga	
aaa	tca		480											
Trp	Lys	Ala	Thr	Arg	Ser	Val	Leu	Arg	Asn	Met	Phe	Asp	Arg	
Lys	Ser													
145					150						155			
160														
att	gac	aag	gta	cat	gat	ttt	gaa	cca	cat	ttc	aaa	acc	ctt	
cag	aaa		528											
Ile	Asp	Lys	Val	His	Asp	Phe	Glu	Pro	His	Phe	Lys	Thr	Leu	
Gln	Lys													
			165							170				
175														
aga	ata	gat	ggg	aag	ggt	gga	tat	ttt	gac	atc	caa	cag	gag	
ttt	tta		576											
Arg	Ile	Asp	Gly	Lys	Val	Gly	Tyr	Phe	Asp	Ile	Gln	Gln	Glu	
Phe	Leu													
			180					185					190	
aaa	tta	gga	ttg	gaa	ttg	agt	att	gag	ttt	att	ttt	ggt	caa	
ggt	gta		624											
Lys	Leu	Gly	Leu	Glu	Leu	Ser	Ile	Glu	Phe	Ile	Phe	Gly	Gln	
Val	Val													
		195				200						205		
tcg	gaa	gat	gtc	cca	cat	tat	gat	gat	ttt	acc	cag	gct	tgg	
gat	aga		672											
Ser	Glu	Asp	Val	Pro	His	Tyr	Asp	Asp	Phe	Thr	Gln	Ala	Trp	
Asp	Arg													
210						215					220			
tgt	caa	gac	tat	atg	atg	cta	aga	tta	ttg	ttg	ggg	gat	ttt	
tat	tgg		720											
Cys	Gln	Asp	Tyr	Met	Met	Leu	Arg	Leu	Leu	Leu	Gly	Asp	Phe	
Tyr	Trp													
225						230					235			
240														
ata	gct	aat	gac	tgg	aga	tat	aaa	cag	tcc	aat	caa	att	gtg	
caa	gct		768											
Ile	Ala	Asn	Asp	Trp	Arg	Tyr	Lys	Gln	Ser	Asn	Gln	Ile	Val	
Gln	Ala													
			245								250			
255														
ttt	tgt	gat	tat	ttg	gtg	caa	aaa	tca	ctt	gaa	aat	aca	tgc	

aac	gac		816										
Phe	Cys	Asp	Tyr	Leu	Val	Gln	Lys	Ser	Leu	Glu	Asn	Thr	Cys
Asn	Asp												
			260					265					270
aaa	ttt	gtc	ttt	gta	cag	gaa	ctt	gca	aaa	cac	acg	acc	aac
aaa	acg		864										
Lys	Phe	Val	Phe	Val	Gln	Glu	Leu	Ala	Lys	His	Thr	Thr	Asn
Lys	Thr												
		275				280						285	
ttc	att	aga	gat	caa	gca	tta	agc	ttg	att	atg	gct	tca	aga
gac	aca		912										
Phe	Ile	Arg	Asp	Gln	Ala	Leu	Ser	Leu	Ile	Met	Ala	Ser	Arg
Asp	Thr												
	290					295					300		
act	gct	gag	ttg	atg	gca	ttc	acc	ata	cta	gaa	tta	tcc	aga
aat	ccc		960										
Thr	Ala	Glu	Leu	Met	Ala	Phe	Thr	Ile	Leu	Glu	Leu	Ser	Arg
Asn	Pro												
305					310					315			
320													
act	atc	tgg	gaa	aga	tta	aga	gag	gaa	ata	gat	gcc	aat	ttt
gga	ttg		1008										
Thr	Ile	Trp	Glu	Arg	Leu	Arg	Glu	Glu	Ile	Asp	Ala	Asn	Phe
Gly	Leu												
				325					330				
335													
gaa	tca	ccc	gac	ttg	ctt	aca	ttt	gat	tca	ctt	cgc	aag	ttc
aaa	tat		1056										
Glu	Ser	Pro	Asp	Leu	Leu	Thr	Phe	Asp	Ser	Leu	Arg	Lys	Phe
Lys	Tyr												
			340					345					350
gtt	caa	gct	atc	ttg	aat	gag	act	ctt	agg	atg	tac	cct	gga
gtt	cca		1104										
Val	Gln	Ala	Ile	Leu	Asn	Glu	Thr	Leu	Arg	Met	Tyr	Pro	Gly
Val	Pro												
		355				360						365	
aga	aat	atg	aaa	act	gct	aaa	tgt	act	act	aca	tta	cca	aaa
gga	gga		1152										
Arg	Asn	Met	Lys	Thr	Ala	Lys	Cys	Thr	Thr	Thr	Leu	Pro	Lys
Gly	Gly												
	370					375					380		
ggg	aaa	gat	ggt	caa	gat	cca	att	cta	gtt	aaa	aag	ggt	caa

tct gtt 1200
Gly Lys Asp Gly Gln Asp Pro Ile Leu Val Lys Lys Gly Gln
Ser Val
385 390 395
400

ggg ttt att tcc ata gct act cat ttg gat ccg gtt tat ttt
ggt agt 1248
Gly Phe Ile Ser Ile Ala Thr His Leu Asp Pro Val Tyr Phe
Gly Ser
405 410
415

gat gcc cat gtg ttt aga cca gac cgc tgg ttt gat tct agt
atg aaa 1296
Asp Ala His Val Phe Arg Pro Asp Arg Trp Phe Asp Ser Ser
Met Lys
420 425 430

aat ttg ggg tgt aaa tac ttg ccc ttt aac gtc ggt cca aga
acg tgt 1344
Asn Leu Gly Cys Lys Tyr Leu Pro Phe Asn Val Gly Pro Arg
Thr Cys
435 440 445

ttg gga caa cag tac act ttg att gag gca agc tac ttg tta
gtt cgt 1392
Leu Gly Gln Gln Tyr Thr Leu Ile Glu Ala Ser Tyr Leu Leu
Val Arg
450 455 460

cta gcg caa aca tat gaa aca gtt gaa tca cat ccc gat tca
gtt tat 1440
Leu Ala Gln Thr Tyr Glu Thr Val Glu Ser His Pro Asp Ser
Val Tyr
465 470 475
480

cca cca agg aag aaa gcg ttg atc aat atg tgt gct gca gac
ggt gtt 1488
Pro Pro Arg Lys Lys Ala Leu Ile Asn Met Cys Ala Ala Asp
Gly Val
485 490
495

gat gtc aag ttc cat aga tta taa
1512
Asp Val Lys Phe His Arg Leu
500

<210> 38
<211> 503
<212> PRT
<213> Candida tropicalis

<400> 38

Met Ser Leu Thr Glu Thr Thr Ala Thr Phe Ile Tyr Asn Tyr
Trp Tyr
1 5 10
15

Ile Ile Phe Ile Ile Phe Tyr Thr Thr Ser Lys Ile Ile Lys
Tyr His
20 25 30

His Thr Thr Tyr Leu Met Ile Lys Phe Lys Ala Ser Pro Pro
Leu Asn
35 40 45

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

Lys His Leu Ile Cys His Thr Ser Ile Asp Tyr Ala Ile Asp
Gln Phe
65 70 75
80

Asn Asn Val Pro Phe Pro His Val His Thr Phe Val Thr Lys
Val Leu
85 90
95

Gly Asn Glu Leu Ile Met Thr Lys Asp Pro Glu Asn Ile Lys
Val Leu
100 105 110

Leu Ser Ser Ser Phe Asp Lys Phe Asp Tyr Gly Thr Arg Ser
Ser Ala
115 120 125

Val Gln Pro Ser Leu Gly Met Gly Ile Phe Thr Leu Glu Gly
Glu Asn
130 135 140

Trp Lys Ala Thr Arg Ser Val Leu Arg Asn Met Phe Asp Arg
Lys Ser
145 150 155
160

Ile Asp Lys Val His Asp Phe Glu Pro His Phe Lys Thr Leu
Gln Lys
165 170
175

Arg Ile Asp Gly Lys Val Gly Tyr Phe Asp Ile Gln Gln Glu
Phe Leu
180 185 190

Lys Leu Gly Leu Glu Leu Ser Ile Glu Phe Ile Phe Gly Gln
Val Val
195 200 205

Ser Glu Asp Val Pro His Tyr Asp Asp Phe Thr Gln Ala Trp
Asp Arg
210 215 220

Cys Gln Asp Tyr Met Met Leu Arg Leu Leu Leu Gly Asp Phe
Tyr Trp
225 230 235
240

Ile Ala Asn Asp Trp Arg Tyr Lys Gln Ser Asn Gln Ile Val
Gln Ala
245 250
255

Phe Cys Asp Tyr Leu Val Gln Lys Ser Leu Glu Asn Thr Cys
Asn Asp
260 265 270

- 156/269 -

Lys	Phe	Val	Phe	Val	Gln	Glu	Leu	Ala	Lys	His	Thr	Thr	Asn
Lys	Thr												
		275					280					285	

Phe	Ile	Arg	Asp	Gln	Ala	Leu	Ser	Leu	Ile	Met	Ala	Ser	Arg
Asp	Thr												
	290					295					300		

Thr	Ala	Glu	Leu	Met	Ala	Phe	Thr	Ile	Leu	Glu	Leu	Ser	Arg
Asn	Pro												
305					310					315			
320													

Thr	Ile	Trp	Glu	Arg	Leu	Arg	Glu	Glu	Ile	Asp	Ala	Asn	Phe
Gly	Leu												
				325					330				
335													

Glu	Ser	Pro	Asp	Leu	Leu	Thr	Phe	Asp	Ser	Leu	Arg	Lys	Phe
Lys	Tyr												
			340					345					350

Val	Gln	Ala	Ile	Leu	Asn	Glu	Thr	Leu	Arg	Met	Tyr	Pro	Gly
Val	Pro												
		355					360					365	

Arg	Asn	Met	Lys	Thr	Ala	Lys	Cys	Thr	Thr	Thr	Leu	Pro	Lys
Gly	Gly												
	370					375					380		

Gly	Lys	Asp	Gly	Gln	Asp	Pro	Ile	Leu	Val	Lys	Lys	Gly	Gln
Ser	Val												
385					390					395			
400													

Gly	Phe	Ile	Ser	Ile	Ala	Thr	His	Leu	Asp	Pro	Val	Tyr	Phe
Gly	Ser												
				405					410				
415													

Asp	Ala	His	Val	Phe	Arg	Pro	Asp	Arg	Trp	Phe	Asp	Ser	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- 157/269 -

Met Lys
420 425 430

Asn Leu Gly Cys Lys Tyr Leu Pro Phe Asn Val Gly Pro Arg
Thr Cys
435 440 445

Leu Gly Gln Gln Tyr Thr Leu Ile Glu Ala Ser Tyr Leu Leu
Val Arg
450 455 460

Leu Ala Gln Thr Tyr Glu Thr Val Glu Ser His Pro Asp Ser
Val Tyr
465 470 475
480

Pro Pro Arg Lys Lys Ala Leu Ile Asn Met Cys Ala Ala Asp
Gly Val
485 490
495

Asp Val Lys Phe His Arg Leu
500

<210> 39
<211> 1554
<212> DNA
<213> Candida tropicalis

<220>
<221> CDS
<222> (1)..(1554)

<400> 39
atg atc gaa caa gtt gtt gaa tac tgg tac gtg gtc tta cca
ttg gta 48
Met Ile Glu Gln Val Val Glu Tyr Trp Tyr Val Val Leu Pro
Leu Val
1 5 10
15

ttt atc ctt cat aaa gta ttt gac atg tgg cac act cgt cgg
ttg atg 96

Met Leu Arg Pro Gln Phe Ala Arg Glu Gln Val Ala His Val
Thr Ser
145 150 155
160

tta gag cca cat ttc caa ttg ttg aaa aaa cat atc ctc aag
aac aaa 528
Leu Glu Pro His Phe Gln Leu Leu Lys Lys His Ile Leu Lys
Asn Lys
165 170
175

gga ggt ttt ttt gat atc cag gaa ttg ttt ttc cga ttc act
gtt gat 576
Gly Gly Phe Phe Asp Ile Gln Glu Leu Phe Phe Arg Phe Thr
Val Asp
180 185 190

tca gct act gag ttt ttg ttt ggt gaa tca gta cac tct ttg
aag gat 624
Ser Ala Thr Glu Phe Leu Phe Gly Glu Ser Val His Ser Leu
Lys Asp
195 200 205

gaa aca att ggg tat aac caa gat gat atc gac ttt gtt ggt
aga aag 672
Glu Thr Ile Gly Tyr Asn Gln Asp Asp Ile Asp Phe Val Gly
Arg Lys
210 215 220

gat ttt gcg gaa tcg ttc aac aag gca caa gag tat ctt gct
att aga 720
Asp Phe Ala Glu Ser Phe Asn Lys Ala Gln Glu Tyr Leu Ala
Ile Arg
225 230 235
240

act ttg gtg caa gat ttt tat tat ctt gta aac aat cag gaa
ttc aga 768
Thr Leu Val Gln Asp Phe Tyr Tyr Leu Val Asn Asn Gln Glu
Phe Arg
245 250
255

gat tgc aat aaa ctg gta cac aag ttt acc aac tac tat gtc
caa aga 816
Asp Cys Asn Lys Leu Val His Lys Phe Thr Asn Tyr Tyr Val
Gln Arg
260 265 270

- 160/269 -

gca ttg gat gcc act cct gaa gag ctt gaa aag caa agt gga
tat gtt 864
Ala Leu Asp Ala Thr Pro Glu Glu Leu Glu Lys Gln Ser Gly
Tyr Val

275

280

285

ttc ttg tat gaa ttg gtt aaa caa acc aga gac cct aat gta
ttg aga 912
Phe Leu Tyr Glu Leu Val Lys Gln Thr Arg Asp Pro Asn Val
Leu Arg
290

295

300

gat caa tca ttg aac atc tta tta gct ggt aga gat acc act
gct ggg 960
Asp Gln Ser Leu Asn Ile Leu Leu Ala Gly Arg Asp Thr Thr
Ala Gly
305 310 315
320

ttg ttg tca ttt gcg gta ttt gaa ctt gct agg aat cca cat
att tgg 1008
Leu Leu Ser Phe Ala Val Phe Glu Leu Ala Arg Asn Pro His
Ile Trp

325

330

335

gcc aaa tta aga gaa gat gtt gaa tcc caa ttt ggt ctt ggt
gaa gaa 1056
Ala Lys Leu Arg Glu Asp Val Glu Ser Gln Phe Gly Leu Gly
Glu Glu

340

345

350

tct cgc att gaa gag att acc ttt gaa agt tta aaa cga tgt
gaa tac 1104
Ser Arg Ile Glu Glu Ile Thr Phe Glu Ser Leu Lys Arg Cys
Glu Tyr

355

360

365

ttg aaa gct ttc ctt aac gaa aca tta cgt gtt tat cca agt
gtt cca 1152
Leu Lys Ala Phe Leu Asn Glu Thr Leu Arg Val Tyr Pro Ser
Val Pro
370

375

380

aga aat ttc aga att gct acc aaa aac acc act tta cca aga
ggt ggt 1200
Arg Asn Phe Arg Ile Ala Thr Lys Asn Thr Thr Leu Pro Arg
Gly Gly

385

390

395

400

ggt tca gac ggc aat tct cct gtt ttg gtc aaa aag ggc gag
gct gtt 1248
Gly Ser Asp Gly Asn Ser Pro Val Leu Val Lys Lys Gly Glu
Ala Val

405

410

415

tca tat ggt ata aat tct act cac tta gat cct gtc tat tat
ggt gac 1296
Ser Tyr Gly Ile Asn Ser Thr His Leu Asp Pro Val Tyr Tyr
Gly Asp

420

425

430

gat gct gca gaa ttt aga cca gaa aga tgg aac gag cca tca
aca aga 1344
Asp Ala Ala Glu Phe Arg Pro Glu Arg Trp Asn Glu Pro Ser
Thr Arg

435

440

445

aaa ttg gga tgg gca tat tta ccg ttc aac gga ggc cca aga
att tgt 1392
Lys Leu Gly Trp Ala Tyr Leu Pro Phe Asn Gly Gly Pro Arg
Ile Cys

450

455

460

tta ggt caa caa ttt gct tta acc gaa gcg ggt tat gta ttg
gtt aga 1440
Leu Gly Gln Gln Phe Ala Leu Thr Glu Ala Gly Tyr Val Leu
Val Arg

465

470

475

480

ttg gcc caa agt ttt gac acc ttg gaa ttg aag cca cca gtt
gtg tat 1488
Leu Ala Gln Ser Phe Asp Thr Leu Glu Leu Lys Pro Pro Val
Val Tyr

485

490

495

cca cca aag aga tta aca aac ttg act atg tct tta caa gac
gga act 1536
Pro Pro Lys Arg Leu Thr Asn Leu Thr Met Ser Leu Gln Asp
Gly Thr

500

505

510

att gtc aag atc gat tag
1554

Ile Val Lys Ile Asp

515

<210> 40
<211> 517
<212> PRT
<213> Candida tropicalis

<400> 40

Met Ile Glu Gln Val Val Glu Tyr Trp Tyr Val Val Leu Pro
Leu Val

1 5 10
15

Phe Ile Leu His Lys Val Phe Asp Met Trp His Thr Arg Arg
Leu Met

20 25 30

Lys Gln Leu Gly Ala Ala Pro Val Thr Asn Gln Leu His Asp
Asn Phe

35 40 45

Phe Gly Ile Ile Asn Gly Trp Lys Ala Leu Lys Phe Lys Lys
Glu Gly

50 55 60

Arg Ala Gln Glu Tyr Asn Asp Tyr Lys Phe Ala Asn Ser Lys
Ile Pro

65 70 75
80

Ser Val Gly Thr Tyr Val Ser Thr Ile Phe Gly Thr Lys Leu
Leu Val

85 90
95

Thr Lys Asp Pro Glu Asn Ile Lys Ala Leu Leu Ala Thr Gln
Phe Ser

100 105 110

Asp Phe Ser Leu Gly Lys Arg His Thr Leu Phe Lys Pro Leu
Leu Gly

115 120 125

Asp	Gly	Ile	Phe	Thr	Leu	Asp	Gly	Glu	Gly	Trp	Lys	His	Ser
Arg	Ala												
	130					135					140		

Met	Leu	Arg	Pro	Gln	Phe	Ala	Arg	Glu	Gln	Val	Ala	His	Val
Thr	Ser												
145					150					155			
160													

Leu	Glu	Pro	His	Phe	Gln	Leu	Leu	Lys	Lys	His	Ile	Leu	Lys
Asn	Lys												
				165					170				
175													

Gly	Gly	Phe	Phe	Asp	Ile	Gln	Glu	Leu	Phe	Phe	Arg	Phe	Thr
Val	Asp												
			180					185					190

Ser	Ala	Thr	Glu	Phe	Leu	Phe	Gly	Glu	Ser	Val	His	Ser	Leu
Lys	Asp												
		195					200					205	

Glu	Thr	Ile	Gly	Tyr	Asn	Gln	Asp	Asp	Ile	Asp	Phe	Val	Gly
Arg	Lys												
	210					215					220		

Asp	Phe	Ala	Glu	Ser	Phe	Asn	Lys	Ala	Gln	Glu	Tyr	Leu	Ala
Ile	Arg												
225					230					235			
240													

Thr	Leu	Val	Gln	Asp	Phe	Tyr	Tyr	Leu	Val	Asn	Asn	Gln	Glu
Phe	Arg												
				245					250				
255													

Asp	Cys	Asn	Lys	Leu	Val	His	Lys	Phe	Thr	Asn	Tyr	Tyr	Val
Gln	Arg												
			260					265					270

Ala Leu Asp Ala Thr Pro Glu Glu Leu Glu Lys Gln Ser Gly
Tyr Val
275 280 285

Phe Leu Tyr Glu Leu Val Lys Gln Thr Arg Asp Pro Asn Val
Leu Arg
290 295 300

Asp Gln Ser Leu Asn Ile Leu Leu Ala Gly Arg Asp Thr Thr
Ala Gly
305 310 315
320

Leu Leu Ser Phe Ala Val Phe Glu Leu Ala Arg Asn Pro His
Ile Trp
325 330
335

Ala Lys Leu Arg Glu Asp Val Glu Ser Gln Phe Gly Leu Gly
Glu Glu
340 345 350

Ser Arg Ile Glu Glu Ile Thr Phe Glu Ser Leu Lys Arg Cys
Glu Tyr
355 360 365

Leu Lys Ala Phe Leu Asn Glu Thr Leu Arg Val Tyr Pro Ser
Val Pro
370 375 380

Arg Asn Phe Arg Ile Ala Thr Lys Asn Thr Thr Leu Pro Arg
Gly Gly
385 390 395
400

Gly Ser Asp Gly Asn Ser Pro Val Leu Val Lys Lys Gly Glu
Ala Val
405 410
415

- 165/269 -

Ser Tyr Gly Ile Asn Ser Thr His Leu Asp Pro Val Tyr Tyr
Gly Asp
420 425 430

Asp Ala Ala Glu Phe Arg Pro Glu Arg Trp Asn Glu Pro Ser
Thr Arg
435 440 445

Lys Leu Gly Trp Ala Tyr Leu Pro Phe Asn Gly Gly Pro Arg
Ile Cys
450 455 460

Leu Gly Gln Gln Phe Ala Leu Thr Glu Ala Gly Tyr Val Leu
Val Arg
465 470 475
480

Leu Ala Gln Ser Phe Asp Thr Leu Glu Leu Lys Pro Pro Val
Val Tyr
485 490
495

Pro Pro Lys Arg Leu Thr Asn Leu Thr Met Ser Leu Gln Asp
Gly Thr
500 505 510

Ile Val Lys Ile Asp
515

<210> 41
<211> 1539
<212> DNA
<213> Candida tropicalis

<220>
<221> CDS
<222> (1)..(1539)

<400> 41
atg att gaa cag gtt tta cat tat tgg tat att gtt tta cct
gca ttt 48
Met Ile Glu Gln Val Leu His Tyr Trp Tyr Ile Val Leu Pro

Thr Arg	Leu Pro	Asp	Gly	Glu	Gly	Trp	Lys	His	Ser	Arg	Ala	Met	Leu
	130					135					140		
cag cca Gln Pro 145 160	ttt cat Phe His	gca Ala	aga Arg 480	gaa Glu	caa Gln	gtt Val	gcc Ala	cat His	gtc Val	act Thr	tct Ser	tta Leu	gaa Glu
					150					155			
ttc ttt Phe Phe 175	caa ttt Gln Phe	ttg Leu	ttg Leu 528	aaa Lys	aag Lys	cat His	atc Ile	ctc Leu	aag Lys	aac Asn	aaa Lys	ggg Gly	ggg Gly
				165					170				
gat act Asp Thr	atc gag Ile Glu	cag Gln	gaa Glu 180	ttg Leu	ttt Phe	ttc Phe	cga Arg	ttc Phe	acc Thr	ggt Val	gat Asp	tca Ser	gct Ala
								185					190
ttt att Phe Ile	ttg ggg Leu Gly	ttt Phe	ggg Gly 624	gaa Glu	tca Ser	gtg Val	aac Asn	tct Ser	ttg Leu	aaa Lys	agt Ser	gca Ala	tca Ser
		195					200				205		
tgt gaa Cys Glu	gac gca Asp Ala 210	gag Glu	gaa Glu 672	acc Thr	gag Glu	ctt Leu	gag Glu	gaa Glu	aga Arg	aag Lys	aaa Lys	ttt Phe	gcg Ala
						215				220			
ttc caa Phe Gln 225 240	aat caa Asn Gln	aaa Lys	gcg Ala 720	caa Gln	gag Glu	tat Tyr	att Ile	tct Ser	act Thr	cga Arg	ggt Val	gct Ala	ttg Leu
					230					235			
tta gaa Leu Glu 255	tat att Tyr Ile	tgg Trp	ttt Phe 768	gtt Val	aat Asn	aat Asn	agc Ser	gaa Glu	ttc Phe	aag Lys	gaa Glu	tgt Cys	aac Asn
				245					250				

- 168/269 -

gtt cat aag ttt acc aat tat tat gta caa aag gca ttg gat
gct act 816
Val His Lys Phe Thr Asn Tyr Tyr Val Gln Lys Ala Leu Asp
Ala Thr

260

265

270

cct gaa gag ctt gaa aag caa agt gga tat gtt ttc ttg tat
gaa ttg 864
Pro Glu Glu Leu Glu Lys Gln Ser Gly Tyr Val Phe Leu Tyr
Glu Leu

275

280

285

gtt aaa caa acc aga gac cct aat gta ttg aga gat caa tca
ttg aat 912
Val Lys Gln Thr Arg Asp Pro Asn Val Leu Arg Asp Gln Ser
Leu Asn

290

295

300

atc tta tta gct ggt aga gat acc act gct ggg ttg ttg tca
ttt gcg 960
Ile Leu Leu Ala Gly Arg Asp Thr Thr Ala Gly Leu Leu Ser
Phe Ala

305

310

315

320

gta ttt gaa ctt gct agg aat cca cat att tgg gcc aaa tta
aga gaa 1008
Val Phe Glu Leu Ala Arg Asn Pro His Ile Trp Ala Lys Leu
Arg Glu

325

330

335

gat gtc gaa tcc caa ttt ggt ctt ggt gaa gaa tct cgc att
gaa gag 1056
Asp Val Glu Ser Gln Phe Gly Leu Gly Glu Glu Ser Arg Ile
Glu Glu

340

345

350

att acc ttt gaa agt tta aaa cga tgt gaa tat ttg aaa gcc
gtg atg 1104
Ile Thr Phe Glu Ser Leu Lys Arg Cys Glu Tyr Leu Lys Ala
Val Met

355

360

365

aat gaa aca ttg aga ttg cat cca agt gtt cca aga aat gct
aga ttt 1152
Asn Glu Thr Leu Arg Leu His Pro Ser Val Pro Arg Asn Ala
Arg Phe

370

375

380

gca ctt aag gat aca act tta cct aga ggt gga ggt cca gat
gga aaa 1200
Ala Leu Lys Asp Thr Thr Leu Pro Arg Gly Gly Gly Pro Asp
Gly Lys
385 390 395
400

gac ccg att tta gtt aga aaa aat gaa gtt gtt caa tat tcc
att tct 1248
Asp Pro Ile Leu Val Arg Lys Asn Glu Val Val Gln Tyr Ser
Ile Ser
405 410
415

ggc aca caa att gat cca aaa cat tat ggc aaa gat gct aaa
ttg ttt 1296
Gly Thr Gln Ile Asp Pro Lys His Tyr Gly Lys Asp Ala Lys
Leu Phe
420 425 430

aga cca gaa aga tgg ttt gaa tca agt aca aga aat tta ggt
tgg gca 1344
Arg Pro Glu Arg Trp Phe Glu Ser Ser Thr Arg Asn Leu Gly
Trp Ala
435 440 445

tac tta cca ttc aac ggg ggt ccg aga att tgt tta ggt caa
caa ttt 1392
Tyr Leu Pro Phe Asn Gly Gly Pro Arg Ile Cys Leu Gly Gln
Gln Phe
450 455 460

gct tta acc gaa gca ggt tac ata ttg gtt aga ttg gct caa
agt ttt 1440
Ala Leu Thr Glu Ala Gly Tyr Ile Leu Val Arg Leu Ala Gln
Ser Phe
465 470 475
480

gac acc ttg gaa ttg aaa cca gat aca gaa tac cct cca cca
aga tta 1488
Asp Thr Leu Glu Leu Lys Pro Asp Thr Glu Tyr Pro Pro Pro
Arg Leu
485 490
495

gcc cat ttg act atg tgt ttg ttt gat ggt gcg ctt gtc aag
atg gat 1536
Ala His Leu Thr Met Cys Leu Phe Asp Gly Ala Leu Val Lys
Met Asp

- 170/269 -

500

505

510

taa
1539

<210> 42
<211> 512
<212> PRT
<213> *Candida tropicalis*

<400> 42

Met Ile Glu Gln Val Leu His Tyr Trp Tyr Ile Val Leu Pro
Ala Phe
1 5 10
15

Ile Ile Phe His Trp Ile Val Ser Ala Ile His Thr Asn Ser
Leu Arg
20 25 30

Arg Lys Leu Gly Ala Lys Pro Phe Thr His Thr Gln Leu Asp
Gly Phe
35 40 45

Tyr Gly Phe Lys Phe Gly Arg Asp Phe Leu Lys Ala Lys Arg
Ile Gly
50 55 60

Arg Gln Val Asp Leu Ile Asn Ser Arg Phe Pro Asp Asp Ile
Asp Thr
65 70 75
80

Phe Ser Ser Tyr Thr Phe Gly Asn His Val Ile Phe Thr Arg
Asp Pro
85 90
95

Glu Asn Ile Lys Ala Leu Leu Ala Thr Gln Phe Asn Asp Phe
Ser Leu
100 105 110

Gly Gly Arg Ile Lys Phe Phe Lys Pro Leu Leu Gly Tyr Gly
Ile Phe
115 120 125

Thr	Leu	Asp	Gly	Glu	Gly	Trp	Lys	His	Ser	Arg	Ala	Met	Leu
Arg	Pro												
	130					135					140		

Gln Phe Ala Arg Glu Gln Val Ala His Val Thr Ser Leu Glu
Pro His
145 150 155
160

Phe Gln Leu Leu Lys Lys His Ile Leu Lys Asn Lys Gly Gly
Phe Phe
165 170
175

Asp Ile Gln Glu Leu Phe Phe Arg Phe Thr Val Asp Ser Ala
Thr Glu
180 185 190

Phe Leu Phe Gly Glu Ser Val Asn Ser Leu Lys Ser Ala Ser
Ile Gly
195 200 205

Cys Asp Glu Glu Thr Glu Leu Glu Glu Arg Lys Lys Phe Ala
Glu Ala
210 215 220

Phe Asn Lys Ala Gln Glu Tyr Ile Ser Thr Arg Val Ala Leu
Gln Gln
225 230 235
240

Leu Tyr Trp Phe Val Asn Asn Ser Glu Phe Lys Glu Cys Asn
Glu Ile
245 250
255

- 172/269 -

Val His Lys Phe Thr Asn Tyr Tyr Val Gln Lys Ala Leu Asp
Ala Thr
260 265 270

Pro Glu Glu Leu Glu Lys Gln Ser Gly Tyr Val Phe Leu Tyr
Glu Leu
275 280 285

Val Lys Gln Thr Arg Asp Pro Asn Val Leu Arg Asp Gln Ser
Leu Asn
290 295 300

Ile Leu Leu Ala Gly Arg Asp Thr Thr Ala Gly Leu Leu Ser
Phe Ala
305 310 315
320

Val Phe Glu Leu Ala Arg Asn Pro His Ile Trp Ala Lys Leu
Arg Glu
325 330
335

Asp Val Glu Ser Gln Phe Gly Leu Gly Glu Glu Ser Arg Ile
Glu Glu
340 345 350

Ile Thr Phe Glu Ser Leu Lys Arg Cys Glu Tyr Leu Lys Ala
Val Met
355 360 365

Asn Glu Thr Leu Arg Leu His Pro Ser Val Pro Arg Asn Ala
Arg Phe
370 375 380

Ala Leu Lys Asp Thr Thr Leu Pro Arg Gly Gly Gly Pro Asp
Gly Lys
385 390 395
400

Asp Pro Ile Leu Val Arg Lys Asn Glu Val Val Gln Tyr Ser
Ile Ser

- 173/269 -

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                                405                                410
415
Gly Thr Gln Ile Asp Pro Lys His Tyr Gly Lys Asp Ala Lys
Leu Phe
                                420                                425                                430

Arg Pro Glu Arg Trp Phe Glu Ser Ser Thr Arg Asn Leu Gly
Trp Ala
                                435                                440                                445

Tyr Leu Pro Phe Asn Gly Gly Pro Arg Ile Cys Leu Gly Gln
Gln Phe
                                450                                455                                460

Ala Leu Thr Glu Ala Gly Tyr Ile Leu Val Arg Leu Ala Gln
Ser Phe
465                                470                                475
480

Asp Thr Leu Glu Leu Lys Pro Asp Thr Glu Tyr Pro Pro Pro
Arg Leu
                                485                                490
495

Ala His Leu Thr Met Cys Leu Phe Asp Gly Ala Leu Val Lys
Met Asp
                                500                                505                                510

<210> 43
<211> 1572
<212> DNA
<213> Candida tropicalis

<220>
<221> CDS
<222> (1)..(1572)

<400> 43
atg att aaa gaa ata gtg tat ttt gta tat tat tat gga att
acc cac 48
Met Ile Lys Glu Ile Val Tyr Phe Val Tyr Tyr Tyr Gly Ile
```


Glu	Asn	Asp	Arg	His	Ile	Lys	Tyr	Lys	Arg	Met	Ile	Asn	Asn	
Leu Tyr	130						135				140			
agt gtt Ser Val	aaa tta Lys Leu	tct Ser	tcc Ser	atc Ile	ttc Phe	tcc Ser	aaa Lys	gaa Glu	aac Asn	cac His	aca Thr	aga Arg	tca Ser	
145 160							150				155			
ttt tct Phe Ser	gac ccg Asp Pro	acc Thr	aca Thr	aaa Lys	aca Thr	tta Leu	gtc Val	gat Asp	gca Ala	gtt Val	gct Ala	aga Arg	gaa Glu	
175	165						170							
tca gtg Ser Val	att gtt Ile Val	gat Asp	gtg Val	ttt Phe	acg Thr	tta Leu	ttt Phe	ggg Gly	tcc Ser	ttg Leu	gcc Ala	atg Met	gat Asp	
		180				185				190				
tca aat Ser Asn	agg cat Arg His	ttt Phe	gaa Glu	cta Leu	ggg Gly	aga Arg	gac Asp	aat Asn	gga Gly	acg Thr	gat Asp	tta Leu	ttg Leu	
		195				200				205				
cca tgt Pro Cys	caa atg Gln Met	gaa Glu	agg Arg	cat His	att Ile	att Ile	gaa Glu	tct Ser	cat His	aga Arg	aag Lys	gtg Val	tct Ser	
		210				215				220				
ggg gca Gly Ala	ttc gca Phe Ala	tgg Trp	aca Thr	aca Thr	ttg Leu	atg Met	cca Pro	agc Ser	ttc Phe	ttt Phe	tgg Trp	aat Asn	ttg Leu	
225 240							230				235			
acc caa Thr Gln	aag ttg Lys Leu	gcc Ala	acc Thr	ttg Leu	caa Gln	gct Ala	gtt Val	gat Asp	gat Asp	att Ile	tgc Cys	aat Asn	ttc Phe	
255	245						250							

- 176/269 -

ggt	tta	tat	aaa	att	gca	gaa	tcc	aat	ctt	gtg	tcc	aat	ggt
aaa	aac		816										
Gly	Leu	Tyr	Lys	Ile	Ala	Glu	Ser	Asn	Leu	Val	Ser	Asn	Gly
Lys	Asn		260					265					270

cta	act	acg	ata	caa	aca	ctc	aag	aag	tac	gga	ttg	gaa	gga
aat	tct		864										
Leu	Thr	Thr	Ile	Gln	Thr	Leu	Lys	Lys	Tyr	Gly	Leu	Glu	Gly
Asn	Ser		275					280					285

gcg	tat	tct	ttt	ctc	acg	gat	aat	tta	ttt	gct	gga	cat	gaa
act	aca		912										
Ala	Tyr	Ser	Phe	Leu	Thr	Asp	Asn	Leu	Phe	Ala	Gly	His	Glu
Thr	Thr							295					300

gct	gtt	caa	ttg	aca	tat	ttg	tgt	tat	gaa	tta	tca	aga	cca
gct	aat		960										
Ala	Val	Gln	Leu	Thr	Tyr	Leu	Cys	Tyr	Glu	Leu	Ser	Arg	Pro
Ala	Asn												
305						310						315	
320													

tac	aaa	att	cag	aat	aga	tta	aga	tat	gag	ctt	caa	gaa	gca
ttt	cca		1008										
Tyr	Lys	Ile	Gln	Asn	Arg	Leu	Arg	Tyr	Glu	Leu	Gln	Glu	Ala
Phe	Pro												
						325						330	
335													

agt	ggt	caa	att	gaa	gat	ttg	gaa	gtg	gtt	gat	aat	ctt	ccg
tat	ctt		1056										
Ser	Gly	Gln	Ile	Glu	Asp	Leu	Glu	Val	Val	Asp	Asn	Leu	Pro
Tyr	Leu												
						340						345	350

aat	gcg	ttg	ttg	tcc	gaa	aat	ggt	cga	att	cac	acc	tca	att
cct	gga		1104										
Asn	Ala	Leu	Leu	Ser	Glu	Asn	Gly	Arg	Ile	His	Thr	Ser	Ile
Pro	Gly												
						355						360	365

gct	gag	cca	cgt	gtg	gtt	gca	aaa	ccg	tat	act	att	ggc	aaa
ttg	ctt		1152										
Ala	Glu	Pro	Arg	Val	Val	Ala	Lys	Pro	Tyr	Thr	Ile	Gly	Lys
Leu	Leu												
						370						375	380

- 177/269 -

att cca gtt ggt acg gtt atc tct tgt ctt cct tat gcg tat
cat aga 1200
Ile Pro Val Gly Thr Val Ile Ser Cys Leu Pro Tyr Ala Tyr
His Arg
385 390 395
400

aat ccg tcg gta ttt acc aat cct gat aaa ttt atc ccc gaa
aga tgg 1248
Asn Pro Ser Val Phe Thr Asn Pro Asp Lys Phe Ile Pro Glu
Arg Trp
405 410
415

tta gtt gac aac gaa gaa gac aag aaa cga gtc aaa caa caa
gcg aag 1296
Leu Val Asp Asn Glu Glu Asp Lys Lys Arg Val Lys Gln Gln
Ala Lys
420 425 430

tat atg atg cca ttt ggt aaa ggt gta aga atg tgt ctt ggg
atg aac 1344
Tyr Met Met Pro Phe Gly Lys Gly Val Arg Met Cys Leu Gly
Met Asn
435 440 445

ttg gca ctc att gaa atg aag ttg gcc att gca agt ttg tat
tta aac 1392
Leu Ala Leu Ile Glu Met Lys Leu Ala Ile Ala Ser Leu Tyr
Leu Asn
450 455 460

ttt tct tct tcc att gac gaa gac tgg tgt ggc aaa gta tta
gaa aat 1440
Phe Ser Ser Ser Ile Asp Glu Asp Trp Cys Gly Lys Val Leu
Glu Asn
465 470 475
480

gat gac ccc ata ggt atc ggg aat tca tgc act cat gag act
gat cag 1488
Asp Asp Pro Ile Gly Ile Gly Asn Ser Cys Thr His Glu Thr
Asp Gln
485 490
495

gat aaa atg aaa atg tac gat gct tat act acg aga cca atg
cta gat 1536
Asp Lys Met Lys Met Tyr Asp Ala Tyr Thr Thr Arg Pro Met
Leu Asp

- 178/269 -

500

505

510

gaa tgt tac ttg aag tgg aca aga tta act cct tga

1572

Glu Cys Tyr Leu Lys Trp Thr Arg Leu Thr Pro

515

520

<210> 44

<211> 523

<212> PRT

<213> Candida tropicalis

<400> 44

Met Ile Lys Glu Ile Val Tyr Phe Val Tyr Tyr Tyr Gly Ile

Thr His

1

5

10

15

Ser Val Ser Val Gln Val Thr Ala Leu Val Leu Ile Val Thr

Tyr Phe

20

25

30

Phe Val Ile Arg Pro Ile Asn Ser Pro Leu Trp Arg Val Pro

Gly Pro

35

40

45

Tyr Leu His Arg Val Thr Tyr Phe Pro Cys Leu Asn Ala Gln

Arg Lys

50

55

60

Gly Glu Trp Ile Ser Lys Val Tyr Asp Leu His Lys Lys Tyr

Gly Asp

65

70

75

80

Val Val Leu Leu Ser Pro Asn Glu Ile Ser Val Asn Gly Asp

Pro Lys

85

90

95

Tyr Leu Thr Asp Ile Tyr Val Lys Asn Leu Pro Lys Ser Lys

Phe Tyr

- 179/269 -

	100		105		110
Glu Asn Phe Arg Asn His Gly Phe Gln Asp Asn Ile Phe Ala					
Ser Leu					
	115		120		125
Glu Asn Asp Arg His Ile Lys Tyr Lys Arg Met Ile Asn Asn					
Leu Tyr					
	130		135		140
Ser Lys Ser Ser Ile Phe Ser Lys Glu Asn His Thr Arg Ser					
Val Leu					
145		150		155	
160					
Phe Asp Thr Thr Lys Thr Leu Val Asp Ala Val Ala Arg Glu					
Ser Pro					
		165		170	
175					
Ser Ile Asp Val Phe Thr Leu Phe Gly Ser Leu Ala Met Asp					
Val Val					
		180		185	190
Ser Arg Phe Glu Leu Gly Arg Asp Asn Gly Thr Asp Leu Leu					
Asn His					
	195		200		205
Pro Gln Glu Arg His Ile Ile Glu Ser His Arg Lys Val Ser					
Cys Met					
	210		215		220
Gly Phe Trp Thr Thr Leu Met Pro Ser Phe Phe Trp Asn Leu					
Ala Ala					
225		230		235	
240					
Thr Lys Ala Thr Leu Gln Ala Val Asp Asp Ile Cys Asn Phe					
Gln Leu					
		245		250	
255					

Gly Leu Tyr Lys Ile Ala Glu Ser Asn Leu Val Ser Asn Gly
Lys Asn
260 265 270

Leu Thr Thr Ile Gln Thr Leu Lys Lys Tyr Gly Leu Glu Gly
Asn Ser
275 280 285

Ala Tyr Ser Phe Leu Thr Asp Asn Leu Phe Ala Gly His Glu
Thr Thr
290 295 300

Ala Val Gln Leu Thr Tyr Leu Cys Tyr Glu Leu Ser Arg Pro
Ala Asn
305 310 315
320

Tyr Lys Ile Gln Asn Arg Leu Arg Tyr Glu Leu Gln Glu Ala
Phe Pro
325 330
335

Ser Gly Gln Ile Glu Asp Leu Glu Val Val Asp Asn Leu Pro
Tyr Leu
340 345 350

Asn Ala Leu Leu Ser Glu Asn Gly Arg Ile His Thr Ser Ile
Pro Gly

355 360 365

Ala Glu Pro Arg Val Val Ala Lys Pro Tyr Thr Ile Gly Lys
Leu Leu
370 375 380

Ile Pro Val Gly Thr Val Ile Ser Cys Leu Pro Tyr Ala Tyr
His Arg
385 390 395
400

- 181/269 -

Asn Pro Ser Val Phe Thr Asn Pro Asp Lys Phe Ile Pro Glu
Arg Trp

405

410

415

Leu Val Asp Asn Glu Glu Asp Lys Lys Arg Val Lys Gln Gln
Ala Lys

420

425

430

Tyr Met Met Pro Phe Gly Lys Gly Val Arg Met Cys Leu Gly
Met Asn

435

440

445

Leu Ala Leu Ile Glu Met Lys Leu Ala Ile Ala Ser Leu Tyr
Leu Asn

450

455

460

Phe Ser Ser Ser Ile Asp Glu Asp Trp Cys Gly Lys Val Leu
Glu Asn

465

470

475

480

Asp Asp Pro Ile Gly Ile Gly Asn Ser Cys Thr His Glu Thr
Asp Gln

485

490

495

Asp Lys Met Lys Met Tyr Asp Ala Tyr Thr Thr Arg Pro Met
Leu Asp

500

505

510

Glu Cys Tyr Leu Lys Trp Thr Arg Leu Thr Pro
515 520

<210> 45

<211> 1728

<212> DNA

<213> Candida tropicalis

<220>

<221> CDS

<222> (1)..(1728)

<400> 45

atg ctt ctg agc ata cca tgg gat caa tca ttg cta acg ttg
cta aca 48
Met Leu Leu Ser Ile Pro Trp Asp Gln Ser Leu Leu Thr Leu
Leu Thr
1 5 10
15

tat ctt gat acc cat cca ata gct acg ata ttc acc att att
tta acc 96
Tyr Leu Asp Thr His Pro Ile Ala Thr Ile Phe Thr Ile Ile
Leu Thr
20 25 30

att tta aca att gga att tta ttt gat tat tgt cta tca cct
aaa gag 144
Ile Leu Thr Ile Gly Ile Leu Phe Asp Tyr Cys Leu Ser Pro
Lys Glu
35 40 45

att gcc aat att ttc agt att cct gga gat ttg cca ttt att
ggt cat 192
Ile Ala Asn Ile Phe Ser Ile Pro Gly Asp Leu Pro Phe Ile
Gly His
50 55 60

tta cat tta ata cta gat aat cca gca ttg att tat tta aca
tgg tat 240
Leu His Leu Ile Leu Asp Asn Pro Ala Leu Ile Tyr Leu Thr
Trp Tyr
65 70 75
80

aaa tta tat aat aaa ctg gtt ttt caa att cgt att gga aat
aaa cgt 288
Lys Leu Tyr Asn Lys Leu Val Phe Gln Ile Arg Ile Gly Asn
Lys Arg
85 90
95

gta gtt gtt gtt aat tca ttt gat gat gtt gtt gga tta tgg
ata aat 336
Val Val Val Val Asn Ser Phe Asp Asp Val Val Gly Leu Trp
Ile Asn
100 105 110

cat agt tgt caa aat aat tca aga cct tta agt tat act ttt
cat gga 384

His	Ser	Cys	Gln	Asn	Asn	Ser	Arg	Pro	Leu	Ser	Tyr	Thr	Phe
His	Gly												
		115					120					125	
tta	ggt	tca	gca	tta	caa	ggt	ttt	aca	ggt	ggt	tct	act	cct
gca	agt		432										
Leu	Val	Ser	Ala	Leu	Gln	Gly	Phe	Thr	Val	Gly	Ser	Thr	Pro
Ala	Ser												
		130				135					140		
tta	aca	ttt	ctg	aga	aag	aag	aaa	ggt	att	tca	ctg	tgt	tta
aga	aag		480										
Leu	Thr	Phe	Leu	Arg	Lys	Lys	Lys	Val	Ile	Ser	Leu	Cys	Leu
Arg	Lys												
145					150					155			
160													
aaa	gaa	att	gat	gaa	aaa	gta	tgt	ctc	ata	gat	aat	gaa	att
tgt	ggt		528										
Lys	Glu	Ile	Asp	Glu	Lys	Val	Cys	Leu	Ile	Asp	Asn	Glu	Ile
Cys	Val												
			165					170					
175													
atg	att	aaa	gaa	ata	att	aaa	aag	aag	gat	ata	tca	act	gat
gta	aat		576										
Met	Ile	Lys	Glu	Ile	Ile	Lys	Lys	Lys	Asp	Ile	Ser	Thr	Asp
Val	Asn												
			180					185				190	
atg	tta	cct	tat	tta	caa	aaa	ttc	ata	tta	aaa	aca	gct	att
ctt	atg		624										
Met	Leu	Pro	Tyr	Leu	Gln	Lys	Phe	Ile	Leu	Lys	Thr	Ala	Ile
Leu	Met												
		195					200				205		
agt	tat	gga	att	gaa	ttg	gat	tgt	tat	aat	aaa	gat	ggt	aaa
tta	tgt		672										
Ser	Tyr	Gly	Ile	Glu	Leu	Asp	Cys	Tyr	Asn	Lys	Asp	Val	Lys
Leu	Cys												
		210				215					220		
caa	gag	att	atc	acc	gtg	gag	aat	aat	atc	ata	aga	tta	aga
tca	cca		720										
Gln	Glu	Ile	Ile	Thr	Val	Glu	Asn	Asn	Ile	Ile	Arg	Leu	Arg
Ser	Pro												
225					230						235		
240													
ata	tct	aat	ctt	caa	gat	tct	gta	cct	ttc	tta	aga	cta	ata

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cca tgg      768
Ile Ser Asn Leu Gln Asp Ser Val Pro Phe Leu Arg Leu Ile
Pro Trp
                245                250
255

ttt aat aat cga gaa ttt gcc ctt cgt tgt gga aat aga agg
aat aaa      816
Phe Asn Asn Arg Glu Phe Ala Leu Arg Cys Gly Asn Arg Arg
Asn Lys
                260                265                270

tat atg gat caa tta tat aat agg tta caa aat gga tta gct
gaa aat      864
Tyr Met Asp Gln Leu Tyr Asn Arg Leu Gln Asn Gly Leu Ala
Glu Asn
                275                280                285

gat cca aat ata gct aat agt att ctt gga caa tta att ctt
aat aat      912
Asp Pro Asn Ile Ala Asn Ser Ile Leu Gly Gln Leu Ile Leu
Asn Asn
                290                295                300

gat aat aat aat tct aac agc tta act agt caa gaa ata caa
agt att      960
Asp Asn Asn Asn Ser Asn Ser Leu Thr Ser Gln Glu Ile Gln
Ser Ile
305                310                315
320

tgt tta aca tta gta agt gct gga tta gat aat acc cca ctt
aat ttg      1008
Cys Leu Thr Leu Val Ser Ala Gly Leu Asp Asn Thr Pro Leu
Asn Leu
                325                330
335

aat tat ctt att gga ata tta tca caa cca aga ata ggt aag
ata ttt      1056
Asn Tyr Leu Ile Gly Ile Leu Ser Gln Pro Arg Ile Gly Lys
Ile Phe
                340                345                350

caa gat aaa gct ata aaa gat att tta aat cat gca aat gga
gat att      1104
Gln Asp Lys Ala Ile Lys Asp Ile Leu Asn His Ala Asn Gly
Asp Ile
                355                360                365

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- 185/269 -

att caa gca tgg aat caa ctg aat gaa gaa aat cga gat tgt
aaa tat 1152
Ile Gln Ala Trp Asn Gln Leu Asn Glu Glu Asn Arg Asp Cys
Lys Tyr
370 375 380

att caa gct tta att ctt gaa act tta aga cat ttt aca gta
tta cca 1200
Ile Gln Ala Leu Ile Leu Glu Thr Leu Arg His Phe Thr Val
Leu Pro
385 390 395
400

tta agt tta cct aga tta act aca aaa cca ata tat tat aaa
aat ttt 1248
Leu Ser Leu Pro Arg Leu Thr Thr Lys Pro Ile Tyr Tyr Lys
Asn Phe
405 410
415

atg att cct aaa aat act cat atg ttt atg aat gca tat tct
gca aat 1296
Met Ile Pro Lys Asn Thr His Met Phe Met Asn Ala Tyr Ser
Ala Asn
420 425 430

cat gat gaa tta ata ttc aaa aat cca ttt aaa ttt gat cca
gaa aga 1344
His Asp Glu Leu Ile Phe Lys Asn Pro Phe Lys Phe Asp Pro
Glu Arg
435 440 445

tgg tta gat tca gaa act aat gaa att aaa tca aaa ata ctt
gct act 1392
Trp Leu Asp Ser Glu Thr Asn Glu Ile Lys Ser Lys Ile Leu
Ala Thr
450 455 460

act tct tcg tct tct tct tcg aca cat cat ggt ggt gga aat
gga ata 1440
Thr Ser Ser Ser Ser Ser Ser Thr His His Gly Gly Gly Asn
Gly Ile
465 470 475
480

aat gta cag aat ttt cat ttt gca ttt ggt gct gga tca aga
atg tgt 1488
Asn Val Gln Asn Phe His Phe Ala Phe Gly Ala Gly Ser Arg
Met Cys
485 490

495

tca ggt tat aat cta gtt atg aaa gaa atg tat atg atg ata
att aaa 1536

Ser Gly Tyr Asn Leu Val Met Lys Glu Met Tyr Met Met Ile
Ile Lys

500

505

510

tta tta tta tta ttt gaa att aat cct cct gat aat aat aat
aat aat 1584

Leu Leu Leu Leu Phe Glu Ile Asn Pro Pro Asp Asn Asn Asn
Asn Asn

515

520

525

ggg aaa tat tta atg gaa atg aat cct ttt gtt aat aat ctg
aat cct 1632

Gly Lys Tyr Leu Met Glu Met Asn Pro Phe Val Asn Asn Leu
Asn Pro

530

535

540

aga ggt act tca ttt gaa cca cga ata cat aat att aaa tta
caa tat 1680

Arg Gly Thr Ser Phe Glu Pro Arg Ile His Asn Ile Lys Leu
Gln Tyr

545

550

555

560

aga aaa cta cct aat tat gaa act cta cac gaa ata gtt ctc
aaa tag 1728

Arg Lys Leu Pro Asn Tyr Glu Thr Leu His Glu Ile Val Leu
Lys

565

570

575

<210> 46

<211> 575

<212> PRT

<213> Candida tropicalis

<400> 46

Met Leu Leu Ser Ile Pro Trp Asp Gln Ser Leu Leu Thr Leu
Leu Thr

1

5

10

15

Tyr Leu Asp Thr His Pro Ile Ala Thr Ile Phe Thr Ile Ile
Leu Thr

- 187/269 -

	20	25	30
Ile Leu Thr Ile Gly Ile Leu Phe Asp Tyr Cys Leu Ser Pro			
Lys Glu			
	35	40	45
Ile Ala Asn Ile Phe Ser Ile Pro Gly Asp Leu Pro Phe Ile			
Gly His			
	50	55	60
Leu His Leu Ile Leu Asp Asn Pro Ala Leu Ile Tyr Leu Thr			
Trp Tyr			
65	70	75	
80			
Lys Leu Tyr Asn Lys Leu Val Phe Gln Ile Arg Ile Gly Asn			
Lys Arg			
	85	90	
95			
Val Val Val Val Asn Ser Phe Asp Asp Val Val Gly Leu Trp			
Ile Asn			
	100	105	110
His Ser Cys Gln Asn Asn Ser Arg Pro Leu Ser Tyr Thr Phe			
His Gly			
	115	120	125
Leu Val Ser Ala Leu Gln Gly Phe Thr Val Gly Ser Thr Pro			
Ala Ser			
	130	135	140
Leu Thr Phe Leu Arg Lys Lys Lys Val Ile Ser Leu Cys Leu			
Arg Lys			
145	150	155	
160			
Lys Glu Ile Asp Glu Lys Val Cys Leu Ile Asp Asn Glu Ile			
Cys Val			
	165	170	
175			

Met Ile Lys Glu Ile Ile Lys Lys Lys Asp Ile Ser Thr Asp
Val Asn
180 185 190

Met Leu Pro Tyr Leu Gln Lys Phe Ile Leu Lys Thr Ala Ile
Leu Met
195 200 205

Ser Tyr Gly Ile Glu Leu Asp Cys Tyr Asn Lys Asp Val Lys
Leu Cys
210 215 220

Gln Glu Ile Ile Thr Val Glu Asn Asn Ile Ile Arg Leu Arg
Ser Pro
225 230 235
240

Ile Ser Asn Leu Gln Asp Ser Val Pro Phe Leu Arg Leu Ile
Pro Trp
245 250
255

Phe Asn Asn Arg Glu Phe Ala Leu Arg Cys Gly Asn Arg Arg
Asn Lys
260 265 270

Tyr Met Asp Gln Leu Tyr Asn Arg Leu Gln Asn Gly Leu Ala
Glu Asn
275 280 285

Asp Pro Asn Ile Ala Asn Ser Ile Leu Gly Gln Leu Ile Leu
Asn Asn
290 295 300

Asp Asn Asn Asn Ser Asn Ser Leu Thr Ser Gln Glu Ile Gln
Ser Ile
305 310 315
320

- 189/269 -

Cys Leu Thr Leu Val Ser Ala Gly Leu Asp Asn Thr Pro Leu
Asn Leu
325 330
335

Asn Tyr Leu Ile Gly Ile Leu Ser Gln Pro Arg Ile Gly Lys
Ile Phe
340 345 350

Gln Asp Lys Ala Ile Lys Asp Ile Leu Asn His Ala Asn Gly
Asp Ile
355 360 365

Ile Gln Ala Trp Asn Gln Leu Asn Glu Glu Asn Arg Asp Cys
Lys Tyr
370 375 380

Ile Gln Ala Leu Ile Leu Glu Thr Leu Arg His Phe Thr Val
Leu Pro
385 390 395
400

Leu Ser Leu Pro Arg Leu Thr Thr Lys Pro Ile Tyr Tyr Lys
Asn Phe
405 410
415

Met Ile Pro Lys Asn Thr His Met Phe Met Asn Ala Tyr Ser
Ala Asn
420 425 430

His Asp Glu Leu Ile Phe Lys Asn Pro Phe Lys Phe Asp Pro
Glu Arg
435 440 445

Trp Leu Asp Ser Glu Thr Asn Glu Ile Lys Ser Lys Ile Leu
Ala Thr
450 455 460

Thr Ser Ser Ser Ser Ser Ser Thr His His Gly Gly Gly Asn
Gly Ile

- 190/269 -

465
480

470

475

Asn Val Gln Asn Phe His Phe Ala Phe Gly Ala Gly Ser Arg
Met Cys

485

490

495

Ser Gly Tyr Asn Leu Val Met Lys Glu Met Tyr Met Met Ile
Ile Lys

500

505

510

Leu Leu Leu Leu Phe Glu Ile Asn Pro Pro Asp Asn Asn Asn
Asn Asn

515

520

525

Gly Lys Tyr Leu Met Glu Met Asn Pro Phe Val Asn Asn Leu
Asn Pro

530

535

540

Arg Gly Thr Ser Phe Glu Pro Arg Ile His Asn Ile Lys Leu
Gln Tyr

545

550

555

560

Arg Lys Leu Pro Asn Tyr Glu Thr Leu His Glu Ile Val Leu
Lys

565

570

575

<210> 47

<211> 1518

<212> DNA

<213> Candida tropicalis

<220>

<221> CDS

<222> (1)..(1518)

<400> 47

atg tat caa tta ttt tgt ttt ctt gct ggt ata att gtt gta
tat aaa 48

Met	Tyr	Gln	Leu	Phe	Cys	Phe	Leu	Ala	Gly	Ile	Ile	Val	Val
Tyr	Lys												
1			5					10					
15													
gca	gca	caa	tac	tac	aag	aga	agg	aca	ctt	gtg	act	aaa	ttt
cat	tgc		96										
Ala	Ala	Gln	Tyr	Tyr	Lys	Arg	Arg	Thr	Leu	Val	Thr	Lys	Phe
His	Cys												
		20					25					30	
aaa	caa	gca	cgt	att	tcc	cca	aac	aag	tca	tgg	ttg	gaa	tat
tta	ggc		144										
Lys	Gln	Ala	Arg	Ile	Ser	Pro	Asn	Lys	Ser	Trp	Leu	Glu	Tyr
Leu	Gly												
		35					40					45	
att	gcc	tcc	gtt	gta	cat	gcc	aat	gaa	atg	att	aga	aaa	gga
gga	ttg		192										
Ile	Ala	Ser	Val	Val	His	Ala	Asn	Glu	Met	Ile	Arg	Lys	Gly
Gly	Leu												
		50				55					60		
tat	tca	gaa	att	gat	gga	aga	ttt	aaa	tcc	ctt	gat	gtt	tca
aca	ttc		240										
Tyr	Ser	Glu	Ile	Asp	Gly	Arg	Phe	Lys	Ser	Leu	Asp	Val	Ser
Thr	Phe												
65					70					75			
80													
aag	tct	ata	act	ttg	gga	aag	aca	acg	tat	gtt	acc	aaa	gat
att	gaa		288										
Lys	Ser	Ile	Thr	Leu	Gly	Lys	Thr	Thr	Tyr	Val	Thr	Lys	Asp
Ile	Glu												
			85						90				
95													
aac	atc	cgt	cat	atc	ttg	agt	gca	acg	gaa	atg	aac	tca	tgg
aat	ctt		336										
Asn	Ile	Arg	His	Ile	Leu	Ser	Ala	Thr	Glu	Met	Asn	Ser	Trp
Asn	Leu												
		100					105					110	
ggt	gcc	cgt	cca	att	gcg	tta	aga	ccc	ttg	att	ggt	gat	gga
att	ttt		384										
Gly	Ala	Arg	Pro	Ile	Ala	Leu	Arg	Pro	Leu	Ile	Gly	Asp	Gly
Ile	Phe												
		115					120					125	
gct	agt	gaa	ggt	caa	tct	tgg	aaa	cat	agt	cga	atc	atg	ctt

aga cca 432
Ala Ser Glu Gly Gln Ser Trp Lys His Ser Arg Ile Met Leu
Arg Pro
130 135 140

gta ttt gca aaa gaa cac gtt aaa caa atc act tca atg gaa
cca tat 480
Val Phe Ala Lys Glu His Val Lys Gln Ile Thr Ser Met Glu
Pro Tyr
145 150 155
160

gta caa ctg ttg atc aaa atc atc aag aac cat gaa ggg gaa
cca tta 528
Val Gln Leu Leu Ile Lys Ile Ile Lys Asn His Glu Gly Glu
Pro Leu
165 170
175

gag ttt caa acc tta gcc cat ctt ttt aca ata gat tat tct
act gat 576
Glu Phe Gln Thr Leu Ala His Leu Phe Thr Ile Asp Tyr Ser
Thr Asp
180 185 190

ttc cta tta ggt gaa agt tgt gat agt ttg aag gat ttc cta
gga gaa 624
Phe Leu Leu Gly Glu Ser Cys Asp Ser Leu Lys Asp Phe Leu
Gly Glu
195 200 205

gag tcc aat tcc aca tta gat aca tcg ttg aga ctg gca ttt
gca tca 672
Glu Ser Asn Ser Thr Leu Asp Thr Ser Leu Arg Leu Ala Phe
Ala Ser
210 215 220

cag ttt aat aaa acc cag cag caa atg aca att cga ttc atg
ttg gga 720
Gln Phe Asn Lys Thr Gln Gln Gln Met Thr Ile Arg Phe Met
Leu Gly
225 230 235
240

aaa ttg gcc ttt ctc atg tat cca aag agt ttt caa aat agt
att caa 768
Lys Leu Ala Phe Leu Met Tyr Pro Lys Ser Phe Gln Asn Ser
Ile Gln
245 250
255

atg caa aag gac ttt gtt gat gaa tat atc gac aga gta gta
ggt atg 816
Met Gln Lys Asp Phe Val Asp Glu Tyr Ile Asp Arg Val Val
Gly Met
260 265 270

tcc gaa gaa gaa ttg aac aat cat cca aag agc tat gtt ttg
ttg tac 864
Ser Glu Glu Glu Leu Asn Asn His Pro Lys Ser Tyr Val Leu
Leu Tyr
275 280 285

caa tta gca aga caa act aag aat cgt gat ata tta caa gat
gaa ttg 912
Gln Leu Ala Arg Gln Thr Lys Asn Arg Asp Ile Leu Gln Asp
Glu Leu
290 295 300

atg tcc att tta ctt gca ggt aga gac acc act gcc agt ttg
ttg act 960
Met Ser Ile Leu Leu Ala Gly Arg Asp Thr Thr Ala Ser Leu
Leu Thr
305 310 315
320

ttt ttg ttt ttc gaa tta agt cac cat cca gaa gta ttt aac
aaa tta 1008
Phe Leu Phe Phe Glu Leu Ser His His Pro Glu Val Phe Asn
Lys Leu
325 330
335

aaa gag gaa atc gaa aga cac ttt cct gat gtt gaa tcc gtt
aca ttt 1056
Lys Glu Glu Ile Glu Arg His Phe Pro Asp Val Glu Ser Val
Thr Phe
340 345 350

gga act atc cag aga tgc gac tat ctt caa tgg tgt att aac
gaa act 1104
Gly Thr Ile Gln Arg Cys Asp Tyr Leu Gln Trp Cys Ile Asn
Glu Thr
355 360 365

atg aga ctc cat cca tca gtt cct ttt aat ttc aga act gca
gcc aat 1152
Met Arg Leu His Pro Ser Val Pro Phe Asn Phe Arg Thr Ala
Ala Asn
370 375 380

gac aca gta ata cca aga ggt gga ggt aaa tcc tgt aca gat
 cct att 1200
 Asp Thr Val Ile Pro Arg Gly Gly Gly Lys Ser Cys Thr Asp
 Pro Ile
 385 390 395
 400

ctt gtc cat aag ggt gaa caa gta tta ttc agt ttc tat tct
 gta aac 1248
 Leu Val His Lys Gly Glu Gln Val Leu Phe Ser Phe Tyr Ser
 Val Asn
 405 410
 415

aga gaa gaa aag tat ttt ggt aca aat acc gac aag ttt gct
 cca gaa 1296
 Arg Glu Glu Lys Tyr Phe Gly Thr Asn Thr Asp Lys Phe Ala
 Pro Glu
 420 425 430

aga tgg agt gaa tca tta agg aga act gag ttc ata cca ttt
 tct gct 1344
 Arg Trp Ser Glu Ser Leu Arg Arg Thr Glu Phe Ile Pro Phe
 Ser Ala
 435 440 445

gga cct cgt gcc tgt ttg ggt caa cag tta gct aga gtt gaa
 gct tca 1392
 Gly Pro Arg Ala Cys Leu Gly Gln Gln Leu Ala Arg Val Glu
 Ala Ser
 450 455 460

tat gtt act att aga ttg ctt caa acc ttt cat ggg ttg cat
 aat gcc 1440
 Tyr Val Thr Ile Arg Leu Leu Gln Thr Phe His Gly Leu His
 Asn Ala
 465 470 475
 480

agt aaa caa tac cca cca aat aga gtg gtt gca gct aca atg
 aga ttg 1488
 Ser Lys Gln Tyr Pro Pro Asn Arg Val Val Ala Ala Thr Met
 Arg Leu
 485 490
 495

act gac ggt tgt aac gtt tgt ttt atc tag
 1518
 Thr Asp Gly Cys Asn Val Cys Phe Ile

- 195/269 -

500

505

<210> 48
<211> 505
<212> PRT
<213> Candida tropicalis

<400> 48

Met Tyr Gln Leu Phe Cys Phe Leu Ala Gly Ile Ile Val Val
Tyr Lys
1 5 10
15

Ala Ala Gln Tyr Tyr Lys Arg Arg Thr Leu Val Thr Lys Phe
His Cys
20 25 30

Lys Gln Ala Arg Ile Ser Pro Asn Lys Ser Trp Leu Glu Tyr
Leu Gly
35 40 45

Ile Ala Ser Val Val His Ala Asn Glu Met Ile Arg Lys Gly
Gly Leu
50 55 60

Tyr Ser Glu Ile Asp Gly Arg Phe Lys Ser Leu Asp Val Ser
Thr Phe
65 70 75
80

Lys Ser Ile Thr Leu Gly Lys Thr Thr Tyr Val Thr Lys Asp
Ile Glu
85 90
95

Asn Ile Arg His Ile Leu Ser Ala Thr Glu Met Asn Ser Trp
Asn Leu
100 105 110

Gly Ala Arg Pro Ile Ala Leu Arg Pro Leu Ile Gly Asp Gly
Ile Phe

- 196/269 -

115	120	125
Ala Ser Glu Gly Gln Ser Trp Lys His Ser Arg Ile Met Leu		
Arg Pro		
130	135	140
Val Phe Ala Lys Glu His Val Lys Gln Ile Thr Ser Met Glu		
Pro Tyr		
145	150	155
160		
Val Gln Leu Leu Ile Lys Ile Ile Lys Asn His Glu Gly Glu		
Pro Leu		
165	170	
175		
Glu Phe Gln Thr Leu Ala His Leu Phe Thr Ile Asp Tyr Ser		
Thr Asp		
180	185	190
Phe Leu Leu Gly Glu Ser Cys Asp Ser Leu Lys Asp Phe Leu		
Gly Glu		
195	200	205
Glu Ser Asn Ser Thr Leu Asp Thr Ser Leu Arg Leu Ala Phe		
Ala Ser		
210	215	220
Gln Phe Asn Lys Thr Gln Gln Gln Met Thr Ile Arg Phe Met		
Leu Gly		
225	230	235
240		
Lys Leu Ala Phe Leu Met Tyr Pro Lys Ser Phe Gln Asn Ser		
Ile Gln		
245	250	
255		
Met Gln Lys Asp Phe Val Asp Glu Tyr Ile Asp Arg Val Val		
Gly Met		
260	265	270

Ser Glu Glu Glu Leu Asn Asn His Pro Lys Ser Tyr Val Leu
Leu Tyr
275 280 285

Gln Leu Ala Arg Gln Thr Lys Asn Arg Asp Ile Leu Gln Asp
Glu Leu
290 295 300

Met Ser Ile Leu Leu Ala Gly Arg Asp Thr Thr Ala Ser Leu
Leu Thr
305 310 315
320

Phe Leu Phe Phe Glu Leu Ser His His Pro Glu Val Phe Asn
Lys Leu
325 330
335

Lys Glu Glu Ile Glu Arg His Phe Pro Asp Val Glu Ser Val
Thr Phe

340 345 350

Gly Thr Ile Gln Arg Cys Asp Tyr Leu Gln Trp Cys Ile Asn
Glu Thr
355 360 365

Met Arg Leu His Pro Ser Val Pro Phe Asn Phe Arg Thr Ala
Ala Asn
370 375 380

Asp Thr Val Ile Pro Arg Gly Gly Gly Lys Ser Cys Thr Asp
Pro Ile
385 390 395
400

Leu Val His Lys Gly Glu Gln Val Leu Phe Ser Phe Tyr Ser
 Val Asn
 405 410
 415

- 198/269 -

Arg Glu Glu Lys Tyr Phe Gly Thr Asn Thr Asp Lys Phe Ala
Pro Glu
420 425 430

Arg Trp Ser Glu Ser Leu Arg Arg Thr Glu Phe Ile Pro Phe
Ser Ala
435 440 445

Gly Pro Arg Ala Cys Leu Gly Gln Gln Leu Ala Arg Val Glu
Ala Ser
450 455 460

Tyr Val Thr Ile Arg Leu Leu Gln Thr Phe His Gly Leu His
Asn Ala
465 470 475
480

Ser Lys Gln Tyr Pro Pro Asn Arg Val Val Ala Ala Thr Met
Arg Leu
485 490
495

Thr Asp Gly Cys Asn Val Cys Phe Ile
500 505

<210> 49
<211> 1584
<212> DNA
<213> Candida tropicalis

<220>
<221> CDS
<222> (1)..(1584)

<400> 49
atg agt gtc aat act act tct cca gtt gtg gat agt att agt
gat aat 48
Met Ser Val Asn Thr Thr Ser Pro Val Val Asp Ser Ile Ser
Asp Asn
1 5 10
15

- 199/269 -

gct	act	aca	tat	ttg	agt	aca	aaa	tat	atc	atc	gat	agt	tta
tat	tca												
Ala	Thr	Thr	Tyr	Leu	Ser	Thr	Lys	Tyr	Ile	Ile	Asp	Ser	Leu
Tyr	Ser												

20

25

30

act	tat	caa	caa	gct	tca	tgg	tta	caa	atc	att	tta	acc	tca
atc	att												
Thr	Tyr	Gln	Gln	Ala	Ser	Trp	Leu	Gln	Ile	Ile	Leu	Thr	Ser
Ile	Ile												

35

40

45

ctc	att	ttg	act	tat	gat	caa	atc	ctg	tat	caa	atc	aat	aaa
ggt	tca												
Leu	Ile	Leu	Thr	Tyr	Asp	Gln	Ile	Leu	Tyr	Gln	Ile	Asn	Lys
Gly	Ser												

50

55

60

att	gct	ggt	cca	aaa	ttc	aaa	ttt	tgg	cca	att	att	ggt	cca
ttc	ttg												
Ile	Ala	Gly	Pro	Lys	Phe	Lys	Phe	Trp	Pro	Ile	Ile	Gly	Pro
Phe	Leu												

65

70

75

80

gaa	tct	tta	gat	cca	aaa	ttc	gaa	gaa	tat	aaa	gct	aaa	tgg
gat	tct												
Glu	Ser	Leu	Asp	Pro	Lys	Phe	Glu	Glu	Tyr	Lys	Ala	Lys	Trp
Asp	Ser												

85

90

95

ggt	gaa	ttg	agt	tgt	ggt	tcc	att	ttc	cat	aaa	ttc	ggt	ggt
att	gct												
Gly	Glu	Leu	Ser	Cys	Val	Ser	Ile	Phe	His	Lys	Phe	Val	Val
Ile	Ala												

100

105

110

tct	tct	cgt	gat	tta	gct	aga	aag	att	tta	gca	tct	cca	aaa
tac	ggt												
Ser	Ser	Arg	Asp	Leu	Ala	Arg	Lys	Ile	Leu	Ala	Ser	Pro	Lys
Tyr	Val												

115

120

125

aaa	cct	tgt	ggt	ggt	gat	ggt	gct	ggt	aaa	att	tta	aga	cct
tca	aat												
Lys	Pro	Cys	Val	Val	Asp	Val	Ala	Val	Lys	Ile	Leu	Arg	Pro
Ser	Asn												

130

135

140

- 200/269 -

tgg gtt ttc tta gac ggt aaa gca cat act gat tac cgt cgt
tct ttg 480
Trp Val Phe Leu Asp Gly Lys Ala His Thr Asp Tyr Arg Arg
Ser Leu
145 150 155
160

aat ggt tta ttc tcc caa aga gct ttg gaa att tac att cca
gtt caa 528
Asn Gly Leu Phe Ser Gln Arg Ala Leu Glu Ile Tyr Ile Pro
Val Gln
165 170
175

gaa aaa tac atg gat att tat tta gat aga ttc tgt aag tac
gac ggt 576
Glu Lys Tyr Met Asp Ile Tyr Leu Asp Arg Phe Cys Lys Tyr
Asp Gly
180 185 190

cca cgt gaa ttc ttc cca gaa ttt aga gaa ttg ttg tgt gct
tta tct 624
Pro Arg Glu Phe Phe Pro Glu Phe Arg Glu Leu Leu Cys Ala
Leu Ser
195 200 205

ttg aga act ttc tgt ggg gat tac atc act gaa gat caa att
gct tta 672
Leu Arg Thr Phe Cys Gly Asp Tyr Ile Thr Glu Asp Gln Ile
Ala Leu
210 215 220

gtt gct gat aac tat tac aga gtc act gct gct ttg gaa ttg
gtc aat 720
Val Ala Asp Asn Tyr Tyr Arg Val Thr Ala Ala Leu Glu Leu
Val Asn
225 230 235
240

ttc cca atc att att cct tac act aaa act tgg tac ggt aag
aag att 768
Phe Pro Ile Ile Ile Pro Tyr Thr Lys Thr Trp Tyr Gly Lys
Lys Ile
245 250
255

gct gat gat acc atg aag att ttt gaa aat tgt gct gct atg
tcc aag 816
Ala Asp Asp Thr Met Lys Ile Phe Glu Asn Cys Ala Ala Met
Ser Lys

			260				265				270			
aaa gat Lys Asp	cac gaa His Glu	att Ile	aat 864 Asn	gaa Glu	aat Asn	aat Asn	ggc Gly	act Thr	cca Pro	ggc Gly	tgt Cys	gtt Val	atg Met	
		275					280					285		
tgg gat Trp Asp	att cca Ile Pro	tac Tyr	ttg 912 Leu	atg Met	aaa Lys	gaa Glu	gct Ala	aaa Lys	gaa Glu	aaa Lys	cac His	tct Ser	gat Asp	
	290					295					300			
gat tcc Asp Ser 305 320	tcc gaa Ser Glu	aaa Lys	tta 960 Leu	ttg Leu	att Ile	aga Arg	gaa Glu	ttc Phe	tcc Ser	aac Asn	cgt Arg	gaa Glu	att Ile	
					310					315				
gcc tct Ala Ser 335	att ttg Ile Leu	ttc Phe	act 1008 Thr	ttc Phe	ttg Leu	ttt Phe	gct Ala	tct Ser	caa Gln	gat Asp	gcc Ala	tct Ser	tct Ser	
				325					330					
gct gtt Ala Val	tgt gcc Cys Ala	tgg Trp	tta 1056 Leu	ttc Phe	caa Gln	att Ile	gtc Val	gcc Ala	gac Asp	aga Arg	cca Pro	gat Asp	gtt Val	
			340					345					350	
aag tct Lys Ser	att gtt Ile Val	aga Arg	gaa 1104 Glu	gaa Glu	caa Gln	ttg Leu	aga Arg	gtt Val	aga Arg	aac Asn	aat Asn	gac Asp	cca Pro	
		355					360					365		
aaa gat Lys Asp	ttg gtt Leu Val	tcc Ser	ttg 1152 Leu	gat Asp	ttg Leu	att Ile	aat Asn	gaa Glu	atg Met	act Thr	tac Tyr	acc Thr	aat Asn	
	370					375					380			
gtt cca Val Pro	aaa tat Lys Tyr	gaa Glu	tct 1200 Ser	ttg Leu	aga Arg	tac Tyr	cgt Arg	cca Pro	cca Pro	gtc Val	ttg Leu	atg Met	gtt Val	

Val Ile Leu Glu Trp Lys Lys Arg Asp Pro Leu Ala Ala Ser
Asn

515

520

525

<210> 50

<211> 527

<212> PRT

<213> Candida tropicalis

<400> 50

Met Ser Val Asn Thr Thr Ser Pro Val Val Asp Ser Ile Ser
Asp Asn

1 5

10

15

Ala Thr Thr Tyr Leu Ser Thr Lys Tyr Ile Ile Asp Ser Leu
Tyr Ser

20

25

30

Thr Tyr Gln Gln Ala Ser Trp Leu Gln Ile Ile Leu Thr Ser
Ile Ile

35

40

45

Leu Ile Leu Thr Tyr Asp Gln Ile Leu Tyr Gln Ile Asn Lys
Gly Ser

50

55

60

Ile Ala Gly Pro Lys Phe Lys Phe Trp Pro Ile Ile Gly Pro
Phe Leu

65

70

75

80

Glu Ser Leu Asp Pro Lys Phe Glu Glu Tyr Lys Ala Lys Trp
Asp Ser

85

90

95

Gly Glu Leu Ser Cys Val Ser Ile Phe His Lys Phe Val Val
Ile Ala

100

105

110

- 204/269 -

Ser	Ser	Arg	Asp	Leu	Ala	Arg	Lys	Ile	Leu	Ala	Ser	Pro	Lys
Tyr	Val												
		115					120					125	

Lys	Pro	Cys	Val	Val	Asp	Val	Ala	Val	Lys	Ile	Leu	Arg	Pro
Ser	Asn												
	130					135					140		

Trp	Val	Phe	Leu	Asp	Gly	Lys	Ala	His	Thr	Asp	Tyr	Arg	Arg
Ser	Leu												
145					150					155			
160													

Asn	Gly	Leu	Phe	Ser	Gln	Arg	Ala	Leu	Glu	Ile	Tyr	Ile	Pro
Val	Gln												
				165					170				
175													

Glu	Lys	Tyr	Met	Asp	Ile	Tyr	Leu	Asp	Arg	Phe	Cys	Lys	Tyr
Asp	Gly												
			180					185					190

Pro	Arg	Glu	Phe	Phe	Pro	Glu	Phe	Arg	Glu	Leu	Leu	Cys	Ala
Leu	Ser												
		195					200					205	

Leu	Arg	Thr	Phe	Cys	Gly	Asp	Tyr	Ile	Thr	Glu	Asp	Gln	Ile
Ala	Leu												
	210					215					220		

Val	Ala	Asp	Asn	Tyr	Tyr	Arg	Val	Thr	Ala	Ala	Leu	Glu	Leu
Val	Asn												
225					230					235			
240													

Phe	Pro	Ile	Ile	Ile	Pro	Tyr	Thr	Lys	Thr	Trp	Tyr	Gly	Lys
Lys	Ile												
				245					250				
255													

Ala	Asp	Asp	Thr	Met	Lys	Ile	Phe	Glu	Asn	Cys	Ala	Ala	Met
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- 205/269 -

Ser	Lys													
		260						265					270	

Lys	His	Ile	Asn	Glu	Asn	Asn	Gly	Thr	Pro	Gly	Cys	Val	Met	
Asp	Glu													
		275					280					285		

Trp	Ile	Tyr	Leu	Met	Lys	Glu	Ala	Lys	Glu	Lys	His	Ser	Asp	
Asp	Pro													
	290					295					300			

Asp	Ser	Lys	Leu	Leu	Ile	Arg	Glu	Phe	Ser	Asn	Arg	Glu	Ile	
Ser	Glu													
305					310					315				
320														

Ala	Ile	Phe	Thr	Phe	Leu	Phe	Ala	Ser	Gln	Asp	Ala	Ser	Ser	
Ser	Leu													
				325					330					
335														

Ala	Cys	Trp	Leu	Phe	Gln	Ile	Val	Ala	Asp	Arg	Pro	Asp	Val	
Val	Ala													
			340					345					350	

Lys	Ile	Arg	Glu	Glu	Gln	Leu	Arg	Val	Arg	Asn	Asn	Asp	Pro	
Ser	Val													
		355					360					365		

Lys	Leu	Ser	Leu	Asp	Leu	Ile	Asn	Glu	Met	Thr	Tyr	Thr	Asn	
Asp	Val													
	370					375					380			

Val	Lys	Glu	Ser	Leu	Arg	Tyr	Arg	Pro	Pro	Val	Leu	Met	Val	
Pro	Tyr													
385					390					395				
400														

Val	Val	Lys	Lys	Ala	Phe	Pro	Val	Thr	Glu	Lys	Tyr	Thr	Ala	
Pro	Lys													
				405					410					

415

Gly Ser Met Leu Ile Pro Thr Leu Tyr Pro Ala Leu His Asp
Pro Glu
420 425 430

Val Tyr Asp Glu Pro Asp Ser Phe Ile Pro Glu Arg Trp Ala
Thr Ala
435 440 445

Ser Gly Asp Met Tyr Lys Arg Asn Trp Leu Val Phe Gly Thr
Gly Pro
450 455 460

His Val Cys Leu Gly Lys Asn Tyr Val Met Met Leu Phe Thr
Gly Met
465 470 475
480

Leu Gly Lys Phe Val Met Asn Ser Asp Ile Ile His His Lys
Thr Ala
485 490
495

Leu Ser Glu Glu Ile Lys Val Phe Ala Thr Ile Phe Pro Lys
Asp Asp
500 505 510

Val Ile Leu Glu Trp Lys Lys Arg Asp Pro Leu Ala Ala Ser
Asn
515 520 525

<210> 51
<211> 1587
<212> DNA
<213> Candida tropicalis

<220>
<221> CDS
<222> (1)..(1587)

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<400> 51
atg gct att gtt gat act gcc att gat ggc atc aat tat ttc
tta tcc 48
Met Ala Ile Val Asp Thr Ala Ile Asp Gly Ile Asn Tyr Phe
Leu Ser
1 5 10
15

tta tca tta act caa caa atc acc atc ttg gtt gtt ttc cca
ttc atc 96
Leu Ser Leu Thr Gln Gln Ile Thr Ile Leu Val Val Phe Pro
Phe Ile
20 25 30

tac aac ata gca tgg caa tta ctt tac tcc tta aga aaa gat
aga gtt 144
Tyr Asn Ile Ala Trp Gln Leu Leu Tyr Ser Leu Arg Lys Asp
Arg Val
35 40 45

cca atg gtt ttc tac tgg atc cca tgg ttt ggt tct gct gct
agt tat 192
Pro Met Val Phe Tyr Trp Ile Pro Trp Phe Gly Ser Ala Ala
Ser Tyr
50 55 60

ggg atg caa cca tac gaa ttc ttt gaa aag tgc aga ttg aaa
tat ggt 240
Gly Met Gln Pro Tyr Glu Phe Phe Glu Lys Cys Arg Leu Lys
Tyr Gly
65 70 75
80

gat gtt ttt tca ttt atg tta tta ggt aaa gtt atg act gtt
tat ttg 288
Asp Val Phe Ser Phe Met Leu Leu Gly Lys Val Met Thr Val
Tyr Leu
85 90
95

ggg cca aaa ggt cac gaa ttc att tac aat gct aaa tta tcc
gat gtt 336
Gly Pro Lys Gly His Glu Phe Ile Tyr Asn Ala Lys Leu Ser
Asp Val
100 105 110

tct gct gaa gaa gct tat acc cat ttg act act cct gtt ttt
ggg aaa 384
Ser Ala Glu Glu Ala Tyr Thr His Leu Thr Thr Pro Val Phe
Gly Lys

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115				120				125					
ggt	ggt	att	tat	gat	tgt	cca	aac	tct	aga	tta	atg	gaa	caa
aag	aag		432										
Gly	Val	Ile	Tyr	Asp	Cys	Pro	Asn	Ser	Arg	Leu	Met	Glu	Gln
Lys	Lys												
	130				135						140		
ttt	gct	aaa	ttt	gct	ttg	act	act	gat	tct	ttc	aaa	acc	tat
ggt	cca		480										
Phe	Ala	Lys	Phe	Ala	Leu	Thr	Thr	Asp	Ser	Phe	Lys	Thr	Tyr
Val	Pro												
145					150						155		
160													
aag	atc	aga	gaa	gaa	ggt	ttg	aat	tat	ttt	ggt	aac	gat	ggt
agt	ttc		528										
Lys	Ile	Arg	Glu	Glu	Val	Leu	Asn	Tyr	Phe	Val	Asn	Asp	Val
Ser	Phe												
					165				170				
175													
aaa	acc	aag	gaa	aga	gac	cat	ggt	ggt	gct	agt	ggt	atg	aaa
act	caa		576										
Lys	Thr	Lys	Glu	Arg	Asp	His	Gly	Val	Ala	Ser	Val	Met	Lys
Thr	Gln												
					180				185				190
cca	gaa	atc	act	att	ttc	act	gct	tct	cgt	tgt	tta	ttt	ggt
gat	gaa		624										
Pro	Glu	Ile	Thr	Ile	Phe	Thr	Ala	Ser	Arg	Cys	Leu	Phe	Gly
Asp	Glu												
					195				200				205
atg	aga	aag	agt	ttc	gac	aga	tca	ttt	gct	caa	ttg	tat	gct
gac	ttg		672										
Met	Arg	Lys	Ser	Phe	Asp	Arg	Ser	Phe	Ala	Gln	Leu	Tyr	Ala
Asp	Leu												
210					215						220		
gat	aaa	ggt	ttc	acc	cca	atc	aac	ttt	ggt	ttc	cca	aac	ttg
cca	tta		720										
Asp	Lys	Gly	Phe	Thr	Pro	Ile	Asn	Phe	Val	Phe	Pro	Asn	Leu
Pro	Leu												
225					230						235		
240													
cct	cat	tac	tgg	aga	cgt	gac	gct	gct	caa	aga	aag	ata	tct
gct	cat		768										
Pro	His	Tyr	Trp	Arg	Arg	Asp	Ala	Ala	Gln	Arg	Lys	Ile	Ser

- 210/269 -

Thr Leu Arg Met His Met Pro Leu His Ser Ile Phe Arg Lys
Val Met
370 375 380

aac cca ttg aga gtc cca aat acc aaa tat gtt att cca aaa
ggt cac 1200
Asn Pro Leu Arg Val Pro Asn Thr Lys Tyr Val Ile Pro Lys
Gly His
385 390 395
400

[illegible]

gaa	cac	cca	gaa	cat	ttc	aac	cca	aga	aga	tgg	gaa	tct	gat
gat	acc		1296										
Glu	His	Pro	Glu	His	Phe	Asn	Pro	Arg	Arg	Trp	Glu	Ser	Asp
Asp	Thr												
			420					425					430

aag gct agt gct gtt tct ttc aat tct gaa gat act gtt gat
tat ggt 1344
Lys Ala Ser Ala Val Ser Phe Asn Ser Glu Asp Thr Val Asp
Tyr Gly
435 440 445

ttc	ggt	aaa	att	tcc	aaa	ggt	gtc	tcc	tct	cca	tac	ttg	cca
ttc	ggt		1392										
Phe	Gly	Lys	Ile	Ser	Lys	Gly	Val	Ser	Ser	Pro	Tyr	Leu	Pro
Phe	Gly												
	450					455					460		

```

ggg ggt aga cac aga tgt att ggt gaa caa ttt gct tat gtt
caa ttg      1440
Gly Gly Arg His Arg Cys Ile Gly Glu Gln Phe Ala Tyr Val
Gln Leu
465              470              475
480

```

gga act att ttg acc act tat atc tac aac ttc aaa tgg aga
tta aac 1488
Gly Thr Ile Leu Thr Thr Tyr Ile Tyr Asn Phe Lys Trp Arg
Leu Asn
485 490
495

- 211/269 -

ggt gat aag gtt cca gat gtt gat tac caa tcc atg gtt acc
tta cca 1536
Gly Asp Lys Val Pro Asp Val Asp Tyr Gln Ser Met Val Thr
Leu Pro

500

505

510

tta gaa cct gct gaa atc gtt tgg gaa aag aga gat act tgt
atg gtt 1584
Leu Glu Pro Ala Glu Ile Val Trp Glu Lys Arg Asp Thr Cys
Met Val

515

520

525

tag
1587

<210> 52
<211> 528
<212> PRT
<213> Candida tropicalis

<400> 52

Met Ala Ile Val Asp Thr Ala Ile Asp Gly Ile Asn Tyr Phe
Leu Ser
1 5 10
15

Leu Ser Leu Thr Gln Gln Ile Thr Ile Leu Val Val Phe Pro
Phe Ile
20 25 30

Tyr Asn Ile Ala Trp Gln Leu Leu Tyr Ser Leu Arg Lys Asp
Arg Val
35 40 45

Pro Met Val Phe Tyr Trp Ile Pro Trp Phe Gly Ser Ala Ala
Ser Tyr
50 55 60

Gly Met Gln Pro Tyr Glu Phe Phe Glu Lys Cys Arg Leu Lys
Tyr Gly
65 70 75
80

- 212/269 -

Asp Val Phe Ser Phe Met Leu Leu Gly Lys Val Met Thr Val
Tyr Leu

85

90

95

Gly Pro Lys Gly His Glu Phe Ile Tyr Asn Ala Lys Leu Ser
Asp Val

100

105

110

Ser Ala Glu Glu Ala Tyr Thr His Leu Thr Thr Pro Val Phe
Gly Lys

115

120

125

Gly Val Ile Tyr Asp Cys Pro Asn Ser Arg Leu Met Glu Gln
Lys Lys

130

135

140

Phe Ala Lys Phe Ala Leu Thr Thr Asp Ser Phe Lys Thr Tyr
Val Pro

145

150

155

160

Lys Ile Arg Glu Glu Val Leu Asn Tyr Phe Val Asn Asp Val
Ser Phe

165

170

175

Lys Thr Lys Glu Arg Asp His Gly Val Ala Ser Val Met Lys
Thr Gln

180

185

190

Pro Glu Ile Thr Ile Phe Thr Ala Ser Arg Cys Leu Phe Gly
Asp Glu

195

200

205

Met Arg Lys Ser Phe Asp Arg Ser Phe Ala Gln Leu Tyr Ala
Asp Leu

210

215

220

Asp Lys Gly Phe Thr Pro Ile Asn Phe Val Phe Pro Asn Leu
Pro Leu

- 213/269 -

225
240

230

235

Pro His Tyr Trp Arg Arg Asp Ala Ala Gln Arg Lys Ile Ser
Ala His

245

250

255

Tyr Met Lys Glu Ile Lys Arg Arg Arg Glu Ser Gly Asp Ile
Asp Pro

260

265

270

Lys Arg Asp Leu Ile Asp Ser Leu Leu Val Asn Ser Thr Tyr
Lys Asp

275

280

285

Gly Val Lys Met Thr Asp Gln Glu Ile Ala Asn Leu Leu Ile
Gly Val

290

295

300

Leu Met Gly Gly Gln His Thr Ser Ala Ser Thr Ser Ala Trp
Phe Leu

305

310

315

320

Leu His Leu Ala Glu Gln Pro Gln Leu Gln Asp Asp Leu Tyr
Glu Glu

325

330

335

Leu Thr Asn Leu Leu Lys Glu Lys Gly Gly Asp Leu Asn Asp
Leu Thr

340

345

350

Tyr Glu Asp Leu Gln Lys Leu Pro Leu Val Asn Asn Thr Ile
Lys Glu

355

360

365

Thr Leu Arg Met His Met Pro Leu His Ser Ile Phe Arg Lys
Val Met

370

375

380

Asn	Pro	Leu	Arg	Val	Pro	Asn	Thr	Lys	Tyr	Val	Ile	Pro	Lys
Gly	His												
385					390					395			
400													

Tyr	Val	Leu	Val	Ser	Ala	Gly	Tyr	Ala	His	Thr	Ser	Asp	Arg
Trp	Phe												
				405					410				
415													

Glu	His	Pro	Glu	His	Phe	Asn	Pro	Arg	Arg	Trp	Glu	Ser	Asp
Asp	Thr												
			420					425					430

Lys	Ala	Ser	Ala	Val	Ser	Phe	Asn	Ser	Glu	Asp	Thr	Val	Asp
Tyr	Gly												
		435					440					445	

Phe	Gly	Lys	Ile	Ser	Lys	Gly	Val	Ser	Ser	Pro	Tyr	Leu	Pro
Phe	Gly												
	450					455					460		

Gly	Gly	Arg	His	Arg	Cys	Ile	Gly	Glu	Gln	Phe	Ala	Tyr	Val
Gln	Leu												
465					470					475			
480													

Gly	Thr	Ile	Leu	Thr	Thr	Tyr	Ile	Tyr	Asn	Phe	Lys	Trp	Arg
Leu	Asn												
				485					490				
495													

Gly	Asp	Lys	Val	Pro	Asp	Val	Asp	Tyr	Gln	Ser	Met	Val	Thr
Leu	Pro												
			500					505				510	

Leu	Glu	Pro	Ala	Glu	Ile	Val	Trp	Glu	Lys	Arg	Asp	Thr	Cys
Met	Val												
		515					520					525	

<210> 53
<211> 2097
<212> DNA
<213> Candida cloacae

<220>
<221> CDS
<222> (1)..(2097)

<400> 53
atg tcc cat caa gtt gaa gac cac gac tta gac gtg ttc tgt
tta ttg 48
Met Ser His Gln Val Glu Asp His Asp Leu Asp Val Phe Cys
Leu Leu
1 5 10
15

gcc gat gcc gtg ctc cat gaa att cct ccc agc gaa atc gtg
gag tac 96
Ala Asp Ala Val Leu His Glu Ile Pro Pro Ser Glu Ile Val
Glu Tyr
20 25 30

ctt cat cct gac ttc ccc aaa gat aag atc gaa gag tat ttg
aca ggc 144
Leu His Pro Asp Phe Pro Lys Asp Lys Ile Glu Glu Tyr Leu
Thr Gly
35 40 45

ttt tcc cgt ccg tct gct gtt cct cag ttt aga caa tgt gcc
aag aag 192
Phe Ser Arg Pro Ser Ala Val Pro Gln Phe Arg Gln Cys Ala
Lys Lys
50 55 60

ctt atc aac aga ggc tcc gag ctg tcg atc aag ttg ttt ttg
tac ttg 240
Leu Ile Asn Arg Gly Ser Glu Leu Ser Ile Lys Leu Phe Leu
Tyr Leu
65 70 75
80

acc act gcg ttg gac tca aga atc ctt gca cct gcc ttg acc
aat tcg 288
Thr Thr Ala Leu Asp Ser Arg Ile Leu Ala Pro Ala Leu Thr
Asn Ser
85 90
95

[illegible]

105

110

aga tca tgg aga gac tct cct tta act gca aaa aga aga tta
 ttt aga 384
 Arg Ser Trp Arg Asp Ser Pro Leu Thr Ala Lys Arg Arg Leu
 Phe Arg

120

125

[illegible]

135

140

ttg cac ttt aag gcg ttg ggc tac cca ggt aga gag ctc aga
acg caa 480
Leu His Phe Lys Ala Leu Gly Tyr Pro Gly Arg Glu Leu Arg
Thr Gln

150

155

160

att caa gac tac gaa gtc gac cct ttt aga tat tcg ttt atg
gag aaa 528
Ile Gln Asp Tyr Glu Val Asp Pro Phe Arg Tyr Ser Phe Met
Glu Lys

170

175

```

ctt aaa cac gag ggc cac gaa ttg ttc ctt cct gat att gac
ggt tta          576
Leu Lys His Glu Gly His Glu Leu Phe Leu Pro Asp Ile Asp
Val Leu

```

185

190

atc atc ggg tcg gga tca gga gca ggt gtg gtt gca caa act
 ctt act 624
 Ile Ile Gly Ser Gly Ser Gly Ala Gly Val Val Ala Gln Thr
 Leu Thr

200

205

gaa agt ggc ctc aaa tca ttg gtt ttg gaa aag ggc aaa tac
 ttt gcc 672
 Glu Ser Gly Leu Lys Ser Leu Val Leu Glu Lys Gly Lys Tyr
 Phe Ala

215

220

agt gaa gaa ttg tgc atg acg gac ttg gac ggt aac gag gca
tta ttc 720
Ser Glu Glu Leu Cys Met Thr Asp Leu Asp Gly Asn Glu Ala
Leu Phe
225 230 235
240

gaa agt gga gga aca att cct tcc acc aac caa caa ttg ttc
atg att 768
Glu Ser Gly Gly Thr Ile Pro Ser Thr Asn Gln Gln Leu Phe
Met Ile
245 250
255

gca ggt tcg act ttt ggt ggt ggt tct aca gtt aat tgg tct
gcc tgt 816
Ala Gly Ser Thr Phe Gly Gly Gly Ser Thr Val Asn Trp Ser
Ala Cys
260 265 270

ttg aag acc cca ttc aaa gta aga aag gaa tgg tat gac gat
ttc gga 864
Leu Lys Thr Pro Phe Lys Val Arg Lys Glu Trp Tyr Asp Asp
Phe Gly
275 280 285

ctt gat ttt gtc gct act caa caa tac gac gat tgt atg gat
tac gtg 912
Leu Asp Phe Val Ala Thr Gln Gln Tyr Asp Asp Cys Met Asp
Tyr Val
290 295 300

tgg aag aaa atg ggt gct tcg acc gaa cat atc gaa cat tct
gct gca 960
Trp Lys Lys Met Gly Ala Ser Thr Glu His Ile Glu His Ser
Ala Ala
305 310 315
320

aat gcc gtc atc atg gac ggg gca gca aaa ctt ggc tac gca
cac aga 1008
Asn Ala Val Ile Met Asp Gly Ala Ala Lys Leu Gly Tyr Ala
His Arg
325 330
335

gca ctt gag cag aat acc ggg ggc cat gtt cac gac tgt ggg
atg tgc 1056
Ala Leu Glu Gln Asn Thr Gly Gly His Val His Asp Cys Gly

Asp	Leu												
465					470					475			
480													
gat	ggc	aag	gcc	cat	gga	aca	aga	att	gaa	gcc	att	ttg	cat
gct	cca		1488										
Asp	Gly	Lys	Ala	His	Gly	Thr	Arg	Ile	Glu	Ala	Ile	Leu	His
Ala	Pro												
				485						490			
495													
tac	gtc	act	gcc	cca	ttt	tac	cca	tgg	caa	tca	ggt	gct	caa
gca	aga		1536										
Tyr	Val	Thr	Ala	Pro	Phe	Tyr	Pro	Trp	Gln	Ser	Gly	Ala	Gln
Ala	Arg												
			500					505					510
aag	aac	ctc	ttg	aaa	tat	aaa	caa	act	gtg	ccg	tta	tta	ctt
ctt	tct		1584										
Lys	Asn	Leu	Leu	Lys	Tyr	Lys	Gln	Thr	Val	Pro	Leu	Leu	Leu
Leu	Ser												
		515					520					525	
aga	gat	aca	tca	tca	ggt	acc	gtt	aca	tat	gat	aaa	caa	aag
cct	gac		1632										
Arg	Asp	Thr	Ser	Ser	Gly	Thr	Val	Thr	Tyr	Asp	Lys	Gln	Lys
Pro	Asp												
	530					535					540		
gta	ttg	gta	gtt	gac	tac	act	gtt	aac	aag	ttt	gac	aga	aat
tcg	att		1680										
Val	Leu	Val	Val	Asp	Tyr	Thr	Val	Asn	Lys	Phe	Asp	Arg	Asn
Ser	Ile												
545					550					555			
560													
tta	caa	ggg	ttt	ttg	gtt	gct	tcc	gac	atc	ttg	tat	att	gaa
ggt	gct		1728										
Leu	Gln	Gly	Phe	Leu	Val	Ala	Ser	Asp	Ile	Leu	Tyr	Ile	Glu
Gly	Ala												
				565						570			
575													
aaa	gag	att	ttg	tca	cca	caa	gct	tgg	gta	cca	acc	ttc	aag
agc	aac		1776										
Lys	Glu	Ile	Leu	Ser	Pro	Gln	Ala	Trp	Val	Pro	Thr	Phe	Lys
Ser	Asn												
			580					585					590
aaa	cca	aaa	cat	gct	aga	tcg	atc	aaa	gac	gaa	gat	tac	gtc

- 220/269 -

aaa tgg 1824
Lys Pro Lys His Ala Arg Ser Ile Lys Asp Glu Asp Tyr Val
Lys Trp
595 600 605

aga gaa acc gtg gcc aag atc cca ttt gac tcc tac ggt tcg
cca tac 1872
Arg Glu Thr Val Ala Lys Ile Pro Phe Asp Ser Tyr Gly Ser
Pro Tyr
610 615 620

ggt tct gct cat caa atg agt tcg tgt aga atg tct ggt aag
gga cca 1920
Gly Ser Ala His Gln Met Ser Ser Cys Arg Met Ser Gly Lys
Gly Pro
625 630 635
640

gga tac ggt gct tgt gac act aaa gga aga tta ttt gaa tgt
aac aac 1968
Gly Tyr Gly Ala Cys Asp Thr Lys Gly Arg Leu Phe Glu Cys
Asn Asn
645 650
655

gtt tac gtt gct gat gct tcg gtt atg cct act gca tcg gga
gtc aat 2016
Val Tyr Val Ala Asp Ala Ser Val Met Pro Thr Ala Ser Gly
Val Asn
660 665 670

cct atg atc act aca atg gct ttt gca aga cat gtg gcc tta
tgt ctt 2064
Pro Met Ile Thr Thr Met Ala Phe Ala Arg His Val Ala Leu
Cys Leu
675 680 685

gct aaa gac ttg caa cca caa act aaa ctt tag
2097
Ala Lys Asp Leu Gln Pro Gln Thr Lys Leu
690 695

<210> 54
<211> 698
<212> PRT
<213> Candida cloacae

<400> 54

- 221/269 -

```
Met Ser His Gln Val Glu Asp His Asp Leu Asp Val Phe Cys
Leu Leu
1          5          10
15
```

Ala Asp Ala Val Leu His Glu Ile Pro Pro Ser Glu Ile Val
Glu Tyr

20 25 30

Leu His Pro Asp Phe Pro Lys Asp Lys Ile Glu Glu Tyr Leu
Thr Gly

35 40 45

Phe Ser Arg Pro Ser Ala Val Pro Gln Phe Arg Gln Cys Ala
Lys Lys
50 55 60

Leu Ile Asn Arg Gly Ser Glu Leu Ser Ile Lys Leu Phe Leu
Tyr Leu
65 70 75
80

Thr Thr Ala Leu Asp Ser Arg Ile Leu Ala Pro Ala Leu Thr
Asn Ser
85 90
95

Leu Thr Leu Ile Arg Asp Met Asp Leu Ser Gln Arg Glu Glu
Leu Leu

100 105 110

Arg Ser Trp Arg Asp Ser Pro Leu Thr Ala Lys Arg Arg Leu
Phe Arg
115 120 125

Val	Tyr	Ala	Ser	Phe	Thr	Leu	Ser	Thr	Phe	Asn	Lys	Leu	Gly
Thr	Asp												
	130					135					140		

Leu His Phe Lys Ala Leu Gly Tyr Pro Gly Arg Glu Leu Arg
Thr Gln

- 222/269 -

145
160

150

155

Ile Gln Asp Tyr Glu Val Asp Pro Phe Arg Tyr Ser Phe Met
Glu Lys

165

170

175

Leu Lys His Glu Gly His Glu Leu Phe Leu Pro Asp Ile Asp
Val Leu

180

185

190

Ile Ile Gly Ser Gly Ser Gly Ala Gly Val Val Ala Gln Thr
Leu Thr

195

200

205

Glu Ser Gly Leu Lys Ser Leu Val Leu Glu Lys Gly Lys Tyr
Phe Ala

210

215

220

Ser Glu Glu Leu Cys Met Thr Asp Leu Asp Gly Asn Glu Ala
Leu Phe

225

230

235

240

Glu Ser Gly Gly Thr Ile Pro Ser Thr Asn Gln Gln Leu Phe
Met Ile

245

250

255

Ala Gly Ser Thr Phe Gly Gly Gly Ser Thr Val Asn Trp Ser
Ala Cys

260

265

270

Leu Lys Thr Pro Phe Lys Val Arg Lys Glu Trp Tyr Asp Asp
Phe Gly

275

280

285

Leu Asp Phe Val Ala Thr Gln Gln Tyr Asp Asp Cys Met Asp
Tyr Val

290

295

300

Trp Lys Lys Met Gly Ala Ser Thr Glu His Ile Glu His Ser
Ala Ala
305 310 315
320

Asn Ala Val Ile Met Asp Gly Ala Ala Lys Leu Gly Tyr Ala
His Arg
325 330
335

Ala Leu Glu Gln Asn Thr Gly Gly His Val His Asp Cys Gly
Met Cys
340 345 350

His Leu Gly Cys Arg Phe Gly Ile Lys Gln Gly Gly Val Asn
Cys Trp
355 360 365

Phe Arg Glu Pro Ser Glu Lys Gly Ser Lys Phe Met Glu Gln
Val Val
370 375 380

Val Glu Lys Ile Leu Gln His Lys Gly Lys Ala Thr Gly Ile
Leu Cys
385 390 395
400

Arg Asp Thr Glu Ser Gly Ile Lys Phe Lys Ile Thr Gly Pro
Lys Lys
405 410
415

Tyr Val Val Ser Gly Gly Ser Leu Gln Thr Pro Val Leu Leu
Gln Lys
420 425 430

Ser Gly Phe Lys Asn Lys His Ile Gly Ala Asn Leu Lys Leu
His Pro
435 440 445

Val	Ser	Val	Ala	Leu	Gly	Asp	Phe	Gly	Asn	Glu	Val	Asp	Phe
Glu	Ala												
	450					455					460		

Tyr	Lys	Arg	Pro	Leu	Met	Thr	Ala	Val	Cys	Asn	Ala	Val	Asp
Asp	Leu												
465					470					475			
480													

Asp	Gly	Lys	Ala	His	Gly	Thr	Arg	Ile	Glu	Ala	Ile	Leu	His
Ala	Pro												
				485					490				
495													

Tyr	Val	Thr	Ala	Pro	Phe	Tyr	Pro	Trp	Gln	Ser	Gly	Ala	Gln
Ala	Arg												
			500					505				510	

Lys	Asn	Leu	Leu	Lys	Tyr	Lys	Gln	Thr	Val	Pro	Leu	Leu	Leu
Leu	Ser												
		515					520					525	

Arg	Asp	Thr	Ser	Ser	Gly	Thr	Val	Thr	Tyr	Asp	Lys	Gln	Lys
Pro	Asp												
	530					535					540		

Val	Leu	Val	Val	Asp	Tyr	Thr	Val	Asn	Lys	Phe	Asp	Arg	Asn
Ser	Ile												
545					550					555			
560													

Leu	Gln	Gly	Phe	Leu	Val	Ala	Ser	Asp	Ile	Leu	Tyr	Ile	Glu
Gly	Ala												
				565					570				
575													

Lys	Glu	Ile	Leu	Ser	Pro	Gln	Ala	Trp	Val	Pro	Thr	Phe	Lys
Ser	Asn												
			580					585				590	

- 225/269 -

Lys Pro Lys His Ala Arg Ser Ile Lys Asp Glu Asp Tyr Val
Lys Trp
595 600 605

Arg Glu Thr Val Ala Lys Ile Pro Phe Asp Ser Tyr Gly Ser
Pro Tyr
610 615 620

Gly Ser Ala His Gln Met Ser Ser Cys Arg Met Ser Gly Lys
Gly Pro
625 630 635
640

Gly Tyr Gly Ala Cys Asp Thr Lys Gly Arg Leu Phe Glu Cys
Asn Asn
645 650
655

Val Tyr Val Ala Asp Ala Ser Val Met Pro Thr Ala Ser Gly
Val Asn
660 665 670

Pro Met Ile Thr Thr Met Ala Phe Ala Arg His Val Ala Leu
Cys Leu
675 680 685

Ala Lys Asp Leu Gln Pro Gln Thr Lys Leu
690 695

<210> 55
<211> 2097
<212> DNA
<213> Candida cloacae

<220>
<221> CDS
<222> (1)..(2097)

<400> 55
atg aat ccc gtt gtt gaa gac agc cat tta gat gtg ttc tgc
ttg tta 48
Met Asn Pro Val Val Glu Asp Ser His Leu Asp Val Phe Cys

Leu Leu
 1 5 10
 15
 gcc gat gct gtg gtc cat gag ata cct cct agt gag atc gta
 gag tac 96
 Ala Asp Ala Val Val His Glu Ile Pro Pro Ser Glu Ile Val
 Glu Tyr
 20 25 30
 tta cat cct gat ttc cca aag gac aag gtt gaa gag tat ttg
 gct gag 144
 Leu His Pro Asp Phe Pro Lys Asp Lys Val Glu Glu Tyr Leu
 Ala Glu
 35 40 45
 ttt tct cat cct tca gca att ccc gaa ttt aga gaa gtt gca
 aaa aga 192
 Phe Ser His Pro Ser Ala Ile Pro Glu Phe Arg Glu Val Ala
 Lys Arg
 50 55 60
 att att aac aaa ggg act gtg ctg tca ata aag ttg ttt ttg
 ctc ttg 240
 Ile Ile Asn Lys Gly Thr Val Leu Ser Ile Lys Leu Phe Leu
 Leu Leu
 65 70 75
 80
 gca act gct cta gac tcg aga atc ctt gct cct gcg ttg acc
 aac tcg 288
 Ala Thr Ala Leu Asp Ser Arg Ile Leu Ala Pro Ala Leu Thr
 Asn Ser
 85 90
 95
 acg acg tta atc aga gat atg gat ctt tct caa aga gaa gaa
 tta ttg 336
 Thr Thr Leu Ile Arg Asp Met Asp Leu Ser Gln Arg Glu Glu
 Leu Leu
 100 105 110
 aga tca tgg aga gac tct cca ttc act aca aaa agg aaa ttg
 ttc agg 384
 Arg Ser Trp Arg Asp Ser Pro Phe Thr Thr Lys Arg Lys Leu
 Phe Arg
 115 120 125
 gtg tat aat tca ttc acc ttg aac gcg ttt agt aag acc gca
 aca gat 432

- 227/269 -

Val	Tyr	Asn	Ser	Phe	Thr	Leu	Asn	Ala	Phe	Ser	Lys	Thr	Ala
Thr	Asp												
	130					135					140		

```
ttg cac ttc aaa gcg ttg gga tat cct ggt aga gag ctc agg  
act caa          480  
Leu His Phe Lys Ala Leu Gly Tyr Pro Gly Arg Glu Leu Arg  
Thr Gln  
145              150              155  
160
```

att cag gac tat gag gtc gat cct ttc aga tat acg ttc ttg
gaa aaa 528
Ile Gln Asp Tyr Glu Val Asp Pro Phe Arg Tyr Thr Phe Leu
Glu Lys
165 170
175

```

ccc caa caa gac ggc cag gag tta cat ttt ccc gac att gat
gtc ttg      576
Pro Gln Gln Asp Gly Gln Glu Leu His Phe Pro Asp Ile Asp
Val Leu
      180      185      190

```

att	atc	ggg	tct	ggt	tcg	gga	gca	gga	gtg	gtt	gct	caa	act
ctt	tcg				624								
Ile	Ile	Gly	Ser	Gly	Ser	Gly	Ala	Gly	Val	Val	Ala	Gln	Thr
Leu	Ser												
		195				200						205	

gaa	aac	gga	ctt	aaa	tca	ttg	gtg	ttg	gaa	aaa	ggt	aaa	tac
ttt	tcc			672									
Glu	Asn	Gly	Leu	Lys	Ser	Leu	Val	Leu	Glu	Lys	Gly	Lys	Tyr
Phe	Ser												
	210					215					220		

aat gat gag ttg acc atg aat gat ttg gaa ggt agt gag gca
tta ttc 720
Asn Asp Glu Leu Thr Met Asn Asp Leu Glu Gly Ser Glu Ala
Leu Phe
225 230 235
240

gaa aat gga ggt gcc ctc agt agt acc aac caa cag ata ttt
ata att 768
Glu Asn Gly Gly Ala Leu Ser Ser Thr Asn Gln Gln Ile Phe
Ile Ile
245 250
255

- 228/269 -

gca ggt tcg act ttt ggg ggt ggt tct aca gtt aat tgg tct
gcc tgt 816
Ala Gly Ser Thr Phe Gly Gly Gly Ser Thr Val Asn Trp Ser
Ala Cys

260

265

270

tta aaa act ccg ttc aaa gta aga aaa gag tgg tat gac aac
ttc gga 864
Leu Lys Thr Pro Phe Lys Val Arg Lys Glu Trp Tyr Asp Asn
Phe Gly

275

280

285

ctt gat ttc gtc gca acc caa tac tac gaa gat tgt atg gat
tat gtt 912
Leu Asp Phe Val Ala Thr Gln Tyr Tyr Glu Asp Cys Met Asp
Tyr Val

290

295

300

tgg aag aaa atg ggt gct tcg aac gaa aat atc gac cat tct
ggt gct 960
Trp Lys Lys Met Gly Ala Ser Asn Glu Asn Ile Asp His Ser
Gly Ala

305

310

315

320

aat agt gtt ata ttg gaa ggg tcc aaa aaa ctt ggc tac cct
cac agg 1008
Asn Ser Val Ile Leu Glu Gly Ser Lys Lys Leu Gly Tyr Pro
His Arg

325

330

335

gcc gtt gaa caa aat aat ggg ggc aaa att cat gac tgt ggt
atg tgt 1056
Ala Val Glu Gln Asn Asn Gly Gly Lys Ile His Asp Cys Gly
Met Cys

340

345

350

cac ttg ggt tgt aga ttt ggt att aaa cag gga agt gta aat
tgc tgg 1104
His Leu Gly Cys Arg Phe Gly Ile Lys Gln Gly Ser Val Asn
Cys Trp

355

360

365

ttc cgt ggt cca agt gaa aac gga tcc aag ttt atg caa caa
gtt ctc 1152
Phe Arg Gly Pro Ser Glu Asn Gly Ser Lys Phe Met Gln Gln
Val Leu

370

375

380

gtg gat aag ata ttg caa cgt gac ggt aaa gca gtc ggt gtt
ttg tgt 1200
Val Asp Lys Ile Leu Gln Arg Asp Gly Lys Ala Val Gly Val
Leu Cys
385 390 395
400

aga gat gtt gta acc ggt gtt aag ttc aag atc act gga cca
aag aaa 1248
Arg Asp Val Val Thr Gly Val Lys Phe Lys Ile Thr Gly Pro
Lys Lys
405 410
415

att gtt gtt ttc tgg tgg ttc ttt gca aac tcc ggt ttt gtt
aca aaa 1296
Ile Val Val Phe Trp Trp Phe Phe Ala Asn Ser Gly Phe Val
Thr Lys
420 425 430

tca ggt ttc aag aat aaa cac att ggt gct aac ttg aag ctc
cat cca 1344
Ser Gly Phe Lys Asn Lys His Ile Gly Ala Asn Leu Lys Leu
His Pro
435 440 445

gtt tca ctt acg ctt gga gac ttc ggt aac aac gtg gat ttc
gaa gct 1392
Val Ser Leu Thr Leu Gly Asp Phe Gly Asn Asn Val Asp Phe
Glu Ala
450 455 460

tac agg aaa cca att atg aca tca att tgt aat aaa gtc gaa
gat tta 1440
Tyr Arg Lys Pro Ile Met Thr Ser Ile Cys Asn Lys Val Glu
Asp Leu
465 470 475
480

gat gga aag gcc cat ggt aca aga att gaa gct atg ttg aat
gct cca 1488
Asp Gly Lys Ala His Gly Thr Arg Ile Glu Ala Met Leu Asn
Ala Pro
485 490
495

tat ggt gtt gca cca ttt ttc ccc tgg aaa tca ggc gct gaa
tca aga 1536
Tyr Gly Val Ala Pro Phe Phe Pro Trp Lys Ser Gly Ala Glu
Ser Arg

500				505				510					
aag	gat	ctc	ttg	aga	tac	aaa	caa	act	gtg	cct	ata	tta	ctt
ctt	tcc		1584										
Lys	Asp	Leu	Leu	Arg	Tyr	Lys	Gln	Thr	Val	Pro	Ile	Leu	Leu
Leu	Ser												
		515				520					525		
aga	gat	act	act	tca	ggg	tct	gtc	aca	tat	gat	aaa	caa	aaa
cca	gat		1632										
Arg	Asp	Thr	Thr	Ser	Gly	Ser	Val	Thr	Tyr	Asp	Lys	Gln	Lys
Pro	Asp												
		530				535					540		
gca	ttg	gtg	att	gat	tac	ctg	tta	aac	aag	ttt	gac	aga	aac
tca	att		1680										
Ala	Leu	Val	Ile	Asp	Tyr	Leu	Leu	Asn	Lys	Phe	Asp	Arg	Asn
Ser	Ile												
545					550						555		
560													
tta	caa	ggg	ttt	ttg	ata	gct	tca	gac	ctt	tta	tat	att	gaa
ggt	gcc		1728										
Leu	Gln	Gly	Phe	Leu	Ile	Ala	Ser	Asp	Leu	Leu	Tyr	Ile	Glu
Gly	Ala												
			565								570		
575													
agt	aga	gat	cat	gtc	acc	tac	aag	ctt	ggg	tac	caa	tgg	ttc
aag	agt		1776										
Ser	Arg	Asp	His	Val	Thr	Tyr	Lys	Leu	Gly	Tyr	Gln	Trp	Phe
Lys	Ser												
		580					585				590		
tct	aaa	cct	aaa	cat	gcc	aga	tcg	att	gaa	gat	gaa	gac	tac
gta	aac		1824										
Ser	Lys	Pro	Lys	His	Ala	Arg	Ser	Ile	Glu	Asp	Glu	Asp	Tyr
Val	Asn												
		595				600					605		
tgg	aga	gct	aaa	gtt	gca	aag	att	cca	ttt	gat	tcc	tac	gga
tca	cca		1872										
Trp	Arg	Ala	Lys	Val	Ala	Lys	Ile	Pro	Phe	Asp	Ser	Tyr	Gly
Ser	Pro												
		610				615					620		
tac	ggt	tca	gct	cac	caa	atg	agt	aca	tgc	aga	atg	tca	ggt
aag	gga		1920										
Tyr	Gly	Ser	Ala	His	Gln	Met	Ser	Thr	Cys	Arg	Met	Ser	Gly
Lys	Gly												

- 231/269 -

625			630						635					
640														
cca	gga	tat	gga	gct	tgt	gat	acc	aaa	gga	aaa	tta	ttt	gaa	
tgt	agc		1968											
Pro	Gly	Tyr	Gly	Ala	Cys	Asp	Thr	Lys	Gly	Lys	Leu	Phe	Glu	
Cys	Ser		645						650					
655														
aat	gtt	tat	gtt	gca	gat	gct	tcc	act	ttg	cct	act	gca	tca	
ggg	gct		2016											
Asn	Val	Tyr	Val	Ala	Asp	Ala	Ser	Thr	Leu	Pro	Thr	Ala	Ser	
Gly	Ala		660						665				670	
aat	cca	atg	gtt	agt	acc	atg	tca	ttt	gca	agg	cac	gtg	tcc	
tta	gga		2064											
Asn	Pro	Met	Val	Ser	Thr	Met	Ser	Phe	Ala	Arg	His	Val	Ser	
Leu	Gly		675				680				685			
att	gtt	aaa	gaa	ttg	caa	caa	agt	aaa	ctt	tag				
2097														
Ile	Val	Lys	Glu	Leu	Gln	Gln	Ser	Lys	Leu					
690			695											

<210>	56
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<212>	PRT
<213>	Candida cloacae

<400> 56

Met Asn Pro Val Val Glu Asp Ser His Leu Asp Val Phe Cys
Leu Leu
1 5 10
15

Ala Asp Ala Val Val His Glu Ile Pro Pro Ser Glu Ile Val
Glu Tyr

20 25 30

Leu His Pro Asp Phe Pro Lys Asp Lys Val Glu Glu Tyr Leu
Ala Glu

35 40 45

Phe	Ser	His	Pro	Ser	Ala	Ile	Pro	Glu	Phe	Arg	Glu	Val	Ala
Lys	Arg												
	50					55					60		

Ile	Ile	Asn	Lys	Gly	Thr	Val	Leu	Ser	Ile	Lys	Leu	Phe	Leu
Leu	Leu												
65					70					75			
80													

Ala	Thr	Ala	Leu	Asp	Ser	Arg	Ile	Leu	Ala	Pro	Ala	Leu	Thr
Asn	Ser												
				85					90				
95													

Thr	Thr	Leu	Ile	Arg	Asp	Met	Asp	Leu	Ser	Gln	Arg	Glu	Glu
Leu	Leu												
			100					105					110

Arg	Ser	Trp	Arg	Asp	Ser	Pro	Phe	Thr	Thr	Lys	Arg	Lys	Leu
Phe	Arg												
		115					120					125	

Val	Tyr	Asn	Ser	Phe	Thr	Leu	Asn	Ala	Phe	Ser	Lys	Thr	Ala
Thr	Asp												
	130					135					140		

Leu	His	Phe	Lys	Ala	Leu	Gly	Tyr	Pro	Gly	Arg	Glu	Leu	Arg
Thr	Gln												
145					150					155			
160													

Ile	Gln	Asp	Tyr	Glu	Val	Asp	Pro	Phe	Arg	Tyr	Thr	Phe	Leu
Glu	Lys												
				165					170				
175													

Pro	Gln	Gln	Asp	Gly	Gln	Glu	Leu	His	Phe	Pro	Asp	Ile	Asp
Val	Leu												
			180					185					190

- 233/269 -

Ile	Ile	Gly	Ser	Gly	Ser	Gly	Ala	Gly	Val	Val	Ala	Gln	Thr
Leu	Ser												
		195					200					205	

Glu	Asn	Gly	Leu	Lys	Ser	Leu	Val	Leu	Glu	Lys	Gly	Lys	Tyr
Phe	Ser												
	210					215					220		

Asn	Asp	Glu	Leu	Thr	Met	Asn	Asp	Leu	Glu	Gly	Ser	Glu	Ala
Leu	Phe												
225					230					235			
240													

Glu	Asn	Gly	Gly	Ala	Leu	Ser	Ser	Thr	Asn	Gln	Gln	Ile	Phe
Ile	Ile												
				245					250				
255													

Ala	Gly	Ser	Thr	Phe	Gly	Gly	Gly	Ser	Thr	Val	Asn	Trp	Ser
Ala	Cys												
			260					265					270

Leu	Lys	Thr	Pro	Phe	Lys	Val	Arg	Lys	Glu	Trp	Tyr	Asp	Asn
Phe	Gly												
		275					280					285	

Leu	Asp	Phe	Val	Ala	Thr	Gln	Tyr	Tyr	Glu	Asp	Cys	Met	Asp
Tyr	Val												
	290					295					300		

Trp	Lys	Lys	Met	Gly	Ala	Ser	Asn	Glu	Asn	Ile	Asp	His	Ser
Gly	Ala												
305					310					315			
320													

Asn	Ser	Val	Ile	Leu	Glu	Gly	Ser	Lys	Lys	Leu	Gly	Tyr	Pro
His	Arg												
			325						330				
335													

Ala	Val	Glu	Gln	Asn	Asn	Gly	Gly	Lys	Ile	His	Asp	Cys	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- 234/269 -

Met Cys
340 345 350

His Leu Gly Cys Arg Phe Gly Ile Lys Gln Gly Ser Val Asn
Cys Trp
355 360 365

Phe Arg Gly Pro Ser Glu Asn Gly Ser Lys Phe Met Gln Gln
Val Leu
370 375 380

Val Asp Lys Ile Leu Gln Arg Asp Gly Lys Ala Val Gly Val
Leu Cys
385 390 395
400

Arg Asp Val Val Thr Gly Val Lys Phe Lys Ile Thr Gly Pro
Lys Lys
405 410
415

Ile Val Val Phe Trp Trp Phe Phe Ala Asn Ser Gly Phe Val
Thr Lys
420 425 430

Ser Gly Phe Lys Asn Lys His Ile Gly Ala Asn Leu Lys Leu
His Pro
435 440 445

Val Ser Leu Thr Leu Gly Asp Phe Gly Asn Asn Val Asp Phe
Glu Ala
450 455 460

Tyr Arg Lys Pro Ile Met Thr Ser Ile Cys Asn Lys Val Glu
Asp Leu
465 470 475
480

Asp Gly Lys Ala His Gly Thr Arg Ile Glu Ala Met Leu Asn
Ala Pro
485 490

495

Tyr Gly Val Ala Pro Phe Phe Pro Trp Lys Ser Gly Ala Glu
Ser Arg

500 505 510

Lys Asp Leu Leu Arg Tyr Lys Gln Thr Val Pro Ile Leu Leu
Leu Ser
515 520 525

Arg Asp Thr Thr Ser Gly Ser Val Thr Tyr Asp Lys Gln Lys
Pro Asp
530 535 540

Ala Leu Val Ile Asp Tyr Leu Leu Asn Lys Phe Asp Arg Asn
Ser Ile
545 550 555
560

Leu Gln Gly Phe Leu Ile Ala Ser Asp Leu Leu Tyr Ile Glu
Gly Ala
565 570
575

Ser Arg Asp His Val Thr Tyr Lys Leu Gly Tyr Gln Trp Phe
Lys Ser
580 585 590

Ser Lys Pro Lys His Ala Arg Ser Ile Glu Asp Glu Asp Tyr
Val Asn
595 600 605

Trp Arg Ala Lys Val Ala Lys Ile Pro Phe Asp Ser Tyr Gly
Ser Pro
610 615 620

Tyr Gly Ser Ala His Gln Met Ser Thr Cys Arg Met Ser Gly
Lys Gly
625 630 635
640

Pro Gly Tyr Gly Ala Cys Asp Thr Lys Gly Lys Leu Phe Glu
Cys Ser

645

650

655

Asn Val Tyr Val Ala Asp Ala Ser Thr Leu Pro Thr Ala Ser
Gly Ala

660

665

670

Asn Pro Met Val Ser Thr Met Ser Phe Ala Arg His Val Ser
Leu Gly

675

680

685

Ile Val Lys Glu Leu Gln Gln Ser Lys Leu

690

695

<210> 57

<211> 948

<212> DNA

<213> Candida tropicalis

<220>

<221> CDS

<222> (1)..(948)

<400> 57

cca ttg caa tac acc gat atc cca gtt cca gtc cct aag cca
aac gaa 48

Pro Leu Gln Tyr Thr Asp Ile Pro Val Pro Val Pro Lys Pro
Asn Glu

1

5

10

15

ttg ctc gtc cac gtc aaa tac tcc ggt gtt tgt cac tca gat
ata cac 96

Leu Leu Val His Val Lys Tyr Ser Gly Val Cys His Ser Asp
Ile His

20

25

30

gtc tgg aag ggt gac tgg ttc cca gca tcg aaa ttg ccc gtt
gtt ggt 144

Val Trp Lys Gly Asp Trp Phe Pro Ala Ser Lys Leu Pro Val
Val Gly

35

40

45

ggt cac gaa ggt gcc ggt gtt gtc gtt gcc att ggt gaa aac
 gtc caa 192
 Gly His Glu Gly Ala Gly Val Val Val Ala Ile Gly Glu Asn
 Val Gln
 50 55 60

ggc tgg aaa gta ggt gac ttg gca ggt ata aag atg ttg aat
 ggt tcc 240
 Gly Trp Lys Val Gly Asp Leu Ala Gly Ile Lys Met Leu Asn
 Gly Ser
 65 70 75
 80

tgt atg aac tgt gaa tac tgt caa caa ggt gct gaa cca aac
 tgt ccc 288
 Cys Met Asn Cys Glu Tyr Cys Gln Gln Gly Ala Glu Pro Asn
 Cys Pro
 85 90
 95

cac gct gat gtc tcg ggt tac tcc cac gac ggt act ttc caa
 cag tac 336
 His Ala Asp Val Ser Gly Tyr Ser His Asp Gly Thr Phe Gln
 Gln Tyr
 100 105 110

gct acc gcc gat gct gtt caa gct gct aaa ttc cca gct ggt
 tct gat 384
 Ala Thr Ala Asp Ala Val Gln Ala Ala Lys Phe Pro Ala Gly
 Ser Asp
 115 120 125

tta gct agc atc gca cct ata tcc tgc gcc ggt gtt act gtt
 tac aaa 432
 Leu Ala Ser Ile Ala Pro Ile Ser Cys Ala Gly Val Thr Val
 Tyr Lys
 130 135 140

gca ttg aaa act gca ggc ttg cag cca ggt caa tgg gtt gcc
 atc tct 480
 Ala Leu Lys Thr Ala Gly Leu Gln Pro Gly Gln Trp Val Ala
 Ile Ser
 145 150 155
 160

ggt gca gct ggt ggt ttg ggt tct ttg gct gtg caa tac gcc
 aag gcc 528
 Gly Ala Ala Gly Gly Leu Gly Ser Leu Ala Val Gln Tyr Ala
 Lys Ala

	165	170
175		
atg ggt ttg aga gtc gtg gcc att gac ggt ggt gac gaa aga		
gga gtg	576	
Met Gly Leu Arg Val Val Ala Ile Asp Gly Gly Asp Glu Arg		
Gly Val		
	180	185
		190
ttt gtc aaa tcg ttg ggt gct gaa gtt ttc gtt gat ttc acc		
aaa gag	624	
Phe Val Lys Ser Leu Gly Ala Glu Val Phe Val Asp Phe Thr		
Lys Glu		
	195	200
		205
gcc aat gtc tct gag gct atc atc aag gct acc gac ggt ggt		
gcc cat	672	
Ala Asn Val Ser Glu Ala Ile Ile Lys Ala Thr Asp Gly Gly		
Ala His		
	210	215
		220
ggc gtc atc aac gtt tcc att tct gaa aaa gcc atc aac cag		
tct gtt	720	
Gly Val Ile Asn Val Ser Ile Ser Glu Lys Ala Ile Asn Gln		
Ser Val		
225	230	235
240		
gaa tat gtt aga act ttg gga act gtt gtc ttg gtt ggt ttg		
cca gct	768	
Glu Tyr Val Arg Thr Leu Gly Thr Val Val Leu Val Gly Leu		
Pro Ala		
	245	250
255		
ggt gca aag ctc gaa gct cct atc ttc aat gcc gtt gcc aaa		
tcc atc	816	
Gly Ala Lys Leu Glu Ala Pro Ile Phe Asn Ala Val Ala Lys		
Ser Ile		
	260	265
		270
caa atc aaa ggt tct tac gtg gga aac aga aga gac act gct		
gag gct	864	
Gln Ile Lys Gly Ser Tyr Val Gly Asn Arg Arg Asp Thr Ala		
Glu Ala		
	275	280
		285
gtt gat ttc ttc gct aga ggt ttg gtc aaa tgt cca att aag		
gtt gtt	912	
Val Asp Phe Phe Ala Arg Gly Leu Val Lys Cys Pro Ile Lys		

- 239/269 -

Val Val
290 295 300

ggg ttg agt gaa ttg cca gag att ttc aaa ttg ttg
948

Gly Leu Ser Glu Leu Pro Glu Ile Phe Lys Leu Leu
305 310 315

<210> 58
<211> 316
<212> PRT
<213> Candida tropicalis

<400> 58

Pro Leu Gln Tyr Thr Asp Ile Pro Val Pro Val Pro Lys Pro
Asn Glu

1 5 10
15

Leu Leu Val His Val Lys Tyr Ser Gly Val Cys His Ser Asp
Ile His
20 25 30

Val Trp Lys Gly Asp Trp Phe Pro Ala Ser Lys Leu Pro Val
Val Gly
35 40 45

Gly His Glu Gly Ala Gly Val Val Val Ala Ile Gly Glu Asn
Val Gln
50 55 60

Gly Trp Lys Val Gly Asp Leu Ala Gly Ile Lys Met Leu Asn
Gly Ser
65 70 75
80

Cys Met Asn Cys Glu Tyr Cys Gln Gln Gly Ala Glu Pro Asn
Cys Pro
85 90
95

His Ala Asp Val Ser Gly Tyr Ser His Asp Gly Thr Phe Gln

- 240/269 -

Gln Tyr

100 105 110

Ala Thr Ala Asp Ala Val Gln Ala Ala Lys Phe Pro Ala Gly
Ser Asp
115 120 125

Leu Ala Ser Ile Ala Pro Ile Ser Cys Ala Gly Val Thr Val
Tyr Lys
130 135 140

Ala Leu Lys Thr Ala Gly Leu Gln Pro Gly Gln Trp Val Ala
Ile Ser
145 150 155
160

Gly Ala Ala Gly Gly Leu Gly Ser Leu Ala Val Gln Tyr Ala
Lys Ala
165
170
175

Met Gly Leu Arg Val Val Ala Ile Asp Gly Gly Asp Glu Arg
Gly Val
180 185 190

Phe Val Lys Ser Leu Gly Ala Glu Val Phe Val Asp Phe Thr
Lys Glu
195 200 205

Ala Asn Val Ser Glu Ala Ile Ile Lys Ala Thr Asp Gly Gly
Ala His
210 215 220

Gly Val Ile Asn Val Ser Ile Ser Glu Lys Ala Ile Asn Gln
Ser Val
225 230 235
240

Glu Tyr Val Arg Thr Leu Gly Thr Val Val Leu Val Gly Leu
Pro Ala

245 250

255

Gly Ala Lys Leu Glu Ala Pro Ile Phe Asn Ala Val Ala Lys
Ser Ile
260 265 270

Gln Ile Lys Gly Ser Tyr Val Gly Asn Arg Arg Asp Thr Ala
Glu Ala
275 280 285

Val Asp Phe Phe Ala Arg Gly Leu Val Lys Cys Pro Ile Lys
Val Val
290 295 300

Gly Leu Ser Glu Leu Pro Glu Ile Phe Lys Leu Leu
305 310 315

<210> 59
<211> 948
<212> DNA
<213> *Candida tropicalis*

<220>
<221> CDS
<222> (1)..(948)

<400> 59
aaa tta gaa tac aag gac atc cca gtt cca aag cca aag cca
aac gaa 48
Lys Leu Glu Tyr Lys Asp Ile Pro Val Pro Lys Pro Lys Pro
Asn Glu
1 5 10
15

ttg ctc atc aac gtc aag tac tcc ggt gtc tgc cac act gat
tta cac 96
Leu Leu Ile Asn Val Lys Tyr Ser Gly Val Cys His Thr Asp
Leu His
20 25 30

gcc tgg aag ggt gac tgg cca ttg gac acc aag ttg cca ttg
gtg ggt 144
Ala Trp Lys Gly Asp Trp Pro Leu Asp Thr Lys Leu Pro Leu
Val Gly

35			40			45							
ggt	cac	gaa	ggt	gct	ggt	ggt	ggt	gcc	att	ggt	gac	aat	
gtc	aag			192									
Gly	His	Glu	Gly	Ala	Gly	Val	Val	Val	Ala	Ile	Gly	Asp	Asn
Val	Lys												
	50					55					60		
gga	tgg	aag	gtc	ggt	gat	ttg	gcc	ggt	gtc	aag	tgg	ttg	aac
ggt	tcc			240									
Gly	Trp	Lys	Val	Gly	Asp	Leu	Ala	Gly	Val	Lys	Trp	Leu	Asn
Gly	Ser												
65					70					75			
80													
tgt	atg	aac	tgt	gag	tac	tgt	caa	cag	ggt	gcc	gaa	cca	aac
tgt	cca			288									
Cys	Met	Asn	Cys	Glu	Tyr	Cys	Gln	Gln	Gly	Ala	Glu	Pro	Asn
Cys	Pro												
				85						90			
95													
cag	gct	gac	ttg	tct	ggt	tac	acc	cac	gac	ggt	tct	ttc	cag
caa	tac			336									
Gln	Ala	Asp	Leu	Ser	Gly	Tyr	Thr	His	Asp	Gly	Ser	Phe	Gln
Gln	Tyr												
			100					105				110	
gcc	act	gca	gat	gcc	gtg	caa	gcc	gct	aga	att	cca	gct	ggt
act	gat			384									
Ala	Thr	Ala	Asp	Ala	Val	Gln	Ala	Ala	Arg	Ile	Pro	Ala	Gly
Thr	Asp												
		115					120				125		
tta	gcc	aac	gtt	gcc	ccc	atc	ttg	tgt	gct	ggt	gtc	act	gtt
tac	aag			432									
Leu	Ala	Asn	Val	Ala	Pro	Ile	Leu	Cys	Ala	Gly	Val	Thr	Val
Tyr	Lys												
	130					135					140		
gcc	ttg	aag	acc	gcc	gac	ttg	cag	cca	ggt	caa	tgg	gtc	gcc
att	tcc			480									
Ala	Leu	Lys	Thr	Ala	Asp	Leu	Gln	Pro	Gly	Gln	Trp	Val	Ala
Ile	Ser												
145					150					155			
160													
ggt	gcc	gct	ggt	ggt	ttg	ggt	tct	ttg	gcc	gtt	caa	tac	gcc
aag	gcc			528									
Gly	Ala	Ala	Gly	Gly	Leu	Gly	Ser	Leu	Ala	Val	Gln	Tyr	Ala

Lys Ala

165

170

175

atg ggc tac aga gtt gtc gcc atc gat ggt ggt gcc gac aag
ggt gag 576
Met Gly Tyr Arg Val Val Ala Ile Asp Gly Gly Ala Asp Lys
Gly Glu

180

185

190

ttc gtc aag tct ttg ggc gct gag gtc ttt gtt gat ttc ctc
aag gaa 624
Phe Val Lys Ser Leu Gly Ala Glu Val Phe Val Asp Phe Leu
Lys Glu

195

200

205

aag gac att gtt ggt gct gtc aag aag gca acc gat ggt ggc
cca cac 672
Lys Asp Ile Val Gly Ala Val Lys Lys Ala Thr Asp Gly Gly
Pro His
210

215

220

ggt gcc gtt aac gtt tcc atc tcc gaa aag gcc atc aac caa
tct gtc 720
Gly Ala Val Asn Val Ser Ile Ser Glu Lys Ala Ile Asn Gln
Ser Val
225 230 235
240

gac tac gtt aga acc ttg ggt aag gtt gtc ttg gtc ggt ttg
cca gct 768
Asp Tyr Val Arg Thr Leu Gly Lys Val Val Leu Val Gly Leu
Pro Ala

245

250

255

ggc tcc aag gtt tct gct cca gtc ttt gac tcc gtc gtc aag
tcc atc 816
Gly Ser Lys Val Ser Ala Pro Val Phe Asp Ser Val Val Lys
Ser Ile

260

265

270

caa atc aag ggt tcc tat gtc ggt aac aga aag gac act gcc
gaa gct 864
Gln Ile Lys Gly Ser Tyr Val Gly Asn Arg Lys Asp Thr Ala
Glu Ala

275

280

285

gtt gac ttt ttc tcc aga ggc ttg atc aag tgt cca atc aag
gtt gtc 912

- 244/269 -

Val Asp Phe Phe Ser Arg Gly Leu Ile Lys Cys Pro Ile Lys
Val Val
290 295 300

ggt ttg agt gaa ttg cca gaa gtc tac aag ttg atg
948
Gly Leu Ser Glu Leu Pro Glu Val Tyr Lys Leu Met
305 310 315

<210> 60
<211> 316
<212> PRT
<213> Candida tropicalis

<400> 60

Lys Leu Glu Tyr Lys Asp Ile Pro Val Pro Lys Pro Lys Pro
Asn Glu
1 5 10
15

Leu Leu Ile Asn Val Lys Tyr Ser Gly Val Cys His Thr Asp
Leu His
20 25 30

Ala Trp Lys Gly Asp Trp Pro Leu Asp Thr Lys Leu Pro Leu
Val Gly
35 40 45

Gly His Glu Gly Ala Gly Val Val Val Ala Ile Gly Asp Asn
Val Lys
50 55 60

Gly Trp Lys Val Gly Asp Leu Ala Gly Val Lys Trp Leu Asn
Gly Ser
65 70 75
80

Cys Met Asn Cys Glu Tyr Cys Gln Gln Gly Ala Glu Pro Asn
Cys Pro
85 90
95

- 245/269 -

Gln Ala Asp Leu Ser Gly Tyr Thr His Asp Gly Ser Phe Gln
Gln Tyr
100 105 110

Ala Thr Ala Asp Ala Val Gln Ala Ala Arg Ile Pro Ala Gly
Thr Asp
115 120 125

Leu Ala Asn Val Ala Pro Ile Leu Cys Ala Gly Val Thr Val
Tyr Lys
130 135 140

Ala Leu Lys Thr Ala Asp Leu Gln Pro Gly Gln Trp Val Ala
Ile Ser
145 150 155
160

Gly Ala Ala Gly Gly Leu Gly Ser Leu Ala Val Gln Tyr Ala
Lys Ala
165 170
175

Met Gly Tyr Arg Val Val Ala Ile Asp Gly Gly Ala Asp Lys
Gly Glu
180 185 190

Phe Val Lys Ser Leu Gly Ala Glu Val Phe Val Asp Phe Leu
Lys Glu
195 200 205

Lys Asp Ile Val Gly Ala Val Lys Lys Ala Thr Asp Gly Gly
Pro His
210 215 220

Gly Ala Val Asn Val Ser Ile Ser Glu Lys Ala Ile Asn Gln
Ser Val
225 230 235
240

Asp Tyr Val Arg Thr Leu Gly Lys Val Val Leu Val Gly Leu
Pro Ala

245														250													
255																											
Gly	Ser	Lys	Val	Ser	Ala	Pro	Val	Phe	Asp	Ser	Val	Val	Lys														
Ser	Ile																										
				260				265				270															
Gln	Ile	Lys	Gly	Ser	Tyr	Val	Gly	Asn	Arg	Lys	Asp	Thr	Ala														
Glu	Ala																										
				275				280				285															
Val	Asp	Phe	Phe	Ser	Arg	Gly	Leu	Ile	Lys	Cys	Pro	Ile	Lys														
Val	Val																										
				290				295				300															
Gly	Leu	Ser	Glu	Leu	Pro	Glu	Val	Tyr	Lys	Leu	Met																
305					310					315																	

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<220>
<221> CDS
<222> (1)..(456)
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gcc gat gcc gtc caa gct gcc aag atc cca gaa ggc gca gac
atg gct 144
Ala Asp Ala Val Gln Ala Ala Lys Ile Pro Glu Gly Ala Asp

```

Met Ala
      35                      40                      45

agt atc gcc ccg atc ttg tgt gct ggt gtg acc gtg tac aag
gct ttg          192
Ser Ile Ala Pro Ile Leu Cys Ala Gly Val Thr Val Tyr Lys
Ala Leu
      50                      55                      60

aag aac gcc gac ttg ttg gct ggc caa tgg gtg gct atc tct
ggt gct          240
Lys Asn Ala Asp Leu Leu Ala Gly Gln Trp Val Ala Ile Ser
Gly Ala
65                      70                      75
80

ggt ggt ggt ttg ggc tcc ttg ggt gtg cag tac gct aaa gcc
atg ggt          288
Gly Gly Gly Leu Gly Ser Leu Gly Val Gln Tyr Ala Lys Ala
Met Gly
      85                      90

95

tac aga gtg tta gcc atc gat ggt ggt gat gag aga gga gag
ttt gtc          336
Tyr Arg Val Leu Ala Ile Asp Gly Gly Asp Glu Arg Gly Glu
Phe Val
      100                      105                      110

aag tca ttg ggc gcc gaa gtg tac att gac ttc ctt aag gaa
cag gac          384
Lys Ser Leu Gly Ala Glu Val Tyr Ile Asp Phe Leu Lys Glu
Gln Asp
      115                      120                      125

att gtt agt gcc att aga aag gca act ggt ggt ggc cca cac
ggt gtt          432
Ile Val Ser Ala Ile Arg Lys Ala Thr Gly Gly Gly Pro His
Gly Val
      130                      135                      140

att aac gtc tcg gtg tcc gaa aag
456
Ile Asn Val Ser Val Ser Glu Lys
145                      150

```

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<210> 62
<211> 152
<212> PRT

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<213> Candida tropicalis

<400> 62

Asn Cys Glu Phe Cys Gln Gln Gly Ala Glu Pro Asn Cys Pro
Arg Ala
1 5 10
15

Asp Met Ser Gly Tyr Thr His Asp Gly Thr Phe Gln Gln Tyr
Ala Thr
20 25 30

Ala Asp Ala Val Gln Ala Ala Lys Ile Pro Glu Gly Ala Asp
Met Ala
35 40 45

Ser Ile Ala Pro Ile Leu Cys Ala Gly Val Thr Val Tyr Lys
Ala Leu
50 55 60

Lys Asn Ala Asp Leu Leu Ala Gly Gln Trp Val Ala Ile Ser
Gly Ala
65 70 75
80

Gly Gly Gly Leu Gly Ser Leu Gly Val Gln Tyr Ala Lys Ala
Met Gly
85 90
95

Tyr Arg Val Leu Ala Ile Asp Gly Gly Asp Glu Arg Gly Glu
Phe Val
100 105 110

Lys Ser Leu Gly Ala Glu Val Tyr Ile Asp Phe Leu Lys Glu
Gln Asp
115 120 125

Ile Val Ser Ala Ile Arg Lys Ala Thr Gly Gly Gly Pro His
Gly Val
130 135 140

Ile Asn Val Ser Val Ser Glu Lys
145 150

<210> 63
<211> 948
<212> DNA
<213> Candida tropicalis

<220>
<221> CDS
<222> (1)..(948)

<400> 63
aag tta gaa tac aaa gac gtg ccg gtc cct gtc cct aaa ccc
aac gaa 48
Lys Leu Glu Tyr Lys Asp Val Pro Val Pro Val Pro Lys Pro
Asn Glu
1 5 10
15

ttg ctt gtc aac gtc aag tac tcg ggt gtg tgt cat tct gac
ttg cat 96
Leu Leu Val Asn Val Lys Tyr Ser Gly Val Cys His Ser Asp
Leu His
20 25 30

gtc tgg aaa ggc gac tgg ccc att cct gcc aag ttg ccc ttg
gtg gga 144
Val Trp Lys Gly Asp Trp Pro Ile Pro Ala Lys Leu Pro Leu
Val Gly
35 40 45

ggt cac gaa ggt gct ggt gtc gtt gtc ggc atg ggt gac aac
gtc aag 192
Gly His Glu Gly Ala Gly Val Val Val Gly Met Gly Asp Asn
Val Lys
50 55 60

ggc tgg aag gtg ggg gac ttg gct ggt atc aag tgg ttg aat
ggt tcg 240
Gly Trp Lys Val Gly Asp Leu Ala Gly Ile Lys Trp Leu Asn
Gly Ser
65 70 75
80

tgt atg aac tgt gag ttt tgc caa cag ggc gca gaa cct aac

tgt tca	288													
Cys Met	Asn	Cys	Glu	Phe	Cys	Gln	Gln	Gly	Ala	Glu	Pro	Asn		
Cys Ser														
			85					90						
95														
aga gcc	gac	atg	tct	ggg	tat	acc	cac	gat	gga	act	ttc	caa		
caa tac		336												
Arg Ala	Asp	Met	Ser	Gly	Tyr	Thr	His	Asp	Gly	Thr	Phe	Gln		
Gln Tyr														
			100					105				110		
gcc act	gct	gat	gct	gtc	caa	gct	gcc	aag	atc	cca	gaa	ggc		
gcc gac		384												
Ala Thr	Ala	Asp	Ala	Val	Gln	Ala	Ala	Lys	Ile	Pro	Glu	Gly		
Ala Asp														
		115						120				125		
atg gct	agt	atc	gcc	ccg	atc	ttg	tgc	gct	ggg	gtg	acc	gtg		
tac aag		432												
Met Ala	Ser	Ile	Ala	Pro	Ile	Leu	Cys	Ala	Gly	Val	Thr	Val		
Tyr Lys														
		130						135				140		
gct ttg	aag	aac	gcc	gac	ttg	ttg	gct	ggc	caa	tgg	gtg	gct		
atc tct		480												
Ala Leu	Lys	Asn	Ala	Asp	Leu	Leu	Ala	Gly	Gln	Trp	Val	Ala		
Ile Ser														
145								150				155		
160														
ggg gct	ggg	ggg	ggg	ttg	ggc	tcc	ttg	ggg	gtg	cag	tac	gct		
aaa gcc		528												
Gly Ala	Gly	Gly	Gly	Leu	Gly	Ser	Leu	Gly	Val	Gln	Tyr	Ala		
Lys Ala														
			165					170						
175														
atg ggt	tac	aga	gtg	ttg	gct	atc	gac	ggg	ggg	gac	gag	aga		
gga gag		576												
Met Gly	Tyr	Arg	Val	Leu	Ala	Ile	Asp	Gly	Gly	Asp	Glu	Arg		
Gly Glu														
			180					185				190		
ttt gtc	aag	tcc	ttg	ggc	gcc	gaa	gtg	tac	att	gac	ttc	ctt		
aag gaa		624												
Phe Val	Lys	Ser	Leu	Gly	Ala	Glu	Val	Tyr	Ile	Asp	Phe	Leu		
Lys Glu														
		195						200				205		

- 251/269 -

cag gac atc gtt agt gct atc aga aag gca act ggt ggt ggt
cca cac 672
Gln Asp Ile Val Ser Ala Ile Arg Lys Ala Thr Gly Gly Gly
Pro His
210 215 220

ggt gtt att aac gtg tca gtg tcc gaa aag gca atc aac cag
tcg gtg 720
Gly Val Ile Asn Val Ser Val Ser Glu Lys Ala Ile Asn Gln
Ser Val
225 230 235
240

gag tac gtc aga act ttg ggg aaa gtg gtt tta gtt agc ttg
ccg gca 768
Glu Tyr Val Arg Thr Leu Gly Lys Val Val Leu Val Ser Leu
Pro Ala
245 250
255

ggt ggt aaa ctc act gct cct ctt ttc gag tct gtt gct aga
tca atc 816
Gly Gly Lys Leu Thr Ala Pro Leu Phe Glu Ser Val Ala Arg
Ser Ile
260 265 270

cag att aga act acg tgt gtt ggc aac aga aag gat act act
gaa gct 864
Gln Ile Arg Thr Thr Cys Val Gly Asn Arg Lys Asp Thr Thr
Glu Ala
275 280 285

att gat ttc ttt gtt aga ggg ttg atc gat tgc cca att aaa
gtc gct 912
Ile Asp Phe Phe Val Arg Gly Leu Ile Asp Cys Pro Ile Lys
Val Ala
290 295 300

ggt tta agt gaa gtg cca gag att ttt gac ttg atg
948
Gly Leu Ser Glu Val Pro Glu Ile Phe Asp Leu Met
305 310 315

<210> 64
<211> 316
<212> PRT
<213> Candida tropicalis

<400> 64

- 252/269 -

Lys Leu Glu Tyr Lys Asp Val Pro Val Pro Val Pro Lys Pro
Asn Glu
1 5 10
15

Leu Leu Val Asn Val Lys Tyr Ser Gly Val Cys His Ser Asp
Leu His
20 25 30

Val Trp Lys Gly Asp Trp Pro Ile Pro Ala Lys Leu Pro Leu
Val Gly
35 40 45

Gly His Glu Gly Ala Gly Val Val Val Gly Met Gly Asp Asn
Val Lys
50 55 60

Gly Trp Lys Val Gly Asp Leu Ala Gly Ile Lys Trp Leu Asn
Gly Ser
65 70 75
80

Cys Met Asn Cys Glu Phe Cys Gln Gln Gly Ala Glu Pro Asn
Cys Ser
85 90
95

Arg Ala Asp Met Ser Gly Tyr Thr His Asp Gly Thr Phe Gln
Gln Tyr
100 105 110

Ala Thr Ala Asp Ala Val Gln Ala Ala Lys Ile Pro Glu Gly
Ala Asp
115 120 125

Met Ala Ser Ile Ala Pro Ile Leu Cys Ala Gly Val Thr Val
Tyr Lys
130 135 140

Ala Leu Lys Asn Ala Asp Leu Leu Ala Gly Gln Trp Val Ala

- 253/269 -

Ile Ser
145
160

150

155

Gly Ala Gly Gly Gly Leu Gly Ser Leu Gly Val Gln Tyr Ala
Lys Ala
165 170
175

Met Gly Tyr Arg Val Leu Ala Ile Asp Gly Gly Asp Glu Arg
Gly Glu
180 185 190

Phe Val Lys Ser Leu Gly Ala Glu Val Tyr Ile Asp Phe Leu
Lys Glu
195 200 205

Gln Asp Ile Val Ser Ala Ile Arg Lys Ala Thr Gly Gly Gly
Pro His
210 215 220

Gly Val Ile Asn Val Ser Val Ser Glu Lys Ala Ile Asn Gln
Ser Val
225 230 235
240

Glu Tyr Val Arg Thr Leu Gly Lys Val Val Leu Val Ser Leu
Pro Ala
245 250
255

Gly Gly Lys Leu Thr Ala Pro Leu Phe Glu Ser Val Ala Arg
Ser Ile
260 265 270

Gln Ile Arg Thr Thr Cys Val Gly Asn Arg Lys Asp Thr Thr
Glu Ala
275 280 285

Ile Asp Phe Phe Val Arg Gly Leu Ile Asp Cys Pro Ile Lys
Val Ala

290

295

300

Gly Leu Ser Glu Val Pro Glu Ile Phe Asp Leu Met
305 310 315

<210> 65
<211> 948
<212> DNA
<213> Candida tropicalis

<220>
<221> CDS
<222> (1)..(948)

<400> 65
gaa tta gaa tac aaa gat atc cca gtg cca acc cca aag gcc
aac gaa 48
Glu Leu Glu Tyr Lys Asp Ile Pro Val Pro Thr Pro Lys Ala
Asn Glu
1 5 10
15

ttg ctc atc aac gtc aaa tac tcg ggt gtc tgc cac act gat
ttg cac 96
Leu Leu Ile Asn Val Lys Tyr Ser Gly Val Cys His Thr Asp
Leu His
20 25 30

gcc tgg aag ggt gac tgg cca ttg gcc acc aag ttg cca ttg
gtt ggt 144
Ala Trp Lys Gly Asp Trp Pro Leu Ala Thr Lys Leu Pro Leu
Val Gly
35 40 45

ggt cac gaa ggt gct ggt gtc gtt gtc ggc atg ggt gaa aac
gtc aag 192
Gly His Glu Gly Ala Gly Val Val Val Gly Met Gly Glu Asn
Val Lys
50 55 60

ggc tgg aag att ggt gac ttc gcc ggt atc aaa tgg ttg aac
ggt tcc 240
Gly Trp Lys Ile Gly Asp Phe Ala Gly Ile Lys Trp Leu Asn
Gly Ser
65 70 75
80

tgt atg tcc tgt gag ttc tgt caa caa ggt gct gaa cca aac
tgt ggt 288
Cys Met Ser Cys Glu Phe Cys Gln Gln Gly Ala Glu Pro Asn
Cys Gly

85

90

95

gag gcc gac ttg tct ggt tac acc cac gat ggt tct ttc gaa
caa tac 336
Glu Ala Asp Leu Ser Gly Tyr Thr His Asp Gly Ser Phe Glu
Gln Tyr

100

105

110

gcc act gct gat gct gtt caa gcc gcc aga atc cca gct ggt
act gat 384
Ala Thr Ala Asp Ala Val Gln Ala Ala Arg Ile Pro Ala Gly
Thr Asp

115

120

125

ttg gcc gaa gtt gcc cca atc ttg tgt gcg ggt gtc acc gtc
tac aaa 432
Leu Ala Glu Val Ala Pro Ile Leu Cys Ala Gly Val Thr Val
Tyr Lys

130

135

140

gcc ttg aag act gcc gac ttg gcc gct ggt caa tgg gtc gct
atc tcc 480
Ala Leu Lys Thr Ala Asp Leu Ala Ala Gly Gln Trp Val Ala
Ile Ser

145

150

155

160

ggg gct ggt ggt ggt ttg ggt tcc ttg gct gtc caa tac gcc
gtc gcc 528
Gly Ala Gly Gly Gly Leu Gly Ser Leu Ala Val Gln Tyr Ala
Val Ala

165

170

175

atg ggc ttg aga gtc gtt gcc att gac ggt ggt gac gaa aag
ggg gcc 576
Met Gly Leu Arg Val Val Ala Ile Asp Gly Gly Asp Glu Lys
Gly Ala

180

185

190

ttt gtc aag tcc ttg ggt gct gaa gcc tac att gat ttc ctc
aag gaa 624
Phe Val Lys Ser Leu Gly Ala Glu Ala Tyr Ile Asp Phe Leu
Lys Glu

195

200

205

aag gac att gtc tct gct gtc aag aag gcc acc gat gga ggt
cca cac 672
Lys Asp Ile Val Ser Ala Val Lys Lys Ala Thr Asp Gly Gly
Pro His
210 215 220

ggt gct atc aat gtt tcc gtt tcc gaa aaa gcc att gac caa
tcc gtc 720
Gly Ala Ile Asn Val Ser Val Ser Glu Lys Ala Ile Asp Gln
Ser Val
225 230 235
240

gag tac gtt aga cca ttg ggt aag gtt gtt ttg gtt ggt ttg
cca gct 768
Glu Tyr Val Arg Pro Leu Gly Lys Val Val Leu Val Gly Leu
Pro Ala
245 250
255

ggc tcc aag gtc act gct ggt gtt ttc gaa gcc gtt gtc aag
tcc att 816
Gly Ser Lys Val Thr Ala Gly Val Phe Glu Ala Val Val Lys
Ser Ile
260 265 270

gaa atc aag ggt tcc tat gtc ggt aac aga aag gat acc gcc
gaa gcc 864
Glu Ile Lys Gly Ser Tyr Val Gly Asn Arg Lys Asp Thr Ala
Glu Ala
275 280 285

gtt gac ttt ttc tcc aga ggc ttg atc aag tgt cca atc aag
att gtt 912
Val Asp Phe Phe Ser Arg Gly Leu Ile Lys Cys Pro Ile Lys
Ile Val
290 295 300

ggc ttg agt gaa ttg cca cag gtc ttc aag ttg atg
948
Gly Leu Ser Glu Leu Pro Gln Val Phe Lys Leu Met
305 310 315

<210> 66
<211> 316
<212> PRT
<213> Candida tropicalis

<400> 66

Glu Leu Glu Tyr Lys Asp Ile Pro Val Pro Thr Pro Lys Ala
Asn Glu

1 5 10

15

Leu Leu Ile Asn Val Lys Tyr Ser Gly Val Cys His Thr Asp
Leu His

20 25 30

Ala Trp Lys Gly Asp Trp Pro Leu Ala Thr Lys Leu Pro Leu
Val Gly

35 40 45

Gly His Glu Gly Ala Gly Val Val Val Gly Met Gly Glu Asn
Val Lys

50 55 60

Gly Trp Lys Ile Gly Asp Phe Ala Gly Ile Lys Trp Leu Asn
Gly Ser

65 70 75

80

Cys Met Ser Cys Glu Phe Cys Gln Gln Gly Ala Glu Pro Asn
Cys Gly

85 90

95

Glu Ala Asp Leu Ser Gly Tyr Thr His Asp Gly Ser Phe Glu
Gln Tyr

100 105 110

Ala Thr Ala Asp Ala Val Gln Ala Ala Arg Ile Pro Ala Gly
Thr Asp

115 120 125

Leu Ala Glu Val Ala Pro Ile Leu Cys Ala Gly Val Thr Val
Tyr Lys

130 135 140

- 258/269 -

Ala Leu Lys Thr Ala Asp Leu Ala Ala Gly Gln Trp Val Ala
Ile Ser
145 150 155
160

Gly Ala Gly Gly Gly Leu Gly Ser Leu Ala Val Gln Tyr Ala
Val Ala
165 170
175

Met Gly Leu Arg Val Val Ala Ile Asp Gly Gly Asp Glu Lys
Gly Ala
180 185 190

Phe Val Lys Ser Leu Gly Ala Glu Ala Tyr Ile Asp Phe Leu
Lys Glu
195 200 205

Lys Asp Ile Val Ser Ala Val Lys Lys Ala Thr Asp Gly Gly
Pro His
210 215 220

Gly Ala Ile Asn Val Ser Val Ser Glu Lys Ala Ile Asp Gln
Ser Val
225 230 235
240

Glu Tyr Val Arg Pro Leu Gly Lys Val Val Leu Val Gly Leu
Pro Ala
245 250
255

Gly Ser Lys Val Thr Ala Gly Val Phe Glu Ala Val Val Lys
Ser Ile
260 265 270

Glu Ile Lys Gly Ser Tyr Val Gly Asn Arg Lys Asp Thr Ala
Glu Ala
275 280 285

Val Asp Phe Phe Ser Arg Gly Leu Ile Lys Cys Pro Ile Lys

Ile Val
290 295 300

Gly Leu Ser Glu Leu Pro Gln Val Phe Lys Leu Met
305 310 315

<210> 67
<211> 1992
<212> DNA
<213> Candida tropicalis

<220>
<221> CDS
<222> (1)..(1992)

<400> 67
ctt atg tta tta tgt gac ggg atc atc cac gaa acc acc gtc
gac caa 48
Leu Met Leu Leu Cys Asp Gly Ile Ile His Glu Thr Thr Val
Asp Gln
1 5 10
15

atc aaa gac gtt att gct cct gac ttc cct gct gac aag tac
gaa gag 96
Ile Lys Asp Val Ile Ala Pro Asp Phe Pro Ala Asp Lys Tyr
Glu Glu
20 25 30

tac gtc agg aca ttc acc aaa ccc tcc gaa acc cca ggg ttc
agg gaa 144
Tyr Val Arg Thr Phe Thr Lys Pro Ser Glu Thr Pro Gly Phe
Arg Glu
35 40 45

acc gtc tac aac aca gtc aac gca aac acc acg gac gca atc
cac cag 192
Thr Val Tyr Asn Thr Val Asn Ala Asn Thr Thr Asp Ala Ile
His Gln
50 55 60

ttc att atc ttg acc aat gtt ttg gca tcc agg gtc ttg gct
cca gct 240
Phe Ile Ile Leu Thr Asn Val Leu Ala Ser Arg Val Leu Ala
Pro Ala
65 70 75
80

ttg acc aac tcg ttg acg cct atc aag gac atg agc ttg gaa
gac cgt 288
Leu Thr Asn Ser Leu Thr Pro Ile Lys Asp Met Ser Leu Glu
Asp Arg

85 90

95

gaa aaa ttg ttg gcc tcg tgg cgc gac tcc cca atc gct gcc
 aaa agg 336
 Glu Lys Leu Leu Ala Ser Trp Arg Asp Ser Pro Ile Ala Ala
 Lys Arg

100

105

110

aaa ttg ttc agg ttg gtt tcc acg ctt acc ttg gtt act ttc
acg aga 384
Lys Leu Phe Arg Leu Val Ser Thr Leu Thr Leu Val Thr Phe
Thr Arg

115

120

125

ttg gcc aat gag ttg cat ttg aaa gcc att cac tat cca gga
aga gaa 432
Leu Ala Asn Glu Leu His Leu Lys Ala Ile His Tyr Pro Gly
Arg Glu

130

135

140

gac cgt gaa aag gct tat gaa acc cag gag att gac cct ttc
aag tac 480
Asp Arg Glu Lys Ala Tyr Glu Thr Gln Glu Ile Asp Pro Phe
Lys Tyr

145

150

155

160

cag ttt atg gaa aag cca aag ttt gac ggc gct gag ttg tac
 ttg cca 528
 Gln Phe Met Glu Lys Pro Lys Phe Asp Gly Ala Glu Leu Tyr
 Leu Pro

165

170

175

gat att gat gtt atc att att gga tct ggt gcc ggt gct ggt
gtt gtg 576
Asp Ile Asp Val Ile Ile Ile Gly Ser Gly Ala Gly Ala Gly
Val Val

180

185

190

gcc cac act ttg gcc aac gat ggc ttc aag agt ttg gtt ttg
gaa aag 624
Ala His Thr Leu Ala Asn Asp Gly Phe Lys Ser Leu Val Leu
Glu Lys

624

- 261/269 -

195				200				205					
ggc	aaa	tac	ttt	agc	aac	tcc	gag	ttg	aac	ttt	gat	gac	aag
gac	ggc		672										
Gly	Lys	Tyr	Phe	Ser	Asn	Ser	Glu	Leu	Asn	Phe	Asp	Asp	Lys
Asp	Gly												
	210				215					220			
ggt	caa	gaa	tta	tac	caa	agt	gga	ggt	act	ttg	act	aca	gtc
aac	caa		720										
Val	Gln	Glu	Leu	Tyr	Gln	Ser	Gly	Gly	Thr	Leu	Thr	Thr	Val
Asn	Gln												
225					230					235			
240													
cag	ttg	ttt	ggt	ctt	gct	ggt	tcc	act	ttt	ggt	ggc	ggt	acc
act	gtc		768										
Gln	Leu	Phe	Val	Leu	Ala	Gly	Ser	Thr	Phe	Gly	Gly	Gly	Thr
Thr	Val												
					245					250			
255													
aat	tgg	tca	gcc	tgt	ctt	aag	acg	cca	ttc	aag	gtg	cgt	aag
gaa	tgg		816										
Asn	Trp	Ser	Ala	Cys	Leu	Lys	Thr	Pro	Phe	Lys	Val	Arg	Lys
Glu	Trp												
					260					265			270
tat	gat	gag	ttt	ggt	ggt	gac	ttt	gct	gct	gat	gaa	gca	tac
gat	aaa		864										
Tyr	Asp	Glu	Phe	Gly	Val	Asp	Phe	Ala	Ala	Asp	Glu	Ala	Tyr
Asp	Lys												
					275					280			285
gcg	cag	gat	tat	ggt	tgg	cag	caa	atg	gga	gct	tct	acc	gaa
ggc	atc		912										
Ala	Gln	Asp	Tyr	Val	Trp	Gln	Gln	Met	Gly	Ala	Ser	Thr	Glu
Gly	Ile												
					290					295			300
acc	cac	tct	ttg	gct	aac	gag	att	att	att	att	gaa	ggt	ggt
aaa	tta		960										
Thr	His	Ser	Leu	Ala	Asn	Glu	Ile	Ile	Ile	Ile	Glu	Gly	Gly
Lys	Leu												
305					310					315			
320													
ggt	tac	aag	gcc	aag	gta	tta	gac	caa	aac	agc	ggt	ggt	cat
cct	cag		1008										
Gly	Tyr	Lys	Ala	Lys	Val	Leu	Asp	Gln	Asn	Ser	Gly	Gly	His

- 264/269 -

cca att ttt gaa tcc gac aag cca aag gat aag aga tca atc
aag gac 1776
Pro Ile Phe Glu Ser Asp Lys Pro Lys Asp Lys Arg Ser Ile
Lys Asp

580

585

590

gag gac tat gtc gaa tgg aga gcc aag gtt gcc aag att cct
ttc gac 1824
Glu Asp Tyr Val Glu Trp Arg Ala Lys Val Ala Lys Ile Pro
Phe Asp

595

600

605

acc tac ggc tca cct tat ggt tcg gca cat caa atg tct tct
tgc cgt 1872
Thr Tyr Gly Ser Pro Tyr Gly Ser Ala His Gln Met Ser Ser
Cys Arg

610

615

620

atg tca ggt aag ggt cct aaa tac ggt gct gtt gac acc gat
ggg aga 1920
Met Ser Gly Lys Gly Pro Lys Tyr Gly Ala Val Asp Thr Asp
Gly Arg

625

630

635

640

ttg ttt gaa tgt tcg aat gtt tat gtt gcc gat gca agt ctt
ttg cca 1968
Leu Phe Glu Cys Ser Asn Val Tyr Val Ala Asp Ala Ser Leu
Leu Pro

645

650

655

act gca agc ggt gct aat cct atg
1992

Thr Ala Ser Gly Ala Asn Pro Met
660

<210> 68

<211> 664

<212> PRT

<213> Candida tropicalis

<400> 68

Leu Met Leu Leu Cys Asp Gly Ile Ile His Glu Thr Thr Val
Asp Gln

1

5

10

15

Ile	Lys	Asp	Val	Ile	Ala	Pro	Asp	Phe	Pro	Ala	Asp	Lys	Tyr
Glu	Glu												
			20					25					30

Tyr	Val	Arg	Thr	Phe	Thr	Lys	Pro	Ser	Glu	Thr	Pro	Gly	Phe
Arg	Glu												
		35					40					45	

Thr	Val	Tyr	Asn	Thr	Val	Asn	Ala	Asn	Thr	Thr	Asp	Ala	Ile
His	Gln												
	50					55					60		

Phe	Ile	Ile	Leu	Thr	Asn	Val	Leu	Ala	Ser	Arg	Val	Leu	Ala
Pro	Ala												
65					70					75			
80													

Leu	Thr	Asn	Ser	Leu	Thr	Pro	Ile	Lys	Asp	Met	Ser	Leu	Glu
Asp	Arg												
				85					90				
95													

Glu	Lys	Leu	Leu	Ala	Ser	Trp	Arg	Asp	Ser	Pro	Ile	Ala	Ala
Lys	Arg												
			100					105					110

Lys	Leu	Phe	Arg	Leu	Val	Ser	Thr	Leu	Thr	Leu	Val	Thr	Phe
Thr	Arg												
		115					120					125	

Leu	Ala	Asn	Glu	Leu	His	Leu	Lys	Ala	Ile	His	Tyr	Pro	Gly
Arg	Glu												
	130					135					140		

Asp	Arg	Glu	Lys	Ala	Tyr	Glu	Thr	Gln	Glu	Ile	Asp	Pro	Phe
Lys	Tyr												
145					150					155			
160													

Gln	Phe	Met	Glu	Lys	Pro	Lys	Phe	Asp	Gly	Ala	Glu	Leu	Tyr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- 266/269 -

Leu Pro

165

170

175

Asp Ile Asp Val Ile Ile Ile Gly Ser Gly Ala Gly Ala Gly
Val Val

180

185

190

Ala His Thr Leu Ala Asn Asp Gly Phe Lys Ser Leu Val Leu
Glu Lys

195

200

205

Gly Lys Tyr Phe Ser Asn Ser Glu Leu Asn Phe Asp Asp Lys
Asp Gly

210

215

220

Val Gln Glu Leu Tyr Gln Ser Gly Gly Thr Leu Thr Thr Val
Asn Gln

225

230

235

240

Gln Leu Phe Val Leu Ala Gly Ser Thr Phe Gly Gly Gly Thr
Thr Val

245

250

255

Asn Trp Ser Ala Cys Leu Lys Thr Pro Phe Lys Val Arg Lys
Glu Trp

260

265

270

Tyr Asp Glu Phe Gly Val Asp Phe Ala Ala Asp Glu Ala Tyr
Asp Lys

275

280

285

Ala Gln Asp Tyr Val Trp Gln Gln Met Gly Ala Ser Thr Glu
Gly Ile

290

295

300

Thr His Ser Leu Ala Asn Glu Ile Ile Ile Glu Gly Gly Lys
Lys Leu

305

310

315

320

Gly Tyr Lys Ala Lys Val Leu Asp Gln Asn Ser Gly Gly His
Pro Gln

325

330

335

His Arg Cys Gly Phe Cys Tyr Leu Gly Cys Lys His Gly Ile
Lys Gln

340

345

350

Gly Ser Val Asn Asn Trp Phe Arg Asp Ala Ala Ala His Gly
Ser Gln

355

360

365

Phe Met Gln Gln Val Arg Val Leu Gln Ile Leu Asn Lys Lys
Gly Ile

370

375

380

Ala Tyr Gly Ile Leu Cys Glu Asp Val Val Thr Gly Ala Lys
Phe Thr

385

390

395

400

Ile Thr Gly Pro Lys Lys Phe Val Val Ala Ala Gly Ala Leu
Asn Thr

405

410

415

Pro Ser Val Leu Val Asn Ser Gly Phe Lys Asn Lys Asn Ile
Gly Lys

420

425

430

Asn Leu Thr Leu His Pro Val Ser Val Val Phe Gly Asp Phe
Gly Lys

435

440

445

Asp Val Gln Ala Asp His Phe His Asn Ser Ile Met Thr Ala
Leu Cys

450

455

460

Ser Glu Ala Ala Asp Leu Asp Gly Lys Gly His Gly Cys Arg
 Ile Glu
 465 470 475
 480

Thr Ile Leu Asn Ala Pro Phe Ile Gln Ala Ser Phe Leu Pro
 Trp Arg
 485 490
 495

Gly Ser Asn Glu Ala Arg Arg Asp Leu Leu Arg Tyr Asn Asn
 Met Val
 500 505 510

Ala Met Leu Leu Leu Ser Arg Asp Thr Thr Ser Gly Ser Val
 Ser Ala
 515 520 525

His Pro Thr Lys Pro Glu Ala Leu Val Val Glu Tyr Asp Val
 Asn Lys
 530 535 540

Phe Asp Arg Asn Ser Ile Leu Gln Ala Leu Leu Val Thr Ala
 Asp Leu
 545 550 555
 560

Leu Tyr Ile Gln Gly Ala Lys Arg Ile Leu Ser Pro Gln Ala
 Trp Val
 565 570
 575

Pro Ile Phe Glu Ser Asp Lys Pro Lys Asp Lys Arg Ser Ile
 Lys Asp
 580 585 590

Glu Asp Tyr Val Glu Trp Arg Ala Lys Val Ala Lys Ile Pro
 Phe Asp
 595 600 605

- 269/269 -

Thr	Tyr	Gly	Ser	Pro	Tyr	Gly	Ser	Ala	His	Gln	Met	Ser	Ser
Cys	Arg												
	610					615					620		

Met	Ser	Gly	Lys	Gly	Pro	Lys	Tyr	Gly	Ala	Val	Asp	Thr	Asp
Gly	Arg												
625					630					635			
640													

Leu	Phe	Glu	Cys	Ser	Asn	Val	Tyr	Val	Ala	Asp	Ala	Ser	Leu
Leu	Pro												
				645					650				
655													

Thr	Ala	Ser	Gly	Ala	Asn	Pro	Met
			660				

Claims

1. A *Candida tropicalis* cell, characterized in that the cell has, compared with its wild type, a reduced activity of at least one of the enzymes that are encoded by the intron-free nucleic acid sequences selected from the two groups A) and B) consisting of
 - A) Seq ID No. 1, Seq ID No. 3, Seq ID No. 5, Seq ID No. 7, Seq ID No. 9, Seq ID No. 11, Seq ID No. 13, Seq ID No. 15, Seq ID No. 17, Seq ID No. 19, Seq ID No. 21, Seq ID No. 23, Seq ID No. 25, Seq ID No. 27, Seq ID No. 29, Seq ID No. 31, Seq ID No. 33, Seq ID No. 35, Seq ID No. 37, Seq ID No. 39, Seq ID No. 41, Seq ID No. 43, Seq ID No. 45, Seq ID No. 47, Seq ID No. 49, Seq ID No. 51, Seq ID No. 53, Seq ID No. 55, Seq ID No. 57, Seq ID No. 59, Seq ID No. 61, Seq ID No. 63, Seq ID No. 65 and Seq ID No. 67
 - B) a sequence that is identical to at least 80% to one of the sequences Seq ID No. 1, Seq ID No. 3, Seq ID No. 5, Seq ID No. 7, Seq ID No. 9, Seq ID No. 11, Seq ID No. 13, Seq ID No. 15, Seq ID No. 17, Seq ID No. 19, Seq ID No. 21, Seq ID No. 23, Seq ID No. 25, Seq ID No. 27, Seq ID No. 29, Seq ID No. 31, Seq ID No. 33, Seq ID No. 35, Seq ID No. 37, Seq ID No. 39, Seq ID No. 41, Seq ID No. 43, Seq ID No. 45, Seq ID No. 47, Seq ID No. 49, Seq ID No. 51, Seq ID No. 53, Seq ID No. 55, Seq ID No. 57, Seq ID No. 59, Seq ID No. 61, Seq ID No. 63, Seq ID No. 65 and Seq ID No. 67.
2. A *Candida tropicalis* cell according to claim 1, characterized in that the decrease in enzymatic activity is achieved by modification of a gene comprising one of the nucleic acid sequences stated in claim 1, the modification being selected

from the group comprising insertion of foreign DNA into the gene, deletion of at least parts of the gene, point mutations in the gene sequence, subjecting the gene to the influence of RNA interference and exchange of parts of the gene with foreign DNA, in particular of the promoter region.

3. A *Candida tropicalis* cell according to claim 2, characterized in that the foreign DNA is a selection marker gene.
4. A *Candida tropicalis* cell according to at least one of the preceding claims, characterized in that the cell is blocked at least partially in its β -oxidation.
5. A *Candida tropicalis* cell according to at least one of the preceding claims, characterized in that the *Candida tropicalis* cell is derived from strains selected from the group comprising *Candida tropicalis* H41, *Candida tropicalis* H41B, *Candida tropicalis* H51, *Candida tropicalis* H45, *Candida tropicalis* H43, *Candida tropicalis* H53, *Candida tropicalis* H534, *Candida tropicalis* 534B, *Candida tropicalis* H435, *Candida tropicalis* ATCC20962 and *Candida tropicalis* HDC100, in particular consisting of *Candida tropicalis* ATCC20962 and *Candida tropicalis* HDC100.
6. Use of the cells according to at least one of the preceding claims for the production of ω -hydroxycarboxylic acids or ω -hydroxycarboxylic acid esters.
7. A method of production of a *C. tropicalis* cell according to at least one of claims 1 to 5 comprising the steps:
 - I) preparation of a *C. tropicalis* cell and

- II) modification of at least one gene comprising one of the sequences selected from the nucleic acid sequence groups A) and B) stated in claim 1 by insertion of foreign DNA, in particular of DNA coding for a selection marker gene, into the gene, deletion at least of parts of the gene, point mutations in the gene sequence, subjecting the gene to the influence of RNA interference and exchange of parts of the gene with foreign DNA, in particular of the promoter region.
8. A method of production of ω -hydroxycarboxylic acids or ω -hydroxycarboxylic acid esters, in particular of ω -hydroxycarboxylic acids or ω -hydroxycarboxylic acid esters with a chain length of the carboxylic acid from 6 to 24 carbon atoms and a chain length of the alcohol component of the ester from 1 to 4 carbon atoms, in particular of 12-hydroxydodecanoic acid or 12-hydroxydodecanoic acid methyl ester comprising the steps
- a) contacting the cell according to at least one of claims 1 to 5 with a medium comprising a carboxylic acid or a carboxylic acid ester,
 - b) cultivating the cell under conditions that enable the cell to form the corresponding ω -hydroxycarboxylic acid or ω -hydroxycarboxylic acid esters from the carboxylic acid or the carboxylic acid ester and
 - c) optionally isolating the ω -hydroxycarboxylic acid or ω -hydroxycarboxylic acid esters that formed.
9. A method according to claim 8, characterized in that cells at least partially blocked in their β -oxidation according to claim 5 are used.
10. Use of the ω -hydroxycarboxylic acid or of the ω -hydroxycarboxylic acid ester obtained by the

method according to claim 8 or 9 for the
production of a polymer.