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THEREOF**(30) **Foreign Application Priority Data**

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Essen (DE)(52) **U.S. Cl. 528/361; 435/254.22; 435/146;**
435/135; 435/471(21) Appl. No.: **12/943,145**(57) **ABSTRACT**(22) Filed: **Nov. 10, 2010**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.

CANDIDA TROPICALIS CELLS AND USE THEREOF

FIELD OF THE INVENTION

[0001] 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.

BACKGROUND OF THE INVENTION

[0002] Owing to its ability to form dicarboxylic acids from alkanes, *Candida tropicalis* is a well-characterized ascomycete.

[0003] 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.

[0004] 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.

[0005] 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.

[0006] 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.

[0007] 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.

[0008] 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

[0009] It was found, surprisingly, that the cells described hereunder make a contribution to solution of this task.

[0010] The object of the present invention is therefore a cell as described in claim 1.

[0011] 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.

[0012] 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.

[0013] 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.

[0014] In this connection, the nucleic acid sequence group that is preferred according to the invention is group A).

[0015] 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".

[0016] 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.

[0017] 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:

[0018] 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 NH₄Cl, 1.5 g Na₂SO₄, 300 ml of a 1 mM potassium phosphate buffer (pH 7.0), 20 mg ZnSO₄×7H₂O, 20 mg MnSO₄×4H₂O, 20 mg nicotinic acid, 20 mg pyridoxine, 8 mg thiamine and 6 mg pantothenate). It is cultivated for 24 h at 30° C.

[0019] 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 0 h, 0.5 h, 1 h, 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 4NH₂SO₄. 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.

[0020] 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. 125×2 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.

[0021] 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%.

[0022] 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.

[0023] “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

[0024] GAP (Deveroy, J. et al., Nucleic Acid Research 12 (1984), page 387, Genetics Computer Group University of Wisconsin, Medicine (Wi), and

[0025] 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 N. Dak. 22894; Altschul S. et al., above).

[0026] The known Smith-Waterman algorithm can also be used for determining nucleotide identity.

[0027] 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

[0028] The above parameters are the default parameters in nucleotide sequence comparison.

[0029] The GAP program is also suitable for use with the above parameters.

[0030] An identity of 80% according to the above algorithm means, in connection with the present invention, 80% identity. The same applies to higher identities.

[0031] 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.

[0032] All stated percentages (%) are percentages by weight unless stated otherwise.

[0033] Methods of lowering enzymatic activities in microorganisms are known by a person skilled in the art.

[0034] 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 September; 11(9):4333-9; Rohrer et al. Appl Microbiol Biotechnol. 1992 February; 36(5):650-4; Picataggio et al. Biotechnology (N Y). 1992 August; 10(8):894-8; Ueda et al. Biochim Biophys Acta. 2003 Mar. 17; 1631(2): 160-8; Ko et al. Appl Environ Microbiol. 2006 June; 72(6): 4207-13; Hara et al. Arch Microbiol. 2001 November; 176 (5):364-9; Kanayama et al. J Bacteriol. 1998 February; 180 (3): 690-8.

[0035] 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.

[0036] 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”.

[0037] 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.

[0038] 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.

[0039] 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.

[0040] 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.

[0041] Other *Candida tropicalis* cells blocked for β -oxidation are described for example in WO03/100013.

[0042] 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.

[0043] 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* HDIC100 described in US2004/0014198.

[0044] 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.

[0045] 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.

[0046] A preferred use is characterized according to the invention in that preferred cells according to the invention as described above are used.

[0047] 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.

[0048] 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.

[0049] Preferred methods according to the invention use cells stated above as being preferred according to the invention.

[0050] 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 ATCC 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.

[0051] 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*.

[0052] These cultivation conditions are described for example in WO00/017380 and WO00/015828.

[0053] 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.

[0054] 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.

[0055] 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.

[0056] 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.

[0057] 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.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 68

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<211> LENGTH: 1575

<212> TYPE: DNA

<213> ORGANISM: *Candida tropicalis*

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(1572)

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Trp Tyr Thr Val Ile Thr Leu Ala Ala Leu Val Phe Leu Ile Ser Ser	
20 25 30	

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Asn Ile Lys Asn Tyr Val Lys Ala Lys Lys Leu Lys Cys Arg Asp Pro	
35 40 45	

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Pro Tyr Phe Lys Gly Ala Gly Trp Thr Gly Ile Ser Pro Leu Ile Glu	
50 55 60	

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Ile Ile Lys Val Lys Gly Asn Gly Arg Leu Ala Arg Phe Trp Pro Ile	
65 70 75 80	

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Lys Thr Phe Asp Asp Tyr Pro Asn His Thr Phe Tyr Met Ser Ile Ile	
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Gly Ala Leu Lys Ile Val Leu Thr Val Ile Gln Glu Asn Ile Lys Ala	
100 105 110	

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Val Leu Ala Thr Gln Phe Thr Asp Phe Ser Leu Gly Thr Arg His Ala	
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Gly Trp Lys His Ser Arg Ala Met Leu Arg Pro Gln Phe Ala Arg Asp	
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Gln Ile Gly His Val Lys Ala Leu Glu Pro His Ile Gln Ile Leu Ala	
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Thr Arg Asp Pro Lys Val Leu Gln Asp Gln Leu Leu Asn Ile Met Val	
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Phe Asn Gly Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe Ala Leu Thr	
465 470 475 480	
gaa gct tct tat gtt att acc aga ttg gta caa atg ttt gaa act gtt	1488
Glu Ala Ser Tyr Val Ile Thr Arg Leu Val Gln Met Phe Glu Thr Val	
485 490 495	
tct tct ccc cca gat gtt gaa tac cct cca cca aaa tgt att cat ttg	1536
Ser Ser Pro Pro Asp Val Glu Tyr Pro Pro Lys Cys Ile His Leu	
500 505 510	
act atg agt cat gat gat ggt gtt ttc gtt aaa atg taa	1575
Thr Met Ser His Asp Asp Gly Val Phe Val Lys Met	
515 520	

<210> SEQ ID NO 2

<211> LENGTH: 524

<212> TYPE: PRT

<213> ORGANISM: Candida tropicalis

<400> SEQUENCE: 2

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 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	

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<210> SEQ ID NO 3
<211> LENGTH: 1572
<212> TYPE: DNA
<213> ORGANISM: Candida tropicalis
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1569)
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atg gcc aca caa gaa atc atc gat tct gta ctt cgg tac ttg 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	

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35	40	45	
cca tac ttg aag gat gcc ggt ctc act ggt att ctg tct ttg atc gcc Pro Tyr Leu Lys Asp Ala Gly Leu Thr Gly Ile Leu Ser Leu Ile Ala 50 55 60			192
gcc atc aag gcc aag aac gac ggt aga ttg gct aac ttt gcc gat gaa Ala Ile Lys Ala Lys Asn Asp Gly Arg Leu Ala Asn Phe Ala Asp Glu 65 70 75 80			240
gtt ttc gac gag tac cca aac cac acc ttc tac ttg tct gtt gcc ggt Val Phe Asp Glu Tyr Pro Asn His Thr Phe Tyr Leu Ser Val Ala Gly 85 90 95			288
gct ttg aag att gtc atg act gtt gac cca gaa aac atc aag gct gtc Ala Leu Lys Ile Val Met Thr Val Asp Pro Glu Asn Ile Lys Ala Val 100 105 110			336
ttg gcc acc caa ttc act gac ttc tcc ttg ggt acc aga cac gcc cac Leu Ala Thr Gln Phe Thr Asp Phe Ser Leu Gly Thr Arg His Ala His 115 120 125			384
ttt gct cct ttg ttg ggt gac ggt atc ttc acc ttg gac gga gaa ggt Phe Ala Pro Leu Leu Gly Asp Gly Ile Phe Thr Leu Asp Gly Glu Gly 130 135 140			432
tggt aag cac tcc aga gct atg ttg aga cca cag ttt gct aga gac cag Trp Lys His Ser Arg Ala Met Leu Arg Pro Gln Phe Ala Arg Asp Gln 145 150 155 160			480
att gga cac gtt aaa gcc ttg gaa cca cac atc caa atc atg gct aag Ile Gly His Val Lys Ala Leu Glu Pro His Ile Gln Ile Met Ala Lys 165 170 175			528
cag atc aag ttg aac cag gga aag act ttc gat atc caa gaa ttg ttc Gln Ile Lys Leu Asn Gln Gly Lys Thr Phe Asp Ile Gln Glu Leu Phe 180 185 190			576
ttt aga ttt acc gtc gac acc gct act gag ttc ttg ttt ggt gaa tcc Phe Arg Phe Thr Val Asp Thr Ala Thr Glu Phe Leu Phe Gly Glu Ser 195 200 205			624
gtt cac tcc ttg tac gat gaa aaa ttg ggc atc cca act cca aac gaa Val His Ser Leu Tyr Asp Glu Lys Leu Gly Ile Pro Thr Pro Asn Glu 210 215 220			672
atc cca gga aga gaa aac ttt gcc gct gct ttc aac gtt tcc caa cac Ile Pro Gly Arg Glu Asn Phe Ala Ala Phe Asn Val Ser Gln His 225 230 235 240			720
tac ttg gcc acc aga agt tac tcc cag act ttt tac ttt ttg acc aac Tyr Leu Ala Thr Arg Ser Tyr Ser Gln Thr Phe Tyr Phe Leu Thr Asn 245 250 255			768
cct aag gaa ttc aga gac tgt aac gcc aag gtc cac cac ttg gcc aag Pro Lys Glu Phe Arg Asp Cys Asn Ala Lys Val His His Leu Ala Lys 260 265 270			816
tac ttt gtc aac aag gcc ttg aac ttt act cct gaa gaa ctc gaa gag Tyr Phe Val Asn Lys Ala Leu Asn Phe Thr Pro Glu Glu Leu Glu Glu 275 280 285			864
aaa tcc aag tcc ggt tac gtt ttc ttg tac gaa ttg gtt aag caa acc Lys Ser Lys Ser Gly Tyr Val Phe Leu Tyr Glu Leu Val Lys Gln Thr 290 295 300			912
aga gat cca aag gtc ttg caa gat caa ttg ttg aac att atg gtt gcc Arg Asp Pro Lys Val Leu Gln Asp Gln Leu Asn Ile Met Val Ala 305 310 315 320			960
gga aga gac acc act gcc ggt ttg ttg tcc ttt gct ttg ttt gaa ttg Gly Arg Asp Thr Ala Gly Leu Leu Ser Phe Ala Leu Phe Glu Leu 325 330 335			1008
gct aga cac cca gag atg tgg tcc aag ttg aga gaa gaa atc gaa gtt Ala Arg His Pro Glu Met Trp Ser Lys Leu Arg Glu Glu Ile Glu Val 340 345 350			1056

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340	345	350	
aac ttt ggt gtt ggt gaa gac tcc cgc gtt gaa gaa att acc ttc gaa Asn Phe Gly Val Gly Glu Asp Ser Arg Val Glu Glu Ile Thr Phe Glu 355 360 365			1104
gcc ttg aag aga tgt gaa tac ttg aag gct atc ctt aac gaa acc ttg Ala Leu Lys Arg Cys Glu Tyr Leu Lys Ala Ile Leu Asn Glu Thr Leu 370 375 380			1152
cgt atg tac cca tct gtt cct gtc aac ttt aga acc gcc acc aga gac Arg Met Tyr Pro Ser Val Pro Val Asn Phe Arg Thr Ala Thr Arg Asp 385 390 395 400			1200
acc act ttg cca aga ggt ggt ggt gct aac ggt acc gac cca atc tac Thr Thr Leu Pro Arg Gly Gly Gly Ala Asn Gly Thr Asp Pro Ile Tyr 405 410 415			1248
att cct aaa ggc tcc act gtt gct tac gtt gtc tac aag acc cac cgt Ile Pro Lys Gly Ser Thr Val Ala Tyr Val Val Tyr Lys Thr His Arg 420 425 430			1296
ttg gaa gaa tac tac ggt aag gac gct aac gac ttc aga cca gaa aga Leu Glu Glu Tyr Tyr Gly Lys Asp Ala Asn Asp Phe Arg Pro Glu Arg 435 440 445			1344
tgg ttt gaa cca tct act aag aag ttg ggc tgg gct tat gtt cca ttc Trp Phe Glu Pro Ser Thr Lys Lys Leu Gly Trp Ala Tyr Val Pro Phe 450 455 460			1392
aac ggt ggt cca aga gtc tgc ttg ggt caa caa ttc gcc ttg act gaa Asn Gly Gly Pro Arg Val Cys Leu Gly Gln Gln Phe Ala Leu Thr Glu 465 470 475 480			1440
gct tct tat gtg atc act aga ttg gcc cag atg ttt gaa act gtc tca Ala Ser Tyr Val Ile Thr Arg Leu Ala Gln Met Phe Glu Thr Val Ser 485 490 495			1488
tct gat cca ggt ctc gaa tac cct cca cca aag tgt att cac ttg acc Ser Asp Pro Gly Leu Glu Tyr Pro Pro Pro Lys Cys Ile His Leu Thr 500 505 510			1536
atg agt cac aac gat ggt gtc ttt gtc aag atg taa Met Ser His Asn Asp Gly Val Phe Val Lys Met 515 520			1572

<210> SEQ ID NO 4

<211> LENGTH: 523

<212> TYPE: PRT

<213> ORGANISM: Candida tropicalis

<400> SEQUENCE: 4

Met Ala Thr Gln Glu Ile Ile Asp Ser Val Leu Pro Tyr Leu Thr Lys
1 5 10 15

Trp Tyr Thr Val Ile Thr Ala Ala Val Leu Val Phe Leu Ile Ser Thr
20 25 30

Asn Ile Lys Asn Tyr Val Lys Ala Lys Lys Leu Lys Cys Val Asp Pro
35 40 45

Pro Tyr Leu Lys Asp Ala Gly Leu Thr Gly Ile Leu Ser Leu Ile Ala
50 55 60

Ala Ile Lys Ala Lys Asn Asp Gly Arg Leu Ala Asn Phe Ala Asp Glu
65 70 75 80

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

Ala Leu Lys Ile Val Met 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

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115	120	125
Phe Ala 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 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 305 310 315 320		
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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<210> SEQ ID NO 5
<211> LENGTH: 1569
<212> TYPE: DNA
<213> ORGANISM: Candida tropicalis
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1566)

<400> SEQUENCE: 5

atg act gta cac gat att atc gcc aca tac ttc acc aaa tgg 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 ggt 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 ggt 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 ggt gat ggt 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

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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 gtt 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 gtt 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 gtt 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	
500 505 510	
ctt ttc gac ggt gcc aat att gag atg tat tag	1569
Leu Phe Asp Gly Ala Asn Ile Glu Met Tyr	
515 520	

<210> SEQ ID NO 6

<211> LENGTH: 522

<212> TYPE: PRT

<213> ORGANISM: Candida tropicalis

<400> SEQUENCE: 6

Met 1	Thr	Val	His	Asp 5	Ile	Ile	Ala	Thr	Tyr 10	Phe	Thr	Lys	Trp	Tyr 15	Val
Ile	Val	Pro	Leu 20	Ala	Leu	Ile	Ala	Tyr 25	Arg	Val	Leu	Asp 30	Tyr	Phe	Tyr
Gly	Arg	Tyr 35	Leu	Met	Tyr	Lys	Leu 40	Gly	Ala	Lys	Pro	Phe 45	Phe	Gln	Lys
Gln	Thr 50	Asp	Gly	Cys	Phe	Gly 55	Phe	Lys	Ala	Pro	Leu 60	Glu	Leu	Leu	Lys
Lys 65	Lys	Ser	Asp	Gly	Thr 70	Leu	Ile	Asp	Phe	Thr 75	Leu	Gln	Arg	Ile	His 80
Asp	Leu	Asp	Arg	Pro 85	Asp	Ile	Pro	Thr	Phe 90	Thr	Phe	Pro	Val	Phe 95	Ser
Ile	Asn	Leu	Val 100	Asn	Thr	Leu	Glu	Pro 105	Glu	Asn	Ile	Lys	Ala 110	Ile	Leu
Ala	Thr	Gln	Phe	Asn	Asp	Phe	Ser 120	Leu	Gly	Thr	Arg	His 125	Ser	His	Phe
Ala	Pro 130	Leu	Leu	Gly	Asp	Gly 135	Ile	Phe	Thr	Leu	Asp 140	Gly	Ala	Gly	Trp
Lys 145	His	Ser	Arg	Ser	Met 150	Leu	Arg	Pro	Gln	Phe 155	Ala	Arg	Glu	Gln	Ile 160
Ser	His	Val	Lys	Leu 165	Leu	Glu	Pro	His	Val 170	Gln	Val	Phe	Phe	Lys 175	His
Val	Arg	Lys	Ala 180	Gln	Gly	Lys	Thr	Phe 185	Asp	Ile	Gln	Glu	Leu 190	Phe	Phe
Arg	Leu	Thr 195	Val	Asp	Ser	Ala	Thr 200	Glu	Phe	Leu	Phe	Gly 205	Glu	Ser	Val
Glu	Ser 210	Leu	Arg	Asp	Glu	Ser 215	Ile	Gly	Met	Ser	Ile 220	Asn	Ala	Leu	Asp
Phe 225	Asp	Gly	Lys	Ala	Gly 230	Phe	Ala	Asp	Ala	Phe 235	Asn	Tyr	Ser	Gln	Asn 240
Tyr	Leu	Ala	Ser	Arg 245	Ala	Val	Met	Gln	Gln	Leu	Tyr	Trp	Val	Leu 255	Asn
Gly	Lys	Lys	Phe 260	Lys	Glu	Cys	Asn	Ala 265	Lys	Val	His	Lys	Phe 270	Ala	Asp
Tyr	Tyr 275	Val	Asn	Lys	Ala	Leu	Asp 280	Leu	Thr	Pro	Glu	Gln 285	Leu	Glu	Lys
Gln	Asp 290	Gly	Tyr	Val	Phe	Leu	Tyr 295	Glu	Leu	Val	Lys 300	Gln	Thr	Arg	Asp
Lys 305	Gln	Val	Leu	Arg	Asp 310	Gln	Leu	Leu	Asn	Ile 315	Met	Val	Ala	Gly	Arg 320
Asp	Thr	Thr	Ala 325	Gly	Leu	Leu	Ser	Phe 330	Val	Phe	Phe	Glu	Leu	Ala 335	Arg
Asn	Pro	Glu	Val 340	Thr	Asn	Lys	Leu	Arg 345	Glu	Glu	Ile	Glu	Asp 350	Lys	Phe
Gly	Leu	Gly 355	Glu	Asn	Ala	Ser	Val 360	Glu	Asp	Ile	Ser	Phe 365	Glu	Ser	Leu
Lys 370	Ser	Cys	Glu	Tyr	Leu	Lys 375	Ala	Val	Leu	Asn	Glu 380	Thr	Leu	Arg	Leu
Tyr 385	Pro	Ser	Val	Pro	Gln 390	Asn	Phe	Arg	Val	Ala 395	Thr	Lys	Asn	Thr	Thr 400
Leu	Pro	Arg	Gly	Gly	Gly	Lys	Asp	Gly	Leu	Ser	Pro	Val	Leu	Val	Arg

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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									
<210> SEQ ID NO 7																
<211> LENGTH: 1569																
<212> TYPE: DNA																
<213> ORGANISM: Candida tropicalis																
<220> FEATURE:																
<221> NAME/KEY: CDS																
<222> LOCATION: (1)..(1566)																
<400> SEQUENCE: 7																
atg	act	gca	cag	gat	att	atc	gcc	aca	tac	atc	acc	aaa	tgg	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	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	ccg	ttt	ttc	cag	aaa	144
Gly	Arg	Tyr	Leu	Met	Tyr	Lys	Leu	Gly	Ala	Lys	Pro	Phe	Phe	Gln	Lys	
			35	40				45								
caa	aca	gac	ggt	tat	ttc	gga	ttc	aaa	gct	cca	ctt	gaa	ttg	tta	aaa	192
Gln	Thr	Asp	Gly	Tyr	Phe	Gly	Phe	Lys	Ala	Pro	Leu	Glu	Leu	Leu	Lys	
			50	55				60								
aag	aag	agt	gac	ggt	acc	ctc	ata	gac	ttc	act	ctc	gag	cgt	atc	caa	240
Lys	Lys	Ser	Asp	Gly	Thr	Leu	Ile	Asp	Phe	Thr	Leu	Glu	Arg	Ile	Gln	
			65	70				75				80				
gcg	ctc	aat	cgt	cca	gat	atc	cca	act	ttt	aca	ttc	cca	atc	ttt	tcc	288
Ala	Leu	Asn	Arg	Pro	Asp	Ile	Pro	Thr	Phe	Thr	Phe	Pro	Ile	Phe	Ser	
			85	90				95								
atc	aac	ctt	atc	agc	acc	ctt	gag	ccg	gag	aac	atc	aag	gct	atc	ttg	336
Ile	Asn	Leu	Ile	Ser	Thr	Leu	Glu	Pro	Glu	Asn	Ile	Lys	Ala	Ile	Leu	
			100	105				110								
gcc	acc	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	ggt	atc	ttt	acc	ttg	gac	ggt	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	atg	cag	gtg	ttc	ttc	aag	cac	528
Ser	His	Val	Lys	Leu	Leu	Glu	Pro	His	Met	Gln	Val	Phe	Phe	Lys	His	

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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	ggg	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	ggt	gcc	ggg	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	ggg	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						
ggg	ctt	ggg	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	ggg	ggg	aag	gac	ggg	tta	tct	cct	ggt	ttg	gtc	aga	1248		
Leu	Pro	Arg	Gly	Gly	Gly	Lys	Asp	Gly	Leu	Ser	Pro	Val	Leu	Val	Arg			
405						410						415						
aag	ggg	caa	acc	gtt	atg	tac	ggg	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	ggg	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	ggg	1392		
Glu	Pro	Glu	Thr	Lys	Lys	Leu	Gly	Trp	Ala	Phe	Leu	Pro	Phe	Asn	Gly			
450						455						460						
ggg	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			

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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> SEQ ID NO 8				
<211> LENGTH: 522				
<212> TYPE: PRT				
<213> ORGANISM: Candida tropicalis				
<400> SEQUENCE: 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	

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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
 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> SEQ ID NO 9
 <211> LENGTH: 1623
 <212> TYPE: DNA
 <213> ORGANISM: Candida tropicalis
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(1620)

<400> SEQUENCE: 9

atg tcg tct tct cca tcg ttt gcc caa gag gtt ctc gct acc act agt	48
Met Ser Ser Ser Pro Ser Phe Ala Gln Glu Val Leu Ala Thr 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	
ata cct ttg gtg ctt ctt tcg ttg aac ttt ata agt ttg ctc cac aca	144
Ile Pro Leu Val Leu Leu Ser Leu Asn Phe Ile Ser Leu Leu His Thr	
35 40 45	
agg tac ttg gaa cgc agg ttc cac gcc aag cca ctc ggt aac ttt gtc	192
Arg Tyr Leu Glu Arg Arg Phe His Ala Lys Pro Leu Gly Asn Phe Val	
50 55 60	
agg gac cct acg ttt ggt atc gct act ccg ttg ctt ttg atc tac ttg	240
Arg Asp Pro Thr Phe Gly Ile Ala Thr Pro Leu Leu Ile Tyr Leu	
65 70 75 80	

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aag tcg aaa ggt acg gtc atg aag ttt gct tgg ggc ctc tgg aac aac	288
Lys Ser Lys Gly Thr Val Met Lys Phe Ala Trp Gly Leu Trp Asn Asn	
85 90 95	
aag tac atc gtc aga gac cca aag tac aag aca act ggg ctc agg att	336
Lys Tyr Ile Val Arg Asp Pro Lys Tyr Lys Thr Thr Gly Leu Arg Ile	
100 105 110	
gtt ggc ctc cca ttg att gaa acc atg gac cca gag aac atc aag gct	384
Val Gly Leu Pro Leu Ile Glu Thr Met Asp Pro Glu Asn Ile Lys Ala	
115 120 125	
gtt ttg gct act cag ttc aat gat ttc tct ttg gga acc 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 ggt gac ggt att ttc 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 cat 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 tct cac gtc aag ttg ttg gag 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 aag cac cgc ggt caa acg ttc 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 agg 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 agg gac gaa tct att gga ttg acc cca acc acc	720
Ser Ala Glu Ser Leu Arg Asp Glu Ser Ile Gly Leu Thr Pro Thr Thr	
225 230 235 240	
aag gat ttc gat ggc aga aga gat ttc gct gac gct ttc aac tat tcg	768
Lys Asp Phe Asp Gly Arg Arg 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 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	
ggc 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	

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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	
tggt 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 gtt aga atg tac taa	1623
Leu Ser Leu Phe Asp Gly Ala Asp Val Arg Met Tyr	
530 535 540	

<210> SEQ ID NO 10

<211> LENGTH: 540

<212> TYPE: PRT

<213> ORGANISM: Candida tropicalis

<400> SEQUENCE: 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	
85 90 95	
Lys Tyr Ile Val Arg Asp Pro Lys Tyr Lys Thr Thr Gly Leu Arg Ile	
100 105 110	
Val Gly Leu Pro Leu Ile Glu Thr Met Asp Pro Glu Asn Ile Lys Ala	
115 120 125	
Val 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	

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145		150		155		160
Gly Trp Lys His Ser Arg Thr Met Leu Arg Pro Gln Phe Ala Arg Glu						
		165		170		175
Gln Val Ser His Val Lys Leu Leu Glu Pro His Val Gln Val Phe Phe						
		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 Glu Ser Ile Gly Leu Thr Pro Thr Thr						
		225		230		235
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
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
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
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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<211> LENGTH: 1623
<212> TYPE: DNA
<213> ORGANISM: Candida tropicalis
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1620)

<400> SEQUENCE: 11

atg tcg tct tct cca tcg ttt gct cag gag gtt ctc gct acc act agt      48
Met Ser Ser Ser Pro Ser Phe Ala Gln Glu Val Leu Ala Thr 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

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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> SEQ ID NO 12

<211> LENGTH: 540

<212> TYPE: PRT

<213> ORGANISM: Candida tropicalis

<400> SEQUENCE: 12

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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			
Lys	Tyr	Leu	Glu	Arg	Arg	Phe	His	Ala	Lys	Pro	Leu	Gly	Asn	Val	Val
	50					55					60				
Leu	Asp	Pro	Thr	Phe	Gly	Ile	Ala	Thr	Pro	Leu	Ile	Leu	Ile	Tyr	Leu
65					70					75					80
Lys	Ser	Lys	Gly	Thr	Val	Met	Lys	Phe	Ala	Trp	Ser	Phe	Trp	Asn	Asn
			85						90					95	
Lys	Tyr	Ile	Val	Lys	Asp	Pro	Lys	Tyr	Lys	Thr	Thr	Gly	Leu	Arg	Ile
		100						105					110		
Val	Gly	Leu	Pro	Leu	Ile	Glu	Thr	Ile	Asp	Pro	Glu	Asn	Ile	Lys	Ala
		115					120					125			
Val	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	
Gln	Val	Ser	His	Val	Lys	Leu	Leu	Glu	Pro	His	Val	Gln	Val	Phe	Phe
		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

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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> SEQ ID NO 13
 <211> LENGTH: 1554
 <212> TYPE: DNA
 <213> ORGANISM: Candida tropicalis
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(1551)

<400> SEQUENCE: 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	

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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 gtt 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				

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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> SEQ ID NO 14

<211> LENGTH: 517

<212> TYPE: PRT

<213> ORGANISM: Candida tropicalis

<400> SEQUENCE: 14

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

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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

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> SEQ ID NO 15

<211> LENGTH: 1554

<212> TYPE: DNA

<213> ORGANISM: Candida tropicalis

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(1551)

<400> SEQUENCE: 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	

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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	80
65 70 75	
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	160
145 150 155	
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	240
225 230 235	
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	270
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	320
305 310 315	
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	

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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> SEQ ID NO 16

<211> LENGTH: 517

<212> TYPE: PRT

<213> ORGANISM: Candida tropicalis

<400> SEQUENCE: 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	

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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			200		205	
	195					
Glu Thr Ile Gly Ile Asn Gln Asp Asp Ile Asp Phe Ala Gly Arg Lys			215		220	
	210					
Asp Phe Ala Glu Ser Phe Asn Lys Ala Gln Glu Tyr Leu Ser Ile Arg			230		235	
	225					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> SEQ ID NO 17

<211> LENGTH: 1539

<212> TYPE: DNA

<213> ORGANISM: Candida tropicalis

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<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1) .. (1536)

<400> SEQUENCE: 17

atg ctc gat cag atc tta cat tac tgg tac att gtc ttg cca 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	

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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	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 ggt 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 ggt ggc ccc aac ggc aag			1200
Ala Ile Lys Asp Thr Thr Leu Pro Arg Gly Gly Gly Pro Asn Gly Lys			
	385	390	395
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
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

<210> SEQ ID NO 18

<211> LENGTH: 512

<212> TYPE: PRT

<213> ORGANISM: Candida tropicalis

<400> SEQUENCE: 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

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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
				405					410					415	
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		

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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

<210> SEQ ID NO 19
 <211> LENGTH: 1539
 <212> TYPE: DNA
 <213> ORGANISM: Candida tropicalis
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(1536)

<400> SEQUENCE: 19

atg ctc gac cag atc ttc cat tac tgg tac att gtc ttg cca 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	tgc	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	
				275			280						285			
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	
				290		295					300					
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	
305				310						315					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	
				325					330					335		
gaa	att	gaa	tca	cac	ttt	ggg	ctg	ggg	gag	gac	tct	cgt	ggt	gaa	gag	1056
Glu	Ile	Glu	Ser	His	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	aaa	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	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	
			370			375					380					
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	
385				390					395					400		
gat	cct	atc	ttg	atc	aga	aag	aat	gag	gtg	gtg	caa	tac	tcc	atc	tgc	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																1536

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<210> SEQ ID NO 20

<211> LENGTH: 512

<212> TYPE: PRT

<213> ORGANISM: *Candida tropicalis*

<400> SEQUENCE: 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

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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			
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			
<210> SEQ ID NO 21			
<211> LENGTH: 390			
<212> TYPE: DNA			
<213> ORGANISM: Candida tropicalis			
<220> FEATURE:			
<221> NAME/KEY: CDS			
<222> LOCATION: (1) .. (387)			
<400> SEQUENCE: 21			
atg acc gac aca gac acc acg acc acc atc tac acc cac gaa gag gtt Met Thr Asp Thr Thr Thr Thr Thr Ile Tyr Thr His Glu Glu Val 1 5 10 15			48
gcc cag cac acc acc cac gac gac ttg tgg gtt att ctc aat ggt aag Ala Gln His Thr Thr His Asp Asp Leu Trp Val Ile Leu Asn Gly Lys 20 25 30			96
gtc tac aac atc tcc aac tat ata gac gag cac cca ggt ggt gaa gaa Val Tyr Asn Ile Ser Asn Tyr Ile Asp Glu His Pro Gly Gly Glu Glu 35 40 45			144
gtc att ctt gat tgc gcc ggc aca gac gcc act gaa gcc ttt gac gac Val Ile Leu Asp Cys Ala Gly Thr Asp Ala Thr Glu Ala Phe Asp Asp 50 55 60			192
att ggc cac tcc gac gag gcc cac gag atc ttg gaa aag ttg tac att Ile Gly His Ser Asp Glu Ala His Glu Ile Leu Glu Lys Leu Tyr Ile 65 70 75 80			240
ggg aac ttg aag ggc gct aag att gtt gag gcc aag cac gcg cag tcg Gly Asn Leu Lys Gly Ala Lys Ile Val Glu Ala Lys His Ala Gln Ser 85 90 95			288
ttc agc acg gaa gaa gac tcg ggt atc aac ttc cca ttg att gct gtt Phe Ser Thr Glu Glu Asp Ser Gly Ile Asn Phe Pro Leu Ile Ala Val 100 105 110			336
ggg gtc ttt ttg gct gct ttc ggt gtc tac tac tac aag acc aac ttt Gly Val Phe Leu Ala Ala Phe Gly Val Tyr Tyr Tyr Lys Thr Asn Phe 115 120 125			384
gcc taa Ala			390

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<210> SEQ ID NO 22
 <211> LENGTH: 129
 <212> TYPE: PRT
 <213> ORGANISM: *Candida tropicalis*

<400> SEQUENCE: 22

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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

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Ala

<210> SEQ ID NO 23
 <211> LENGTH: 2115
 <212> TYPE: DNA
 <213> ORGANISM: *Candida tropicalis*
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(2112)

<400> SEQUENCE: 23

```

atg gct cca ttt ttg ccc gac cag gtc gac tac aaa cac gtc 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

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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 gcc 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 gga tct ggg gcc ggt gct ggt gtc gtg	
195 200 205	
gcc cac act ttg acc aac gac gcc ttc aag agt ttg gtt ttg gaa aag	672
Ala His Thr Leu Thr Asn Asp Gly Phe Lys Ser Leu Val Leu Glu Lys	
210 215 220	
ggc aga tac ttt agc aac tcc gag ttg aac ttt gat gac aag gac ggg	720
Gly Arg Tyr Phe Ser Asn Ser Glu Leu Asn Phe Asp Asp Lys Asp Gly	
225 230 235 240	
gtt caa gaa tta tac caa agt gga ggt act ttg acc acc gtc aac cag	768
Val Gln Glu Leu Tyr Gln Ser Gly Gly Thr Leu Thr Thr Val Asn Gln	
245 250 255	
cag ttg ttt gtt ctt gct ggt tcc act ttt ggt ggt ggt acc act gtc	816
Gln Leu Phe Val Leu Ala Gly Ser Thr Phe Gly Gly Gly Thr Thr Val	
260 265 270	
aat tgg tcg gcc tgt ctt aaa acg cca ttc aag gtg cgt aag gaa tgg	864
Asn Trp Ser Ala Cys Leu Lys Thr Pro Phe Lys Val Arg Lys Glu Trp	
275 280 285	
tat gat gag ttt ggc gtt gac ttt gct gcc gat gaa gcc tac gac aaa	912
Tyr Asp Glu Phe Gly Val Asp Phe Ala Ala Asp Glu Ala Tyr Asp Lys	
290 295 300	
gca cag gat tat gtt tgg cag caa atg gga gct tct acc gaa ggc atc	960
Ala Gln Asp Tyr Val Trp Gln Gln Met Gly Ala Ser Thr Glu Gly Ile	
305 310 315 320	
acc cac tct ttg gct aac gag att att att gaa ggt ggc aag aaa tta	1008
Thr His Ser Leu Ala Asn Glu Ile Ile Ile Glu Gly Gly Lys Lys Leu	
325 330 335	
ggg 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 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	

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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 ggt 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 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 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 ggt 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> SEQ ID NO 24

<211> LENGTH: 704

<212> TYPE: PRT

<213> ORGANISM: Candida tropicalis

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<400> SEQUENCE: 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

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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> SEQ ID NO 25
 <211> LENGTH: 2115
 <212> TYPE: DNA
 <213> ORGANISM: Candida tropicalis
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(2112)

<400> SEQUENCE: 25

atg aat acc ttc ttg cca gac gtg ctc gaa tac aaa cac gtc gac acc	48
Met Asn Thr Phe Leu Pro Asp Val Leu Glu Tyr Lys His Val Asp Thr	
1 5 10 15	
ctt ttg tta ttg tgt gac ggg atc atc cac gaa acc aca gtc gat cag	96
Leu Leu Leu Leu Cys Asp Gly Ile Ile His Glu Thr Thr Val Asp Gln	
20 25 30	

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atc aag gac gcc att gct ccc gac ttc cct gag gac cag tac gag gag Ile Lys Asp Ala Ile Ala Pro Asp Phe Pro Glu Asp Gln Tyr Glu Glu 35 40 45	144
tat ctc aag acc ttc acc aag cca tct gag acc cct ggg ttc aga gaa Tyr Leu Lys Thr Phe Thr Lys Pro Ser Glu Thr Pro Gly Phe Arg Glu 50 55 60	192
gcc gtc tac gac acg atc aac gcc acc cca acc gat gcc gtg cac atg Ala Val Tyr Asp Thr Ile Asn Ala Thr Pro Thr Asp Ala Val His Met 65 70 75 80	240
tgt att gtc ttg acc acc gca ttg gac tcc aga atc ttg gcc ccc acg Cys Ile Val Leu Thr Thr Ala Leu Asp Ser Arg Ile Leu Ala Pro Thr 85 90 95	288
ttg acc aac tcg ttg acg cct atc aag gat atg acc ttg aag gag cgt Leu Thr Asn Ser Leu Thr Pro Ile Lys Asp Met Thr Leu Lys Glu Arg 100 105 110	336
gaa caa ttg ttg gcc tct tgg cgt gat tcc ccg att gcg gca aag aga Glu Gln Leu Leu Ala Ser Trp Arg Asp Ser Pro Ile Ala Ala Lys Arg 115 120 125	384
aga ttg ttc aga ttg att tcc tcg ctt acc ttg acg acg ttt acg aga Arg Leu Phe Arg Leu Ile Ser Ser Leu Thr Leu Thr Thr Phe Thr Arg 130 135 140	432
ttg gcc agc gaa ttg cac ttg aaa gcc atc cac tac cct ggc aga gac Leu Ala Ser Glu Leu His Leu Lys Ala Ile His Tyr Pro Gly Arg Asp 145 150 155 160	480
ttg cgt gaa aag gcg tat gaa acc cag gtg gtt gac cct ttc agg tac Leu Arg Glu Lys Ala Tyr Glu Thr Gln Val Val Asp Pro Phe Arg Tyr 165 170 175	528
ctg ttt atg gag aaa cca aag ttt gac ggc gcc gaa ttg tac ttg cca Leu Phe Met Glu Lys Pro Lys Phe Asp Gly Ala Glu Leu Tyr Leu Pro 180 185 190	576
gat atc gac gtc atc atc att gga tca ggc gcc ggt gct ggt gtc atg Asp Ile Asp Val Ile Ile Ile Gly Ser Gly Ala Gly Ala Gly Val Met 195 200 205	624
gcc cac act ctc gcc aac gac ggg ttc aag acc ttg gtt ttg gaa aag Ala His Thr Leu Ala Asn Asp Gly Phe Lys Thr Leu Val Leu Glu Lys 210 215 220	672
gga aag tat ttc agc aac tcc gag ttg aac ttt aat gac gct gat ggc Gly Lys Tyr Phe Ser Asn Ser Glu Leu Asn Phe Asn Asp Ala Asp Gly 225 230 235 240	720
gtg aaa gag ttg tac caa ggt aaa ggt gct ttg gcc acc acc aat cag Val Lys Glu Leu Tyr Gln Gly Lys Gly Ala Leu Ala Thr Thr Asn Gln 245 250 255	768
cag atg ttt att ctt gcc ggt tcc act ttg ggc ggt ggt acc act gtc Gln Met Phe Ile Leu Ala Gly Ser Thr Leu Gly Gly Gly Thr Thr Val 260 265 270	816
aac tgg tct gct tgc ctt aaa aca cca ttt aaa gtg cgt aag gag tgg Asn Trp Ser Ala Cys Leu Lys Thr Pro Phe Lys Val Arg Lys Glu Trp 275 280 285	864
tac gac gag ttt ggt ctt gaa ttt gct gcc gat gaa gcc tac gac aaa Tyr Asp Glu Phe Gly Leu Glu Phe Ala Ala Asp Glu Ala Tyr Asp Lys 290 295 300	912
gcg cag gat tat gtt tgg aaa caa atg ggt gct tca aca gat gga atc Ala Gln Asp Tyr Val Trp Lys Gln Met Gly Ala Ser Thr Asp Gly Ile 305 310 315 320	960
act cac tcc ttg gcc aac gaa gtt gtg gtt gaa gga ggt aag aag ttg Thr His Ser Leu Ala Asn Glu Val Val Glu Gly Gly Lys Lys Leu 325 330 335	1008

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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	
ggg 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 ggt 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 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 act gtg ttg acc aac tcc gga ttc aag aac aag cac att 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 tcc 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 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
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	

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atg tcc gga aag ggt cct aaa tac ggt gct gtt gat act 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	
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

<210> SEQ ID NO 26

<211> LENGTH: 704

<212> TYPE: PRT

<213> ORGANISM: Candida tropicalis

<400> SEQUENCE: 26

Met Asn Thr Phe Leu Pro Asp Val Leu Glu Tyr Lys His Val Asp Thr	
1 5 10 15	
Leu Leu Leu Leu Cys Asp Gly Ile Ile His Glu Thr Thr Val Asp Gln	
20 25 30	
Ile Lys Asp Ala Ile Ala Pro Asp Phe Pro Glu Asp Gln Tyr Glu Glu	
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 Ala Thr Pro Thr Asp 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 Ser 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 Glu Leu His Leu Lys 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 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	

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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					310					315					320	
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	
		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	
			500					505					510			
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			

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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
690 695 700

<210> SEQ ID NO 27
<211> LENGTH: 2115
<212> TYPE: DNA
<213> ORGANISM: *Candida tropicalis*
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(2112)

<400> SEQUENCE: 27

atg aat acc ttc ttg cca gac gtg ctc gaa tac aaa cac gtc gat acc	48
Met Asn Thr Phe Leu Pro Asp Val Leu Glu Tyr Lys His Val Asp Thr	
1 5 10 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	
195 200 205	
gcc cac act tta gcc aac gac ggg tac aag acc ttg gtt ttg gaa aag	672
Ala His Thr Leu Ala Asn Asp Gly Tyr Lys Thr Leu Val Leu Glu Lys	
210 215 220	
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	

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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 Met Phe Ile Leu Ala Gly Ser Thr Leu Gly Gly Gly Thr Thr Val	260	265	270	
aac tgg tct gct tgt 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 gac 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	
gca caa gac tat gtt tgg aaa caa atg ggc gct tct acc gaa gga atc				960
Ala Gln Asp Tyr Val Trp Lys Gln Met Gly Ala Ser Thr Glu Gly Ile	305	310	315	320
act cac tct ttg gcg aac gcg gtt gtg gtt gaa gga ggt aag aag ttg				1008
Thr His Ser Leu Ala Asn Ala Val Val Val Glu Gly Gly Lys Lys Leu	325	330	335	
ggc tac aag agc aag gaa atc gag cag aac aat ggt ggc cat cct gac				1056
Gly Tyr Lys Ser Lys Glu Ile Glu Gln Asn Asn Gly Gly His Pro Asp	340	345	350	
cac ccc tgt ggt ttc tgt tac ttg ggc tgt aag tac ggt att aag cag				1104
His Pro Cys Gly Phe Cys Tyr Leu Gly Cys Lys Tyr Gly Ile Lys Gln	355	360	365	
ggc tct gtg aat aac tgg ttt aga gac gca gct gcc cac ggc tcc aag				1152
Gly Ser Val Asn Asn Trp Phe Arg Asp Ala Ala His Gly Ser Lys	370	375	380	
ttc atg caa caa gtc aga gtt gtg caa atc ctc cac aat aaa ggc gtc				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 Gly 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 agc 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 acc cgt gac 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				

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530	535	540	
gac cca aag aag ccc gac gct ttg att gtc gac tat gac atc aac aag			1680
Asp Pro Lys Lys Pro Asp Ala Leu Ile Val Asp Tyr Asp Ile Asn Lys			
545	550	555	560
ttt gac aag aat gcc atc ttg caa gct ttc ttg atc acc 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 atc gaa ggt gcc aag aga atc ctc agt cca cag gca tgg gtg			1776
Leu Tyr Ile Glu Gly Ala Lys Arg Ile Leu Ser Pro Gln Ala Trp Val			
	580	585	590
cca atc ttt gag tcg aac aag cca aag gag caa aga aca 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 gtc gaa tgg aga gcc aag gct gcc aag ata cct ttc gac			1872
Lys Asp Tyr Val Glu Trp Arg Ala Lys Ala Ala Lys Ile Pro Phe Asp			
	610	615	620
acc tac ggt tct gcc 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
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			
	660	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			
	675	680	685
cag att gcg tta ggt ttg gct gac tct 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
<210> SEQ ID NO 28			
<211> LENGTH: 704			
<212> TYPE: PRT			
<213> ORGANISM: Candida tropicalis			
<400> SEQUENCE: 28			
Met Asn Thr Phe Leu Pro Asp Val Leu Glu Tyr Lys His Val Asp Thr			
1	5	10	15
Leu Leu Leu Leu Cys Asp Gly Ile Ile His Glu Thr Thr Val Asp Gln			
	20	25	30
Ile Arg Asp Ala Ile Ala Pro Asp Phe Pro Glu Asp Gln Tyr Glu Glu			
	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
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

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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
		500						505					510		
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

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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
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	
	690	695	700
<210> SEQ ID NO 29			
<211> LENGTH: 1446			
<212> TYPE: DNA			
<213> ORGANISM: Candida tropicalis			
<220> FEATURE:			
<221> NAME/KEY: CDS			
<222> LOCATION: (1) .. (1443)			
<400> SEQUENCE: 29			
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Met Ile Met Phe Asp Ile Val Lys Tyr Thr Leu Ile Gly Leu Phe Ser			
1 5 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 ggt gct			144
Pro Lys Asn Ile Pro Thr Ile Pro Phe Tyr Val Ser Phe Leu Gly Ala			
35 40 45			
tac act aac ttg gat cag agg gat att tac aat ttg tat ttg aga gag			192
Tyr Thr Asn Leu Asp Gln Arg Asp Ile Tyr Asn Leu Tyr Leu Arg Glu			
50 55 60			
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			
65 70 75 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 gtt att gcc aaa agt att caa ttt ccc			432

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Leu	Trp	Lys	Leu	Tyr	Arg	Glu	Val	Ile	Ala	Lys	Ser	Ile	Gln	Phe	Pro	
130						135					140					
gat	ttt	gaa	cca	att	acg	aaa	aat	act	aaa	tca	tta	ctt	gaa	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	tggt	tat	ggg	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				
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	ggt	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	tggt	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	tggt	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	
				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

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Ala	Leu	Tyr	Glu	Val	Lys	Glu	Leu	Leu	Thr	Ser	Ile	Leu	Gly	His	Tyr		
	435						440					445					
aaa	ggt	act	tta	gat	gca	agt	tggt	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	gggt	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> SEQ ID NO 30
 <211> LENGTH: 481
 <212> TYPE: PRT
 <213> ORGANISM: Candida tropicalis

<400> SEQUENCE: 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				
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			
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					

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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> SEQ ID NO 31
 <211> LENGTH: 1623
 <212> TYPE: DNA
 <213> ORGANISM: Candida tropicalis
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(1620)

<400> SEQUENCE: 31

atg	tcg	tcg	tct	cca	tct	att	gct	caa	gaa	ttt	ctc	gca	acc	att	act	48
Met	Ser	Ser	Ser	Ser	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	tggtac	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	cgg	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	ggg	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	ggg	acc	gtg	atg	caa	ttt	gcc	tgt	gat	tta	tggtac	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	ggg	ctt	aag	att	336
Lys	Leu	Ile	Val	Ser	Asp	Pro	Lys	Ala	Lys	Thr	Ile	Gly	Leu	Lys	Ile	
		100					105					110				

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tta ggt att cca ttg att gaa act aaa gac cca gag aat gtc aag gct Leu Gly Ile Pro Leu Ile Glu Thr Lys Asp Pro Glu Asn Val Lys Ala 115 120 125	384
att tta gcc acc cag ttt aat gat ttt tct ttg gga act aga cat gat Ile Leu Ala Thr Gln Phe Asn Asp Phe Ser Leu Gly Thr Arg His Asp 130 135 140	432
ttc ttg tat tca ttg tta gga gat ggt att ttc act tta gat ggt gct Phe Leu Tyr Ser Leu Leu Gly Asp Gly Ile Phe Thr Leu Asp Gly Ala 145 150 155 160	480
ggc tgg aaa cac agc aga acc atg ttg aga cca caa ttc gct aga gag Gly Trp Lys His Ser Arg Thr Met Leu Arg Pro Gln Phe Ala Arg Glu 165 170 175	528
caa gtt tcg cat gta aag ttg ttg gaa ccc cat atg caa gtt tta ttt Gln Val Ser His Val Lys Leu Leu Glu Pro His Met Gln Val Leu Phe 180 185 190	576
aaa cac att aga aaa cat cat ggc caa act ttt gat atc caa gaa ttg Lys His Ile Arg Lys His His Gly Gln Thr Phe Asp Ile Gln Glu Leu 195 200 205	624
ttt ttc aga tta act gtt gat tcg gct act gag ttt ttg ttt ggt gaa Phe Phe Arg Leu Thr Val Asp Ser Ala Thr Glu Phe Leu Phe Gly Glu 210 215 220	672
tct gct gaa tct tta aga gac gag tct gtc ggt tta act cca aca acc Ser Ala Glu Ser Leu Arg Asp Glu Ser Val Gly Leu Thr Pro Thr Thr 225 230 235 240	720
aaa gat ttt gat ggt aga aat gag ttt gcc gat gcg ttc aac tat tct Lys Asp Phe Asp Gly Arg Asn Glu Phe Ala Asp Ala Phe Asn Tyr Ser 245 250 255	768
caa act tac caa gcg tac aga ttc ttg ttg caa caa atg tat tgg att Gln Thr Tyr Gln Ala Tyr Arg Phe Leu Leu Gln Gln Met Tyr Trp Ile 260 265 270	816
ttg aat ggt tct gaa ttt aga aaa tct att gct att gtc cac aag ttt Leu Asn Gly Ser Glu Phe Arg Lys Ser Ile Ala Ile Val His Lys Phe 275 280 285	864
gct gac cac tat gtt caa aag gca ttg gaa tta act gat gaa gat ttg Ala Asp His Tyr Val Gln Lys Ala Leu Glu Leu Thr Asp Glu Asp Leu 290 295 300	912
gaa aag aaa gaa ggc tat gta ttt tta ttc gag tta gcc aaa caa acc Glu Lys Lys Glu Gly Tyr Val Phe Leu Phe Glu Leu Ala Lys Gln Thr 305 310 315 320	960
aga gat cca aag gtt ttg aga gat caa ttg tta aat atc ttg gtt gct Arg Asp Pro Lys Val Leu Arg Asp Gln Leu Leu Asn Ile Leu Val Ala 325 330 335	1008
ggt aga gat acc aca gct ggc ttg ttg tcg ttt ctt ttc ttt gaa ttg Gly Arg Asp Thr Thr Ala Gly Leu Leu Ser Phe Leu Phe Phe Glu Leu 340 345 350	1056
tct aga aac cca gaa ata ttt gca aaa ttg aga gaa gaa atc gaa aac Ser Arg Asn Pro Glu Ile Phe Ala Lys Leu Arg Glu Glu Ile Glu Asn 355 360 365	1104
aag ttt ggt ctt gga caa gat gct cgt gtt gaa gag att tct ttt gaa Lys Phe Gly Leu Gly Gln Asp Ala Arg Val Glu Glu Ile Ser Phe Glu 370 375 380	1152
aca ttg aaa tct tgt gaa tac ttg aag gct gtt atc aat gaa act ttg Thr Leu Lys Ser Cys Glu Tyr Leu Lys Ala Val Ile Asn Glu Thr Leu 385 390 395 400	1200
aga att tat cct tcc gtc cca cat aat ttt aga gtt gct act aga aac Arg Ile Tyr Pro Ser Val Pro His Asn Phe Arg Val Ala Thr Arg Asn 405 410 415	1248

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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	
450 455 460	
tggttt 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> SEQ ID NO 32

<211> LENGTH: 540

<212> TYPE: PRT

<213> ORGANISM: Candida tropicalis

<400> SEQUENCE: 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	
Gln Val Ser His Val Lys Leu Leu Glu Pro His Met Gln Val Leu Phe	
180 185 190	

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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 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> SEQ ID NO 33
 <211> LENGTH: 1569
 <212> TYPE: DNA
 <213> ORGANISM: Candida tropicalis
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(1566)

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<400> SEQUENCE: 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 Gln Ser	
35 40 45	
caa acc gac ggt tat ctt ggt ttc aga gtt cca ttt gaa ttg atg gga	192
Gln Thr Asp Gly Tyr Leu Gly Phe Arg Val Pro Phe Glu Leu Met Gly	
50 55 60	
aag aag agt gaa ggt aca ctt ata gac ttt aca tat caa cgt act ttg	240
Lys Lys Ser Glu Gly Thr Leu Ile Asp Phe Thr Tyr Gln Arg Thr Leu	
65 70 75 80	
gag ctt gac aat ccc gat att cca aca ttt aca ttc cca ata ttt tct	288
Glu Leu Asp Asn Pro Asp Ile Pro Thr Phe Thr Phe Pro Ile Phe Ser	
85 90 95	
gtt ctg att atc tca act ctt gaa cca gac aac atc aaa gct att ttg	336
Val Leu Ile Ile Ser Thr Leu Glu Pro Asp Asn Ile Lys Ala Ile Leu	
100 105 110	
gcc aca caa ttc aat gac ttt tca tta ggt aca aga cat tca cat ttt	384
Ala Thr Gln Phe Asn Asp Phe Ser Leu Gly Thr Arg His Ser His Phe	
115 120 125	
gct cct tta tta ggt gac ggt att ttc act tta gat ggt gct ggt tgg	432
Ala Pro Leu Leu Gly Asp Gly Ile Phe Thr Leu Asp Gly Ala Gly Trp	
130 135 140	
aaa cat agt aga tct atg ttg aga cca caa ttt gca aga gaa cag gtt	480
Lys His Ser Arg Ser Met Leu Arg Pro Gln Phe Ala Arg Glu Gln Val	
145 150 155 160	
tct cac gtt aag ttg ttg gaa cca cat atg caa gtt ttt ttc aaa cat	528
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 gtt	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 gtt 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 gtt gaa aaa gca ttg gaa tta act ccg gac caa ttg gaa aaa	864
Tyr Tyr Val Glu Lys Ala Leu Glu Thr Pro Asp Gln Leu Glu Lys	
275 280 285	
caa gat ggg tat gtt 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	

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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	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
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 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> SEQ ID NO 34			
<211> LENGTH: 522			
<212> TYPE: PRT			
<213> ORGANISM: Candida tropicalis			
<400> SEQUENCE: 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			

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50					55					60				
Lys 65	Lys	Ser	Glu	Gly	Thr 70	Leu	Ile	Asp	Phe	Thr 75	Tyr	Gln	Arg	Thr 80
Glu	Leu	Asp	Asn	Pro 85	Asp	Ile	Pro	Thr	Phe 90	Thr	Phe	Pro	Ile	Phe 95
Val	Leu	Ile	Ile	Ser 100	Thr	Leu	Glu	Pro 105	Asp	Asn	Ile	Lys	Ala	Ile 110
Ala	Thr	Gln	Phe	Asn 115	Asp	Phe	Ser	Leu 120	Gly	Thr	Arg	His 125	Ser	His 130
Ala	Pro	Leu	Leu	Gly 130	Asp	Gly	Ile	Phe 135	Thr	Leu	Asp	Gly	Ala	Gly 140
Lys 145	His	Ser	Arg	Ser 150	Met	Leu	Arg	Pro	Gln	Phe 155	Ala	Arg	Glu	Gln 160
Ser	His	Val	Lys	Leu 165	Leu	Glu	Pro	His	Met 170	Gln	Val	Phe	Phe	Lys 175
Ile	Arg	Lys	His 180	His	Gly	Gln	Thr	Phe 185	Asp	Ile	Gln	Glu	Leu	Phe 190
Arg	Leu	Thr	Val 195	Asp	Ser	Ala	Thr	Glu 200	Phe	Leu	Phe	Gly	Glu	Ser 205
Glu	Ser	Leu	Arg	Asp 210	Glu	Ser	Ile	Gly 215	Met	Leu	Asn	Asp	Ala	Leu 220
Phe 225	Asp	Gly	Lys	Ala 230	Gly	Phe	Ala	Asp	Ala 235	Phe	Asn	Tyr	Ser	Gln 240
Tyr	Leu	Ala	Ser 245	Arg	Ala	Leu	Met	Gln 250	Gln	Met	Tyr	Trp	Ile	Leu 255
Gly	Lys	Lys	Phe 260	Lys	Glu	Cys	Asn	Ala 265	Lys	Val	His	Lys	Phe	Ala 270
Tyr	Tyr	Val	Glu 275	Lys	Ala	Leu	Glu	Leu 280	Thr	Pro	Asp	Gln	Leu	Glu 285
Gln	Asp	Gly	Tyr 290	Val	Phe	Leu	Tyr	Glu 295	Leu	Val	Lys	Gln	Thr	Arg 300
Arg 305	Gln	Val	Leu	Arg 310	Asp	Gln	Leu	Leu	Asn 315	Ile	Leu	Val	Ala	Gly 320
Asp	Thr	Thr	Ala 325	Gly	Leu	Leu	Ser	Phe 330	Val	Phe	Phe	Glu	Leu	Ala 335
Thr	Pro	Arg	Val 340	Ala	Asn	Lys	Leu	Arg 345	Glu	Glu	Ile	Glu	Asp	Lys 350
Gly	Leu	Gly	Gln 355	Asp	Ala	Arg	Val	Glu 360	Glu	Ile	Ser	Phe	Glu	Ser 365
Lys 370	Ser	Cys	Glu	Tyr 375	Leu	Lys	Ala	Val	Leu	Asn	Glu	Cys	Leu	Arg 380
Tyr 385	Pro	Ser	Val	Pro 390	Gln	Asn	Phe	Arg	Val 395	Ala	Thr	Arg	Asn	Thr 400
Leu	Pro	Arg	Gly 405	Gly	Lys	Asp	Gly	Leu 410	Ser	Pro	Val	Leu	Val	Arg 415
Lys	Gly	Gln	Thr 420	Val	Met	Tyr	Ser	Val 425	Tyr	Ala	Ala	His	Arg	Asn 430
Gln	Ile	Tyr	Gly 435	Glu	Asp	Ala	Leu	Glu 440	Phe	Arg	Pro	Glu	Arg	Trp 445
Glu	Pro	Glu	Thr 450	Lys	Lys	Leu	Gly	Trp 455	Ala	Phe	Leu	Pro	Phe	Asn 460

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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> SEQ ID NO 35

<211> LENGTH: 1572

<212> TYPE: DNA

<213> ORGANISM: Candida tropicalis

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1) .. (1569)

<400> SEQUENCE: 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

tggtat act gtt atc act tta gca gct ttg gtt ttc tta att tca tct 96
 Trp Tyr Thr Val Ile Thr Leu 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 ttg 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
 65 70 75 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 gtt gat cca gaa aat att aaa gct gtt 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

tggtat 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

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ggt 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 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	
tggt ttt gaa cca tca act aaa aag tta ggt tggt 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	

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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

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<210> SEQ ID NO 36
<211> LENGTH: 523
<212> TYPE: PRT
<213> ORGANISM: Candida tropicalis

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<400> SEQUENCE: 36

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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

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

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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	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> SEQ ID NO 37

<211> LENGTH: 1512

<212> TYPE: DNA

<213> ORGANISM: Candida tropicalis

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(1509)

<400> SEQUENCE: 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 gtt cat act ttt gta acc aaa gtt ctt	288
Asn Asn Val Pro Phe Pro His Val His Thr Phe Val Thr Lys Val Leu	
85 90 95	
ggg aat gag tta atc atg aca aaa gat cct gaa aat att aaa gtt tta	336
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	384
Leu Ser Ser Ser Phe Asp Lys Phe Asp Tyr Gly Thr Arg Ser Ser Ala	

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115	120	125	
gtg caa cca tct tta gga atg ggg ata ttc act ctt gaa gga gaa aat			432
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 gtt 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 gtt 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 gtt 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			

-continued

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> SEQ ID NO 38

<211> LENGTH: 503

<212> TYPE: PRT

<213> ORGANISM: Candida tropicalis

<400> SEQUENCE: 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			

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245					250					255						
Phe	Cys	Asp	Tyr	Leu	Val	Gln	Lys	Ser	Leu	Glu	Asn	Thr	Cys	Asn	Asp	
				260					265					270		
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		
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		
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	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		
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> SEQ ID NO 39

<211> LENGTH: 1554

<212> TYPE: DNA

<213> ORGANISM: Candida tropicalis

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1) .. (1551)

<400> SEQUENCE: 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
Phe Ile Leu His Lys Val Phe Asp Met Trp His Thr Arg Arg Leu Met	
20 25 30	
aag caa ttg ggc gct gct cct gtc aca aac caa tta cac gac aat ttt	144
Lys Gln Leu Gly Ala Ala Pro Val Thr Asn Gln Leu His Asp Asn Phe	
35 40 45	
ttt ggt att atc aac gga tgg aaa gca ctt aag ttc aag aaa gaa ggt	192
Phe Gly Ile Ile Asn Gly Trp Lys Ala Leu Lys Phe Lys Lys Glu Gly	
50 55 60	

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aga gct caa gaa tat aat gat tat aaa ttt gcc aat tcg aaa att cca	240
Arg Ala Gln Glu Tyr Asn Asp Tyr Lys Phe Ala Asn Ser Lys Ile Pro	
65 70 75 80	
agt gtg ggt act tat gtt agt acc atc ttt gga aca aag ctc ctc gtc	288
Ser Val Gly Thr Tyr Val Ser Thr Ile Phe Gly Thr Lys Leu Leu Val	
85 90 95	
aca aaa gat ccg gag aat atc aaa gct tta tta gca acc caa ttc agt	336
Thr Lys Asp Pro Glu Asn Ile Lys Ala Leu Leu Ala Thr Gln Phe Ser	
100 105 110	
gat ttt tcc ttg ggt aag agg cat aca ctt ttc aaa cca tta tta ggt	384
Asp Phe Ser Ser Leu Gly Lys Arg His Thr Leu Phe Lys Pro Leu Leu Gly	
115 120 125	
gac ggt att ttc act ttg gat gga gaa ggt tgg aaa cat agt cga gct	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 gca aga gaa caa gtt gcc cat gtc act tct	480
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	
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	

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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> SEQ ID NO 40

<211> LENGTH: 517

<212> TYPE: PRT

<213> ORGANISM: Candida tropicalis

<400> SEQUENCE: 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	

<210> SEQ ID NO 41
<211> LENGTH: 1539
<212> TYPE: DNA

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<213> ORGANISM: *Candida tropicalis*

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1) .. (1536)

<400> SEQUENCE: 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 Ala Phe	
1 5 10 15	
ata att ttt cat tgg att gta tct gca att cat aca aat tcc ttg cgt	96
Ile Ile Phe His Trp Ile Val Ser Ala Ile His Thr Asn Ser Leu Arg	
20 25 30	
aga aaa cta ggt gcc aaa cct ttc act cat aca caa ctt gat ggt ttt	144
Arg Lys Leu Gly Ala Lys Pro Phe Thr His Thr Gln Leu Asp Gly Phe	
35 40 45	
tat gga ttt aaa ttt ggc cgt gat ttt ctt aaa gct aaa agg att ggt	192
Tyr Gly Phe Lys Phe Gly Arg Asp Phe Leu Lys Ala Lys Arg Ile Gly	
50 55 60	
agg caa gtt gat tta atc aat tcc cgt ttc cca gac gat att gac aca	240
Arg Gln Val Asp Leu Ile Asn Ser Arg Phe Pro Asp Asp Ile Asp Thr	
65 70 75 80	
ttt tca agt tat act ttc ggc aac cac gtg att ttt aca cgt gat cca	288
Phe Ser Ser Tyr Thr Phe Gly Asn His Val Ile Phe Thr Arg Asp Pro	
85 90 95	
gaa aat atc aaa gct tta ttg gca aca caa ttt aat gat ttt tca tta	336
Glu Asn Ile Lys Ala Leu Leu Ala Thr Gln Phe Asn Asp Phe Ser Leu	
100 105 110	
ggg ggt aga att aag ttt ttc aaa cca ttg ttg gga tat gga atc ttt	384
Gly Gly Arg Ile Lys Phe Phe Lys Pro Leu Leu Gly Tyr Gly Ile Phe	
115 120 125	
act ttg gat gga gaa ggt tgg aaa cat agt cga gct 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 gca aga gaa caa gtt gcc cat gtc act tct tta 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 caa ttg ttg aaa aag cat atc ctc aag aac aaa ggt ggg ttt ttt	528
Phe Gln Leu Leu Lys Lys His Ile Leu Lys Asn Lys Gly Gly Phe Phe	
165 170 175	
gat atc cag gaa ttg ttt ttc cga ttc acc gtt gat tca gct act gag	576
Asp Ile Gln Glu Leu Phe Phe Arg Phe Thr Val Asp Ser Ala Thr Glu	
180 185 190	
ttt ttg ttt ggt gaa tca gtg aac tct ttg aaa agt gca tca att ggt	624
Phe Leu Phe Gly Glu Ser Val Asn Ser Leu Lys Ser Ala Ser Ile Gly	
195 200 205	
tgt gac gag gaa acc gag ctt gag gaa aga aag aaa ttt gcg gaa gca	672
Cys Asp Glu Glu Thr Glu Leu Glu Glu Arg Lys Lys Phe Ala Glu Ala	
210 215 220	
ttc aat aaa gcg caa gag tat att tct act cga gtt gct ttg caa caa	720
Phe Asn Lys Ala Gln Glu Tyr Ile Ser Thr Arg Val Ala Leu Gln Gln	
225 230 235 240	
tta tat tgg ttt gtt aat aat agc gaa ttc aag gaa tgt aac gaa att	768
Leu Tyr Trp Phe Val Asn Asn Ser Glu Phe Lys Glu Cys Asn Glu Ile	
245 250 255	
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

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<210> SEQ ID NO 42
<211> LENGTH: 512
<212> TYPE: PRT
<213> ORGANISM: Candida tropicalis

<400> SEQUENCE: 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

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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	
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
				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			

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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> SEQ ID NO 43
 <211> LENGTH: 1572
 <212> TYPE: DNA
 <213> ORGANISM: Candida tropicalis
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1) .. (1569)

<400> SEQUENCE: 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 Thr His	
1 5 10 15	
tca gtt tca gtg cag gtc acc gct ctt gtc ctt atc gtg aca tac ttt	96
Ser Val Ser Val Gln Val Thr Ala Leu Val Leu Ile Val Thr Tyr Phe	
20 25 30	
ttt gtt att cgt cca att aac tca cct tta tgg aga gtt ccc gga cca	144
Phe Val Ile Arg Pro Ile Asn Ser Pro Leu Trp Arg Val Pro Gly Pro	
35 40 45	
tat tta cat cgg gta act tac ttt cca tgt tta aat gcc caa cga aag	192
Tyr Leu His Arg Val Thr Tyr Phe Pro Cys Leu Asn Ala Gln Arg Lys	
50 55 60	
gga gaa tgg atc tcc aaa gtt tat gat ttg cac aag aaa tat ggt gat	240
Gly Glu Trp Ile Ser Lys Val Tyr Asp Leu His Lys Lys Tyr Gly Asp	
65 70 75 80	
gta gtt tta ctt tct cca aat gaa atc agc gtc aat ggt gac cca aaa	288
Val Val Leu Leu Ser Pro Asn Glu Ile Ser Val Asn Gly Asp Pro Lys	
85 90 95	
tat ttg act gat att tat gta aag aac ctc cca aag tca aag ttt tat	336
Tyr Leu Thr Asp Ile Tyr Val Lys Asn Leu Pro Lys Ser Lys Phe Tyr	
100 105 110	
gaa aac ttt aga aat cat gga ttc cag gat aat att ttt gcc agt ttg	384
Glu Asn Phe Arg Asn His Gly Phe Gln Asp Asn Ile Phe Ala Ser Leu	
115 120 125	
gaa aat gat aga cat atc aag tat aaa aga atg ata aat aac ttg tac	432
Glu Asn Asp Arg His Ile Lys Tyr Lys Arg Met Ile Asn Asn Leu Tyr	
130 135 140	
agt aaa tct tcc atc ttc tcc aaa gaa aac cac aca aga tca gtt tta	480
Ser Lys Ser Ser Ile Phe Ser Lys Glu Asn His Thr Arg Ser Val Leu	
145 150 155 160	
ttt gac acc aca aaa aca tta gtc gat gca gtt gct aga gaa tct ccg	528
Phe Asp Thr Thr Lys Thr Leu Val Asp Ala Val Ala Arg Glu Ser Pro	
165 170 175	
tca att gat gtg ttt acg tta ttt ggt tcc ttg gcc atg gat gtg gtt	576
Ser Ile Asp Val Phe Thr Leu Phe Gly Ser Leu Ala Met Asp Val Val	
180 185 190	
tca agg ttt gaa ctt ggt aga gac aat gga acg gat tta ttg aat cat	624
Ser Arg Phe Glu Leu Gly Arg Asp Asn Gly Thr Asp Leu Leu Asn His	
195 200 205	

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cca	caa	gaa	agg	cat	att	att	gaa	tct	cat	aga	aag	gtg	tct	tgt	atg	672
Pro	Gln	Glu	Arg	His	Ile	Ile	Glu	Ser	His	Arg	Lys	Val	Ser	Cys	Met	
210					215					220						
ggg	ttc	tgg	aca	aca	ttg	atg	cca	agc	ttc	ttt	tgg	aat	ttg	gca	gca	720
Gly	Phe	Trp	Thr	Thr	Leu	Met	Pro	Ser	Phe	Phe	Trp	Asn	Leu	Ala	Ala	
225					230					235				240		
acc	aag	gcc	acc	ttg	caa	gct	ggt	gat	gat	att	tgc	aat	ttc	caa	ttg	768
Thr	Lys	Ala	Thr	Leu	Gln	Ala	Val	Asp	Asp	Ile	Cys	Asn	Phe	Gln	Leu	
			245					250						255		
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	
	290					295				300						
gct	ggt	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	ggt	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	ggt	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				
att	cca	ggt	ggt	acg	ggt	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	ggt	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	
		500						505						510		

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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

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<210> SEQ ID NO 44
<211> LENGTH: 523
<212> TYPE: PRT
<213> ORGANISM: Candida tropicalis

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<400> SEQUENCE: 44

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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
      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

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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
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> SEQ ID NO 45

<211> LENGTH: 1728

<212> TYPE: DNA

<213> ORGANISM: Candida tropicalis

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1) .. (1725)

<400> SEQUENCE: 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	

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115	120	125	
tta gtt tca gca tta caa ggt ttt aca gtt 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 gtt 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 gtt			528
Lys Glu Ile Asp 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 gtt 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 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	
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			

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420	425	430	
cat gat gaa tta ata ttc aaa aat cca ttt aaa ttt gat cca gaa aga His Asp Glu Leu Ile Phe Lys Asn Pro Phe Lys Phe Asp Pro Glu Arg 435 440 445			1344
tgg tta gat tca gaa act aat gaa att aaa tca aaa ata ctt gct act Trp Leu Asp Ser Glu Thr Asn Glu Ile Lys Ser Lys Ile Leu Ala Thr 450 455 460			1392
act tct tcg tct tct tct tcg aca cat cat ggt ggt gga aat gga ata Thr Ser Ser Ser Ser Ser Ser Thr His His Gly Gly Gly Asn Gly Ile 465 470 475 480			1440
aat gta cag aat ttt cat ttt gca ttt ggt gct gga tca aga atg tgt Asn Val Gln Asn Phe His Phe Ala Phe Gly Ala Gly Ser Arg Met Cys 485 490 495			1488
tca ggt tat aat cta gtt atg aaa gaa atg tat atg atg ata att aaa Ser Gly Tyr Asn Leu Val Met Lys Glu Met Tyr Met Met Ile Ile Lys 500 505 510			1536
tta tta tta tta ttt gaa att aat cct cct gat aat aat aat aat aat Leu Leu Leu Leu Phe Glu Ile Asn Pro Pro Asp Asn Asn Asn Asn Asn 515 520 525			1584
ggg aaa tat tta atg gaa atg aat cct ttt gtt aat aat ctg aat cct Gly Lys Tyr Leu Met Glu Met Asn Pro Phe Val Asn Asn Leu Asn Pro 530 535 540			1632
aga ggt act tca ttt gaa cca cga ata cat aat att aaa tta caa tat Arg Gly Thr Ser Phe Glu Pro Arg Ile His Asn Ile Lys Leu Gln Tyr 545 550 555 560			1680
aga aaa cta cct aat tat gaa act cta cac gaa ata gtt ctc aaa tag Arg Lys Leu Pro Asn Tyr Glu Thr Leu His Glu Ile Val Leu Lys 565 570 575			1728

<210> SEQ ID NO 46

<211> LENGTH: 575

<212> TYPE: PRT

<213> ORGANISM: Candida tropicalis

<400> SEQUENCE: 46

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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
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

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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
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	465	470	475	480
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					

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565	570	575	
<210> SEQ ID NO 47			
<211> LENGTH: 1518			
<212> TYPE: DNA			
<213> ORGANISM: Candida tropicalis			
<220> FEATURE:			
<221> NAME/KEY: CDS			
<222> LOCATION: (1) .. (1515)			
<400> SEQUENCE: 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			

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atg caa aag gac ttt gtt gat gaa tat atc gac aga gta gta ggt atg Met Gln Lys Asp Phe Val Asp Glu Tyr Ile Asp Arg Val Val Gly Met 260 265 270	816
tcc gaa gaa gaa ttg aac aat cat cca aag agc tat gtt ttg ttg tac Ser Glu Glu Glu Leu Asn Asn His Pro Lys Ser Tyr Val Leu Leu Tyr 275 280 285	864
caa tta gca aga caa act aag aat cgt gat ata tta caa gat gaa ttg Gln Leu Ala Arg Gln Thr Lys Asn Arg Asp Ile Leu Gln Asp Glu Leu 290 295 300	912
atg tcc att tta ctt gca ggt aga gac acc act gcc agt ttg ttg act Met Ser Ile Leu Leu Ala Gly Arg Asp Thr Thr Ala Ser Leu Leu Thr 305 310 315 320	960
ttt ttg ttt ttc gaa tta agt cac cat cca gaa gta ttt aac aaa tta Phe Leu Phe Phe Glu Leu Ser His His Pro Glu Val Phe Asn Lys Leu 325 330 335	1008
aaa gag gaa atc gaa aga cac ttt cct gat gtt gaa tcc gtt aca ttt Lys Glu Glu Ile Glu Arg His Phe Pro Asp Val Glu Ser Val Thr Phe 340 345 350	1056
gga act atc cag aga tgc gac tat ctt caa tgg tgt att aac gaa act Gly Thr Ile Gln Arg Cys Asp Tyr Leu Gln Trp Cys Ile Asn Glu Thr 355 360 365	1104
atg aga ctc cat cca tca gtt cct ttt aat ttc aga act gca gcc aat Met Arg Leu His Pro Ser Val Pro Phe Asn Phe Arg Thr Ala Ala Asn 370 375 380	1152
gac aca gta ata cca aga ggt gga ggt aaa tcc tgt aca gat cct att Asp Thr Val Ile Pro Arg Gly Gly Lys Ser Cys Thr Asp Pro Ile 385 390 395 400	1200
ctt gtc cat aag ggt gaa caa gta tta ttc agt ttc tat tct gta aac Leu Val His Lys Gly Glu Gln Val Leu Phe Ser Phe Tyr Ser Val Asn 405 410 415	1248
aga gaa gaa aag tat ttt ggt aca aat acc gac aag ttt gct cca gaa Arg Glu Glu Lys Tyr Phe Gly Thr Asn Thr Asp Lys Phe Ala Pro Glu 420 425 430	1296
aga tgg agt gaa tca tta agg aga act gag ttc ata cca ttt tct gct Arg Trp Ser Glu Ser Leu Arg Arg Thr Glu Phe Ile Pro Phe Ser Ala 435 440 445	1344
gga cct cgt gcc tgt ttg ggt caa cag tta gct aga gtt gaa gct tca Gly Pro Arg Ala Cys Leu Gly Gln Leu Ala Arg Val Glu Ala Ser 450 455 460	1392
tat gtt act att aga ttg ctt caa acc ttt cat ggg ttg cat aat gcc Tyr Val Thr Ile Arg Leu Leu Gln Thr Phe His Gly Leu His Asn Ala 465 470 475 480	1440
agt aaa caa tac cca cca aat aga gtg gtt gca gct aca atg aga ttg Ser Lys Gln Tyr Pro Pro Asn Arg Val Val Ala Ala Thr Met Arg Leu 485 490 495	1488
act gac ggt tgt aac gtt tgt ttt atc tag Thr Asp Gly Cys Asn Val Cys Phe Ile 500 505	1518

<210> SEQ ID NO 48

<211> LENGTH: 505

<212> TYPE: PRT

<213> ORGANISM: Candida tropicalis

<400> SEQUENCE: 48

Met	Tyr	Gln	Leu	Phe	Cys	Phe	Leu	Ala	Gly	Ile	Ile	Val	Val	Tyr	Lys
1				5					10					15	

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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
		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	
Arg	Glu	Glu	Lys	Tyr	Phe	Gly	Thr	Asn	Thr	Asp	Lys	Phe	Ala	Pro	Glu

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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> SEQ ID NO 49			
<211> LENGTH: 1584			
<212> TYPE: DNA			
<213> ORGANISM: Candida tropicalis			
<220> FEATURE:			
<221> NAME/KEY: CDS			
<222> LOCATION: (1) .. (1581)			
 <400> SEQUENCE: 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
gct act aca tat ttg agt aca aaa tat atc atc gat agt tta tat tca			96
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			144
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			192
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			240
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			288
Glu Ser Leu Asp Pro Lys Phe Glu Glu Tyr Lys Ala Lys Trp Asp Ser			
	85	90	95
ggt gaa ttg agt tgt gtt tcc att ttc cat aaa ttc gtt gtt att gct			336
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 gtt			384
Ser Ser Arg Asp Leu Ala Arg Lys Ile Leu Ala Ser Pro Lys Tyr Val			
	115	120	125
aaa cct tgt gtt gtt gat gtt gct gtt aaa att tta aga cct tca aat			432
Lys Pro Cys Val Val Asp Val Ala Val Lys Ile Leu Arg Pro Ser Asn			
	130	135	140
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

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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	ggg	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	cac	att	aat	gaa	aat	aat	ggg	act	cca	ggg	tgt	gtt	atg	gat	gaa	864
Lys	His	Ile	Asn	Glu	Asn	Asn	Gly	Thr	Pro	Gly	Cys	Val	Met	Asp	Glu	
		275					280					285				
tgg	att	tac	ttg	atg	aaa	gaa	gct	aaa	gaa	aaa	cac	tct	gat	gat	cca	912
Trp	Ile	Tyr	Leu	Met	Lys	Glu	Ala	Lys	Glu	Lys	His	Ser	Asp	Asp	Pro	
		290				295					300					
gat	tcc	aaa	tta	ttg	att	aga	gaa	ttc	tcc	aac	cgt	gaa	att	tcc	gaa	960
Asp	Ser	Lys	Leu	Leu	Ile	Arg	Glu	Phe	Ser	Asn	Arg	Glu	Ile	Ser	Glu	
		305				310				315					320	
gcc	att	ttc	act	ttc	ttg	ttt	gct	tct	caa	gat	gcc	tct	tct	tct	ttg	1008
Ala	Ile	Phe	Thr	Phe	Leu	Phe	Ala	Ser	Gln	Asp	Ala	Ser	Ser	Ser	Leu	
			325						330						335	
gct	tgt	tgg	tta	ttc	caa	att	gtc	gcc	gac	aga	cca	gat	gtt	gtt	gcc	1056
Ala	Cys	Trp	Leu	Phe	Gln	Ile	Val	Ala	Asp	Arg	Pro	Asp	Val	Val	Ala	
		340					345						350			
aag	att	aga	gaa	gaa	caa	ttg	aga	gtt	aga	aac	aat	gac	cca	tct	gtt	1104
Lys	Ile	Arg	Glu	Glu	Gln	Leu	Arg	Val	Arg	Asn	Asn	Asp	Pro	Ser	Val	
		355					360					365				
aaa	ttg	tcc	ttg	gat	ttg	att	aat	gaa	atg	act	tac	acc	aat	gat	gtt	1152
Lys	Leu	Ser	Leu	Asp	Leu	Ile	Asn	Glu	Met	Thr	Tyr	Thr	Asn	Asp	Val	
		370				375					380					
gtt	aaa	gaa	tct	ttg	aga	tac	cgt	cca	cca	gtc	ttg	atg	gtt	cca	tat	1200
Val	Lys	Glu	Ser	Leu	Arg	Tyr	Arg	Pro	Pro	Val	Leu	Met	Val	Pro	Tyr	
		385				390				395					400	
gtt	gtt	aag	aaa	gct	ttc	cca	gtt	act	gaa	aaa	tac	act	gct	cca	aag	1248
Val	Val	Lys	Lys	Ala	Phe	Pro	Val	Thr	Glu	Lys	Tyr	Thr	Ala	Pro	Lys	
			405						410					415		
ggg	tct	atg	ctt	atc	cca	act	ttg	tac	cct	gct	tta	cat	gat	cct	gaa	1296
Gly	Ser	Met	Leu	Ile	Pro	Thr	Leu	Tyr	Pro	Ala	Leu	His	Asp	Pro	Glu	
			420				425						430			
gtt	tat	gat	gaa	cca	gat	tct	ttc	att	cca	gaa	aga	tgg	gcc	act	gct	1344
Val	Tyr	Asp	Glu	Pro	Asp	Ser	Phe	Ile	Pro	Glu	Arg	Trp	Ala	Thr	Ala	
		435				440						445				
tct	ggg	gat	atg	tac	aaa	cgt	aac	tgg	ttg	gtc	ttc	ggg	act	ggg	cca	1392
Ser	Gly	Asp	Met	Tyr	Lys	Arg	Asn	Trp	Leu	Val	Phe	Gly	Thr	Gly	Pro	
		450				455						460				
cac	gtt	tgt	ttg	ggg	aag	aac	tat	gtc	atg	atg	ttg	ttt	act	ggg	atg	1440
His	Val	Cys	Leu	Gly	Lys	Asn	Tyr	Val	Met	Met	Leu	Phe	Thr	Gly	Met	
		465				470				475					480	
ttg	ggg	aaa	ttt	gtc	atg	aac	tct	gat	atc	att	cat	cac	aaa	act	gca	1488
Leu	Gly	Lys	Phe	Val	Met	Asn	Ser	Asp	Ile	Ile	His	His	Lys	Thr	Ala	
				485					490					495		

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tta tct gaa gaa atc aaa gtt ttc gct act att ttc cct aag gac gat      1536
Leu Ser Glu Glu Ile Lys Val Phe Ala Thr Ile Phe Pro Lys Asp Asp
           500                505                510

ggt att tta gaa tgg aaa aag aga gat ccg tta gct gct tct aat taa      1584
Val Ile Leu Glu Trp Lys Lys Arg Asp Pro Leu Ala Ala Ser Asn
           515                520                525

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<210> SEQ ID NO 50

<211> LENGTH: 527

<212> TYPE: PRT

<213> ORGANISM: Candida tropicalis

<400> SEQUENCE: 50

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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 Glu 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

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 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

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<210> SEQ ID NO 51		
<211> LENGTH: 1587		
<212> TYPE: DNA		
<213> ORGANISM: Candida tropicalis		
<220> FEATURE:		
<221> NAME/KEY: CDS		
<222> LOCATION: (1)..(1584)		
<400> SEQUENCE: 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		

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100					105					110						
tct	gct	gaa	gaa	gct	tat	acc	cat	ttg	act	act	cct	ggt	ttt	ggt	aaa	384
Ser	Ala	Glu	Glu	Ala	Tyr	Thr	His	Leu	Thr	Thr	Pro	Val	Phe	Gly	Lys	
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	Ala	His	
245					250					255						
tac	atg	aag	gaa	att	aag	aga	aga	aga	gaa	agc	ggt	gat	att	gat	cca	816
Tyr	Met	Lys	Glu	Ile	Lys	Arg	Arg	Arg	Glu	Ser	Gly	Asp	Ile	Asp	Pro	
260					265					270						
aag	aga	gat	ttg	att	gat	tcc	ttg	ttg	ggt	aac	tct	act	tat	aaa	gat	864
Lys	Arg	Asp	Leu	Ile	Asp	Ser	Leu	Leu	Val	Asn	Ser	Thr	Tyr	Lys	Asp	
275					280					285						
ggt	ggt	aaa	atg	act	gat	caa	gaa	att	gct	aac	ctt	tta	att	ggt	ggt	912
Gly	Val	Lys	Met	Thr	Asp	Gln	Glu	Ile	Ala	Asn	Leu	Leu	Ile	Gly	Val	
290					295					300						
ttg	atg	ggt	ggt	caa	cat	act	tct	gct	tcc	act	tct	gcc	tgg	ttc	ttg	960
Leu	Met	Gly	Gly	Gln	His	Thr	Ser	Ala	Ser	Thr	Ser	Ala	Trp	Phe	Leu	
305					310					315					320	
ttg	cat	ttg	gct	gaa	caa	cca	caa	tta	caa	gat	gat	ctt	tac	gaa	gaa	1008
Leu	His	Leu	Ala	Glu	Gln	Pro	Gln	Leu	Gln	Asp	Asp	Leu	Tyr	Glu	Glu	
325					330					335						
ttg	acc	aac	ttg	ttg	aaa	gaa	aag	ggt	ggt	gac	ttg	aac	gat	ttg	act	1056
Leu	Thr	Asn	Leu	Leu	Lys	Glu	Lys	Gly	Gly	Asp	Leu	Asn	Asp	Leu	Thr	
340					345					350						
tac	gaa	gac	ttg	caa	aaa	tta	cca	ttg	ggt	aac	aac	act	att	aaa	gaa	1104
Tyr	Glu	Asp	Leu	Gln	Lys	Leu	Pro	Leu	Val	Asn	Asn	Thr	Ile	Lys	Glu	
355					360					365						
act	ttg	aga	atg	cac	atg	cca	ttg	cat	tct	att	ttc	aga	aaa	ggt	atg	1152
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	ggt	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	
tat	gtc	tta	ggt	tct	gcc	ggt	tat	gct	cat	acc	agt	gat	aga	tgg	ttt	1248
Tyr	Val	Leu	Val	Ser	Ala	Gly	Tyr	Ala	His	Thr	Ser	Asp	Arg	Trp	Phe	

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405	410	415	
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	
ggt 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	
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> SEQ ID NO 52

<211> LENGTH: 528

<212> TYPE: PRT

<213> ORGANISM: Candida tropicalis

<400> SEQUENCE: 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	
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	

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<210> SEQ ID NO 53
<211> LENGTH: 2097
<212> TYPE: DNA
<213> ORGANISM: Candida cloacae
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(2094)
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atg tcc cat caa gtt gaa gac cac gac tta gac gtg ttc tgt tta ttg
Met Ser His Gln Val Glu Asp His Asp Leu Asp Val Phe Cys Leu Leu

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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
ttg act ttg atc agg gat atg gat ctt tcc caa aga gag gag ttg ttg				336
Leu Thr Leu Ile Arg Asp Met Asp Leu Ser Gln Arg Glu Glu Leu Leu				
	100	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				
	115	120	125	
gtg tat gcc tct ttt acc ttg tct act ttt aac aag ttg gga aca gac				432
Val Tyr Ala Ser Phe Thr Leu Ser Thr Phe Asn Lys Leu Gly Thr Asp				
	130	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				
	145	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				
	165	170	175	
ctt aaa cac gag ggc cac gaa ttg ttc ctt cct gat att gac gtt tta				576
Leu Lys His Glu Gly His Glu Leu Phe Leu Pro Asp Ile Asp Val Leu				
	180	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				
	195	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				
	210	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	
tggt 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				

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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 Met Cys				
	340	345	350	
cac ttg gga tgt aga ttc ggt atc aaa caa ggt ggt gta aat tgc tgg				1104
His Leu Gly Cys Arg Phe Gly Ile Lys Gln Gly Gly Val Asn Cys Trp				
	355	360	365	
ttc cgt gaa cct agt gaa aag ggt tct aag ttc atg gaa caa gtt gtt				1152
Phe Arg Glu Pro Ser Glu Lys Gly Ser Lys Phe Met Glu Gln Val Val				
	370	375	380	
gtt gaa aag att ttg cag cac aag ggt aaa gct act ggg att ttg tgt				1200
Val Glu Lys Ile Leu Gln His Lys Gly Lys Ala Thr Gly Ile Leu Cys				
	385	390	395	400
aga gat act gaa agt ggg att aaa ttc aaa atc act gga cca aag aaa				1248
Arg Asp Thr Glu Ser Gly Ile Lys Phe Lys Ile Thr Gly Pro Lys Lys				
	405	410	415	
tac gtt gtt tcc ggt ggt tct ttg caa acc cca gtt ttg tta caa aaa				1296
Tyr Val Val Ser Gly Gly Ser Leu Gln Thr Pro Val Leu Leu Gln Lys				
	420	425	430	
tct ggt ttc aag aat aaa cat att gga gct aac tta aaa ctt cac cca				1344
Ser Gly Phe Lys Asn Lys His Ile Gly Ala Asn Leu Lys Leu His Pro				
	435	440	445	
gtc tcg gtt gcc ctt ggg gac ttt ggt aat gaa gtg gac ttt gaa gcc				1392
Val Ser Val Ala Leu Gly Asp Phe Gly Asn Glu Val Asp Phe Glu Ala				
	450	455	460	
tac aag aga cca ctt atg acc gcc gtt tgt aat gcc gtc gat gat tta				1440
Tyr Lys Arg Pro Leu Met Thr Ala Val Cys Asn Ala Val Asp 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 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				

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610	615	620	
ggt tct gct cat caa atg agt 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 tct gtt atg cct act gca tct 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> SEQ ID NO 54

<211> LENGTH: 698

<212> TYPE: PRT

<213> ORGANISM: Candida cloacae

<400> SEQUENCE: 54

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
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			
	145	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
Glu Ser Gly Gly Thr Ile Pro Ser Thr Asn Gln Gln Leu Phe Met Ile			

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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						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						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						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				
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						640				
Gly	Tyr	Gly	Ala	Cys	Asp	Thr	Lys	Gly	Arg	Leu	Phe	Glu	Cys	Asn	Asn		
			645				650						655				

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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> SEQ ID NO 55
<211> LENGTH: 2097
<212> TYPE: DNA
<213> ORGANISM: Candida cloacae
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1) .. (2094)

<400> SEQUENCE: 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
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

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aat gat gag ttg acc atg aat gat ttg gaa ggt agt gag gca tta ttc Asn Asp Glu Leu Thr Met Asn Asp Leu Glu Gly Ser Glu Ala Leu Phe 225 230 235 240	720
gaa aat gga ggt gcc ctc agt agt acc aac caa cag ata ttt ata att Glu Asn Gly Gly Ala Leu Ser Ser Thr Asn Gln Gln Ile Phe Ile Ile 245 250 255	768
gca ggt tcg act ttt ggg ggt ggt tct aca gtt aat tgg tct gcc tgt Ala Gly Ser Thr Phe Gly Gly Gly Ser Thr Val Asn Trp Ser Ala Cys 260 265 270	816
tta aaa act ccg ttc aaa gta aga aaa gag tgg tat gac aac ttc gga Leu Lys Thr Pro Phe Lys Val Arg Lys Glu Trp Tyr Asp Asn Phe Gly 275 280 285	864
ctt gat ttc gtc gca acc caa tac tac gaa gat tgt atg gat tat gtt Leu Asp Phe Val Ala Thr Gln Tyr Tyr Glu Asp Cys Met Asp Tyr Val 290 295 300	912
tgg aag aaa atg ggt gct tcg aac gaa aat atc gac cat tct ggt gct Trp Lys Lys Met Gly Ala Ser Asn Glu Asn Ile Asp His Ser Gly Ala 305 310 315 320	960
aat agt gtt ata ttg gaa ggg tcc aaa aaa ctt ggc tac cct cac agg Asn Ser Val Ile Leu Glu Gly Ser Lys Lys Leu Gly Tyr Pro His Arg 325 330 335	1008
gcc gtt gaa caa aat aat ggg ggc aaa att cat gac tgt ggt atg tgt Ala Val Glu Gln Asn Asn Gly Gly Lys Ile His Asp Cys Gly Met Cys 340 345 350	1056
cac ttg ggt tgt aga ttt ggt att aaa cag gga agt gta aat tgc tgg His Leu Gly Cys Arg Phe Gly Ile Lys Gln Gly Ser Val Asn Cys Trp 355 360 365	1104
ttc cgt ggt cca agt gaa aac gga tcc aag ttt atg caa caa gtt ctc Phe Arg Gly Pro Ser Glu Asn Gly Ser Lys Phe Met Gln Gln Val Leu 370 375 380	1152
gtg gat aag ata ttg caa cgt gac ggt aaa gca gtc ggt gtt ttg tgt Val Asp Lys Ile Leu Gln Arg Asp Gly Lys Ala Val Gly Val Leu Cys 385 390 395 400	1200
aga gat gtt gta acc ggt gtt aag ttc aag atc act gga cca aag aaa Arg Asp Val Val Thr Gly Val Lys Phe Lys Ile Thr Gly Pro Lys Lys 405 410 415	1248
att gtt gtt ttc tgg tgg ttc ttt gca aac tcc ggt ttt gtt aca aaa Ile Val Val Phe Trp Trp Phe Phe Ala Asn Ser Gly Phe Val Thr Lys 420 425 430	1296
tca ggt ttc aag aat aaa cac att ggt gct aac ttg aag ctc cat cca Ser Gly Phe Lys Asn Lys His Ile Gly Ala Asn Leu Lys Leu His Pro 435 440 445	1344
gtt tca ctt acg ctt gga gac ttc ggt aac aac gtg gat ttc gaa gct Val Ser Leu Thr Leu Gly Asp Phe Gly Asn Asn Val Asp Phe Glu Ala 450 455 460	1392
tac agg aaa cca att atg aca tca att tgt aat aaa gtc gaa gat tta Tyr Arg Lys Pro Ile Met Thr Ser Ile Cys Asn Lys Val Glu Asp Leu 465 470 475 480	1440
gat gga aag gcc cat ggt aca aga att gaa gct atg ttg aat gct cca Asp Gly Lys Ala His Gly Thr Arg Ile Glu Ala Met Leu Asn Ala Pro 485 490 495	1488
tat ggt gtt gca cca ttt ttc ccc tgg aaa tca ggc gct gaa tca aga Tyr Gly Val Ala Pro Phe Phe Pro Trp Lys Ser Gly Ala Glu Ser Arg 500 505 510	1536
aag gat ctc ttg aga tac aaa caa act gtg cct ata tta ctt ctt tcc Lys Asp Leu Leu Arg Tyr Lys Thr Val Pro Ile Leu Leu Leu Ser 515 520 525	1584

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<210> SEQ ID NO 56
<211> LENGTH: 698
<212> TYPE: PRT
<213> ORGANISM: Candida cloacae
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<400> SEQUENCE: 56

Met 1	Asn	Pro	Val	Val 5	Glu	Asp	Ser	His	Leu 10	Asp	Val	Phe	Cys	Leu 15	Leu
Ala	Asp	Ala	Val	Val 20	His	Glu	Ile	Pro 25	Pro	Ser	Glu	Ile	Val 30	Glu	Tyr
Leu	His	Pro	Asp	Phe 35	Pro	Lys	Asp 40	Lys	Val	Glu	Glu	Tyr 45	Leu	Ala	Glu
Phe	Ser 50	His	Pro	Ser	Ala	Ile 55	Pro	Glu	Phe	Arg	Glu 60	Val	Ala	Lys	Arg
Ile 65	Ile	Asn	Lys	Gly	Thr 70	Val	Leu	Ser	Ile	Lys 75	Leu	Phe	Leu	Leu	Leu 80
Ala	Thr	Ala	Leu	Asp 85	Ser	Arg	Ile	Leu	Ala 90	Pro	Ala	Leu	Thr	Asn 95	Ser
Thr	Thr	Leu	Ile 100	Arg	Asp	Met	Asp	Leu 105	Ser	Gln	Arg	Glu 110	Glu	Leu	Leu
Arg	Ser	Trp 115	Arg	Asp	Ser	Pro	Phe 120	Thr	Thr	Lys	Arg 125	Lys	Leu	Phe	Arg

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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		
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	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			

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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> SEQ ID NO 57

<211> LENGTH: 948

<212> TYPE: DNA

<213> ORGANISM: Candida tropicalis

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(948)

<400> SEQUENCE: 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	

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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 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> SEQ ID NO 58

<211> LENGTH: 316

<212> TYPE: PRT

<213> ORGANISM: Candida tropicalis

<400> SEQUENCE: 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 Gln Tyr	
100 105 110	

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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> SEQ ID NO 59

<211> LENGTH: 948

<212> TYPE: DNA

<213> ORGANISM: Candida tropicalis

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(948)

<400> SEQUENCE: 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 gtt gtt gtt 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

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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	ggt	gcc	ccc	atc	ttg	tgt	gct	ggt	gtc	act	ggt	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	ggt	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	ggt	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	ggt	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	ggt	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	ggt	aac	ggt	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	ggt	aga	acc	ttg	ggt	aag	ggt	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	ggt	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					
ggt	gac	ttt	ttc	tcc	aga	ggc	ttg	atc	aag	tgt	cca	atc	aag	ggt	gtc	912	
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> SEQ ID NO 60

<211> LENGTH: 316

<212> TYPE: PRT

<213> ORGANISM: Candida tropicalis

<400> SEQUENCE: 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

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65	70	75	80
Cys Met Asn Cys Glu Tyr Cys Gln Gln Gly Ala Glu Pro Asn Cys Pro	85	90	95
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
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
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

<210> SEQ ID NO 61
 <211> LENGTH: 456
 <212> TYPE: DNA
 <213> ORGANISM: Candida tropicalis
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(456)

<400> SEQUENCE: 61

aac tgt gag ttt tgc caa cag ggc gct gaa cct aat tgt cca aga gcc	48
Asn Cys Glu Phe Cys Gln Gln Gly Ala Glu Pro Asn Cys Pro Arg Ala	
1 5 10 15	
gac atg tct gga tat acc cac gat ggg act ttc caa caa tat gct acc	96
Asp Met Ser Gly Tyr Thr His Asp Gly Thr Phe Gln Gln Tyr Ala Thr	
20 25 30	
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	

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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			

<210> SEQ ID NO 62

<211> LENGTH: 152

<212> TYPE: PRT

<213> ORGANISM: Candida tropicalis

<400> SEQUENCE: 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
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> SEQ ID NO 63

<211> LENGTH: 948

<212> TYPE: DNA

<213> ORGANISM: Candida tropicalis

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(948)

<400> SEQUENCE: 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

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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				
ggc	cac	gaa	ggc	gct	ggc	gtc	gtt	gtc	ggc	atg	ggc	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	ggc	atc	aag	tgg	ttg	aat	ggc	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	ggc	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		
ggc	gct	ggc	ggc	ggc	ttg	ggc	tcc	ttg	ggc	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	ggc	tac	aga	gtg	ttg	gct	atc	gac	ggc	ggc	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				
cag	gac	atc	gtt	agt	gct	atc	aga	aag	gca	act	ggc	ggc	ggc	cca	cac	672
Gln	Asp	Ile	Val	Ser	Ala	Ile	Arg	Lys	Ala	Thr	Gly	Gly	Gly	Pro	His	
	210					215					220					
ggc	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		
ggc	ggc	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					
ggc	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						

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<210> SEQ ID NO 64
<211> LENGTH: 316
<212> TYPE: PRT
<213> ORGANISM: Candida tropicalis

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<400> SEQUENCE: 64

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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 Ile Ser
145     150     155     160
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

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<210> SEQ ID NO 65
<211> LENGTH: 948
<212> TYPE: DNA
<213> ORGANISM: Candida tropicalis
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(948)

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<400> SEQUENCE: 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 gcc 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	
ggt 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 ggt 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	

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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> SEQ ID NO 66
 <211> LENGTH: 316
 <212> TYPE: PRT
 <213> ORGANISM: Candida tropicalis

<400> SEQUENCE: 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
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> SEQ ID NO 67

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<211> LENGTH: 1992
<212> TYPE: DNA
<213> ORGANISM: Candida tropicalis
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1992)

<400> SEQUENCE: 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
          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

gtt 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 gtt 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

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tat gat gag ttt ggt gtt gac ttt gct gct gat gaa gca tac gat aaa Tyr Asp Glu Phe Gly Val Asp Phe Ala Ala Asp Glu Ala Tyr Asp Lys 275 280 285	864
gcg cag gat tat gtt tgg cag caa atg gga gct tct acc gaa ggc atc Ala Gln Asp Tyr Val Trp Gln Gln Met Gly Ala Ser Thr Glu Gly Ile 290 295 300	912
acc cac tct ttg gct aac gag att att att gaa ggt ggt aag aaa tta Thr His Ser Leu Ala Asn Glu Ile Ile Ile Glu Gly Gly Lys Lys Leu 305 310 315 320	960
ggg tac aag gcc aag gta tta gac caa aac agc ggt ggt cat cct cag Gly Tyr Lys Ala Lys Val Leu Asp Gln Asn Ser Gly Gly His Pro Gln 325 330 335	1008
cac aga tgc ggt ttc tgt tat ttg gcc tgt aag cac ggt atc aag cag His Arg Cys Gly Phe Cys Tyr Leu Gly Cys Lys His Gly Ile Lys Gln 340 345 350	1056
ggg tct gtt aat aac tgg ttt aga gac gca gct gcc cac ggt tcc cag Gly Ser Val Asn Asn Trp Phe Arg Asp Ala Ala Ala His Gly Ser Gln 355 360 365	1104
ttc atg caa cag gtt aga gtt ttg caa ata ctt aac aag aag ggg atc Phe Met Gln Gln Val Arg Val Leu Gln Ile Leu Asn Lys Lys Gly Ile 370 375 380	1152
gct tac ggt atc ttg tgt gag gat gtt gta acc gcc gcc aag ttc acc Ala Tyr Gly Ile Leu Cys Glu Asp Val Val Thr Gly Ala Lys Phe Thr 385 390 395 400	1200
att act ggc ccc aaa aag ttt gtt gtt gct gcc ggt gct ttg aac act Ile Thr Gly Pro Lys Lys Phe Val Val Ala Ala Gly Ala Leu Asn Thr 405 410 415	1248
cca tct gtg ttg gtc aac tcc ggc ttc aag aac aag aac atc ggt aag Pro Ser Val Leu Val Asn Ser Gly Phe Lys Asn Lys Asn Ile Gly Lys 420 425 430	1296
aac tta act ttg cac cca gtt tct gtc gtg ttt ggt gat ttt ggc aaa Asn Leu Thr Leu His Pro Val Ser Val Val Phe Gly Asp Phe Gly Lys 435 440 445	1344
gac gtt caa gca gac cac ttc cac aac tcc atc atg act gcc ctt tgt Asp Val Gln Ala Asp His Phe His Asn Ser Ile Met Thr Ala Leu Cys 450 455 460	1392
tca gaa gcc gct gat tta gac ggc aag ggc cat gga tgc aga att gaa Ser Glu Ala Ala Asp Leu Asp Gly Lys Gly His Gly Cys Arg Ile Glu 465 470 475 480	1440
acc atc ttg aac gct cca ttc atc cag gct tca ttc tta cca tgg aga Thr Ile Leu Asn Ala Pro Phe Ile Gln Ala Ser Phe Leu Pro Trp Arg 485 490 495	1488
ggg agt aac gag gct aga cga gac ttg ttg cgt tac aac aac atg gtg Gly Ser Asn Glu Ala Arg Arg Asp Leu Leu Arg Tyr Asn Asn Met Val 500 505 510	1536
gcg atg ttg ctc ctt agt cgt gac acc acc agt ggt tcc gtt tct gct Ala Met Leu Leu Leu Ser Arg Asp Thr Thr Ser Gly Ser Val Ser Ala 515 520 525	1584
cat cca acc aaa cct gaa gct ttg gtt gtc gag tac gac gtg aac aag His Pro Thr Lys Pro Glu Ala Leu Val Val Glu Tyr Asp Val Asn Lys 530 535 540	1632
ttt gac aga aac tcg atc ttg cag gca ttg ttg gtc act gct gac ttg Phe Asp Arg Asn Ser Ile Leu Gln Ala Leu Val Thr Ala Asp Leu 545 550 555 560	1680
ttg tat atc caa ggt gcc aag aga atc ctt agt cca cag gca tgg gtg Leu Tyr Ile Gln Gly Ala Lys Arg Ile Leu Ser Pro Gln Ala Trp Val 565 570 575	1728

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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 ggt 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

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<210> SEQ ID NO 68

<211> LENGTH: 664

<212> TYPE: PRT

<213> ORGANISM: Candida tropicalis

<400> SEQUENCE: 68

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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 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

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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
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

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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			

1. A mutant *Candida tropicalis* cell, which has, compared with a wild type *Candida tropicalis* cell, a reduced activity of at least one of enzyme that is encoded by an intron-free nucleic acid sequence selected from groups A) and B)

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 80% identical to at least to one sequence selected from the group consisting of 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. The *Candida tropicalis* cell according to claim 1, wherein the decrease in enzymatic activity is achieved by modification of the nucleic acid sequence in the cell, wherein the modification is selected from the group consisting of insertion of foreign DNA into the nucleic acid sequence in the cell, deletion of at least parts of the nucleic acid sequence in the cell, a point mutation in the nucleic acid sequence in the cell, subjecting the nucleic acid sequence in the cell to RNA interference and exchanging a part of the nucleic acid sequence in the cell with foreign DNA.

3. The *Candida tropicalis* cell according to claim 2, wherein the foreign DNA is a selection marker gene.

4. The *Candida tropicalis* cell according to claim 1, wherein the cell is blocked at least partially in its β -oxidation.

5. The *Candida tropicalis* cell according to claim 1, which is derived from a strain selected from the group consisting of *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* ATCC20962 and *Candida tropicalis* HDC100.

6. The *Candida tropicalis* cell according to claim 5, which is derived from *Candida tropicalis* ATCC20962 or *Candida tropicalis* HDC100.

7. A method for producing ω -hydroxycarboxylic acid or ω -hydroxycarboxylic acid ester, the method comprising

- contacting the *Candida tropicalis* cell according to claim 1 with a medium comprising a carboxylic acid or a carboxylic acid ester,
- cultivating the cell under conditions to form the corresponding ω -hydroxycarboxylic acid or ω -hydroxycarboxylic acid esters from the carboxylic acid or the carboxylic acid ester and
- optionally isolating the ω -hydroxycarboxylic acid or ω -hydroxycarboxylic acid esters that formed.

8. A method of producing a *C. tropicalis* cell according to claim 1, the method comprising:

- preparing a *C. tropicalis* cell and
- modifying 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 into the gene, deletion at least of a part of the gene, a point mutation in the gene sequence, subjecting the gene to RNA interference and exchanging a part of the gene with foreign DNA.

9. The method according to claim 7, wherein the ω -hydroxycarboxylic acid or ω -hydroxycarboxylic acid ester is a ω -hydroxycarboxylic acid or ω -hydroxycarboxylic acid ester 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

10. The method according to claim 7, wherein the ω -hydroxycarboxylic acid or ω -hydroxycarboxylic acid ester is a 12-hydroxydodecanoic acid or 12-hydroxydodecanoic acid methyl ester.

11. A method according to claim 7, wherein the *Candida tropicalis* cells are derived from a strain selected from the group consisting of *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 and wherein the cells are at least partially blocked in their β -oxidation.

12. A method of manufacturing a polymer, the method comprising polymerizing the ω -hydroxycarboxylic acid or of the ω -hydroxycarboxylic acid ester obtained by the method according to claim 7.

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