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DESCRIPCIÓN

Células de *Candida tropicalis* y su empleo

Campo de la invención

5 Son objeto de la invención células de *Candida tropicalis* modificadas mediante técnica génica, su empleo, así como un procedimiento para la producción de ácidos ω -hidroxi-carboxílicos y ω -hidroxi-carboxilatos.

Estado de la técnica

Debido a su capacidad para formar ácidos dicarboxílicos a partir de alcanos, *Candida tropicalis* es un ascomiceto convenientemente caracterizado.

10 El documento WO91/006660 describe células de *Candida tropicalis* completamente inhibidas mediante interrupción de genes POX4 y/o POX5 en la β -oxidación, que alcanzan rendimientos elevados en ácidos α,ω -dicarboxílicos.

El documento WO00/020566 describe citocromo P450 monooxigenasas y NADPH citocromo P450 oxidorreductasas de *Candida tropicalis* y su empleo para la influencia de la ω -hidroxilación, el primer paso de la ω -oxidación.

15 El documento WO03/089610 describe enzimas de *Candida tropicalis*, que catalizan el segundo paso de la ω -oxidación, la reacción de un alcohol graso para dar un aldehído, así como su empleo para la producción mejorada de ácidos dicarboxílicos.

DATABASE EMBL, accession no. GU056287, Ness J.E., da a conocer la secuencia génica parcial del gen de *Candida tropicalis* hebra H5343 clon B11 alcohol dehidrogenasa (ADH).

20 El documento DE102007060705 describe células que se han modificado mediante técnica génica frente a su tipo salvaje, de tal manera que, en comparación con su tipo salvaje, son capaces de producir más ácidos [omega]-aminocarboxílicos o más lactamas de ácidos carboxílicos o carboxilatos derivadas de ácidos [omega]-aminocarboxílicos.

Fabritius et al., Identification and production of 3-hydroxy-DELTA-9-cis-1,18-octadecenedioic acid by mutants of *Candida tropicalis*, Appl Microbiol Biotechnol. 1996, 45, 432-438, da a conocer ácidos omega-hidroxi-carboxílicos y omega-hidroxi-carboxilatos, y su empleo para la producción de polímeros.

25 Las células y los procedimientos descritos hasta la fecha son inapropiados para la producción de ácidos ω -hidroxi-carboxílicos o sus ésteres, ya que los ácidos ω -hidroxi-carboxílicos se presentan siempre como producto intermedio a corto plazo, y se metabolizan ulteriormente de manera inmediata.

Los ácidos ω -hidroxi-carboxílicos y sus ésteres son compuestos significativos como precursores de polímeros desde el punto de vista económico, mediante lo cual se justifica la aplicación industrial de la presente invención.

30 Era tarea de la invención encontrar una posibilidad de poner a disposición ácidos ω -hidroxi-carboxílicos, o bien ω -hidroxi-carboxilatos, por vía fermentativa en cantidades suficientes, en especial en el medio que rodea las células.

Descripción de la invención

Sorprendentemente se descubrió que las células descritas a continuación contribuyen a la solución de la tarea planteada.

35 Por lo tanto, es objeto de la presente invención una célula como se describe en la reivindicación 1. Otro objeto de la invención es el empleo de la célula según la invención, así como un procedimiento para la producción de ácidos ω -hidroxi-carboxílicos y ω -hidroxi-carboxilatos, bajo empleo de las células según la invención.

40 Son ventajas de la invención la reacción cuidadosa del educto empleado para dar los ácidos ω -hidroxi-carboxílicos y ésteres correspondientes, así como una especificidad elevada del procedimiento, y rendimientos elevados que acompañan a la misma, respecto al educto empleado.

Un objeto de la presente invención es una célula de *Candida tropicalis*, en especial una de la cepa ATCC 20336, que está caracterizada por que la célula, en comparación con su tipo salvaje, presenta una actividad reducida de al menos uno de los enzimas, que se codifican a través de las secuencias de ácido nucleico exentas de intrón,

seleccionadas a partir de ambos grupos constituidos por

A) Seq ID Nr. 63,

B) una secuencia que es idéntica a Seq ID Nr. 63 en al menos un 80 %, de modo especialmente preferente en al menos un 90 %, además preferentemente en al menos un 95 %, y en el más preferente de los casos en al menos un 99 %, debiéndose entender por la actividad del enzima la actividad enzimática que cataliza las reacciones de ácido 12-hidroxi-dodecanoico para dar diácido 1,12-dodecanoico a través de la célula total, además caracterizada por que la reducción de la actividad enzimática se obtiene mediante modificación de un gen que comprende una de las secuencias de ácido nucleico citadas anteriormente, seleccionándose la modificación a partir del grupo que comprende inserción de ADN ajeno en el gen, delección al menos de partes del gen, mutaciones puntuales en la secuencia génica, exposición del gen a la influencia de la interferencia de ARN e intercambio de partes del gen por ADN ajeno, en especial de la zona del promotor.

En este contexto, el grupo de secuencias de ácido nucleico preferente según la invención es el grupo A).

En relación con la presente invención, se entiende por un "tipo salvaje" de una célula preferentemente la cepa de partida a partir de la cual procede la célula según la invención mediante manipulación en los elementos (como por ejemplo los genes que comprenden las citadas secuencias de ácido nucleico que codifican para el correspondiente enzima, o los promotores contenidos en el gen correspondiente, que están enlazados funcionalmente con las citadas secuencias de ácido nucleico), que influyen sobre las actividades del enzima codificado por la citada secuencia ID Nr. de ácido nucleico. A modo de ejemplo, si se reduce la actividad del enzima codificado por la secuencia ID Nr. 1 en la cepa ATCC 20336 mediante interrupción del gen correspondiente, se debe considerar "tipo salvaje" la cepa ATCC 20336 no modificada y empleada para la correspondiente manipulación.

En relación con la presente invención, bajo el concepto "gen" se entiende no solo la región de ADN codificante, o bien transcrita en el mRNA, el "gen estructural", sino, además, regiones de promotor, posibles regiones de intrón, intensificador, y otras regiones de secuencia de regulador, así como de terminador.

En relación con la invención, bajo el concepto "actividad de un enzima" se debe entender siempre la actividad enzimática que cataliza las reacciones de ácido 12-hidroxi-dodecanoico para dar diácido 1,12-dodecanoico a través de la célula total. Esta actividad se determina preferentemente según el siguiente procedimiento:

Partiendo de una colonia aislada se cultiva un matraz Erlenmeyer de 100 ml con 10 ml de medio YM (0,3 % de extracto de levadura, 0,3 % de extracto de malta, 0,5 % de peptona y 1,0 % (w/w) de glucosa) a 30°C y 90 rpm durante 24 horas. Partiendo de este cultivo se inoculan a continuación 10 ml en un matraz Erlenmeyer de 1 l con 100 ml de medio de producción (para 1 l: 25 g de glucosa, 7,6 g de NH_4Cl , 1,5 g de Na_2SO_4 , 300 ml de un tampón fosfato potásico 1 mM (pH 7,0), 20 mg de $\text{ZnSO}_4 \times 7 \text{ H}_2\text{O}$, 20 mg de $\text{MnSO}_4 \times 4 \text{ H}_2\text{O}$, 20 mg de ácido nicotínico, 20 mg de piridoxina, 8 mg de tiamina y 6 mg de pantotenato). El cultivo se efectúa durante 24 h a 30 °C.

Después de 24 h se añade con dosificación la suspensión celular de ácido 12-hidroxi-dodecanoico, de modo que la concentración no asciende a más de 0,5 g/l. Además se añade glucosa o glicerina como co-substrato, de modo que la concentración de co-substrato no se reduce a menos de 0,2 g/l. Después de 0 h, 0,5 h, 1 h, y después hasta 24 h de tiempo de cultivo se extrajeron cada hora muestras (1 ml) para la medida de ácido 12-hidroxi-dodecanoico, ácido 12-oxo-dodecanoico y de diácido 1,12-dodecanoico, y los correspondientes metilésteres, así como para la verificación del número de células. El valor de pH se mantiene entre 5,0 y 6,5 tras cada medida con NaOH 6 N, o bien H_2SO_4 4 N. Durante el cultivo se verifica el crecimiento celular mediante control de "Colony Forming Units"(CFU). El descenso de ácido 12-hidroxi-dodecanoico y la producción de diácido 1,12-dodecanoico, o bien de los correspondientes metilésteres se verifica por medio de LC-MS. A tal efecto se ajustan 500 µl de caldo de cultivo a pH 1, y a continuación se extrae con el mismo volumen de dietiléter o acetato de etilo y se analiza por medio de LC-MS. El sistema de medida está constituido por un HP1100 HPLC (Agilent Technologies, Waldbronn, D) con desgasificador, automuestreador y horno de columna, acoplado a un detector Cuadrupol MSD (Agilent Technologies, Waldbronn, D). La separación cromatográfica se consigue en una fase inversa, por ejemplo columna de 125x2 mm Luna C18(2) (Phenomenex, Aschaffenburg, D) a 40°C. La elución en gradiente se efectúa con un flujo de 0,3 ml/min (A: 0.02% de ácido fórmico en agua y B: 0.02% de ácido fórmico en acetonitrilo). Alternativamente se analizan los extractos orgánicos por medio de GC-FID (Perkin Elmer, Rodgau-Jügesheim, D). La separación cromatográfica se efectúa en una fase de metilpolisiloxano (5 % de fenilo), por ejemplo Elite 5, 30 m, 0,25 mm ID, 0,25 µm FD (Perkin Elmer, Rodgau-Jügesheim, D). Antes de la medida, los ácidos libres se mezclan con un reactivo de metilación, por ejemplo hidróxido de trimetilsulfonio "TMSH" (Macherey-Nagel GmbH & Co. KG, Düren, D), y se transforman en los correspondientes metilésteres en la inyección. Mediante cálculo de la concentración medida de diácido 1,12-dodecanoico y el número de células en el momento de toma de muestras, se puede determinar la tasa de producción específica de diácido 1,12-dodecanoico a partir de ácido 12-hidroxi-dodecanoico, y por consiguiente se puede determinar la "actividad de enzima" en una célula definida anteriormente. Bajo la formulación "actividad

5 reducida en comparación con su tipo salvaje“ se entiende preferentemente una actividad reducida respecto a la actividad de tipo salvaje en al menos un 50 %, de modo especialmente preferente en al menos un 90 %, además preferentemente en al menos un 99,9 %, además de modo aún más preferente en al menos un 99,99 %, y del modo más preferente en al menos un 99,999 %. La reducción de la actividad de la célula según la invención en comparación con su tipo salvaje se determina según procedimientos descritos anteriormente para la determinación de la actividad bajo empleo de números de células/concentraciones iguales en lo posible, cultivándose las células bajo las mismas condiciones, como por ejemplo medio, gasificación, agitación.

10 La “identidad de nucleótido“ relativa a las secuencias indicadas se puede determinar con ayuda de procedimientos conocidos. Generalmente se emplean programas de ordenador especiales con algoritmos, bajo consideración de requisitos especiales. Los procedimientos preferentes para la determinación de la identidad generan en primer lugar la máxima coincidencia entre las secuencias a comparar. No obstante, los programas de ordenador para la determinación de la identidad no están limitados al paquete de programas GCG, que incluye

- GAP (Deveroy, J. et al., Nucleic Acid Research 12 (1984), página 387, Genetics Computer Group University of Wisconsin, Medicine (Wi), y
- 15 • BLASTP, BLASTN und FASTA (Altschul, S. et al., Journal of Molecular Biology 215 (1990), páginas 403-410. El programa BLAST se puede obtener en el National Center For Biotechnology Information (NCBI) y a partir de otras fuentes (BLAST Handbuch, Altschul S. et al., NCBI NLM NIH Bethesda ND 22894; Altschul S. et al., véase más arriba).

20 El conocido algoritmo de Smith-Waterman se puede emplear también para la determinación de la identidad de nucleótidos.

Son parámetros preferentes para la determinación de la “identidad de nucleótidos“, en el caso de empleo del programa BLASTN (Altschul, S. et al., Journal of Molecular Biology 215 (1990), páginas 403-410:

Umbral esperado:	10
Medida de palabra:	28
Puntuación de emparejamiento:	1
Puntuación de desemparejamiento:	-2
Costes de huecos:	Lineal

25 Los anteriores parámetros son los parámetros predeterminados en comparación con la secuencia de nucleótidos. El programa GAP es apropiado igualmente para empleo con los anteriores parámetros. Una identidad de un 80 % según el anterior algoritmo significa un 80 % de identidad en relación con la presente invención. Lo mismo es válido para identidades superiores.

30 Mediante el concepto “que se codifican por las secuencias de ácido nucleico exentas de intrón“ se manifiesta claramente que, en una comparación de secuencias con las secuencias indicadas en este caso, las secuencias de ácido nucleico a comparar se deben aclarar previamente en eventuales intrones.

Si no se indica lo contrario, todos los porcentajes indicados (%) son porcentajes en masa.

35 Los procedimientos para la reducción de actividades enzimáticas en microorganismos son conocidos por el especialista. En especial se ofrecen técnicas de biología molecular en este caso. El especialista encuentra instrucciones para la modificación y reducción de expresiones proteicas y reducción de la actividad enzimática que acompaña a la misma especialmente para *Candida tropicalis*, en especial para la interrupción de genes especiales, en los documentos WO91/006660; WO03/100013; Picataggio et al. Mol Cell Biol. 1991 Sep;11(9):4333-9; Rohrer et al. Appl Microbiol Biotechnol. 1992 Feb;36(5):650-4; Picataggio et al. Biotechnology (N Y). 1992 Aug;10(8):894-8; Ueda et al. Biochim Biophys Acta. 2003 Mar 17;1631(2):160-8; Ko et al. Appl Environ Microbiol. 2006 Jun;72(6):4207-13; Hara et al. Arch Microbiol. 2001 Nov;176(5):364-9; Kanayama et al. J Bacteriol. 1998

Feb;180(3):690-8.

Las células según la invención están caracterizadas por que la reducción de la actividad enzimática se obtiene mediante modificación de al menos un gen que comprende una de las secuencias seleccionadas a partir de los grupos de secuencias de ácido nucleico A) y B) citadas anteriormente, seleccionándose la modificación a partir del grupo que comprende, preferentemente constituido por inserción de ADN ajeno en el gen, delección al menos de partes del gen, mutaciones puntuales en la secuencia génica y exposición del gen a la influencia de la interferencia de ARN, o intercambio de partes del gen con ADN ajeno, en especial de la zona del promotor. En este contexto se debe entender por ADN ajeno cualquier secuencia de ADN que sea "ajena" al gen (y no al organismo), es decir, también secuencias de ADN endógenas de *Candida tropicalis* pueden actuar como "ADN ajeno" en este contexto. En este contexto es especialmente preferente que el gen se interrumpa mediante inserción de un gen marcador de selección, por consiguiente, el ADN ajeno es un gen marcador de selección, efectuándose la inserción mediante recombinación homóloga en el lugar génico. En este contexto puede ser ventajoso que el gen marcador de selección se amplíe mediante otras funcionalidades, que posibilitan a su vez una subsiguiente eliminación a partir del gen, esto se puede conseguir, a modo de ejemplo, mediante un sistema Cre/loxP, mediante *Flippase Recognition Targets* (FRT) o recombinaciones homólogas.

Las células preferentes según la invención están caracterizadas por que están bloqueadas al menos parcialmente, de modo preferente por completo, en su β -Oxidation, ya que esto impide el flujo de sustrato, y por consiguiente posibilita títulos superiores. En el documento EP0499622 se describen ejemplos de células de *Candida tropicalis* bloqueados parcialmente en su β -oxidación como cepas H41, H41B, H51, H45, H43, H53, H534, H534B y H435, de las que se deriva una célula de *Candida tropicalis* preferente según la invención. Otras células de *Candida tropicalis* bloqueadas en la β -Oxidation se describen, a modo de ejemplo, en el documento WO03/100013. En este contexto son preferentes células en las que la β -oxidación se ocasiona mediante una función defectuosa de al menos uno de los genes POX2, POX4 o POX5. Por consiguiente, en este contexto son preferentes células que están caracterizadas por que una célula de *Candida tropicalis* preferente según la invención se deriva de cepas seleccionadas a partir del grupo constituido por ATCC 20962 y la *Candida tropicalis* HDC 100 descrita en el documento US2004/0014198.

El empleo de las células según la invención para la producción de ácidos ω -hidroxi-carboxílicos o ω -hidroxi-carboxilatos contribuye adicionalmente a la solución de la tarea planteada por la invención.

En especial es ventajoso el empleo de las células según la invención para la producción de ácidos ω -hidroxi-carboxílicos o ω -hidroxi-carboxilatos con una longitud de cadena de ácido carboxílico de 6 a 24, preferentemente 8 a 18, y de modo especialmente preferente 10 a 16 átomos de carbono, que son lineales, saturados e insaturados, y una longitud de cadena de componente alcohólico del éster de 1 a 4, en especial de 1 o 2 átomos de carbono. En este contexto es preferente que, en el caso de los ácidos ω -hidroxi-carboxílicos se trate de ácido 12-hidroxi-dodecanoico, y en el caso del o ω -hidroxi-carboxilato se trate de 12-hidroxi-dodecanoato de metilo. Según la invención, el empleo preferente está caracterizado por que las células preferentes según la invención se emplean como se describe anteriormente.

Contribuye adicionalmente a la solución de la tarea planteada por la invención un procedimiento para la producción de la célula de *C. Tropicalis* descrita anteriormente según la invención, que comprende los siguientes pasos:

I) puesta a disposición de una célula de *C. tropicalis*, preferentemente una célula bloqueada al menos parcialmente, de modo preferente por completo, en su β -oxidación,

II) modificación de al menos un gen que comprende una de las secuencias de ácido nucleico exentas de intrón, seleccionadas a partir de los grupos de secuencias de ácido nucleico A) y B) citadas anteriormente, mediante inserción de ADN ajeno, en especial de ADN que codifica para un gen marcador de selección, en el gen, delección al menos de partes del gen, mutaciones puntuales en la secuencia génica, y exposición del gen a la influencia de la interferencia de ARN, o intercambio de partes del gen por ADN ajeno, en especial de la zona del promotor.

Contribuye adicionalmente a la solución de la tarea planteada por la invención un procedimiento para la producción de ácidos ω -hidroxi-carboxílicos o ω -hidroxi-carboxilatos, en especial de ácidos ω -hidroxi-carboxílicos o ω -hidroxi-carboxilatos con una longitud de cadena de ácido carboxílico de 6 a 24, preferentemente 8 a 18, y de modo especialmente preferente 10 a 16 átomos de carbono, que son preferentemente lineales, saturados, y no están substituidos, y una longitud de cadena de componente alcohólico del éster de 1 a 4, en especial de 1 o 2 átomos de carbono, en especial de ácido 12-hidroxi-dodecanoico o 12-hidroxi-dodecanoato de metilo, que comprende los pasos de procedimiento:

A) puesta en contacto de una célula descrita anteriormente según la invención con un medio que contiene un ácido carboxílico, o bien un carboxilato, en especial un ácido carboxílico o un carboxilato con una longitud de cadena de ácido carboxílico de 6 a 24, preferentemente 8 a 18, y de modo especialmente preferente 10 a 16 átomos de

carbono, que son preferentemente lineales, saturadas, y no están substituidas, y una longitud de cadena de componente alcohólico del éster de 1 a 4 átomos de carbono, en especial ácido dodecanoico o dodecanoato de metilo,

5 B) cultivo de la célula bajo condiciones que posibiliten a la célula formar el correspondiente ácido ω -hidroxicarboxílico o ω -hidroxicarboxilato a partir del ácido carboxílico, o bien del carboxilato, y

C) en caso dado aislamiento del ácido ω -hidroxicarboxílico o ω -hidroxicarboxilato formado.

Los procedimientos preferentes según la invención emplean las células citadas anteriormente como preferentes según la invención.

10 Por consiguiente, es muy especialmente preferente, a modo de ejemplo, un procedimiento para la producción de ácido 12-hidroxi-dodecanoico o 12-hidroxi-dodecanoato de metilo, que comprende los pasos de procedimiento:

15 a) puesta en contacto de una célula de *Candida tropicalis* de la cepa ATTC 20336, bloqueada al menos parcialmente en su β -oxidación, que presenta, en comparación con su tipo salvaje, una actividad reducida de al menos uno de los enzimas, que se codifican mediante las secuencias de ácido nucleico exentas de intrón seleccionadas a partir de los grupos de secuencias de ácido nucleico A) y B) citados anteriormente, obteniéndose la reducción de la actividad enzimática mediante modificación de un gen que comprende una de las secuencias de ácido nucleico seleccionadas a partir de los grupos de secuencias de ácido nucleico A) y B) citados anteriormente, estando constituida la modificación por inserción de un gen marcador de selección en el gen, con un medio que contiene ácido dodecanoico o dodecanoato de metilo,

20 b) cultivo de la célula bajo condiciones que posibilitan a la célula formar el correspondiente ácido ω -hidroxicarboxílico o ω -hidroxicarboxilato a partir del ácido carboxílico, o bien del carboxilato, y

c) en caso dado aislamiento del ácido ω -hidroxicarboxílico o ω -hidroxicarboxilato formado.

Las condiciones de cultivo apropiadas para *Candida tropicalis* son conocidas por el especialista. Condiciones apropiadas para el paso de procedimiento b) son aquellas que son conocidas por el especialista de procedimientos de bioconversión para la producción de ácidos dicarboxílicos con *Candida tropicalis*.

25 Tales condiciones de cultivo se describen, a modo de ejemplo, en los documentos WO00/017380 y WO00/015828.

Por el especialista son conocidos procedimientos para el aislamiento del ácido ω -hidroxicarboxílico o del ω -hidroxicarboxilato formado. Estos son procedimientos estándar para el aislamiento de ácidos carboxílicos de cadena larga a partir de disolución acuosa, como por ejemplo destilación o extracción, y se pueden extraer, a modo de ejemplo, también del documento WO2009/077461.

30 Es ventajoso emplear los ácidos ω -hidroxicarboxílicos o ω -hidroxicarboxilatos producidos mediante el procedimiento según la invención para la producción de polímeros, en especial poliésteres. Por lo demás, a partir de los ácidos ω -hidroxicarboxílicos se pueden producir también lactonas, que, por ejemplo, se pueden emplear de nuevo para la producción de poliésteres. Otro empleo ventajoso es transformar los ácidos ω -hidroxicarboxílicos o ω -hidroxicarboxilatos en ácidos ω -amino-carboxílicos o ω -amino-carboxilatos, para obtener poliamidas como polímero. Los ácidos ω -amino-carboxílicos o ω -amino-carboxilatos también se pueden hacer reaccionar primeramente para dar las correspondientes lactamas, que se pueden transformar de nuevo por vía aniónica, o también mediante catálisis ácida, para dar una poliamida. Es muy especialmente ventajoso transformar ácidos ω -hidroxicarboxílicos o correspondientes ésteres en los ácidos ω -oxo-carboxílicos o los correspondientes ésteres en un primer paso de reacción, y llevar a cabo a continuación la aminación del grupo oxo, por ejemplo en el transcurso de una aminación reductiva.

En este contexto es especialmente preferente el empleo de ácido 12-hidroxi-dodecanoico o 12-hidroxi-dodecanoato de metilo para la producción de polímeros, en especial de poliamida 12.

LISTA DE SECUENCIAS

<110> Evonik Degussa GmbH

<120> Células de Candida tropicalis y su empleo

5 <130> 200900334

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<210> 1

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tggttat 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 aga ttt ttg ccg ata	240
Ile Ile Lys Val Lys Gly Asn Gly Arg Leu Ala Arg Phe Trp Pro Ile	
65 70 75 80	
aaa aca ttc gac gac tat cca aac cat act ttt tac atg tct att att	288
Lys Thr Phe Asp Asp Tyr Pro Asn His Thr Phe Tyr Met Ser Ile Ile	
85 90 95	
ggt gct ttg aaa atc gtc ttg act gtg atc caa gaa aat att aaa gct	336
Gly Ala Leu Lys Ile Val Leu Thr Val Ile Gln Glu Asn Ile Lys Ala	
100 105 110	
gtt ttg gct act caa ttt act gat ttc tcc tta ggt act aga cat gcc	384
Val Leu Ala Thr Gln Phe Thr Asp Phe Ser Leu Gly Thr Arg His Ala	
115 120 125	
cat ttc tat cca tta tta ggt gat ggt att ttt act ttg gat ggt gaa	432
His Phe Tyr Pro Leu Leu Gly Asp Gly Ile Phe Thr Leu Asp Gly Glu	
130 135 140	
ggt ttg aaa cat agt aga gct atg ttg aga cca caa ttt gct aga gat	480
Gly Trp Lys His Ser Arg Ala Met Leu Arg Pro Gln Phe Ala Arg Asp	
145 150 155 160	

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

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Phe Ile Pro Lys Gly Ser Thr Val Ala Tyr Ile Val Tyr Lys Thr His	
420 425 430	
cgt tta gaa gaa tat tat ggt aaa gat gct gat gat ttc aga cca gaa	1344
Arg Leu Glu Glu Tyr Tyr Gly Lys Asp Ala Asp Asp Phe Arg Pro Glu	
435 440 445	
aga tgg ttt gaa cca tca act aaa aag tta ggt tgg gct tat gtt cca	1392
Arg Trp Phe Glu Pro Ser Thr Lys Lys Leu Gly Trp Ala Tyr Val Pro	
450 455 460	
ttt aat ggt ggt cca aga att tgt tta ggc caa caa ttt gct tta act	1440
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 Pro Lys Cys Ile His Leu	
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5 <213> Candida tropicalis

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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	

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Val	Leu	Ala	Thr	Gln	Phe	Thr	Asp	Phe	Ser	Leu	Gly	Thr	Arg	His	Ala
115120125															
His	Phe	Tyr	Pro	Leu	Leu	Gly	Asp	Gly	Ile	Phe	Thr	Leu	Asp	Gly	Glu
130135140															
Gly	Trp	Lys	His	Ser	Arg	Ala	Met	Leu	Arg	Pro	Gln	Phe	Ala	Arg	Asp
145150155160															
Gln	Ile	Gly	His	Val	Lys	Ala	Leu	Glu	Pro	His	Ile	Gln	Ile	Leu	Ala
165170175															
Lys	Gln	Ile	Lys	Leu	Asn	Lys	Gly	Lys	Thr	Phe	Asp	Ile	Gln	Glu	Leu
180185190															
Phe	Phe	Arg	Phe	Thr	Val	Asp	Thr	Ala	Thr	Glu	Phe	Leu	Phe	Gly	Glu
195200205															
Ser	Val	His	Ser	Leu	Tyr	Asp	Glu	Lys	Leu	Gly	Ile	Pro	Thr	Pro	Asn
210215220															
Glu	Ile	Pro	Gly	Arg	Asp	Asn	Phe	Ala	Thr	Ala	Phe	Asn	Thr	Ser	Gln
225230235240															
His	Tyr	Leu	Ala	Thr	Arg	Thr	Tyr	Ser	Gln	Thr	Phe	Tyr	Phe	Leu	Thr
245250255															
Asn	Pro	Lys	Glu	Phe	Arg	Asp	Cys	Asn	Ala	Lys	Val	His	Tyr	Leu	Ala
260265270															
Lys	Tyr	Phe	Val	Asn	Lys	Ala	Leu	Asn	Phe	Thr	Pro	Glu	Glu	Ile	Glu
275280285															
Glu	Lys	Ser	Lys	Ser	Gly	Tyr	Val	Phe	Leu	Tyr	Glu	Leu	Val	Lys	Gln
290295300															
Thr	Arg	Asp	Pro	Lys	Val	Leu	Gln	Asp	Gln	Leu	Leu	Asn	Ile	Met	Val
305310315320															
Ala	Gly	Arg	Asp	Thr	Thr	Ala	Gly	Leu	Leu	Ser	Phe	Ala	Met	Phe	Glu
325330335															
Leu	Ala	Arg	His	Pro	Glu	Ile	Trp	Ser	Lys	Leu	Arg	Glu	Glu	Ile	Glu
340345350															
Val	Asn	Phe	Gly	Val	Gly	Glu	Glu	Ser	Arg	Val	Glu	Glu	Ile	Thr	Phe

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355		360		365
Glu Ser Leu Lys Arg Cys Glu Tyr Leu Lys Ala Ile Leu Asn Glu Thr				
370		375		380
Leu Arg Met Tyr Pro Ser Val Pro Val Asn Ser Arg Thr Ala Thr Arg				
385		390		400
Asp Thr Thr Leu Pro Arg Gly Gly Gly Pro Asn Gly Thr Asp Pro Ile				
	405		410	415
Phe Ile Pro Lys Gly Ser Thr Val Ala Tyr Ile Val Tyr Lys Thr His				
	420		425	430
Arg Leu Glu Glu Tyr Tyr Gly Lys Asp Ala Asp Asp Phe Arg Pro Glu				
	435		440	445
Arg Trp Phe Glu Pro Ser Thr Lys Lys Leu Gly Trp Ala Tyr Val Pro				
	450		455	460
Phe Asn Gly Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe Ala Leu Thr				
	465		470	475
Glu Ala Ser Tyr Val Ile Thr Arg Leu Val Gln Met Phe Glu Thr Val				
	485		490	495
Ser Ser Pro Pro Asp Val Glu Tyr Pro Pro Pro Lys Cys Ile His Leu				
	500		505	510
Thr Met Ser His Asp Asp Gly Val Phe Val Lys Met				
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tggtac actgtg 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	
10 aac atc aag aac tac gtc aag gca aag aaa ttg aaa tgt gtc gat cca	144

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

aaa tcc aag tcc ggt tac gtt ttc ttg tac gaa ttg gtt aag caa acc	912
Lys Ser Lys Ser Gly Tyr Val Phe Leu Tyr Glu Leu Val Lys Gln Thr	
290 295 300	
aga gat cca aag gtc ttg caa gat caa ttg ttg aac att atg gtt gcc	960
Arg Asp Pro Lys Val Leu Gln Asp Gln Leu Leu Asn Ile Met Val Ala	
305 310 315 320	
gga aga gac acc act gcc ggt ttg ttg tcc ttt gct ttg ttt gaa ttg	1008
Gly Arg Asp Thr Thr Ala Gly Leu Leu Ser Phe Ala Leu Phe Glu Leu	
325 330 335	
gct aga cac cca gag atg tgg tcc aag ttg aga gaa gaa atc gaa gtt	1056
Ala Arg His Pro Glu Met Trp Ser Lys Leu Arg Glu Glu Ile Glu Val	
340 345 350	
aac ttt ggt gtt ggt gaa gac tcc cgc gtt gaa gaa att acc ttc gaa	1104
Asn Phe Gly Val Gly Glu Asp Ser Arg Val Glu Glu Ile Thr Phe Glu	
355 360 365	
gcc ttg aag aga tgt gaa tac ttg aag gct atc ctt aac gaa acc ttg	1152
Ala Leu Lys Arg Cys Glu Tyr Leu Lys Ala Ile Leu Asn Glu Thr Leu	
370 375 380	
cgt atg tac cca tct gtt cct gtc aac ttt aga acc gcc acc aga gac	1200
Arg Met Tyr Pro Ser Val Pro Val Asn Phe Arg Thr Ala Thr Arg Asp	
385 390 395 400	
acc act ttg cca aga ggt ggt ggt gct aac ggt acc gac cca atc tac	1248
Thr Thr Leu Pro Arg Gly Gly Gly Ala Asn Gly Thr Asp Pro Ile Tyr	
405 410 415	
att cct aaa ggc tcc act gtt gct tac gtt gtc tac aag acc cac cgt	1296
Ile Pro Lys Gly Ser Thr Val Ala Tyr Val Val Tyr Lys Thr His Arg	
420 425 430	
ttg gaa gaa tac tac ggt aag gac gct aac gac ttc aga cca gaa aga	1344
Leu Glu Glu Tyr Tyr Gly Lys Asp Ala Asn Asp Phe Arg Pro Glu Arg	
435 440 445	
tgg ttt gaa cca tct act aag aag ttg ggc tgg gct tat gtt cca ttc	1392
Trp Phe Glu Pro Ser Thr Lys Lys Leu Gly Trp Ala Tyr Val Pro Phe	
450 455 460	
aac ggt ggt cca aga gtc tgc ttg ggt caa caa ttc gcc ttg act gaa	1440
Asn Gly Gly Pro Arg Val Cys Leu Gly Gln Gln Phe Ala Leu Thr Glu	
465 470 475 480	
gct tct tat gtg atc act aga ttg gcc cag atg ttt gaa act gtc tca	1488
Ala Ser Tyr Val Ile Thr Arg Leu Ala Gln Met Phe Glu Thr Val Ser	
485 490 495	
tct gat cca ggt ctc gaa tac cct cca cca aag tgt att cac ttg acc	1536
Ser Asp Pro Gly Leu Glu Tyr Pro Pro Pro Lys Cys Ile His Leu Thr	
500 505 510	
atg agt cac aac gat ggt gtc ttt gtc aag atg taa	1572
Met Ser His Asn Asp Gly Val Phe Val Lys Met	
515 520	

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5 <213> Candida tropicalis

<400> 4

ES 2 626 442 T3

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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	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

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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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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
    
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10

ES 2 626 442 T3

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	ggg	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	tg	gtg	ttg	aac	768
Tyr	Leu	Ala	Ser	Arg	Ala	Val	Met	Gln	Leu	Tyr	Trp	Val	Leu	Asn		
			245					250						255		
ggg	aaa	aag	ttt	aag	gag	tgc	aac	gct	aaa	gtg	cac	aag	ttt	gct	gac	816
Gly	Lys	Lys	Phe	Lys	Glu	Cys	Asn	Ala	Lys	Val	His	Lys	Phe	Ala	Asp	
		260					265					270				
tac	tac	gtc	aac	aag	gct	ttg	gac	ttg	acg	cct	gaa	caa	ttg	gaa	aag	864
Tyr	Tyr	Val	Asn	Lys	Ala	Leu	Asp	Leu	Thr	Pro	Glu	Gln	Leu	Glu	Lys	
		275					280					285				
cag	gat	ggg	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	ggt	gct	ggg	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	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	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	ggg	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	ggg	ggg	ggg	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		

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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> 6

<211> 522

<212> PRT

5 <213> Candida tropicalis

<400> 6

Met Thr Val His Asp Ile Ile Ala Thr Tyr Phe 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 Cys Phe Gly Phe Lys Ala Pro Leu Glu Leu Leu Lys
 50 55 60

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

Asp Leu Asp Arg Pro Asp Ile Pro Thr Phe Thr Phe Pro Val Phe Ser
 85 90 95

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

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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
Ser His Val Lys Leu Leu Glu Pro His Val Gln Val Phe Phe Lys His	165	170	175
Val Arg Lys Ala Gln Gly Lys Thr Phe Asp Ile Gln Glu Leu Phe Phe	180	185	190
Arg Leu Thr Val Asp Ser Ala Thr Glu Phe Leu Phe Gly Glu Ser Val	195	200	205
Glu Ser Leu Arg Asp Glu Ser Ile Gly Met Ser Ile Asn Ala Leu Asp	210	215	220
Phe Asp Gly Lys Ala Gly Phe Ala Asp Ala Phe Asn Tyr Ser Gln Asn	225	230	235
Tyr Leu Ala Ser Arg Ala Val Met Gln Gln Leu Tyr Trp Val Leu Asn	245	250	255
Gly Lys Lys Phe Lys Glu Cys Asn Ala Lys Val His Lys Phe Ala Asp	260	265	270
Tyr Tyr Val Asn Lys Ala Leu Asp Leu Thr Pro Glu Gln Leu Glu Lys	275	280	285
Gln Asp Gly Tyr Val Phe Leu Tyr Glu Leu Val Lys Gln Thr Arg Asp	290	295	300
Lys Gln Val Leu Arg Asp Gln Leu Leu Asn Ile Met Val Ala Gly Arg	305	310	315
Asp Thr Thr Ala Gly Leu Leu Ser Phe Val Phe Phe Glu Leu Ala Arg	325	330	335
Asn Pro Glu Val Thr Asn Lys Leu Arg Glu Glu Ile Glu Asp Lys Phe	340	345	350
Gly Leu Gly Glu Asn Ala Ser Val Glu Asp Ile Ser Phe Glu Ser Leu	355	360	365

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

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

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

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

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

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

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

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

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

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

<210> 7
< 211> 1569
< 212> DNA
5 < 213> Candida tropicalis

<220>
< 221> CDS
< 222> (1)..(1569)

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

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

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Gln Asp Gly Tyr Val Phe Leu Tyr Glu Leu Val Lys Gln Thr Arg Asp	
290 295 300	
agg caa gtg ttg aga gac cag ttg ttg aac atc atg gtt gcc ggt aga	960
Arg Gln Val Leu Arg Asp Gln Leu Leu Asn Ile Met Val Ala Gly Arg	
305 310 315 320	
gac acc acc gcc ggt ttg ttg tcg ttt gtt ttc ttt gaa ttg gcc aga	1008
Asp Thr Thr Ala Gly Leu Leu Ser Phe Val Phe Phe Glu Leu Ala Arg	
325 330 335	
aac cca gag gtg acc aac aag ttg aga gaa gaa atc gag gac aag ttt	1056
Asn Pro Glu Val Thr Asn Lys Leu Arg Glu Glu Ile Glu Asp Lys Phe	
340 345 350	
ggt ctt ggt gag aat gct cgt gtt gaa gac att tcc ttt gag tcg ttg	1104
Gly Leu Gly Glu Asn Ala Arg Val Glu Asp Ile Ser Phe Glu Ser Leu	
355 360 365	
aag tca tgt gaa tac ttg aag gct gtt ctc aac gaa act ttg aga ttg	1152
Lys Ser Cys Glu Tyr Leu Lys Ala Val Leu Asn Glu Thr Leu Arg Leu	
370 375 380	
tac cca tcc gtg cca cag aat ttc aga gtt gcc acc aaa aac act acc	1200
Tyr Pro Ser Val Pro Gln Asn Phe Arg Val Ala Thr Lys Asn Thr Thr	
385 390 395 400	
ctt cca agg gga ggt ggt aag gac ggg tta tct cct gtt ttg gtc aga	1248
Leu Pro Arg Gly Gly Gly Lys Asp Gly Leu Ser Pro Val Leu Val Arg	
405 410 415	
aag ggt caa acc gtt atg tac ggt gtc tac gct gcc cac aga aac cca	1296
Lys Gly Gln Thr Val Met Tyr Gly Val Tyr Ala Ala His Arg Asn Pro	
420 425 430	
gct gtc tac ggt aag gac gcc ctt gag ttt aga cca gag agg tgg ttt	1344
Ala Val Tyr Gly Lys Asp Ala Leu Glu Phe Arg Pro Glu Arg Trp Phe	
435 440 445	
gag cca gag aca aag aag ctt ggc tgg gcc ttc ctt cca ttc aac ggt	1392
Glu Pro Glu Thr Lys Lys Leu Gly Trp Ala Phe Leu Pro Phe Asn Gly	
450 455 460	
ggt cca aga att tgc ttg gga cag cag ttt gcc ttg aca gaa gct tcg	1440
Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe Ala Leu Thr Glu Ala Ser	
465 470 475 480	
tat gtc act gtc aga ttg ctc caa gag ttt gga cac ttg tct atg gac	1488
Tyr Val Thr Val Arg Leu Leu Gln Glu Phe Gly His Leu Ser Met Asp	
485 490 495	
ccc aac acc gaa tat cca cct agg aaa atg tcg cat ttg acc atg tcc	1536
Pro Asn Thr Glu Tyr Pro Pro Arg Lys Met Ser His Leu Thr Met Ser	
500 505 510	
ctt ttc gac ggt gcc aac att gag atg tat tag	1569
Leu Phe Asp Gly Ala Asn Ile Glu Met Tyr	
515 520	

<210> 8

<211> 522

<212> PRT

5 <213> Candida tropicalis

<400> 8

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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

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Tyr Leu Ala Ser Arg Ala Val Met Gln Gln Leu Tyr Trp Val Leu Asn
 245 250 255
 Gly Lys Lys Phe Lys Glu Cys Asn Ala Lys Val His Lys Phe Ala Asp
 260 265 270
 Tyr Tyr Val Ser Lys Ala Leu Asp Leu Thr Pro Glu Gln Leu Glu Lys
 275 280 285
 Gln Asp Gly Tyr Val Phe Leu Tyr Glu Leu Val Lys Gln Thr Arg Asp
 290 295 300
 Arg Gln Val Leu Arg Asp Gln Leu Leu Asn Ile Met Val Ala Gly Arg
 305 310 315 320
 Asp Thr Thr Ala Gly Leu Leu Ser Phe Val Phe Phe Glu Leu Ala Arg
 325 330 335
 Asn Pro Glu Val Thr Asn Lys Leu Arg Glu Glu Ile Glu Asp Lys Phe
 340 345 350
 Gly Leu Gly Glu Asn Ala Arg Val Glu Asp Ile Ser Phe Glu Ser Leu
 355 360 365
 Lys Ser Cys Glu Tyr Leu Lys Ala Val Leu Asn Glu Thr Leu Arg Leu
 370 375 380
 Tyr Pro Ser Val Pro Gln Asn Phe Arg Val Ala Thr Lys Asn Thr Thr
 385 390 395 400
 Leu Pro Arg Gly Gly Gly Lys Asp Gly Leu Ser Pro Val Leu Val Arg
 405 410 415
 Lys Gly Gln Thr Val Met Tyr Gly Val Tyr Ala Ala His Arg Asn Pro
 420 425 430
 Ala Val Tyr Gly Lys Asp Ala Leu Glu Phe Arg Pro Glu Arg Trp Phe
 435 440 445
 Glu Pro Glu Thr Lys Lys Leu Gly Trp Ala Phe Leu Pro Phe Asn Gly
 450 455 460
 Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe Ala Leu Thr Glu Ala Ser
 465 470 475 480
 Tyr Val Thr Val Arg Leu Leu Gln Glu Phe Gly His Leu Ser Met Asp
 485 490 495
 Pro Asn Thr Glu Tyr Pro Pro Arg Lys Met Ser His Leu Thr Met Ser
 500 505 510
 Leu Phe Asp Gly Ala Asn Ile Glu Met Tyr
 515 520

<210> 9
 <211> 1623
 <212> DNA

< 213> Candida tropicalis

<220>

< 221> CDS

< 222> (1)..(1623)

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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 Leu Ile Tyr Leu
65          70          75          80

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

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ES 2 626 442 T3

165	170	175	
cag gtt tct cac gtc aag ttg ttg gag cca cac gtt cag gtg ttc ttc Gln Val Ser His Val Lys Leu Leu Gln Thr Phe Val Gln Val Phe Phe 180 185 190			576
aag cac gtt aga aag cac cgc ggt caa acg ttc gac atc caa gaa ttg Lys His Val Arg Lys His Arg Gly Gln Thr Phe Asp Ile Gln Glu Leu 195 200 205			624
ttc ttc agg ttg acc gtc gac tcc gcc acc gag ttc ttg ttt ggt gag Phe Phe Arg Leu Thr Val Asp Ser Ala Thr Glu Phe Leu Phe Gly Glu 210 215 220			672
tct gct gaa tcc ttg agg gac gaa tct att gga ttg acc cca acc acc Ser Ala Glu Ser Leu Arg Asp Glu Ser Ile Gly Leu Thr Pro Thr Thr 225 230 235 240			720
aag gat ttc gat ggc aga aga gat ttc gct gac gct ttc aac tat tcg Lys Asp Phe Asp Gly Arg Arg Asp Phe Ala Asp Ala Phe Asn Tyr Ser 245 250 255			768
cag act tac cag gcc tac aga ttt ttg ttg caa caa atg tac tgg atc Gln Thr Tyr Gln Ala Tyr Arg Phe Leu Gln Gln Met Tyr Trp Ile 260 265 270			816
ttg aat ggc tcg gaa ttc aga aag tcg att gct gtc gtg cac aag ttt Leu Asn Gly Ser Glu Phe Arg Lys Ser Ile Ala Val Val His Lys Phe 275 280 285			864
gct gac cac tat gtg caa aag gct ttg gag ttg acc gac gat gac ttg Ala Asp His Tyr Val Gln Lys Ala Leu Glu Leu Thr Asp Asp Asp Leu 290 295 300			912
cag aaa caa gac ggc tat gtg ttc ttg tac gag ttg gct aag caa acc Gln Lys Gln Asp Gly Tyr Val Phe Leu Tyr Glu Leu Ala Lys Gln Thr 305 310 315 320			960
aga gac cca aag gtc ttg aga gac cag tta ttg aac att ttg gtt gcc Arg Asp Pro Lys Val Leu Arg Asp Gln Leu Leu Asn Ile Leu Val Ala 325 330 335			1008
ggt aga gac acg acc gcc ggt ttg ttg tca ttt gtt ttc tac gag ttg Gly Arg Asp Thr Thr Ala Gly Leu Leu Ser Phe Val Phe Tyr Glu Leu 340 345 350			1056
tca aga aac cct gag gtg ttt gct aag ttg aga gag gag gtg gaa aac Ser Arg Asn Pro Glu Val Phe Ala Lys Leu Arg Glu Glu Val Glu Asn 355 360 365			1104
aga ttt gga ctc ggt gaa gaa gct cgt gtt gaa gag atc tcg ttt gag Arg Phe Gly Leu Gly Glu Glu Ala Arg Val Glu Glu Ile Ser Phe Glu 370 375 380			1152
tcc ttg aag tct tgt gag tac ttg aag gct gtc atc aat gaa acc ttg Ser Leu Lys Ser Cys Glu Tyr Leu Lys Ala Val Ile Asn Glu Thr Leu 385 390 395 400			1200
aga ttg tac cca tcg gtt cca cac aac ttt aga gtt gct acc aga aac Arg Leu Tyr Pro Ser Val Pro His Asn Phe Arg Val Ala Thr Arg Asn 405 410 415			1248
act acc ctc cca aga ggt ggt ggt gaa gat gga tac tcg cca att gtc			1296

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Thr	Thr	Leu	Pro	Arg	Gly	Gly	Gly	Glu	Asp	Gly	Tyr	Ser	Pro	Ile	Val		
			420					425					430				
gtc	aag	aag	ggt	caa	ggt	gtc	atg	tac	act	gtt	att	gct	acc	cac	aga		1344
Val	Lys	Lys	Gly	Gln	Val	Val	Met	Tyr	Thr	Val	Ile	Ala	Thr	His	Arg		
		435					440					445					
gac	cca	agt	atc	tac	ggt	gcc	gac	gct	gac	gtc	ttc	aga	cca	gaa	aga		1392
Asp	Pro	Ser	Ile	Tyr	Gly	Ala	Asp	Ala	Asp	Val	Phe	Arg	Pro	Glu	Arg		
		450				455					460						
tgg	ttt	gaa	cca	gaa	act	aga	aag	ttg	ggc	tgg	gca	tac	gtt	cca	ttc		1440
Trp	Phe	Glu	Pro	Glu	Thr	Arg	Lys	Leu	Gly	Trp	Ala	Tyr	Val	Pro	Phe		
465					470					475					480		
aat	ggt	ggt	cca	aga	atc	tgt	ttg	ggt	caa	cag	ttt	gcc	ttg	acc	gaa		1488
Asn	Gly	Gly	Pro	Arg	Ile	Cys	Leu	Gly	Gln	Gln	Phe	Ala	Leu	Thr	Glu		
				485					490					495			
gct	tca	tac	gtc	act	gtc	aga	ttg	ctc	cag	gag	ttt	gca	cac	ttg	tct		1536
Ala	Ser	Tyr	Val	Thr	Val	Arg	Leu	Leu	Gln	Glu	Phe	Ala	His	Leu	Ser		
			500					505					510				
atg	gac	cca	gac	acc	gaa	tat	cca	cca	aaa	ttg	cag	aac	acc	ttg	acc		1584
Met	Asp	Pro	Asp	Thr	Glu	Tyr	Pro	Pro	Lys	Leu	Gln	Asn	Thr	Leu	Thr		
		515					520					525					
ttg	tgc	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> 10

<211> 540

<212> PRT

5 <213> Candida tropicalis

<400> 10

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

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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
 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
 225 230 235 240

Lys Asp Phe Asp Gly Arg Arg Asp Phe Ala Asp Ala Phe Asn Tyr Ser
 245 250 255

Gln Thr Tyr Gln Ala Tyr Arg Phe Leu Leu Gln Gln Met Tyr Trp Ile
 260 265 270

Leu Asn Gly Ser Glu Phe Arg Lys Ser Ile Ala Val Val His Lys Phe
 275 280 285

Ala Asp His Tyr Val Gln Lys Ala Leu Glu Leu Thr Asp Asp Asp Leu
 290 295 300

Gln Lys Gln Asp Gly Tyr Val Phe Leu Tyr Glu Leu Ala Lys Gln Thr
 305 310 315 320

Arg Asp Pro Lys Val Leu Arg Asp Gln Leu Leu Asn Ile Leu Val Ala
 325 330 335

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 11

< 211> 1623

< 212> DNA

5 < 213> Candida tropicalis

<220>

< 221> CDS

< 222> (1)..(1623)

<400> 11

atg tcg tct tct cca tcg ttt gct cag gag gtt ctc gct acc act agt
Met Ser Ser Ser Pro Ser Phe Ala Gln Glu Val Leu Ala Thr Thr Ser
1 5 10 15

48

10

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cct tac atc gag tac ttt ctt gac aac tac acc aga tgg tac tac ttc Pro Tyr Ile Glu Tyr Phe Leu Asp Asn Tyr Thr Arg Trp Tyr Tyr Phe 20 25 30	96
atc cct ttg gtg ctt ctt tcg ttg aac ttc atc agc ttg ctc cac aca Ile Pro Leu Val Leu Leu Ser Leu Asn Phe Ile Ser Leu Leu His Thr 35 40 45	144
aag tac ttg gaa cgc agg ttc cac gcc aag ccg ctc ggt aac gtc gtg Lys Tyr Leu Glu Arg Arg Phe His Ala Lys Pro Leu Gly Asn Val Val 50 55 60	192
ttg gat cct acg ttt ggt atc gct act ccg ttg atc ttg atc tac tta Leu Asp Pro Thr Phe Gly Ile Ala Thr Pro Leu Ile Leu Ile Tyr Leu 65 70 75 80	240
aag tcg aaa ggt aca gtc atg aag ttt gcc tgg agc ttc tgg aac aac Lys Ser Lys Gly Thr Val Met Lys Phe Ala Trp Ser Phe Trp Asn Asn 85 90 95	288
aag tac att gtc aaa gac cca aag tac aag acc act ggc ctt aga att Lys Tyr Ile Val Lys Asp Pro Lys Tyr Lys Thr Thr Gly Leu Arg Ile 100 105 110	336
gtc ggc ctc cca ttg att gaa acc ata gac cca gag aac atc aaa gct Val Gly Leu Pro Leu Ile Glu Thr Ile Asp Pro Glu Asn Ile Lys Ala 115 120 125	384
gtg ttg gct act cag ttc aac gat ttc tcc ttg gga act aga cac gat Val Leu Ala Thr Gln Phe Asn Asp Phe Ser Leu Gly Thr Arg His Asp 130 135 140	432
ttc ttg tac tcc ttg ttg ggc gat ggt att ttt acc ttg gac 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 agt aga act atg ttg aga cca cag ttt gct aga gaa Gly Trp Lys His Ser Arg Thr Met Leu Arg Pro Gln Phe Ala Arg Glu 165 170 175	528
cag gtt tcc cac gtc aag ttg ttg gaa cca cac gtt cag gtg ttc ttc Gln Val Ser His Val Lys Leu Leu Glu Pro His Val Gln Val Phe Phe 180 185 190	576
aag cac gtt aga aaa cac cgc ggt cag act ttt gac atc caa gaa ttg Lys His Val Arg Lys His Arg Gly Gln Thr Phe Asp Ile Gln Glu Leu 195 200 205	624
ttc ttc aga ttg acc gtc gac tcc gcc acc gag ttc ttg ttt ggt gag Phe Phe Arg Leu Thr Val Asp Ser Ala Thr Glu Phe Leu Phe Gly Glu 210 215 220	672
tct gct gaa tcc ttg aga gac gac tct gtt ggt ttg acc cca acc acc Ser Ala Glu Ser Leu Arg Asp Asp Ser Val Gly Leu Thr Pro Thr Thr 225 230 235 240	720
aag gat ttc gaa ggc aga gga gat ttc gct gac gct ttc aac tac tcg Lys Asp Phe Glu Gly Arg Gly Asp Phe Ala Asp Ala Phe Asn Tyr Ser 245 250 255	768
cag act tac cag gcc tac aga ttt ttg ttg caa caa atg tac tgg att Gln Thr Tyr Gln Ala Tyr Arg Phe Leu Leu Gln Gln Met Tyr Trp Ile	816

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260	265	270	
ttg aat ggc gcg gaa ttc aga aag tcg att gcc atc gtg cac aag ttt Leu Asn Gly Ala Glu Phe Arg Lys Ser Ile Ala Ile Val His Lys Phe 275 280 285			864
gct gac cac tat gtg caa aag gct ttg gag ttg acc gac gat gac ttg Ala Asp His Tyr Val Gln Lys Ala Leu Glu Leu Thr Asp Asp Asp Leu 290 295 300			912
cag aaa caa gac ggc tat gtg ttc ttg tac gag ttg gct aag caa act Gln Lys Gln Asp Gly Tyr Val Phe Leu Tyr Glu Leu Ala Lys Gln Thr 305 310 315 320			960
aga gac cca aag gtc ttg aga gac cag ttg ttg aac att ttg gtt gcc Arg Asp Pro Lys Val Leu Arg Asp Gln Leu Leu Asn Ile Leu Val Ala 325 330 335			1008
ggg aga gac acg acc gcc ggt ttg ttg tcg ttt gtg ttc tac gag ttg Gly Arg Asp Thr Ala Gly Leu Ser Phe Val Phe Tyr Glu Leu 340 345 350			1056
tcg aga aac cct gaa gtg ttt gcc aag ttg aga gag gag gtg gaa aac Ser Arg Asn Pro Glu Val Phe Ala Lys Leu Arg Glu Glu Val Glu Asn 355 360 365			1104
aga ttt gga ctc ggc gaa gag gct cgt gtt gaa gag atc tct ttt gag Arg Phe Gly Leu Gly Glu Ala Arg Val Glu Glu Ile Ser Phe Glu 370 375 380			1152
tcc ttg aag tcc tgt gag tac ttg aag gct gtc atc aat gaa gcc ttg Ser Leu Lys Ser Cys Glu Tyr Leu Lys Ala Val Ile Asn Glu Ala Leu 385 390 395 400			1200
aga ttg tac cca tct gtt cca cac aac ttc aga gtt gcc acc aga aac Arg Leu Tyr Pro Ser Val Pro His Asn Phe Arg Val Ala Thr Arg Asn 405 410 415			1248
act acc ctt cca aga ggc ggt ggt aaa gac gga tgc tcg cca att gtt Thr Thr Leu Pro Arg Gly Gly Gly Lys Asp Gly Cys Ser Pro Ile Val 420 425 430			1296
gtc aag aag ggt caa gtt gtc atg tac act gtc att ggt acc cac aga Val Lys Lys Gly Gln Val Val Met Tyr Thr Val Ile Gly Thr His Arg 435 440 445			1344
gac cca agt atc tac ggt gcc gac gcc gac gtc ttc aga cca gaa aga Asp Pro Ser Ile Tyr Gly Ala Asp Ala Asp Val Phe Arg Pro Glu Arg 450 455 460			1392
tgg ttc gag cca gaa act aga aag ttg ggc tgg gca tat gtt cca ttc Trp Phe Glu Pro Glu Thr Arg Lys Leu Gly Trp Ala Tyr Val Pro Phe 465 470 475 480			1440
aat ggt ggt cca aga atc tgt ttg ggt cag cag ttt gcc ttg act gaa Asn Gly Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe Ala Leu Thr Glu 485 490 495			1488
gct tca tac gtc act gtc aga ttg ctc caa gag ttt gga aac ttg tcc Ala Ser Tyr Val Thr Val Arg Leu Leu Gln Glu Phe Gly Asn Leu Ser 500 505 510			1536
ctg gat cca aac gct gag tac cca cca aaa ttg cag aac acc ttg acc Leu Asp Pro Asn Ala Glu Tyr Pro Pro Lys Leu Gln Asn Thr Leu Thr 515 520 525			1584
ttg tca ctc ttt gat ggt gct gac gtt aga atg ttc taa Leu Ser Leu Phe Asp Gly Ala Asp Val Arg Met Phe 530 535 540			1623

<210> 12
<211> 540
<212> PRT

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< 213> Candida tropicalis

<400> 12

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

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Lys His Val Arg Lys His Arg Gly Gln Thr Phe Asp Ile Gln Glu Leu
 195 200 205
 Phe Phe Arg Leu Thr Val Asp Ser Ala Thr Glu Phe Leu Phe Gly Glu
 210 215 220
 Ser Ala Glu Ser Leu Arg Asp Asp Ser Val Gly Leu Thr Pro Thr Thr
 225 230 235 240
 Lys Asp Phe Glu Gly Arg Gly Asp Phe Ala Asp Ala Phe Asn Tyr Ser
 245 250 255
 Gln Thr Tyr Gln Ala Tyr Arg Phe Leu Leu Gln Gln Met Tyr Trp Ile
 260 265 270
 Leu Asn Gly Ala Glu Phe Arg Lys Ser Ile Ala Ile Val His Lys Phe
 275 280 285
 Ala Asp His Tyr Val Gln Lys Ala Leu Glu Leu Thr Asp Asp Asp Leu
 290 295 300
 Gln Lys Gln Asp Gly Tyr Val Phe Leu Tyr Glu Leu Ala Lys Gln Thr
 305 310 315 320
 Arg Asp Pro Lys Val Leu Arg Asp Gln Leu Leu Asn Ile Leu Val Ala
 325 330 335
 Gly Arg Asp Thr Thr Ala Gly Leu Leu Ser Phe Val Phe Tyr Glu Leu
 340 345 350
 Ser Arg Asn Pro Glu Val Phe Ala Lys Leu Arg Glu Glu Val Glu Asn
 355 360 365
 Arg Phe Gly Leu Gly Glu Glu Ala Arg Val Glu Glu Ile Ser Phe Glu
 370 375 380
 Ser Leu Lys Ser Cys Glu Tyr Leu Lys Ala Val Ile Asn Glu Ala Leu
 385 390 395 400
 Arg Leu Tyr Pro Ser Val Pro His Asn Phe Arg Val Ala Thr Arg Asn
 405 410 415
 Thr Thr Leu Pro Arg Gly Gly Gly Lys Asp Gly Cys Ser Pro Ile Val
 420 425 430
 Val Lys Lys Gly Gln Val Val Met Tyr Thr Val Ile Gly Thr His Arg
 435 440 445

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

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

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

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

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

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

<210> 13

<211> 1554

<212> DNA

5 <213> Candida tropicalis

<220>

<221> CDS

<222> (1)..(1554)

<400> 13

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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	

10

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

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355	360	365	
ttg aaa gcg ttc ctt aat gaa acc ttg cgt att tac cca agt gtc cca			1152
Leu Lys Ala Phe Leu Asn Glu Thr Leu Arg Ile Tyr Pro Ser Val Pro			
370	375	380	
aga aac ttc aga atc gcc acc aag aac acg aca ttg cca agg ggc ggt			1200
Arg Asn Phe Arg Ile Ala Thr Lys Asn Thr Thr Leu Pro Arg Gly Gly			
385	390	395	400
ggt tca gac ggt acc tcg cca atc ttg atc caa aag gga gaa gct gtg			1248
Gly Ser Asp Gly Thr Ser Pro Ile Leu Ile Gln Lys Gly Glu Ala Val			
	405	410	415
tcg tat ggt atc aac tct act cat ttg gac cct gtc tat tac ggc cct			1296
Ser Tyr Gly Ile Asn Ser Thr His Leu Asp Pro Val Tyr Tyr Gly Pro			
	420	425	430
gat gct gct gag ttc aga cca gag aga tgg ttt gag cca tca acc aaa			1344
Asp Ala Ala Glu Phe Arg Pro Glu Arg Trp Phe Glu Pro Ser Thr Lys			
	435	440	445
aag ctc ggc tgg gct tac ttg cca ttc aac ggt ggt cca aga atc tgt			1392
Lys Leu Gly Trp Ala Tyr Leu Pro Phe Asn Gly Gly Pro Arg Ile Cys			
	450	455	460
ttg ggt cag cag ttt gcc ttg acg gaa gct ggc tat gtg ttg gtt aga			1440
Leu Gly Gln Gln Phe Ala Leu Thr Glu Ala Gly Tyr Val Leu Val Arg			
	465	470	475
ttg gtg caa gag ttc tcc cac gtt agg ctg gac cca gac gag gtg tac			1488
Leu Val Gln Glu Phe Ser His Val Arg Leu Asp Pro Asp Glu Val Tyr			
	485	490	495
ccg cca aag agg ttg acc aac ttg acc atg tgt ttg cag gat ggt gct			1536
Pro Pro Lys Arg Leu Thr Asn Leu Thr Met Cys Leu Gln Asp Gly Ala			
	500	505	510
att gtc aag ttt gac tag			1554
Ile Val Lys Phe Asp			
	515		

<210> 14

<211> 517

<212> PRT

5 <213> Candida tropicalis

<400> 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
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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

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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
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5 <213> Candida tropicalis

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<222> (1)..(1554)

<400> 15

ES 2 626 442 T3

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tac atc atc aaa caa ctc att gcc tac agc aag act cgc gtc ttg atg Tyr Ile Ile Lys Gln Leu Ile Ala Tyr Ser Lys Thr Arg Val Leu Met 20 25 30	96
aaa cag ttg ggt gct gct cca atc aca aac cag ttg tac gac aac gtt Lys Gln Leu Gly Ala Ala Pro Ile Thr Asn Gln Leu Tyr Asp Asn Val 35 40 45	144
ttc ggt atc gtc aac gga tgg aag gct ctc cag ttc aag aaa gag ggc Phe Gly Ile Val Asn Gly Trp Lys Ala Leu Gln Phe Lys Lys Glu Gly 50 55 60	192
aga gct caa gag tac aac gat cac aag ttt gac agc tcc aag aac cca Arg Ala Gln Glu Tyr Asn Asp His Lys Phe Asp Ser Ser Lys Asn Pro 65 70 75 80	240
agc gtc ggc acc tat gtc agt att ctt ttt ggc acc aag att gtc gtg Ser Val Gly Thr Tyr Val Ser Ile Leu Phe Gly Thr Lys Ile Val Val 85 90 95	288
acc aag gat cca gag aat atc aaa gct att ttg gca acc cag ttt ggc Thr Lys Asp Pro Glu Asn Ile Lys Ala Ile Leu Ala Thr Gln Phe Gly 100 105 110	336
gat ttt tct ttg ggc aag aga cac gct ctt ttt aaa cct ttg tta ggt Asp Phe Ser Leu Gly Lys Arg His Ala Leu Phe Lys Pro Leu Leu Gly 115 120 125	384
gat ggg atc ttc acc ttg gac ggc gaa ggc tgg aag cat agc aga tcc Asp Gly Ile Phe Thr Leu Asp Gly Glu Gly Trp Lys His Ser Arg Ser 130 135 140	432
atg tta aga cca cag ttt gcc aga gaa caa gtt gct cat gtg acg tcg Met Leu Arg Pro Gln Phe Ala Arg Glu Gln Val Ala His Val Thr Ser 145 150 155 160	480
ttg gaa cca cac ttc cag ttg ttg aag aag cat atc ctt aaa cac aag Leu Glu Pro His Phe Gln Leu Leu Lys Lys His Ile Leu Lys His Lys 165 170 175	528
ggt gag tac ttt gat atc cag gaa ttg ttc ttt aga ttt act gtc gac Gly Glu Tyr Phe Asp Ile Gln Glu Leu Phe Phe Arg Phe Thr Val Asp 180 185 190	576
tcg gcc acg gag ttc tta ttt ggt gag tcc gtg cac tcc tta aag gac Ser Ala Thr Glu Phe Leu Phe Gly Glu Ser Val His Ser Leu Lys Asp 195 200 205	624
gaa act atc ggt atc aac caa gac gat ata gat ttt gct ggt aga aag Glu Thr Ile Gly Ile Asn Gln Asp Asp Ile Asp Phe Ala Gly Arg Lys 210 215 220	672
gac ttt gct gag tcg ttc aac aaa gcc cag gag tat ttg tct att aga Asp Phe Ala Glu Ser Phe Asn Lys Ala Gln Glu Tyr Leu Ser Ile Arg 225 230 235 240	720

ES 2 626 442 T3

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gac tgt acc aag ctg gtg cac aag ttt acc aac tac tat gtt cag aaa Asp Cys Thr Lys Leu Val His Lys Phe Thr Asn Tyr Tyr Val Gln Lys 260 265 270	816
gct ttg gat gct acc cca gag gaa ctt gaa aag caa ggc ggg tat gtg Ala Leu Asp Ala Thr Pro Glu Glu Leu Glu Lys Gln Gly Gly Tyr Val 275 280 285	864
ttc ttg tat gag ctt gtc aag cag acg aga gac ccc aag gtg ttg cgt Phe Leu Tyr Glu Leu Val Lys Gln Thr Arg Asp Pro Lys Val Leu Arg 290 295 300	912
gac cag tct ttg aac atc ttg ttg gca gga aga gac acc act gct ggg Asp Gln Ser Leu Asn Ile Leu Leu Ala Gly Arg Asp Thr Thr Ala Gly 305 310 315 320	960
ttg ttg tcc ttt gct gtg ttt gag ttg gcc aga aac cca cac atc tgg Leu Leu Ser Phe Ala Val Phe Glu Leu Ala Arg Asn Pro His Ile Trp 325 330 335	1008
gcc aag ttg aga gag gaa att gaa cag cag ttt ggt ctt gga gaa gac Ala Lys Leu Arg Glu Glu Ile Glu Gln Gln Phe Gly Leu Gly Glu Asp 340 345 350	1056
tct cgt gtt gaa gag att acc ttt gag agc ttg aag aga tgt gag tac Ser Arg Val Glu Glu Ile Thr Phe Glu Ser Leu Lys Arg Cys Glu Tyr 355 360 365	1104
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tcg tat ggt atc aac tct acc cac tta gat cct gtc tat tat ggc cct Ser Tyr Gly Ile Asn Ser Thr His Leu Asp Pro Val Tyr Tyr Gly Pro 420 425 430	1296
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aag ctc ggc tgg gct tac ttg cca ttc aac ggt ggg cca cga atc tgt Lys Leu Gly Trp Ala Tyr Leu Pro Phe Asn Gly Gly Pro Arg Ile Cys 450 455 460	1392
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cca cca aag agg ttg acc aac ttg acc atg tgt ttg cag gat ggt gct Pro Pro Lys Arg Leu Thr Asn Leu Thr Met Cys Leu Gln Asp Gly Ala 500 505 510	1536
att gtc aag ttt gac tag Ile Val Lys Phe Asp 515	1554

ES 2 626 442 T3

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 < 211> 517
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 Lys Gln Leu Gly Ala Ala Pro Ile Thr Asn Gln Leu Tyr Asp Asn Val
 35 40 45
 Phe Gly Ile Val Asn Gly Trp Lys Ala Leu Gln Phe Lys Lys Glu Gly
 50 55 60
 Arg Ala Gln Glu Tyr Asn Asp His Lys Phe Asp Ser Ser Lys Asn Pro
 65 70 75 80
 Ser Val Gly Thr Tyr Val Ser Ile Leu Phe Gly Thr Lys Ile Val Val
 85 90 95
 Thr Lys Asp Pro Glu Asn Ile Lys Ala Ile Leu Ala Thr Gln Phe Gly
 100 105 110
 Asp Phe Ser Leu Gly Lys Arg His Ala Leu Phe Lys Pro Leu Leu Gly
 115 120 125
 Asp Gly Ile Phe Thr Leu Asp Gly Glu Gly Trp Lys His Ser Arg Ser
 130 135 140
 Met Leu Arg Pro Gln Phe Ala Arg Glu Gln Val Ala His Val Thr Ser
 145 150 155 160
 Leu Glu Pro His Phe Gln Leu Leu Lys Lys His Ile Leu Lys His Lys
 165 170 175
 Gly Glu Tyr Phe Asp Ile Gln Glu Leu Phe Phe Arg Phe Thr Val Asp

ES 2 626 442 T3

[illegible]

ES 2 626 442 T3

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
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Ile Val Lys Phe Asp
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<210> 17

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1			5						10					15		

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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					

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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	
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ES 2 626 442 T3

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

ES 2 626 442 T3

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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                               400

gat cct atc ttg atc agg aag gat gag gtg gtg cag tac tcc atc tcg      1248
Asp Pro Ile Leu Ile Arg Lys Asp Glu Val Val Gln Tyr Ser Ile Ser
405                               410                               415

gca act cag aca aat cct gct tat tat ggc gcc gat gct gct gat ttt      1296
Ala Thr Gln Thr Asn Pro Ala Tyr Tyr Gly Ala Asp Ala Ala Asp Phe
420                               425                               430

aga ccg gaa aga tgg ttt gaa cca tca act aga aac ttg gga tgg gct      1344
Arg Pro Glu Arg Trp Phe Glu Pro Ser Thr Arg Asn Leu Gly Trp Ala
435                               440                               445

ttc ttg cca ttc aac ggt ggt cca aga atc tgt ttg gga caa cag ttt      1392
Phe Leu Pro Phe Asn Gly Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe
450                               455                               460

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

cca aac ttg tca caa gac ccc gaa acc aag tac cca cca cct aga ttg      1488
Pro Asn Leu Ser Gln Asp Pro Glu Thr Lys Tyr Pro Pro Pro Arg Leu
485                               490                               495

gca cac ttg acg atg tgc ttg ttt gac ggt gca cac gtc aag atg tca      1536
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500                               505                               510

tag                                                                    1539

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20                               25                               30

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

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

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ES 2 626 442 T3

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

ES 2 626 442 T3

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

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> 19

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< 212> DNA

5 < 213> Candida tropicalis

<220>

< 221> CDS

< 222> (1)..(1539)

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1 5 10 15

48

10

ES 2 626 442 T3

gtc att atc aag cag atc gtg gct cat gcc agg acc aat tat ttg atg Val Ile Ile Lys Gln Ile Val Ala His Ala Arg Thr Asn Tyr Leu Met 20 25 30	96
aag aag ttg ggc gct aag cca ttc aca cat gtc caa cta gac ggg tgg Lys Lys Leu Gly Ala Lys Pro Phe Thr His Val Gln Leu Asp Gly Trp 35 40 45	144
ttt ggc ttc aaa ttt ggc cgt gaa ttc ctc aaa gct aaa agt gct ggg Phe Gly Phe Lys Phe Gly Arg Glu Phe Leu Lys Ala Lys Ser Ala Gly 50 55 60	192
agg cag gtt gat tta atc atc tcc cgt ttc cac gat aat gag gac act Arg Gln Val Asp Leu Ile Ile Ser Arg Phe His Asp Asn Glu Asp Thr 65 70 75 80	240
ttc tcc agc tat gct ttt ggc aac cat gtg gtg ttc acc agg gac ccc Phe Ser Ser Tyr Ala Phe Gly Asn His Val Val Phe Thr Arg Asp Pro 85 90 95	288
gag aat atc aag gcg ctt ttg gca acc cag ttt ggt gat ttt tca ttg Glu Asn Ile Lys Ala Leu Leu Ala Thr Gln Phe Gly Asp Phe Ser Leu 100 105 110	336
gga agc agg gtc aaa ttc ttc aaa cca ttg ttg ggg tac ggt atc ttc Gly Ser Arg Val Lys Phe Phe Lys Pro Leu Leu Gly Tyr Gly Ile Phe 115 120 125	384
acc ttg gac ggc gaa ggc tgg aag cac agc aga gcc atg ttg aga cca Thr Leu Asp Gly Glu Gly Trp Lys His Ser Arg Ala Met Leu Arg Pro 130 135 140	432
cag ttt gcc aga gag caa gtt gct cat gtg acg tcg ttg gaa cca cat Gln Phe Ala Arg Glu Gln Val Ala His Val Thr Ser Leu Glu Pro His 145 150 155 160	480
ttc cag ttg ttg aag aag cat att ctt aag cac aag ggt gaa tac ttt Phe Gln Leu Leu Lys Lys His Ile Leu Lys His Lys Gly Glu Tyr Phe 165 170 175	528
gat atc cag gaa ttg ttc ttt aga ttt acc gtt gat tca gcg acg gag Asp Ile Gln Glu Leu Phe Phe Arg Phe Thr Val Asp Ser Ala Thr Glu 180 185 190	576
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tac gat acg aag gac atg gct gaa gaa aga cgc aaa ttt gcc gac gcg Tyr Asp Thr Lys Asp Met Ala Glu Glu Arg Arg Lys Phe Ala Asp Ala 210 215 220	672
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ttg tac tgg ttg gtc aac aac aaa gag ttc aag gag tgc aac gac att Leu Tyr Trp Leu Val Asn Asn Lys Glu Phe Lys Glu Cys Asn Asp Ile 245 250 255	768
gtc cac aag ttc acc aac tac tat gtt cag aaa gcc ttg gat gct acc Val His Lys Phe Thr Asn Tyr Tyr Val Gln Lys Ala Leu Asp Ala Thr	816

ES 2 626 442 T3

260	265	270	
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gcc aag cag acg aaa gac ccc aat gtg ttg cgt gac cag tct ttg aac Ala Lys Gln Thr Lys Asp Pro Asn Val Leu Arg Asp Gln Ser Leu Asn 290 295 300			912
atc ttg ttg gct gga agg gac acc act gct ggg ttg ttg tcc ttt gct Ile Leu Leu Ala Gly Arg Asp Thr Thr Ala Gly Leu Leu Ser Phe Ala 305 310 315 320			960
gtg ttt gag ttg gcc agg aac cca cac atc tgg gcc aag ttg aga gag Val Phe Glu Leu Arg Asn Pro His Ile Trp Ala Lys Leu Arg Glu 325 330 335			1008
gaa att gaa tca cac ttt ggg ctg ggt gag gac tct cgt gtt gaa gag Glu Ile Glu Ser His Phe Gly Leu Glu Asp Ser Arg Val Glu Glu 340 345 350			1056
att acc ttt gag agc ttg aag aga tgt gag tac ttg aaa gcc gtg ttg Ile Thr Phe Glu Ser Leu Lys Arg Cys Glu Tyr Leu Lys Ala Val Leu 355 360 365			1104
aac gaa acg ttg aga tta cac cca agt gtc cca aga aac gca aga ttt Asn Glu Thr Leu Arg Leu His Pro Ser Val Pro Arg Asn Ala Arg Phe 370 375 380			1152
gcg att aaa gac acg act tta cca aga ggc ggt gcc ccc aac gcc aag Ala Ile Lys Asp Thr Thr Leu Pro Arg Gly Gly Gly Pro Asn Gly Lys 385 390 395 400			1200
gat cct atc ttg atc aga aag aat gag gtg gtg caa tac tcc atc tcg Asp Pro Ile Leu Ile Arg Lys Asn Glu Val Val Gln Tyr Ser Ile Ser 405 410 415			1248
gca act cag aca aat cct gct tat tat ggc gcc gat gct gct gat ttt Ala Thr Gln Thr Asn Pro Ala Tyr Tyr Gly Ala Asp Ala Ala Asp Phe 420 425 430			1296
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tac ttg cca ttc aac ggt ggt cca aga atc tgc ttg gga caa cag ttt Tyr Leu Pro Phe Asn Gly Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe 450 455 460			1392
gct ttg acc gaa gcc ggt tac gtt ttg gtt aga ctt gtt cag gaa ttc Ala Leu Thr Glu Ala Gly Tyr Val Leu Val Arg Leu Val Gln Glu Phe 465 470 475 480			1440
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gca cac ttg acg atg tgc ttg ttt gac ggg gca tac gtc aag atg caa Ala His Leu Thr Met Cys Leu Phe Asp Gly Ala Tyr Val Lys Met Gln 500 505 510			1536
tag			1539

<210> 20

<211> 512

<212> PRT

5 <213> Candida tropicalis

<400> 20

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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	

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Phe Asn Lys Ser Gln Val Tyr Leu Ser Thr Arg Val Ala Leu Gln Thr
 225 230 235 240
 Leu Tyr Trp Leu Val Asn Asn Lys Glu Phe Lys Glu Cys Asn Asp Ile
 245 250 255
 Val His Lys Phe Thr Asn Tyr Tyr Val Gln Lys Ala Leu Asp Ala Thr
 260 265 270
 Pro Glu Glu Leu Glu Lys Gln Gly Gly Tyr Val Phe Leu Tyr Glu Leu
 275 280 285
 Ala Lys Gln Thr Lys Asp Pro Asn Val Leu Arg Asp Gln Ser Leu Asn
 290 295 300
 Ile Leu Leu Ala Gly Arg Asp Thr Thr Ala Gly Leu Leu Ser Phe Ala
 305 310 315 320
 Val Phe Glu Leu Ala Arg Asn Pro His Ile Trp Ala Lys Leu Arg Glu
 325 330 335
 Glu Ile Glu Ser His Phe Gly Leu Gly Glu Asp Ser Arg Val Glu Glu
 340 345 350
 Ile Thr Phe Glu Ser Leu Lys Arg Cys Glu Tyr Leu Lys Ala Val Leu
 355 360 365
 Asn Glu Thr Leu Arg Leu His Pro Ser Val Pro Arg Asn Ala Arg Phe
 370 375 380
 Ala Ile Lys Asp Thr Thr Leu Pro Arg Gly Gly Gly Pro Asn Gly Lys
 385 390 395 400
 Asp Pro Ile Leu Ile Arg Lys Asn Glu Val Val Gln Tyr Ser Ile Ser
 405 410 415
 Ala Thr Gln Thr Asn Pro Ala Tyr Tyr Gly Ala Asp Ala Ala Asp Phe
 420 425 430
 Arg Pro Glu Arg Trp Phe Glu Pro Ser Thr Arg Asn Leu Gly Trp Ala
 435 440 445
 Tyr Leu Pro Phe Asn Gly Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe
 450 455 460
 Ala Leu Thr Glu Ala Gly Tyr Val Leu Val Arg Leu Val Gln Glu Phe
 465 470 475 480
 Pro Ser Leu Ser Gln Asp Pro Glu Thr Glu Tyr Pro Pro Pro Arg Leu
 485 490 495
 Ala His Leu Thr Met Cys Leu Phe Asp Gly Ala Tyr Val Lys Met Gln
 500 505 510

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 < 211> 390
 < 212> DNA
 < 213> Candida tropicalis

5 <220>
 < 221> CDS
 < 222> (1)..(390)

<400> 21
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 Met Thr Asp Thr Asp Thr Thr Thr Thr Ile Tyr Thr His Glu Glu Val
 1 5 10 15
 gcc cag cac acc acc cac gac gac ttg tgg gtt att ctc aat ggt aag 96
 Ala Gln His Thr Thr His Asp Asp Leu Trp Val Ile Leu Asn Gly Lys
 20 25 30
 gtc tac aac atc tcc aac tat ata gac gag cac cca ggt ggt gaa gaa 144
 Val Tyr Asn Ile Ser Asn Tyr Ile Asp Glu His Pro Gly Gly Glu Glu
 35 40 45
 gtc att ctt gat tgc gcc ggc aca gac gcc act gaa gcc ttt gac gac 192
 Val Ile Leu Asp Cys Ala Gly Thr Asp Ala Thr Glu Ala Phe Asp Asp
 50 55 60
 att ggc cac tcc gac gag gcc cac gag atc ttg gaa aag ttg tac att 240
 Ile Gly His Ser Asp Glu Ala His Glu Ile Leu Glu Lys Leu Tyr Ile
 65 70 75 80
 ggt aac ttg aag ggc gct aag att gtt gag gcc aag cac gcg cag tcg 288
 Gly Asn Leu Lys Gly Ala Lys Ile Val Glu Ala Lys His Ala Gln Ser
 85 90 95
 ttc agc acg gaa gaa gac tcg ggt atc aac ttc cca ttg att gct gtt 336
 Phe Ser Thr Glu Glu Asp Ser Gly Ile Asn Phe Pro Leu Ile Ala Val
 100 105 110
 ggt gtg ttt ttg gct gct ttc ggt gtc tac tac tac aag acc aac ttt 384
 Gly Val Phe Leu Ala Ala Phe Gly Val Tyr Tyr Tyr Lys Thr Asn Phe
 115 120 125
 gcc taa 390
 Ala

10 <210> 22
 < 211> 129
 < 212> PRT
 < 213> Candida tropicalis

<400> 22

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

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

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

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

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

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

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

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

Ala

<210> 23

<211> 2115

<212> DNA

5 <213> Candida tropicalis

<220>

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<222> (1)..(2115)

<400> 23

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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

10 tac gtc agg aca ttc acc aaa ccc tcc gaa acc cca ggg ttc agg gaa 192

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Tyr	Val	Arg	Thr	Phe	Thr	Lys	Pro	Ser	Glu	Thr	Pro	Gly	Phe	Arg	Glu	
50						55					60					
acc	gtc	tac	aac	acc	gtc	aac	gca	aac	acc	atg	gat	gca	atc	cac	cag	240
Thr	Val	Tyr	Asn	Thr	Val	Asn	Ala	Asn	Thr	Met	Asp	Ala	Ile	His	Gln	
65					70					75					80	
ttc	att	atc	ttg	acc	aat	gtt	ttg	gga	tca	agg	gtc	ttg	gca	cca	gct	288
Phe	Ile	Ile	Leu	Thr	Asn	Val	Leu	Gly	Ser	Arg	Val	Leu	Ala	Pro	Ala	
				85					90					95		
ttg	acc	aac	tcg	ttg	act	cct	atc	aag	gac	atg	agc	ttg	gaa	gac	cgt	336
Leu	Thr	Asn	Ser	Leu	Thr	Pro	Ile	Lys	Asp	Met	Ser	Leu	Glu	Asp	Arg	
			100					105					110			
gaa	aag	ttg	tta	gcc	tcg	tgg	cgt	gac	tcc	cct	att	gct	gct	aaa	agg	384
Glu	Lys	Leu	Leu	Ala	Ser	Trp	Arg	Asp	Ser	Pro	Ile	Ala	Ala	Lys	Arg	
		115					120					125				
aag	ttg	ttc	agg	ttg	gtt	tct	acg	ctt	acc	ttg	gtc	acg	ttc	acg	aga	432
Lys	Leu	Phe	Arg	Leu	Val	Ser	Thr	Leu	Thr	Leu	Val	Thr	Phe	Thr	Arg	
	130					135						140				
ttg	gcc	aat	gag	ttg	cat	ttg	aaa	gcc	att	cat	tat	cca	gga	aga	gaa	480
Leu	Ala	Asn	Glu	Leu	His	Leu	Lys	Ala	Ile	His	Tyr	Pro	Gly	Arg	Glu	
145					150					155					160	
gac	cgt	gaa	aag	gct	tat	gaa	acc	cag	gag	att	gac	cct	ttt	aag	tac	528
Asp	Arg	Glu	Lys	Ala	Tyr	Glu	Thr	Gln	Glu	Ile	Asp	Pro	Phe	Lys	Tyr	
				165					170					175		
cag	ttt	ttg	gaa	aaa	ccg	aag	ttt	tac	ggc	gct	gag	ttg	tac	ttg	cca	576
Gln	Phe	Leu	Glu	Lys	Pro	Lys	Phe	Tyr	Gly	Ala	Glu	Leu	Tyr	Leu	Pro	
			180					185					190			
gat	att	gat	gtg	atc	att	att	gga	tct	ggg	gcc	ggg	gct	ggg	gtc	gtg	624
Asp	Ile	Asp	Val	Ile	Ile	Ile	Gly	Ser	Gly	Ala	Gly	Ala	Gly	Val	Val	
		195					200					205				
gcc	cac	act	ttg	acc	aac	gac	ggc	ttc	aag	agt	ttg	gtt	ttg	gaa	aag	672
Ala	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	ggg	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	ggg	tcc	act	ttt	ggg	ggg	ggg	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					

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

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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> 24

<211> 704

<212> PRT

5 <213> Candida tropicalis

<400> 24

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

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

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

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

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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

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Thr His Ser Leu Ala Asn Glu Ile Ile Ile Glu Gly Gly Lys Lys Leu
 325 330 335
 Gly Tyr Lys Ala Lys Val Leu Asp Gln Asn Ser Gly Gly His Pro His
 340 345 350
 His Arg Cys Gly Phe Cys Tyr Leu Gly Cys Lys His Gly Ile Lys Gln
 355 360 365
 Gly Ser Val Asn Asn Trp Phe Arg Asp Ala Ala Ala His Gly Ser Gln
 370 375 380
 Phe Met Gln Gln Val Arg Val Leu Gln Ile Leu Asn Lys Lys Gly Ile
 385 390 395 400
 Ala Tyr Gly Ile Leu Cys Glu Asp Val Val Thr Gly Ala Lys Phe Thr
 405 410 415
 Ile Thr Gly Pro Lys Lys Phe Val Val Ala Ala Gly Ala Leu Asn Thr
 420 425 430
 Pro Ser Val Leu Val Asn Ser Gly Phe Lys Asn Lys Asn Ile Gly Lys
 435 440 445
 Asn Leu Thr Leu His Pro Val Ser Val Val Phe Gly Asp Phe Gly Lys
 450 455 460
 Asp Val Gln Ala Asp His Phe His Asn Ser Ile Met Thr Ala Leu Cys
 465 470 475 480
 Ser Glu Ala Ala Asp Leu Asp Gly Lys Gly His Gly Cys Arg Ile Glu
 485 490 495
 Thr Ile Leu Asn Ala Pro Phe Ile Gln Ala Ser Phe Leu Pro Trp Arg
 500 505 510
 Gly Ser Asn Glu Ala Arg Arg Asp Leu Leu Arg Tyr Asn Asn Met Val
 515 520 525
 Ala Met Leu Leu Leu Ser Arg Asp Thr Thr Ser Gly Ser Val Ser Ser
 530 535 540
 His Pro Thr Lys Pro Glu Ala Leu Val Val Glu Tyr Asp Val Asn Lys
 545 550 555 560
 Phe Asp Arg Asn Ser Ile Leu Gln Ala Leu Leu Val Thr Ala Asp Leu
 565 570 575

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

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

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

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

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

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

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

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

<210> 25

< 211> 2115

< 212> DNA

5 < 213> Candida tropicalis

<220>

< 221> CDS

< 222> (1)..(2115)

<400> 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

atc aag gac gcc att gct ccc gac ttc cct gag gac cag tac gag gag 144
Ile Lys 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 gcc acc cca acc gat gcc gtg cac atg 240
Ala Val Tyr Asp Thr Ile Asn Ala Thr Pro Thr Asp Ala Val His Met
10

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

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Thr	His	Ser	Leu	Ala	Asn	Glu	Val	Val	Val	Glu	Gly	Gly	Lys	Lys	Leu	
				325					330					335		
ggc	tac	aag	agc	aag	gaa	att	gag	cag	aac	aac	ggg	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	ggg	ttc	tgt	tac	ttg	ggc	tgt	aag	tac	ggg	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	ggg	atc	ttg	tgt	gag	gat	gtc	gaa	acc	gga	gtc	agg	ttc	act	1248
Ala	Tyr	Gly	Ile	Leu	Cys	Glu	Asp	Val	Glu	Thr	Gly	Val	Arg	Phe	Thr	
			405					410						415		
att	agt	ggc	ccc	aaa	aag	ttt	gtt	gtt	tct	gct	ggg	tct	ttg	aac	acg	1296
Ile	Ser	Gly	Pro	Lys	Lys	Phe	Val	Val	Ser	Ala	Gly	Ser	Leu	Asn	Thr	
			420					425					430			
cca	act	gtg	ttg	acc	aac	tcc	gga	ttc	aag	aac	aag	cac	att	ggg	aag	1344
Pro	Thr	Val	Leu	Thr	Asn	Ser	Gly	Phe	Lys	Asn	Lys	His	Ile	Gly	Lys	
		435					440					445				
aac	ttg	acg	ttg	cac	cca	gtt	tcc	acc	gtg	ttt	ggg	gac	ttt	ggc	aga	1392
Asn	Leu	Thr	Leu	His	Pro	Val	Ser	Thr	Val	Phe	Gly	Asp	Phe	Gly	Arg	
	450					455					460					
gac	gtg	caa	gcc	gac	cat	ttc	cac	aaa	tct	att	atg	act	tcg	ctt	tgt	1440
Asp	Val	Gln	Ala	Asp	His	Phe	His	Lys	Ser	Ile	Met	Thr	Ser	Leu	Cys	
465					470					475					480	
tac	gag	gtt	gct	gac	ttg	gac	ggc	aag	ggc	cac	gga	tgc	aga	atc	gaa	1488
Tyr	Glu	Val	Ala	Asp	Leu	Asp	Gly	Lys	Gly	His	Gly	Cys	Arg	Ile	Glu	
			485					490						495		
acc	atc	ttg	aac	gct	cca	ttc	atc	caa	gct	tct	ttg	ttg	cca	tgg	aga	1536
Thr	Ile	Leu	Asn	Ala	Pro	Phe	Ile	Gln	Ala	Ser	Leu	Leu	Pro	Trp	Arg	
			500					505					510			
gga	agt	gac	gag	gtc	aga	aga	gac	ttg	ttg	cgt	tac	aac	aac	atg	gtg	1584
Gly	Ser	Asp	Glu	Val	Arg	Arg	Asp	Leu	Leu	Arg	Tyr	Asn	Asn	Met	Val	
		515					520					525				
gcc	atg	ttg	ctt	atc	acg	cgt	gat	acc	acc	agt	ggg	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		

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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	
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

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 5 <213> Candida tropicalis

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 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

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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				
			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							

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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

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Pro Ile Phe Glu Ser Asn Lys Pro Lys Glu Gln Arg Thr Ile Lys Asp
595 600 605

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

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

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

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

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

Gln Ile Ala Leu Gly Leu Ala Asp Ser Leu Lys Thr Lys Pro Lys Leu
690 695 700

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5 <213> Candida tropicalis

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Met Asn Thr Phe Leu Pro Asp Val Leu Glu Tyr Lys His Val Asp Thr	
1 5 10 15	

ott 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	

10

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ttg acc aac tcg ttg acg cct atc aag gat atg acc ttg aaa 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 gct gcc tgg cgt gat tcc ccg atc gcg gcc aag aga Glu Gln Leu Leu Ala Ala Trp Arg Asp Ser Pro Ile Ala Ala Lys Arg 115 120 125	384
aga ttg ttc aga ttg att tcc tca ctt acc ttg acg acc 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 gac ttg cac ttg aga gcc atc cac tac cct ggc aga gac Leu Ala Ser Asp Leu His Leu Arg Ala Ile His Tyr Pro Gly Arg Asp 145 150 155 160	480
ttg cgt gaa aag gca 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 gaa aaa cca aag ttt gac ggc acc gag ttg tac ttg cca Leu Phe Met Glu Lys Pro Lys Phe Asp Gly Thr Glu Leu Tyr Leu Pro 180 185 190	576
gat atc gac gtc atc atc att gga tcc ggt 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 tta gcc aac gac ggg tac aag acc ttg gtt ttg gaa aag Ala His Thr Leu Ala Asn Asp Gly Tyr Lys Thr Leu Val Leu Glu Lys 210 215 220	672
gga aag tat ttc agc aac tcc gag ttg aac ttt aat gat gcc gat ggt Gly Lys Tyr Phe Ser Asn Ser Glu Leu Asn Phe Asn Asp Ala Asp Gly 225 230 235 240	720
atg aaa gag ttg tac caa ggt aaa tgt gcg ttg acc acc acg aac cag Met Lys Glu Leu Tyr Gln Gly Lys Cys Ala Leu Thr Thr Thr Asn Gln 245 250 255	768
cag atg ttt att ctt gcc ggt tcc act ttg ggc ggt ggt acc act gtt Gln Met Phe Ile Leu Ala Gly Ser Thr Leu Gly Gly Gly Thr Thr Val 260 265 270	816
aac tgg tct gct tgt 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 gac 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
gca caa gac tat gtt tgg aaa caa atg ggc gct tct acc gaa gga atc Ala Gln Asp Tyr Val Trp Lys Gln Met Gly Ala Ser Thr Glu Gly Ile 305 310 315 320	960
act cac tct ttg gcg aac gcg gtt gtg gtt gaa gga ggt aag aag ttg Thr His Ser Leu Ala Asn Ala Val Val Val Glu Gly Gly Lys Lys Leu 325 330 335	1008
ggt tac aag agc aag gaa atc gag cag aac aat ggt ggc cat cct gac Gly Tyr Lys Ser Lys Glu Ile Glu Gln Asn Asn Gly Gly His Pro Asp 1056	

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340	345	350	
cac ccc tgt ggt ttc tgt tac ttg ggc tgt aag tac ggt att aag cag His Pro Cys Gly Phe Cys Tyr Leu Gly Cys Lys Tyr Gly Ile Lys Gln 355 360 365			1104
ggt tct gtg aat aac tgg ttt aga gac gca gct gcc cac ggg tcc aag Gly Ser Val Asn Asn Trp Phe Arg Asp Ala Ala His Gly Ser Lys 370 375 380			1152
ttc atg caa caa gtc aga gtt gtg caa atc ctc cac aat aaa ggc gtc Phe Met Gln Gln Val Arg Val Val Gln Ile Leu His Asn Lys Gly Val 385 390 395 400			1200
gct tat ggc atc ttg tgt gag gat gtc gag acc gga gtc aaa ttc act Ala Tyr Gly Ile Leu Cys Glu Asp Val Glu Thr Gly Val Lys Phe Thr 405 410 415			1248
atc agt ggc ccc aaa aag ttt gtt gtt tct gca ggt tct ttg aac acg Ile Ser Gly Pro Lys Lys Phe Val Val Ser Ala Gly Ser Leu Asn Thr 420 425 430			1296
cca acg gtg ttg acc aac tcc gga ttc aag aac aaa cac atc ggt aag Pro Thr Val Leu Thr Asn Ser Gly Phe Lys Asn Lys His Ile Gly Lys 435 440 445			1344
aac ttg acg ttg cac cca gtt tcg acc gtg ttt ggt gac ttt ggc aga Asn Leu Thr Leu His Pro Val Ser Thr Val Phe Gly Asp Phe Gly Arg 450 455 460			1392
gac gtg caa gcc gac cat ttc cac aaa tct att atg act tcg ctc tgt Asp Val Gln Ala Asp His Phe His Lys Ser Ile Met Thr Ser Leu Cys 465 470 475 480			1440
tac gaa gtc gct gac ttg gac ggc aag ggc cac gga tgc aga atc gag Tyr Glu Val Ala Asp Leu Asp Gly Lys Gly His Gly Cys Arg Ile Glu 485 490 495			1488
acc atc ttg aac gct cca ttc atc caa gct tct ttg ttg cca tgg aga Thr Ile Leu Asn Ala Pro Phe Ile Gln Ala Ser Leu Leu Pro Trp Arg 500 505 510			1536
gga agc gac gag gtc aga aga gac ttg ttg cgt tac aac aac atg gtg Gly Ser Asp Glu Val Arg Arg Asp Leu Leu Arg Tyr Asn Asn Met Val 515 520 525			1584
gcc atg ttg ctt atc acc cgt gac acc acc agt ggt tca gtt tct gct Ala Met Leu Leu Ile Thr Arg Asp Thr Thr Ser Gly Ser Val Ser Ala 530 535 540			1632
gac cca aag aag ccc gac gct ttg att gtc gac tat gac atc aac aag Asp Pro Lys Lys Pro Asp Ala Leu Ile Val Asp Tyr Asp Ile Asn Lys 545 550 555 560			1680
ttt gac aag aat gcc atc ttg caa gct ttc ttg atc acc tcc gac atg Phe Asp Lys Asn Ala Ile Leu Gln Ala Phe Leu Ile Thr Ser Asp Met 565 570 575			1728
ttg tac atc gaa ggt gcc aag aga atc ctc agt cca cag gca tgg gtg Leu Tyr Ile Glu Gly Ala Lys Arg Ile Leu Ser Pro Gln Ala Trp Val 580 585 590			1776
cca atc ttt gag tcg aac aag cca aag gag caa aga aca atc aag gac			1824

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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					640		
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	tgc	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	

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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					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	

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

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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
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
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 Asp Ile Asn Lys				
545		550		555
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

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

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

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

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

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

Gln Ile Ala Leu Gly Leu Ala Asp Ser Leu Lys Thr Lys Pro Lys Leu
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5 < 213> Candida tropicalis

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Met Ile Met Phe Asp Ile Val Lys Tyr Thr Leu Ile Gly Leu Phe Ser
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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

10

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

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tac tgt ggc tat aat aat ttt ggt acg ggt aga gac aga aat gtt tgg	1152
Tyr Cys Gly Tyr Asn Asn Phe Gly Thr Gly Arg Asp Arg Asn Val Trp	
370 375 380	
gga cca gac tcg gat gag ttt aaa cca gag aga tgg gga agg gat aat	1200
Gly Pro Asp Ser Asp Glu Phe Lys Pro Glu Arg Trp Gly Arg Asp Asn	
385 390 395 400	
att gaa gaa ata aat cgc aat tat gct aat gcc aaa aga tca gct gaa	1248
Ile Glu Glu Ile Asn Arg Asn Tyr Ala Asn Ala Lys Arg Ser Ala Glu	
405 410 415	
tta cct gcg ttt cat ggc aga aag aga gct tgt tta gga gaa aag tat	1296
Leu Pro Ala Phe His Gly Arg Lys Arg Ala Cys Leu Gly Glu Lys Tyr	
420 425 430	
gcc tta tat gaa gtt aaa gaa ttg cta act agt att tta gga cat tac	1344
Ala Leu Tyr Glu Val Lys Glu Leu Leu Thr Ser Ile Leu Gly His Tyr	
435 440 445	
aaa gtt act tta gat gca agt tgg aaa gag aaa ata acc cct gct gga	1392
Lys Val Thr Leu Asp Ala Ser Trp Lys Glu Lys Ile Thr Pro Ala Gly	
450 455 460	
cct att agt cca ttt ggt ttg aag gtg aaa ttt gaa aag ctt att gtt	1440
Pro Ile Ser Pro Phe Gly Leu Lys Val Lys Phe Glu Lys Leu Ile Val	
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gca taa	1446
Ala	

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<211> 481

<212> PRT

5 <213> Candida tropicalis

<400> 30

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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

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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
 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
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[illegible]

Ala

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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					
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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	tgg	gac	aag	288
Lys	Ser	Lys	Gly	Thr	Val	Met	Gln	Phe	Ala	Cys	Asp	Leu	Trp	Asp	Lys	
				85					90					95		
aaa	ctc	att	gtc	agt	gat	cca	aag	gca	aag	act	att	ggg	ctt	aag	att	336
Lys	Leu	Ile	Val	Ser	Asp	Pro	Lys	Ala	Lys	Thr	Ile	Gly	Leu	Lys	Ile	
			100					105					110			
tta	ggg	att	cca	ttg	att	gaa	act	aaa	gac	cca	gag	aat	gtc	aag	gct	384
Leu	Gly	Ile	Pro	Leu	Ile	Glu	Thr	Lys	Asp	Pro	Glu	Asn	Val	Lys	Ala	
		115				120						125				
att	tta	gcc	acc	cag	ttt	aat	gat	ttt	tct	ttg	gga	act	aga	cat	gat	432
Ile	Leu	Ala	Thr	Gln	Phe	Asn	Asp	Phe	Ser	Leu	Gly	Thr	Arg	His	Asp	
	130					135					140					
ttc	ttg	tat	tca	ttg	tta	gga	gat	ggg	att	ttc	act	tta	gat	ggg	gct	480
Phe	Leu	Tyr	Ser	Leu	Leu	Gly	Asp	Gly	Ile	Phe	Thr	Leu	Asp	Gly	Ala	
145				150					155						160	
ggc	tgg	aaa	cac	agc	aga	acc	atg	ttg	aga	cca	caa	ttc	gct	aga	gag	528
Gly	Trp	Lys	His	Ser	Arg	Thr	Met	Leu	Arg	Pro	Gln	Phe	Ala	Arg	Glu	
				165					170					175		
caa	gtt	tcg	cat	gta	aag	ttg	ttg	gaa	ccc	cat	atg	caa	gtt	tta	ttt	576
Gln	Val	Ser	His	Val	Lys	Leu	Leu	Glu	Pro	His	Met	Gln	Val	Leu	Phe	
			180					185					190			
aaa	cac	att	aga	aaa	cat	cat	ggc	caa	act	ttt	gat	atc	caa	gaa	ttg	624
Lys	His	Ile	Arg	Lys	His	His	Gly	Gln	Thr	Phe	Asp	Ile	Gln	Glu	Leu	
		195					200					205				
ttt	ttc	aga	tta	act	gtt	gat	tcg	gct	act	gag	ttt	ttg	ttt	ggg	gaa	672
Phe	Phe	Arg	Leu	Thr	Val	Asp	Ser	Ala	Thr	Glu	Phe	Leu	Phe	Gly	Glu	
	210					215					220					
tct	gct	gaa	tct	tta	aga	gac	gag	tct	gtc	ggg	tta	act	cca	aca	acc	720
Ser	Ala	Glu	Ser	Leu	Arg	Asp	Glu	Ser	Val	Gly	Leu	Thr	Pro	Thr	Thr	
225					230					235					240	
aaa	gat	ttt	gat	ggg	aga	aat	gag	ttt	gcc	gat	gcg	ttc	aac	tat	tct	768
Lys	Asp	Phe	Asp	Gly	Arg	Asn	Glu	Phe	Ala	Asp	Ala	Phe	Asn	Tyr	Ser	
				245					250					255		
caa	act	tac	caa	gcg	tac	aga	ttc	ttg	ttg	caa	caa	atg	tat	tgg	att	816
Gln	Thr	Tyr	Gln	Ala	Tyr	Arg	Phe	Leu	Leu	Gln	Gln	Met	Tyr	Trp	Ile	
			260					265					270			
ttg	aat	ggg	tct	gaa	ttt	aga	aaa	tct	att	gct	att	gtc	cac	aag	ttt	864
Leu	Asn	Gly	Ser	Glu	Phe	Arg	Lys	Ser	Ile	Ala	Ile	Val	His	Lys	Phe	
		275					280					285				
gct	gac	cac	tat	gtt	caa	aag	gca	ttg	gaa	tta	act	gat	gaa	gat	ttg	912
Ala	Asp	His	Tyr	Val	Gln	Lys	Ala	Leu	Glu	Leu	Thr	Asp	Glu	Asp	Leu	
	290					295					300					

gaa aag aaa gaa ggc tat gta ttt tta ttc gag tta gcc aaa caa acc 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
ggg aga gat acc aca gct ggc ttg ttg tgc 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
aca act tta cca aga ggt ggt ggt gaa ggt ggt tta tcc cca att gct Thr Thr Leu Pro Arg Gly Gly Gly Glu Gly Gly Leu Ser Pro Ile Ala 420 425 430	1296
att aag aag ggc caa gtt gtt atg tac acg att ctt gct act cac aga Ile Lys Lys Gly Gln Val Val Met Tyr Thr Ile Leu Ala Thr His Arg 435 440 445	1344
gat aaa gac att tat ggt gaa gat gct tat gtt ttc agg cca gaa aga Asp Lys Asp Ile Tyr Gly Glu Asp Ala Tyr Val Phe Arg Pro Glu Arg 450 455 460	1392
tgg ttt gaa cct gaa acc aga aaa ttg ggc tgg gca tat gtt cca ttc Trp Phe Glu Pro Glu Thr Arg Lys Leu Gly Trp Ala Tyr Val Pro Phe 465 470 475 480	1440
aat ggc ggt cca aga att tgt ttg ggt caa cag ttt gct tta act gaa Asn Gly Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe Ala Leu Thr Glu 485 490 495	1488
gca tca tat gtc act gtt aga ttg ctt caa gaa ttt ggt aac ttg aaa Ala Ser Tyr Val Thr Val Arg Leu Leu Gln Glu Phe Gly Asn Leu Lys 500 505 510	1536
caa gat cca aat act gaa tat cca cca aaa tta caa aac aca ttg act Gln Asp Pro Asn Thr Glu Tyr Pro Pro Lys Leu Gln Asn Thr Leu Thr 515 520 525	1584
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<212> PRT

5 <213> Candida tropicalis

<400> 32

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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	
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

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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

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	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			
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	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			
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Lys 145	His	Ser	Arg	Ser	Met 150	Leu	Arg	Pro	Gln	Phe 155	Ala	Arg	Glu	Gln	Val 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	tggt	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	Leu	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	
	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	
					390					395					400	

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tta cca aga ggt ggt ggc aag gat ggt tta tca cca gta tta gtt aga    1248
Leu Pro Arg Gly Gly Gly Lys Asp Gly Leu Ser Pro Val Leu Val Arg
                                405                                410                                415

aag ggt caa act gtg atg tac agt gtg tat gct gcc cat aga aac aaa    1296
Lys Gly Gln Thr Val Met Tyr Ser Val Tyr Ala Ala His Arg Asn Lys
                                420                                425                                430

caa att tat ggt gaa gac gca ctt gaa ttc agg cca gaa aga tgg ttt    1344
Gln Ile Tyr Gly Glu Asp Ala Leu Glu Phe Arg Pro Glu Arg Trp Phe
                                435                                440                                445

gaa cca gag aca aag aaa ttg ggc tgg gcc ttc tta cct ttt aat ggt    1392
Glu Pro Glu Thr Lys Lys Leu Gly Trp Ala Phe Leu Pro Phe Asn Gly
                                450                                455                                460

ggt cca aga att tgt ttg ggt caa caa ttt gct ttg act gaa gct tct    1440
Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe Ala Leu Thr Glu Ala Ser
                                465                                470                                475                                480

tat gtt act gtt aga tta ctt caa gag ttt agc cac ttg aca atg gat    1488
Tyr Val Thr Val Arg Leu Leu Gln Glu Phe Ser His Leu Thr Met Asp
                                485                                490                                495

cca aac act gaa tac ccg cca aag aaa atg tcc cat ttg aca atg tct    1536
Pro Asn Thr Glu Tyr Pro Pro Lys Lys Met Ser His Leu Thr Met Ser
                                500                                505                                510

cta ttt gat ggt gcc aac att caa atg tat tag    1569
Leu Phe Asp Gly Ala Asn Ile Gln Met Tyr
                                515                                520

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<210> 34

<211> 522

<212> PRT

5 <213> Candida tropicalis

<400> 34

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Met Ser Ile Gln Asp Ile Val Glu Thr Tyr Ser Thr Lys Trp Tyr Val
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Val Val Leu Val Ala Leu Ile Val Tyr Lys Val Phe Asp Phe Phe Tyr
                                20                                25                                30

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

Gln Thr Asp Gly Tyr Leu Gly Phe Arg Val Pro Phe Glu Leu Met Gly
                                50                                55                                60

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

Glu Leu Asp Asn Pro Asp Ile Pro Thr Phe Thr Phe Pro Ile Phe Ser
                                85                                90                                95

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

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

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

Tyr Pro Ser Val Pro Gln Asn Phe Arg Val Ala Thr Arg 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 Ser Val Tyr Ala Ala His Arg Asn Lys
420 425 430

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

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5 < 213> Candida tropicalis

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< 222> (1)..(1572)

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tgg tat act gtt atc act tta gca gct ttg gtt ttc tta att tca tct 96
10 Trp Tyr Thr Val Ile Thr Leu Ala Ala Leu Val Phe Leu Ile Ser Ser

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20	25	30	
aat att aaa aat tac gtc aag gct aag aag ttg aaa tgc aga gat cct Asn Ile Lys Asn Tyr Val Lys Ala Lys Lys Leu Lys Cys Arg Asp Pro 35 40 45			144
cca tat ttc aaa gga gcc ggt tgg aca ggt att agt cca tta att gaa Pro Tyr Phe Lys Gly Ala Gly Trp Thr Gly Ile Ser Pro Leu Ile Glu 50 55 60			192
att att aaa gtt aaa ggt aat ggt aga ttg gca gat ttt gcc gat aaa Ile Ile Lys Val Lys Gly Asn Gly Arg Leu Ala Asp Phe Ala Asp Lys 65 70 75 80			240
aca ttc gac gac tat cca aac cat act ttt tac atg tct att att ggt Thr Phe Asp Asp Tyr Pro Asn His Thr Phe Tyr Met Ser Ile Ile Gly 85 90 95			288
gct ttg aaa atc gtc ttg act gtt gat cca gaa aat att aaa gct gtt Ala Leu Lys Ile Val Leu Thr Val Asp Pro Glu Asn Ile Lys Ala Val 100 105 110			336
ttg gct act caa ttt act gat ttc tcc tta ggt acc aga cat gct cat Leu Ala Thr Gln Phe Thr Asp Phe Ser Leu Gly Thr Arg His Ala His 115 120 125			384
ttc tat cca tta tta ggt gat ggt att ttt act ttg gat ggt gaa ggt Phe Tyr Pro Leu Leu Gly Gly Ile Phe Thr Leu Asp Gly Glu Gly 130 135 140			432
tggt aaa cat agt aga gct atg ttg aga cca caa ttt gct aga gat caa Trp Lys His Ser Arg Ala Met Leu Arg Pro Gln Phe Ala Arg Asp Gln 145 150 155 160			480
att ggt cat gtt aaa gct ttg gaa cca cat att caa atc ttg gcc aaa Ile Gly His Val Lys Ala Leu Glu Pro His Ile Gln Ile Leu Ala Lys 165 170 175			528
caa att aaa ttg aat aaa ggt aaa act ttt gat att caa gaa ttg ttt Gln Ile Lys Leu Asn Lys Gly Lys Thr Phe Asp Ile Gln Glu Leu Phe 180 185 190			576
ttc aga ttt act gtt gat act gct act gaa ttc ttg ttt ggt gaa tct Phe Arg Phe Thr Val Asp Thr Ala Thr Glu Phe Leu Phe Gly Glu Ser 195 200 205			624
gtt cac tct ttg tat gat gaa aaa tta ggt att cct act cca aat gaa Val His Ser Leu Tyr Asp Glu Lys Leu Gly Ile Pro Thr Pro Asn Glu 210 215 220			672
att cca ggt aga gat aat ttt gca act gct ttt aac act tct caa cat Ile Pro Gly Arg Asp Asn Phe Ala Thr Ala Phe Asn Thr Ser Gln His 225 230 235 240			720
tat ttg gct acc aga aca tac tcc caa act ttc tac ttt tta act aac Tyr Leu Ala Thr Arg Thr Tyr Ser Gln Thr Phe Tyr Phe Leu Thr Asn 245 250 255			768
cct aag gaa ttt aga gac tgt aat gct aaa gtt cat tac ttg gct aaa Pro Lys Glu Phe Arg Asp Cys Asn Ala Lys Val His Tyr Leu Ala Lys 260 265 270			816
tat ttt gtc aat aaa gct ttg aat ttc act ccg gaa gaa att gaa gaa			864

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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	ggt	ttc	ttg	tat	gaa	ttg	ggt	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	ggt	tta	caa	gat	caa	tta	ttg	aac	att	atg	ggt	gcc	960	
Arg	Asp	Pro	Lys	Val	Leu	Gln	Asp	Gln	Leu	Leu	Asn	Ile	Met	Val	Ala		
305					310					315					320		
ggt	aga	gat	acc	act	gct	ggt	tta	tta	tca	ttt	gca	atg	ttt	gaa	tta	1008	
Gly	Arg	Asp	Thr	Thr	Ala	Gly	Leu	Leu	Ser	Phe	Ala	Met	Phe	Glu	Leu		
				325					330					335			
gct	aga	cat	cca	gaa	att	tgg	tct	aaa	tta	aga	gaa	gaa	att	gaa	ggt	1056	
Ala	Arg	His		Glu	Ile	Trp	Ser	Lys	Leu	Arg	Glu	Glu	Ile	Glu	Val		
			340					345					350				
aac	ttt	ggt	ggt	ggt	gaa	gaa	tct	cgt	ggt	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	ggt	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	ggt	gct	tat	att	ggt	tac	aaa	act	cat	cgt	1296	
Ile	Pro	Lys	Gly	Ser	Thr	Val	Ala	Tyr	Ile	Val	Tyr	Lys	Thr	His	Arg		
		420					425					430					
tta	gaa	gaa	tat	tat	ggt	aaa	gat	gct	gat	gat	ttc	aga	cca	gaa	aga	1344	
Leu	Glu	Glu	Tyr	Tyr	Gly	Lys	Asp	Ala	Asp	Asp	Phe	Arg	Pro	Glu	Arg		
		435				440					445						
tgg	ttt	gaa	cca	tca	act	aaa	aag	tta	ggt	tgg	gct	tat	ggt	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	ggt	att	acc	aga	ttg	gta	caa	atg	ttt	gaa	act	ggt	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	ggt	gaa	tac	cct	cca	cca	aaa	tgt	att	cat	ttg	act	1536	
Ser	Ser	Pro	Asp	Val	Glu	Tyr	Pro	Pro	Pro	Lys	Cys	Ile	His	Leu	Thr		
		500						505					510				
atg	agt	cat	gat	gat	ggt	ggt	ttc	ggt	aaa	atg	taa					1572	
Met	Ser	His	Asp	Asp	Gly	Val	Phe	Val	Lys	Met							
		515				520											

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<211> 523

<212> PRT

5 <213> Candida tropicalis

<400> 36

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 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

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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
 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
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5 <220>
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 < 222> (1)..(1512)

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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
          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
    
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10

ES 2 626 442 T3

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

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Gly Phe Ile Ser Ile Ala Thr His Leu Asp Pro Val Tyr Phe Gly Ser	
405 410 415	
gat gcc cat gtg ttt aga cca gac cgc tgg ttt gat tct agt atg aaa	1296
Asp Ala His Val Phe Arg Pro Asp Arg Trp Phe Asp Ser Ser Met Lys	
420 425 430	
aat ttg ggg tgt aaa tac ttg ccc ttt aac gtc ggt cca aga acg tgt	1344
Asn Leu Gly Cys Lys Tyr Leu Pro Phe Asn Val Gly Pro Arg Thr Cys	
435 440 445	
ttg gga caa cag tac act ttg att gag gca agc tac ttg tta gtt cgt	1392
Leu Gly Gln Gln Tyr Thr Leu Ile Glu Ala Ser Tyr Leu Leu Val Arg	
450 455 460	
cta gcg caa aca tat gaa aca gtt gaa tca cat ccc gat tca gtt tat	1440
Leu Ala Gln Thr Tyr Glu Thr Val Glu Ser His Pro Asp Ser Val Tyr	
465 470 475 480	
cca cca agg aag aaa gcg ttg atc aat atg tgt gct gca gac ggt gtt	1488
Pro Pro Arg Lys Lys Ala Leu Ile Asn Met Cys Ala Ala Asp Gly Val	
485 490 495	
gat gtc aag ttc cat aga tta taa	1512
Asp Val Lys Phe His Arg Leu	
500	

<210> 38

<211> 503

<212> PRT

5 <213> Candida tropicalis

<400> 38

Met Ser Leu Thr Glu Thr Thr Ala Thr Phe Ile Tyr Asn Tyr Trp Tyr	
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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	

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

ES 2 626 442 T3

Arg Asn Met Lys Thr Ala Lys Cys Thr Thr Thr Leu Pro Lys Gly Gly
370 375 380

Gly Lys Asp Gly Gln Asp Pro Ile Leu Val Lys Lys Gly Gln Ser Val
385 390 395 400

Gly Phe Ile Ser Ile Ala Thr His Leu Asp Pro Val Tyr Phe Gly Ser
405 410 415

Asp Ala His Val Phe Arg Pro Asp Arg Trp Phe Asp Ser Ser Met Lys
420 425 430

Asn Leu Gly Cys Lys Tyr Leu Pro Phe Asn Val Gly Pro Arg Thr Cys
435 440 445

Leu Gly Gln Gln Tyr Thr Leu Ile Glu Ala Ser Tyr Leu Leu Val Arg
450 455 460

Leu Ala Gln Thr Tyr Glu Thr Val Glu Ser His Pro Asp Ser Val Tyr
465 470 475 480

Pro Pro Arg Lys Lys Ala Leu Ile Asn Met Cys Ala Ala Asp Gly Val
485 490 495

Asp Val Lys Phe His Arg Leu
500

<210> 39
< 211> 1554
< 212> DNA
< 213> Candida tropicalis

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

<400> 39
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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

ES 2 626 442 T3

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

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305	310	315	320	
ttg ttg tca ttt gcg gta ttt gaa ctt gct agg aat cca cat att tgg				1008
Leu Leu Ser Phe	Ala Val Phe Glu	Leu Ala Arg Asn Pro	His Ile Trp	
	325	330	335	
gcc aaa tta aga gaa gat gtt gaa tcc caa ttt ggt ctt ggt gaa gaa				1056
Ala Lys Leu Arg	Glu Asp Val Glu	Ser Gln Phe Gly	Leu Gly Glu Glu	
	340	345	350	
tct cgc att gaa gag att acc ttt gaa agt tta aaa cga tgt gaa tac				1104
Ser Arg Ile Glu	Glu Ile Thr Phe	Glu Ser Leu Lys	Arg Cys Glu Tyr	
	355	360	365	
ttg aaa gct ttc ctt aac gaa aca tta cgt gtt tat cca agt gtt cca				1152
Leu Lys Ala Phe	Leu Asn Glu Thr	Leu Arg Val Tyr	Pro Ser Val Pro	
	370	375	380	
aga aat ttc aga att gct acc aaa aac acc act tta cca aga ggt ggt				1200
Arg Asn Phe Arg	Ile Ala Thr Lys	Asn Thr Thr Leu	Pro Arg Gly Gly	
	385	390	400	
ggt tca gac ggc aat tct cct gtt ttg gtc aaa aag ggc gag gct gtt				1248
Gly Ser Asp Gly	Asn Ser Pro Val	Leu Val Lys Lys	Gly Glu Ala Val	
	405	410	415	
tca tat ggt ata aat tct act cac tta gat cct gtc tat tat ggt gac				1296
Ser Tyr Gly Ile	Asn Ser Thr His	Leu Asp Pro Val	Tyr Tyr Gly Asp	
	420	425	430	
gat gct gca gaa ttt aga cca gaa aga tgg aac gag cca tca aca aga				1344
Asp Ala Ala Glu	Phe Arg Pro Glu	Arg Trp Asn Glu	Pro Ser Thr Arg	
	435	440	445	
aaa ttg gga tgg gca tat tta ccg ttc aac gga ggc cca aga att tgt				1392
Lys Leu Gly Trp	Ala Tyr Leu Pro	Phe Asn Gly Gly	Pro Arg Ile Cys	
	450	455	460	
tta ggt caa caa ttt gct tta acc gaa gcg ggt tat gta ttg gtt aga				1440
Leu Gly Gln Gln	Phe Ala Leu Thr	Glu Ala Gly Tyr	Val Leu Val Arg	
	465	470	475	480
ttg gcc caa agt ttt gac acc ttg gaa ttg aag cca cca gtt gtg tat				1488
Leu Ala Gln Ser	Phe Asp Thr Leu	Glu Leu Lys Pro	Pro Val Val Tyr	
	485	490	495	
cca cca aag aga tta aca aac ttg act atg tct tta caa gac gga act				1536
Pro Pro Lys Arg	Leu Thr Asn Leu	Thr Met Ser Leu	Gln Asp Gly Thr	
	500	505	510	
att gtc aag atc gat tag				1554
Ile Val Lys Ile Asp				
	515			

<210> 40

<211> 517

<212> PRT

5 <213> Candida tropicalis

<400> 40

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

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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
Ser Val Gly Thr Tyr Val Ser Thr Ile Phe Gly Thr Lys Leu Leu Val	85	90	95
Thr Lys Asp Pro Glu Asn Ile Lys Ala Leu Leu Ala Thr Gln Phe Ser	100	105	110
Asp Phe Ser Leu Gly Lys Arg His Thr Leu Phe Lys Pro Leu Leu Gly	115	120	125
Asp Gly Ile Phe Thr Leu Asp Gly Glu Gly Trp Lys His Ser Arg Ala	130	135	140
Met Leu Arg Pro Gln Phe Ala Arg Glu Gln Val Ala His Val Thr Ser	145	150	155
Leu Glu Pro His Phe Gln Leu Leu Lys Lys His Ile Leu Lys Asn Lys	165	170	175
Gly Gly Phe Phe Asp Ile Gln Glu Leu Phe Phe Arg Phe Thr Val Asp	180	185	190
Ser Ala Thr Glu Phe Leu Phe Gly Glu Ser Val His Ser Leu Lys Asp	195	200	205
Glu Thr Ile Gly Tyr Asn Gln Asp Asp Ile Asp Phe Val Gly Arg Lys	210	215	220
Asp Phe Ala Glu Ser Phe Asn Lys Ala Gln Glu Tyr Leu Ala Ile Arg	225	230	235
Thr Leu Val Gln Asp Phe Tyr Tyr Leu Val Asn Asn Gln Glu Phe Arg	245	250	255

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Asp Cys Asn Lys Leu Val His Lys Phe Thr Asn Tyr Tyr Val Gln Arg
 260 265 270
 Ala Leu Asp Ala Thr Pro Glu Glu Leu Glu Lys Gln Ser Gly Tyr Val
 275 280 285
 Phe Leu Tyr Glu Leu Val Lys Gln Thr Arg Asp Pro Asn Val Leu Arg
 290 295 300
 Asp Gln Ser Leu Asn Ile Leu Leu Ala Gly Arg Asp Thr Thr Ala Gly
 305 310 315 320
 Leu Leu Ser Phe Ala Val Phe Glu Leu Ala Arg Asn Pro His Ile Trp
 325 330 335
 Ala Lys Leu Arg Glu Asp Val Glu Ser Gln Phe Gly Leu Gly Glu Glu
 340 345 350
 Ser Arg Ile Glu Glu Ile Thr Phe Glu Ser Leu Lys Arg Cys Glu Tyr
 355 360 365
 Leu Lys Ala Phe Leu Asn Glu Thr Leu Arg Val Tyr Pro Ser Val Pro
 370 375 380
 Arg Asn Phe Arg Ile Ala Thr Lys Asn Thr Thr Leu Pro Arg Gly Gly
 385 390 395 400
 Gly Ser Asp Gly Asn Ser Pro Val Leu Val Lys Lys Gly Glu Ala Val
 405 410 415
 Ser Tyr Gly Ile Asn Ser Thr His Leu Asp Pro Val Tyr Tyr Gly Asp
 420 425 430
 Asp Ala Ala Glu Phe Arg Pro Glu Arg Trp Asn Glu Pro Ser Thr Arg
 435 440 445
 Lys Leu Gly Trp Ala Tyr Leu Pro Phe Asn Gly Gly Pro Arg Ile Cys
 450 455 460
 Leu Gly Gln Gln Phe Ala Leu Thr Glu Ala Gly Tyr Val Leu Val Arg
 465 470 475 480
 Leu Ala Gln Ser Phe Asp Thr Leu Glu Leu Lys Pro Pro Val Val Tyr
 485 490 495
 Pro Pro Lys Arg Leu Thr Asn Leu Thr Met Ser Leu Gln Asp Gly Thr
 500 505 510
 Ile Val Lys Ile Asp
 515

<210> 41
 <211> 1539
 <212> DNA
 <213> Candida tropicalis

<220>

< 221> CDS
< 222> (1)..(1539)

<400> 41

atg att gaa cag gtt tta cat tat tgg tat att gtt tta cct gca ttt	48
Met Ile Glu Gln Val Leu His Tyr Trp Tyr Ile Val Leu Pro 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	

ES 2 626 442 T3

ttt ttg ttt ggt gaa tca gtg aac tct ttg aaa agt gca tca att ggt Phe Leu Phe Gly Glu Ser Val Asn Ser Leu Lys Ser Ala Ser Ile Gly 195 200 205	624
tgt gac gag gaa acc gag ctt gag gaa aga aag aaa ttt gcg gaa gca Cys Asp Glu Glu Thr Glu Leu Glu Glu Arg Lys Lys Phe Ala Glu Ala 210 215 220	672
ttc aat aaa gcg caa gag tat att tct act cga gtt gct ttg caa caa Phe Asn Lys Ala Gln Glu Tyr Ile Ser Thr Arg Val Ala Leu Gln Gln 225 230 235 240	720
tta tat tgg ttt gtt aat aat agc gaa ttc aag gaa tgt aac gaa att Leu Tyr Trp Phe Val Asn Asn Ser Glu Phe Lys Glu Cys Asn Glu Ile 245 250 255	768
gtt cat aag ttt acc aat tat tat gta caa aag gca ttg gat gct act Val His Lys Phe Thr Asn Tyr Tyr Val Gln Lys Ala Leu Asp Ala Thr 260 265 270	816
cct gaa gag ctt gaa aag caa agt gga tat gtt ttc ttg tat gaa ttg Pro Glu Glu Leu Glu Lys Gln Ser Gly Tyr Val Phe Leu Tyr Glu Leu 275 280 285	864
gtt aaa caa acc aga gac cct aat gta ttg aga gat caa tca ttg aat Val Lys Gln Thr Arg Asp Pro Asn Val Leu Arg Asp Gln Ser Leu Asn 290 295 300	912
atc tta tta gct ggt aga gat acc act gct ggg ttg ttg tca ttt gcg Ile Leu Leu Ala Gly Arg Asp Thr Thr Ala Gly Leu Leu Ser Phe Ala 305 310 315 320	960
gta ttt gaa ctt gct agg aat cca cat att tgg gcc aaa tta aga gaa Val Phe Glu Leu Ala Arg Asn Pro His Ile Trp Ala Lys Leu Arg Glu 325 330 335	1008
gat gtc gaa tcc caa ttt ggt ctt ggt gaa gaa tct cgc att gaa gag Asp Val Glu Ser Gln Phe Gly Leu Gly Glu Glu Ser Arg Ile Glu Glu 340 345 350	1056
att acc ttt gaa agt tta aaa cga tgt gaa tat ttg aaa gcc gtg atg Ile Thr Phe Glu Ser Leu Lys Arg Cys Glu Tyr Leu Lys Ala Val Met 355 360 365	1104
aat gaa aca ttg aga ttg cat cca agt gtt cca aga aat gct aga ttt Asn Glu Thr Leu Arg Leu His Pro Ser Val Pro Arg Asn Ala Arg Phe 370 375 380	1152
gca ctt aag gat aca act tta cct aga ggt gga ggt cca gat gga aaa Ala Leu Lys Asp Thr Thr Leu Pro Arg Gly Gly Gly Pro Asp Gly Lys 385 390 395 400	1200
gac ccg att tta gtt aga aaa aat gaa gtt gtt caa tat tcc att tct Asp Pro Ile Leu Val Arg Lys Asn Glu Val Val Gln Tyr Ser Ile Ser 405 410 415	1248
ggc aca caa att gat cca aaa cat tat ggc aaa gat gct aaa ttg ttt Gly Thr Gln Ile Asp Pro Lys His Tyr Gly Lys Asp Ala Lys Leu Phe 420 425 430	1296
aga cca gaa aga tgg ttt gaa tca agt aca aga aat tta ggt tgg gca Arg Pro Glu Arg Trp Phe Glu Ser Ser Thr Arg Asn Leu Gly Trp Ala 435 440 445	1344

ES 2 626 442 T3

435	440	445	
tac tta cca ttc aac ggg ggt ccg aga att tgt tta ggt caa caa ttt			1392
Tyr Leu Pro Phe Asn Gly Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe			
450	455	460	
gct tta acc gaa gca ggt tac ata ttg gtt aga ttg gct caa agt ttt			1440
Ala Leu Thr Glu Ala Gly Tyr Ile Leu Val Arg Leu Ala Gln Ser Phe			
465	470	475	480
gac acc ttg gaa ttg aaa cca gat aca gaa tac cct cca cca aga tta			1488
Asp Thr Leu Glu Leu Lys Pro Asp Thr Glu Tyr Pro Pro Pro Arg Leu			
485	490	495	
gcc cat ttg act atg tgt ttg ttt gat ggt gcg ctt gtc aag atg gat			1536
Ala His Leu Thr Met Cys Leu Phe Asp Gly Ala Leu Val Lys Met Asp			
500	505	510	
taa			1539

<210> 42
 <211> 512
 <212> PRT
 <213> Candida tropicalis

5

<400> 42
 Met Ile Glu Gln Val Leu His Tyr Trp Tyr Ile Val Leu Pro Ala Phe
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Ile Ile Phe His Trp Ile Val Ser Ala Ile His Thr Asn Ser Leu Arg
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Arg Lys Leu Gly Ala Lys Pro Phe Thr His Thr Gln Leu Asp Gly Phe
 35 40 45

Tyr Gly Phe Lys Phe Gly Arg Asp Phe Leu Lys Ala Lys Arg Ile Gly
 50 55 60

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

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

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

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

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

ES 2 626 442 T3

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

ES 2 626 442 T3

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

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

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

Asp Thr Leu Glu Leu Lys Pro Asp Thr Glu Tyr Pro Pro Pro Arg Leu
485 490 495

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

<210> 43

<211> 1572

<212> DNA

5 <213> Candida tropicalis

<220>

<221> CDS

<222> (1)..(1572)

<400> 43

atg att aaa gaa ata gtg tat ttt gta tat tat tat gga att acc cac 48
Met Ile Lys Glu Ile Val Tyr Phe Val Tyr Tyr Tyr Gly Ile 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

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85	90	95	
tat ttg act gat att tat gta aag aac ctc cca aag tca aag ttt tat Tyr Leu Thr Asp Ile Tyr Val Lys Asn Leu Pro Lys Ser Lys Phe Tyr 100 105 110			336
gaa aac ttt aga aat cat gga ttc cag gat aat att ttt gcc agt ttg Glu Asn Phe Arg Asn His Gly Phe Gln Asp Asn Ile Phe Ala Ser Leu 115 120 125			384
gaa aat gat aga cat atc aag tat aaa aga atg ata aat aac ttg tac Glu Asn Asp Arg His Ile Lys Tyr Lys Arg Met Ile Asn Asn Leu Tyr 130 135 140			432
agt aaa tct tcc atc ttc tcc aaa gaa aac cac aca aga tca gtt tta Ser Lys Ser Ser Ile Phe Ser Lys Glu Asn His Thr Arg Ser Val Leu 145 150 155 160			480
ttt gac acc aca aaa aca tta gtc gat gca gtt gct aga gaa tct ccg Phe Asp Thr Thr Lys Thr Leu Val Asp Gly Ala Val Ala Arg Glu Ser Pro 165 170 175			528
tca att gat gtg ttt acg tta ttt ggt tcc ttg gcc atg gat gtg gtt Ser Ile Asp Val Phe Thr Leu Phe Gly Ser Leu Ala Met Asp Val Val 180 185 190			576
tca agg ttt gaa ctt ggt aga gac aat gga acg gat tta ttg aat cat Ser Arg Phe Glu Leu Gly Arg Asp Asn Gly Thr Asp Leu Leu Asn His 195 200 205			624
cca caa gaa agg cat att att gaa tct cat aga aag gtg tct tgt atg Pro Gln Glu Arg His Ile Ile Glu Ser His Arg Lys Val Ser Cys Met 210 215 220			672
ggg ttc tgg aca aca ttg atg cca agc ttc ttt tgg aat ttg gca gca Gly Phe Trp Thr Thr Leu Met Pro Ser Phe Phe Trp Asn Leu Ala Ala 225 230 235 240			720
acc aag gcc acc ttg caa gct gtt gat gat att tgc aat ttc caa ttg Thr Lys Ala Thr Leu Gln Ala Val Asp Asp Ile Cys Asn Phe Gln Leu 245 250 255			768
ggt tta tat aaa att gca gaa tcc aat ctt gtg tcc aat ggt aaa aac Gly Leu Tyr Lys Ile Ala Glu Ser Asn Leu Val Ser Asn Gly Lys Asn 260 265 270			816
cta act acg ata caa aca ctc aag aag tac gga ttg gaa gga aat tct Leu Thr Thr Ile Gln Thr Leu Lys Lys Tyr Gly Leu Glu Gly Asn Ser 275 280 285			864
gcg tat tct ttt ctc acg gat aat tta ttt gct gga cat gaa act aca Ala Tyr Ser Phe Leu Thr Asp Asn Leu Phe Ala Gly His Glu Thr Thr 290 295 300			912
gct gtt caa ttg aca tat ttg tgt tat gaa tta tca aga cca gct aat Ala Val Gln Leu Thr Tyr Leu Cys Tyr Glu Leu Ser Arg Pro Ala Asn 305 310 315 320			960
tac aaa att cag aat aga tta aga tat gag ctt caa gaa gca ttt cca Tyr Lys Ile Gln Asn Arg Leu Arg Tyr Glu Leu Gln Glu Ala Phe Pro 325 330 335			1008
agt ggt caa att gaa gat ttg gaa gtg gtt gat aat ctt ccg tat ctt			1056

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

<210> 44

< 211> 523

< 212> PRT

5 < 213> Candida tropicalis

<400> 44

Met Ile Lys Glu Ile Val Tyr Phe Val Tyr Tyr Tyr Gly Ile Thr His
1 5 10 15

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

ES 2 626 442 T3

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

ES 2 626 442 T3

Ala Tyr Ser Phe Leu Thr Asp Asn Leu Phe Ala Gly His Glu Thr Thr
290 295 300

Ala Val Gln Leu Thr Tyr Leu Cys Tyr Glu Leu Ser Arg Pro Ala Asn
305 310 315 320

Tyr Lys Ile Gln Asn Arg Leu Arg Tyr Glu Leu Gln Glu Ala Phe Pro
325 330 335

Ser Gly Gln Ile Glu Asp Leu Glu Val Val Asp Asn Leu Pro Tyr Leu
340 345 350

Asn Ala Leu Leu Ser Glu Asn Gly Arg Ile His Thr Ser Ile Pro Gly
355 360 365

Ala Glu Pro Arg Val Val Ala Lys Pro Tyr Thr Ile Gly Lys Leu Leu
370 375 380

Ile Pro Val Gly Thr Val Ile Ser Cys Leu Pro Tyr Ala Tyr His Arg
385 390 395 400

Asn Pro Ser Val Phe Thr Asn Pro Asp Lys Phe Ile Pro Glu Arg Trp
405 410 415

Leu Val Asp Asn Glu Glu Asp Lys Lys Arg Val Lys Gln Gln Ala Lys
420 425 430

Tyr Met Met Pro Phe Gly Lys Gly Val Arg Met Cys Leu Gly Met Asn
435 440 445

Leu Ala Leu Ile Glu Met Lys Leu Ala Ile Ala Ser Leu Tyr Leu Asn
450 455 460

Phe Ser Ser Ser Ile Asp Glu Asp Trp Cys Gly Lys Val Leu Glu Asn
465 470 475 480

Asp Asp Pro Ile Gly Ile Gly Asn Ser Cys Thr His Glu Thr Asp Gln
485 490 495

Asp Lys Met Lys Met Tyr Asp Ala Tyr Thr Thr Arg Pro Met Leu Asp
500 505 510

Glu Cys Tyr Leu Lys Trp Thr Arg Leu Thr Pro
515 520

<210> 45

< 211> 1728

< 212> DNA

5 < 213> Candida tropicalis

<220>

< 221> CDS

< 222> (1)..(1728)

<400> 45

ES 2 626 442 T3

atg ctt ctg agc ata cca tgg gat caa tca ttg cta acg ttg cta aca Met Leu Leu Ser Ile Pro Trp Asp Gln Ser Leu Leu Thr Leu Leu Thr 1 5 10 15	48
tat ctt gat acc cat cca ata gct acg ata ttc acc att att tta acc Tyr Leu Asp Thr His Pro Ile Ala Thr Ile Phe Thr Ile Ile Leu Thr 20 25 30	96
att tta aca att gga att tta ttt gat tat tgt cta tca cct aaa gag Ile Leu Thr Ile Gly Ile Leu Phe Asp Tyr Cys Leu Ser Pro Lys Glu 35 40 45	144
att gcc aat att ttc agt att cct gga gat ttg cca ttt att ggt cat Ile Ala Asn Ile Phe Ser Ile Pro Gly Asp Leu Pro Phe Ile Gly His 50 55 60	192
tta cat tta ata cta gat aat cca gca ttg att tat tta aca tgg tat Leu His Leu Ile Leu Asp Asn Pro Ala Leu Ile Tyr Leu Thr Trp Tyr 65 70 75 80	240
aaa tta tat aat aaa ctg gtt ttt caa att cgt att gga aat aaa cgt Lys Leu Tyr Asn Lys Leu Val Phe Gln Ile Arg Ile Gly Asn Lys Arg 85 90 95	288
gta gtt gtt gtt aat tca ttt gat gat gtt gtt gga tta tgg ata aat Val Val Val Val Asn Ser Phe Asp Asp Val Val Gly Leu Trp Ile Asn 100 105 110	336
cat agt tgt caa aat aat tca aga cct tta agt tat act ttt cat gga His Ser Cys Gln Asn Asn Ser Arg Pro Leu Ser Tyr Thr Phe His Gly 115 120 125	384
tta gtt tca gca tta caa ggt ttt aca gtt ggt tct act cct gca agt Leu Val Ser Ala Leu Gln Gly Phe Thr Val Gly Ser Thr Pro Ala Ser 130 135 140	432
tta aca ttt ctg aga aag aag aaa gtt att tca ctg tgt tta aga aag Leu Thr Phe Leu Arg Lys Lys Lys Val Ile Ser Leu Cys Leu Arg Lys 145 150 155 160	480
aaa gaa att gat gaa aaa gta tgt ctc ata gat aat gaa att tgt gtt Lys Glu Ile Asp Glu Lys Val Cys Leu Ile Asp Asn Glu Ile Cys Val 165 170 175	528
atg att aaa gaa ata att aaa aag aag gat ata tca act gat gta aat Met Ile Lys Glu Ile Ile Lys Lys Lys Asp Ile Ser Thr Asp Val Asn 180 185 190	576
atg tta cct tat tta caa aaa ttc ata tta aaa aca gct att ctt atg Met Leu Pro Tyr Leu Gln Lys Phe Ile Leu Lys Thr Ala Ile Leu Met 195 200 205	624
agt tat gga att gaa ttg gat tgt tat aat aaa gat gtt aaa tta tgt Ser Tyr Gly Ile Glu Leu Asp Cys Tyr Asn Lys Asp Val Lys Leu Cys	672

ES 2 626 442 T3

210	215	220	
caa gag att atc acc gtg gag aat aat atc ata aga tta aga tca cca Gln Glu Ile Ile Thr Val Glu Asn Asn Ile Ile Arg Leu Arg Ser Pro 225 230 235 240			720
ata tct aat ctt caa gat tct gta cct ttc tta aga cta ata cca tgg Ile Ser Asn Leu Glu Asn Ser Val Pro Phe Leu Arg Leu Ile Pro Trp 245 250 255			768
ttt aat aat cga gaa ttt gcc ctt cgt tgt gga aat aga agg aat aaa Phe Asn Asn Arg Glu Phe Ala Leu Arg Cys Gly Asn Arg Arg Asn Lys 260 265 270			816
tat atg gat caa tta tat aat agg tta caa aat gga tta gct gaa aat Tyr Met Asp Gln Leu Tyr Asn Arg Leu Gln Asn Gly Leu Ala Glu Asn 275 280 285			864
gat cca aat ata gct aat agt att ctt gga caa tta att ctt aat aat Asp Pro Asn Ile Ala Asn Ser Ile Leu Gly Gln Leu Ile Leu Asn Asn 290 295 300			912
gat aat aat aat tct aac agc tta act agt caa gaa ata caa agt att Asp Asn Asn Asn Ser Asn Ser Leu Thr Ser Gln Glu Ile Gln Ser Ile 305 310 315 320			960
tgt tta aca tta gta agt gct gga tta gat aat acc cca ctt aat ttg Cys Leu Thr Leu Val Ser Ala Gly Leu Asp Asn Thr Pro Leu Asn Leu 325 330 335			1008
aat tat ctt att gga ata tta tca caa cca aga ata ggt aag ata ttt Asn Tyr Leu Ile Gly Ile Leu Ser Pro Arg Ile Gly Lys Ile Phe 340 345 350			1056
caa gat aaa gct ata aaa gat att tta aat cat gca aat gga gat att Gln Asp Lys Ala Ile Lys Asp Ile Leu Asn His Ala Asn Gly Asp Ile 355 360 365			1104
att caa gca tgg aat caa ctg aat gaa gaa aat cga gat tgt aaa tat Ile Gln Ala Trp Asn Gln Leu Asn Glu Glu Asn Arg Asp Cys Lys Tyr 370 375 380			1152
att caa gct tta att ctt gaa act tta aga cat ttt aca gta tta cca Ile Gln Ala Leu Ile Leu Glu Thr Leu Arg His Phe Thr Val Leu Pro 385 390 395 400			1200
tta agt tta cct aga tta act aca aaa cca ata tat tat aaa aat ttt Leu Ser Leu Pro Arg Leu Thr Thr Lys Pro Ile Tyr Tyr Lys Asn Phe 405 410 415			1248
atg att cct aaa aat act cat atg ttt atg aat gca tat tct gca aat Met Ile Pro Lys Asn Thr His Met Phe Met Asn Ala Tyr Ser Ala Asn 420 425 430			1296
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			1440

ES 2 626 442 T3

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

<210> 46

<211> 575

<212> PRT

5 <213> Candida tropicalis

<400> 46

Met Leu Leu Ser Ile Pro Trp Asp Gln Ser Leu Leu Thr Leu Leu Thr	
1 5 10 15	
Tyr Leu Asp Thr His Pro Ile Ala Thr Ile Phe Thr Ile Ile Leu Thr	
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	

ES 2 626 442 T3

His	Ser	Cys	Gln	Asn	Asn	Ser	Arg	Pro	Leu	Ser	Tyr	Thr	Phe	His	Gly
		115					120				125				
Leu	Val	Ser	Ala	Leu	Gln	Gly	Phe	Thr	Val	Gly	Ser	Thr	Pro	Ala	Ser
130						135				140					
Leu	Thr	Phe	Leu	Arg	Lys	Lys	Lys	Val	Ile	Ser	Leu	Cys	Leu	Arg	Lys
145					150				155		160				
Lys	Glu	Ile	Asp	Glu	Lys	Val	Cys	Leu	Ile	Asp	Asn	Glu	Ile	Cys	Val
				165				170						175	
Met	Ile	Lys	Glu	Ile	Ile	Lys	Lys	Lys	Asp	Ile	Ser	Thr	Asp	Val	Asn
		180					185						190		
Met	Leu	Pro	Tyr	Leu	Gln	Lys	Phe	Ile	Leu	Lys	Thr	Ala	Ile	Leu	Met
195						200					205				
Ser	Tyr	Gly	Ile	Glu	Leu	Asp	Cys	Tyr	Asn	Lys	Asp	Val	Lys	Leu	Cys
210						215					220				
Gln	Glu	Ile	Ile	Thr	Val	Glu	Asn	Asn	Ile	Ile	Arg	Leu	Arg	Ser	Pro
225					230				235		240				
Ile	Ser	Asn	Leu	Gln	Asp	Ser	Val	Pro	Phe	Leu	Arg	Leu	Ile	Pro	Trp
				245				250						255	
Phe	Asn	Asn	Arg	Glu	Phe	Ala	Leu	Arg	Cys	Gly	Asn	Arg	Arg	Asn	Lys
		260					265						270		
Tyr	Met	Asp	Gln	Leu	Tyr	Asn	Arg	Leu	Gln	Asn	Gly	Leu	Ala	Glu	Asn
275						280						285			
Asp	Pro	Asn	Ile	Ala	Asn	Ser	Ile	Leu	Gly	Gln	Leu	Ile	Leu	Asn	Asn
290						295				300					
Asp	Asn	Asn	Asn	Ser	Asn	Ser	Leu	Thr	Ser	Gln	Glu	Ile	Gln	Ser	Ile
305					310				315		320				
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				

ES 2 626 442 T3

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
515 520 525

Gly Lys Tyr Leu Met Glu Met Asn Pro Phe Val Asn Asn Leu Asn Pro
530 535 540

Arg Gly Thr Ser Phe Glu Pro Arg Ile His Asn Ile Lys Leu Gln Tyr
545 550 555 560

Arg Lys Leu Pro Asn Tyr Glu Thr Leu His Glu Ile Val Leu Lys
565 570 575

<210> 47

<211> 1518

<212> DNA

5 <213> Candida tropicalis

<220>

<221> CDS

<222> (1)..(1518)

<400> 47

ES 2 626 442 T3

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gca gca caa tac tac aag aga agg aca ctt gtg act aaa ttt cat tgc Ala Ala Gln Tyr Tyr Lys Arg Arg Thr Leu Val Thr Lys Phe His Cys 20 25 30	96
aaa caa gca cgt att tcc cca aac aag tca tgg ttg gaa tat tta ggc Lys Gln Ala Arg Ile Ser Pro Asn Lys Ser Trp Leu Glu Tyr Leu Gly 35 40 45	144
att gcc tcc gtt gta cat gcc aat gaa atg att aga aaa gga gga ttg Ile Ala Ser Val Val His Ala Asn Glu Met Ile Arg Lys Gly Gly Leu 50 55 60	192
tat tca gaa att gat gga aga ttt aaa tcc ctt gat gtt tca aca ttc Tyr Ser Glu Ile Asp Gly Arg Phe Lys Ser Leu Asp Val Ser Thr Phe 65 70 75 80	240
aag tct ata act ttg gga aag aca acg tat gtt acc aaa gat att gaa Lys Ser Ile Thr Leu Gly Lys Thr Thr Tyr Val Thr Lys Asp Ile Glu 85 90 95	288
aac atc cgt cat atc ttg agt gca acg gaa atg aac tca tgg aat ctt Asn Ile Arg His Ile Leu Ser Ala Thr Glu Met Asn Ser Trp Asn Leu 100 105 110	336
ggt gcc cgt cca att gcg tta aga ccc ttg att ggt gat gga att ttt Gly Ala Arg Pro Ile Ala Leu Arg Pro Leu Ile Gly Asp Gly Ile Phe 115 120 125	384
gct agt gaa ggt caa tct tgg aaa cat agt cga atc atg ctt aga cca Ala Ser Glu Gly Gln Ser Trp Lys His Ser Arg Ile Met Leu Arg Pro 130 135 140	432
gta ttt gca aaa gaa cac gtt aaa caa atc act tca atg gaa cca tat Val Phe Ala Lys Glu His Val Lys Gln Ile Thr Ser Met Glu Pro Tyr 145 150 155 160	480
gta caa ctg ttg atc aaa atc atc aag aac cat gaa ggg gaa cca tta Val Gln Leu Leu Ile Lys Ile Ile Lys Asn His Glu Gly Glu Pro Leu 165 170 175	528
gag ttt caa acc tta gcc cat ctt ttt aca ata gat tat tct act gat Glu Phe Gln Thr Leu Ala His Leu Phe Thr Ile Asp Tyr Ser Thr Asp 180 185 190	576
ttc cta tta ggt gaa agt tgt gat agt ttg aag gat ttc cta gga gaa Phe Leu Leu Gly Glu Ser Cys Asp Ser Leu Lys Asp Phe Leu Gly Glu 195 200 205	624
gag tcc aat tcc aca tta gat aca tcg ttg aga ctg gca ttt gca tca Glu Ser Asn Ser Thr Leu Asp Thr Ser Leu Arg Leu Ala Phe Ala Ser 210 215 220	672
cag ttt aat aaa acc cag cag caa atg aca att cga ttc atg ttg gga Gln Phe Asn Lys Thr Gln Gln Gln Met Thr Ile Arg Phe Met Leu Gly 225 230 235 240	720
aaa ttg gcc ttt ctc atg tat cca aag agt ttt caa aat agt att caa Lys Leu Ala Phe Leu Met Tyr Pro Lys Ser Phe Gln Asn Ser Ile Gln	768

ES 2 626 442 T3

	245	250	255	
atg caa aag gac ttt gtt gat gaa tat atc gac aga gta gta ggt atg				816
Met Gln Lys Asp Phe Val Asp Glu Tyr	260	265	270	
tcc gaa gaa gaa ttg aac aat cat cca aag agc tat gtt ttg ttg tac				864
Ser Glu Glu Glu Leu Asn Asn His Pro Lys Ser Tyr	275	280	285	
caa tta gca aga caa act aag aat cgt gat ata tta caa gat gaa ttg				912
Gln Leu Ala Arg Gln Thr Lys Asn Arg Asp Ile	290	295	300	
atg tcc att tta ctt gca ggt aga gac acc act gcc agt ttg ttg act				960
Met Ser Ile Leu Leu Gly Arg Asp Thr Thr Ala Ser Leu Leu Thr	305	310	315	320
ttt ttg ttt ttc gaa tta agt cac cat cca gaa gta ttt aac aaa tta				1008
Phe Leu Phe Phe Glu Leu Ser His His Pro Glu Val Phe Asn Lys Leu	325	330	335	
aaa gag gaa atc gaa aga cac ttt cct gat gtt gaa tcc gtt aca ttt				1056
Lys Glu Glu Ile Glu Arg His Phe Pro Asp Val Glu Ser Val Thr Phe	340	345	350	
gga act atc cag aga tgc gac tat ctt caa tgg tgt att aac gaa act				1104
Gly Thr Ile Gln Arg Cys Asp Tyr Leu Gln Trp Cys Ile Asn Glu Thr	355	360	365	
atg aga ctc cat cca tca gtt cct ttt aat ttc aga act gca gcc aat				1152
Met Arg Leu His Pro Ser Val Pro Phe Asn Phe Arg Thr Ala Ala Asn	370	375	380	
gac aca gta ata cca aga ggt gga ggt aaa tcc tgt aca gat cct att				1200
Asp Thr Val Ile Pro Arg Gly Gly Gly Lys Ser Cys Thr Asp Pro Ile	385	390	395	400
ctt gtc cat aag ggt gaa caa gta tta ttc agt ttc tat tct gta aac				1248
Leu Val His Lys Gly Glu Gln Val Leu Phe Ser Phe Tyr Ser Val Asn	405	410	415	
aga gaa gaa aag tat ttt ggt aca aat acc gac aag ttt gct cca gaa				1296
Arg Glu Glu Lys Tyr Phe Gly Thr Asn Thr Asp Lys Phe Ala Pro Glu	420	425	430	
aga tgg agt gaa tca tta agg aga act gag ttc ata cca ttt tct gct				1344
Arg Trp Ser Glu Ser Leu Arg Arg Thr Glu Phe Ile Pro Phe Ser Ala	435	440	445	
gga cct cgt gcc tgt ttg ggt caa cag tta gct aga gtt gaa gct tca				1392
Gly Pro Arg Ala Cys Leu Leu Gln Gln Leu Ala Arg Val Glu Ala Ser	450	455	460	
tat gtt act att aga ttg ctt caa acc ttt cat ggg ttg cat aat gcc				1440
Tyr Val Thr Ile Arg Leu Leu Gln Thr Phe His Gly Leu His Asn Ala	465	470	475	480
agt aaa caa tac cca cca aat aga gtg gtt gca gct aca atg aga ttg				1488
Ser Lys Gln Tyr Pro Pro Asn Arg Val Val Ala Ala Thr Met Arg Leu	485	490	495	
act gac ggt tgt aac gtt tgt ttt atc tag				1518
Thr Asp Gly Cys Asn Val Cys Phe Ile	500	505		

<210> 48
 <211> 505
 <212> PRT
 <213> Candida tropicalis

<400> 48

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

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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
 420 425 430
 Arg Trp Ser Glu Ser Leu Arg Arg Thr Glu Phe Ile Pro Phe Ser Ala
 435 440 445
 Gly Pro Arg Ala Cys Leu Gly Gln Gln Leu Ala Arg Val Glu Ala Ser
 450 455 460
 Tyr Val Thr Ile Arg Leu Leu Gln Thr Phe His Gly Leu His Asn Ala
 465 470 475 480
 Ser Lys Gln Tyr Pro Pro Asn Arg Val Val Ala Ala Thr Met Arg Leu
 485 490 495
 Thr Asp Gly Cys Asn Val Cys Phe Ile
 500 505

<210> 49
 < 211> 1584
 < 212> DNA
 < 213> Candida tropicalis

5 <220>
 < 221> CDS
 < 222> (1)..(1584)

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<400> 49
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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
    
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10

ES 2 626 442 T3

aat ggt tta ttc tcc caa aga gct ttg gaa att tac att cca gtt caa Asn Gly Leu Phe Ser Gln Arg Ala Leu Glu Ile Tyr Ile Pro Val Gln 165 170 175	528
gaa aaa tac atg gat att tat tta gat aga ttc tgt aag tac gac ggt Glu Lys Tyr Met Asp Ile Tyr Leu Asp Arg Phe Cys Lys Tyr Asp Gly 180 185 190	576
cca cgt gaa ttc ttc cca gaa ttt aga gaa ttg ttg tgt gct tta tct Pro Arg Glu Phe Phe Pro Glu Phe Arg Glu Leu Leu Cys Ala Leu Ser 195 200 205	624
ttg aga act ttc tgt ggg gat tac atc act gaa gat caa att gct tta Leu Arg Thr Phe Cys Gly Asp Tyr Ile Thr Glu Asp Gln Ile Ala Leu 210 215 220	672
ggt gct gat aac tat tac aga gtc act gct gct ttg gaa ttg gtc aat Val Ala Asp Asn Tyr Tyr Arg Val Thr Ala Ala Leu Glu Leu Val Asn 225 230 235 240	720
ttc cca atc att att cct tac act aaa act tgg tac ggt aag aag att Phe Pro Ile Ile Ile Pro Tyr Thr Lys Thr Trp Tyr Gly Lys Lys Ile 245 250 255	768
gct gat gat acc atg aag att ttt gaa aat tgt gct gct atg tcc aag Ala Asp Asp Thr Met Lys Ile Phe Glu Asn Cys Ala Ala Met Ser Lys 260 265 270	816
aaa cac att aat gaa aat aat ggt act cca ggt tgt gtt atg gat gaa Lys His Ile Asn Glu Asn Asn Gly Thr Pro Gly Cys Val Met Asp Glu 275 280 285	864
tgg att tac ttg atg aaa gaa gct aaa gaa aaa cac tct gat gat cca Trp Ile Tyr Leu Met Lys Glu Ala Lys Glu Lys His Ser Asp Asp Pro 290 295 300	912
gat tcc aaa tta ttg att aga gaa ttc tcc aac cgt gaa att tcc gaa Asp Ser Lys Leu Leu Ile Arg Glu Phe Ser Asn Arg Glu Ile Ser Glu 305 310 315 320	960
gcc att ttc act ttc ttg ttt gct tct caa gat gcc tct tct tct ttg Ala Ile Phe Thr Phe Leu Phe Ala Ser Gln Asp Ala Ser Ser Ser Leu 325 330 335	1008
gct tgt tgg tta ttc caa att gtc gcc gac aga cca gat gtt gtt gcc Ala Cys Trp Leu Phe Gln Ile Val Ala Asp Arg Pro Asp Val Val Ala 340 345 350	1056
aag att aga gaa gaa caa ttg aga gtt aga aac aat gac cca tct gtt Lys Ile Arg Glu Glu Gln Leu Arg Val Arg Asn Asn Asp Pro Ser Val 355 360 365	1104
aaa ttg tcc ttg gat ttg att aat gaa atg act tac acc aat gat gtt Lys Leu Ser Leu Asp Leu Ile Asn Glu Met Thr Tyr Thr Asn Asp Val 370 375 380	1152
ggt aaa gaa tct ttg aga tac cgt cca cca gtc ttg atg gtt cca tat Val Lys Glu Ser Leu Arg Tyr Arg Pro Pro Val Leu Met Val Pro Tyr 385 390 395 400	1200
ggt gtt aag aaa gct ttc cca gtt act gaa aaa tac act gct cca aag Val Val Lys Lys Ala Phe Pro Val Thr Glu Lys Tyr Thr Ala Pro Lys	1248

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405										410					415					
ggt	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	tggt	gcc	act	gct	1344				
Val	Tyr	Asp	Glu	Pro	Asp	Ser	Phe	Ile	Pro	Glu	Arg	Trp	Ala	Thr	Ala					
		435					440						445							
tct	ggt	gat	atg	tac	aaa	cgt	aac	tggt	ttg	gtc	ttc	ggt	act	ggt	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	ggt	aag	aac	tat	gtc	atg	atg	ttg	ttt	act	ggt	atg	1440				
His	Val	Cys	Leu	Gly	Lys	Asn	Tyr	Val	Met	Met	Leu	Phe	Thr	Gly	Met					
					470				475						480					
ttg	ggt	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						
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							
gtt	att	tta	gaa	tggt	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								

<210> 50

<211> 527

<212> PRT

5 <213> Candida tropicalis

<400> 50

Met	Ser	Val	Asn	Thr	Thr	Ser	Pro	Val	Val	Asp	Ser	Ile	Ser	Asp	Asn
1				5					10					15	

Ala	Thr	Thr	Tyr	Leu	Ser	Thr	Lys	Tyr	Ile	Ile	Asp	Ser	Leu	Tyr	Ser
			20					25					30		

Thr	Tyr	Gln	Gln	Ala	Ser	Trp	Leu	Gln	Ile	Ile	Leu	Thr	Ser	Ile	Ile
		35					40					45			

Leu	Ile	Leu	Thr	Tyr	Asp	Gln	Ile	Leu	Tyr	Gln	Ile	Asn	Lys	Gly	Ser
	50					55					60				

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

Glu	Ser	Leu	Asp	Pro	Lys	Phe	Glu	Glu	Tyr	Lys	Ala	Lys	Trp	Asp	Ser
				85					90					95	

Gly	Glu	Leu	Ser	Cys	Val	Ser	Ile	Phe	His	Lys	Phe	Val	Val	Ile	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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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
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
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
Ala Ile Phe Thr Phe Leu Phe Ala Ser Gln Asp Ala Ser Ser Ser Leu		
325	330	335
Ala Cys Trp Leu Phe Gln Ile Val Ala Asp Arg Pro Asp Val Val Ala		
340	345	350

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Lys Ile Arg Glu Glu Gln Leu Arg Val Arg Asn Asn Asp Pro Ser Val
355 360 365

Lys Leu Ser Leu Asp Leu Ile Asn Glu Met Thr Tyr Thr Asn Asp Val
370 375 380

Val Lys Glu Ser Leu Arg Tyr Arg Pro Pro Val Leu Met Val Pro Tyr
385 390 395 400

Val Val Lys Lys Ala Phe Pro Val Thr Glu Lys Tyr Thr Ala Pro Lys
405 410 415

Gly Ser Met Leu Ile Pro Thr Leu Tyr Pro Ala Leu His Asp Pro Glu
420 425 430

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

Ser Gly Asp Met Tyr Lys Arg Asn Trp Leu Val Phe Gly Thr Gly Pro
450 455 460

His Val Cys Leu Gly Lys Asn Tyr Val Met Met Leu Phe Thr Gly Met
465 470 475 480

Leu Gly Lys Phe Val Met Asn Ser Asp Ile Ile His His Lys Thr Ala
485 490 495

Leu Ser Glu Glu Ile Lys Val Phe Ala Thr Ile Phe Pro Lys Asp Asp
500 505 510

Val Ile Leu Glu Trp Lys Lys Arg Asp Pro Leu Ala Ala Ser Asn
515 520 525

<210> 51

< 211> 1587

< 212> DNA

5 < 213> Candida tropicalis

<220>

< 221> CDS

< 222> (1)..(1587)

<400> 51

atg gct att gtt gat act gcc att gat ggc atc aat tat ttc tta tcc	48
Met Ala Ile Val Asp Thr Ala Ile Asp Gly Ile Asn Tyr Phe Leu Ser	
1 5 10 15	

tta tca tta act caa caa atc acc atc ttg gtt gtt ttc cca ttc atc	96
Leu Ser Leu Thr Gln Gln Ile Thr Ile Leu Val Val Phe Pro Phe Ile	
20 25 30	

10

tac aac ata gca tgg caa tta ctt tac tcc tta aga aaa gat aga gtt Tyr Asn Ile Ala Trp Gln Leu Leu Tyr Ser Leu Arg Lys Asp Arg Val 35 40 45	144
cca atg gtt ttc tac tgg atc cca tgg ttt ggt tct gct gct agt tat Pro Met Val Phe Tyr Trp Ile Pro Trp Phe Gly Ser Ala Ala Ser Tyr 50 55 60	192
ggt atg caa cca tac gaa ttc ttt gaa aag tgc aga ttg aaa tat ggt Gly Met Gln Pro Tyr Glu Phe Phe Glu Lys Cys Arg Leu Lys Tyr Gly 65 70 75 80	240
gat gtt ttt tca ttt atg tta tta ggt aaa gtt atg act gtt tat ttg Asp Val Phe Ser Phe Met Leu Leu Gly Lys Val Met Thr Val Tyr Leu 85 90 95	288
ggt cca aaa ggt cac gaa ttc att tac aat gct aaa tta tcc gat gtt Gly Pro Lys Gly His Glu Phe Ile Tyr Asn Ala Lys Leu Ser Asp Val 100 105 110	336
tct gct gaa gaa gct tat acc cat ttg act act cct gtt ttt ggt aaa Ser Ala Glu Glu Ala Tyr Thr His Leu Thr Thr Pro Val Phe Gly Lys 115 120 125	384
ggt gtt att tat gat tgt cca aac tct aga tta atg gaa caa aag aag Gly Val Ile Tyr Asp Cys Pro Asn Ser Arg Leu Met Glu Gln Lys Lys 130 135 140	432
ttt gct aaa ttt gct ttg act act gat tct ttc aaa acc tat gtt cca Phe Ala Lys Phe Ala Leu Thr Thr Asp Ser Phe Lys Thr Tyr Val Pro 145 150 155 160	480
aag atc aga gaa gaa gtt ttg aat tat ttt gtt aac gat gtt agt ttc Lys Ile Arg Glu Glu Val Leu Asn Tyr Phe Val Asn Asp Val Ser Phe 165 170 175	528
aaa acc aag gaa aga gac cat ggt gtt gct agt gtt atg aaa act caa Lys Thr Lys Glu Arg Asp His Gly Val Ala Ser Val Met Lys Thr Gln 180 185 190	576
cca gaa atc act att ttc act gct tct cgt tgt tta ttt ggt gat gaa Pro Glu Ile Thr Ile Phe Thr Ala Ser Arg Cys Leu Phe Gly Asp Glu 195 200 205	624
atg aga aag agt ttc gac aga tca ttt gct caa ttg tat gct gac ttg Met Arg Lys Ser Phe Asp Arg Ser Phe Ala Gln Leu Tyr Ala Asp Leu 210 215 220	672
gat aaa ggt ttc acc cca atc aac ttt gtt ttc cca aac ttg cca tta Asp Lys Gly Phe Thr Pro Ile Asn Phe Val Phe Pro Asn Leu Pro Leu 225 230 235 240	720
cct cat tac tgg aga cgt gac gct gct caa aga aag ata tct gct cat Pro His Tyr Trp Arg Arg Asp Ala Ala Gln Arg Lys Ile Ser Ala His 245 250 255	768
tac atg aag gaa att aag aga aga aga gaa agc ggt gat att gat cca Tyr Met Lys Glu Ile Lys Arg Arg Arg Glu Ser Gly Asp Ile Asp Pro 260 265 270	816
aag aga gat ttg att gat tcc ttg ttg gtt aac tct act tat aaa gat Lys Arg Asp Leu Ile Asp Ser Leu Leu Val Asn Ser Thr Tyr Lys Asp 275 280 285	864

ES 2 626 442 T3

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ggt gtt aaa atg act gat caa gaa att gct aac ctt tta att ggt gtt      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 gtt 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 gtt 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 gtt att cca aaa ggt cac      1200
Asn Pro Leu Arg Val Pro Asn Thr Lys Tyr Val Ile Pro Lys Gly His
385                               390                               395                               400

tat gtc tta gtt 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
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

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<210> 52

< 211> 528

< 212> PRT

5 < 213> Candida tropicalis

<400> 52

ES 2 626 442 T3

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	
Pro	Glu	Ile	Thr	Ile	Phe	Thr	Ala	Ser	Arg	Cys	Leu	Phe	Gly	Asp	Glu	195	200	205	
Met	Arg	Lys	Ser	Phe	Asp	Arg	Ser	Phe	Ala	Gln	Leu	Tyr	Ala	Asp	Leu	210	215	220	

Asp Lys Gly Phe Thr Pro Ile Asn Phe Val Phe Pro Asn Leu Pro Leu
225 230 235 240

Pro His Tyr Trp Arg Arg Asp Ala Ala Gln Arg Lys Ile Ser Ala His
245 250 255

Tyr Met Lys Glu Ile Lys Arg Arg Arg Glu Ser Gly Asp Ile Asp Pro
260 265 270

Lys Arg Asp Leu Ile Asp Ser Leu Leu Val Asn Ser Thr Tyr Lys Asp
275 280 285

Gly Val Lys Met Thr Asp Gln Glu Ile Ala Asn Leu Leu Ile Gly Val
290 295 300

Leu Met Gly Gly Gln His Thr Ser Ala Ser Thr Ser Ala Trp Phe Leu
305 310 315 320

Leu His Leu Ala Glu Gln Pro Gln Leu Gln Asp Asp Leu Tyr Glu Glu
325 330 335

Leu Thr Asn Leu Leu Lys Glu Lys Gly Gly Asp Leu Asn Asp Leu Thr
340 345 350

Tyr Glu Asp Leu Gln Lys Leu Pro Leu Val Asn Asn Thr Ile Lys Glu
355 360 365

Thr Leu Arg Met His Met Pro Leu His Ser Ile Phe Arg Lys Val Met
370 375 380

Asn Pro Leu Arg Val Pro Asn Thr Lys Tyr Val Ile Pro Lys Gly His
385 390 395 400

Tyr Val Leu Val Ser Ala Gly Tyr Ala His Thr Ser Asp Arg Trp Phe
405 410 415

Glu His Pro Glu His Phe Asn Pro Arg Arg Trp Glu Ser Asp Asp Thr
420 425 430

Lys Ala Ser Ala Val Ser Phe Asn Ser Glu Asp Thr Val Asp Tyr Gly
435 440 445

Phe Gly Lys Ile Ser Lys Gly Val Ser Ser Pro Tyr Leu Pro Phe Gly
450 455 460

Gly Gly Arg His Arg Cys Ile Gly Glu Gln Phe Ala Tyr Val Gln Leu
465 470 475 480

Gly Thr Ile Leu Thr Thr Tyr Ile Tyr Asn Phe Lys Trp Arg Leu Asn
485 490 495

Gly Asp Lys Val Pro Asp Val Asp Tyr Gln Ser Met Val Thr Leu Pro
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Leu Glu Pro Ala Glu Ile Val Trp Glu Lys Arg Asp Thr Cys Met Val
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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	

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

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Arg	Asp	Thr	Glu	Ser	Gly	Ile	Lys	Phe	Lys	Ile	Thr	Gly	Pro	Lys	Lys	
				405					410					415		
tac	ggt	ggt	tcc	ggt	ggt	tct	ttg	caa	acc	cca	ggt	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	ggt	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	ggt	tgt	aat	gcc	gtc	gat	gat	tta	1440
Tyr	Lys	Arg	Pro	Leu	Met	Thr	Ala	Val	Cys	Asn	Ala	Val	Asp	Asp	Leu	
					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	ggt	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	ggt	gac	tac	act	ggt	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	ggt	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	
		610				615					620					
ggt	tct	gct	cat	caa	atg	agt	tcg	tgt	aga	atg	tct	ggt	aag	gga	cca	1920
Gly	Ser	Ala	His	Gln	Met	Ser	Ser	Cys	Arg	Met	Ser	Gly	Lys	Gly	Pro	
				625		630				635				640		
gga	tac	ggt	gct	tgt	gac	act	aaa	gga	aga	tta	ttt	gaa	tgt	aac	aac	1968
Gly	Tyr	Gly	Ala	Cys	Asp	Thr	Lys	Gly	Arg	Leu	Phe	Glu	Cys	Asn	Asn	
				645				650						655		

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gtt tac gtt gct gat gct tcg gtt atg cct act gca tcg gga gtc aat 2016
Val Tyr Val Ala Asp Ala Ser Val Met Pro Thr Ala Ser Gly Val Asn
660 665 670

cct atg atc act aca atg gct ttt gca aga cat gtg gcc tta tgt ctt 2064
Pro Met Ile Thr Thr Met Ala Phe Ala Arg His Val Ala Leu Cys Leu
675 680 685

gct aaa gac ttg caa cca caa act aaa ctt tag 2097
Ala Lys Asp Leu Gln Pro Gln Thr Lys Leu
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<211> 698

<212> PRT

5 <213> Candida cloacae

<400> 54

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Leu His Pro Asp Phe Pro Lys Asp Lys Ile Glu Glu Tyr Leu Thr Gly
35 40 45

Phe Ser Arg Pro Ser Ala Val Pro Gln Phe Arg Gln Cys Ala Lys Lys
50 55 60

Leu Ile Asn Arg Gly Ser Glu Leu Ser Ile Lys Leu Phe Leu Tyr Leu
65 70 75 80

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

Leu Thr Leu Ile Arg Asp Met Asp Leu Ser Gln Arg Glu Glu Leu Leu
100 105 110

Arg Ser Trp Arg Asp Ser Pro Leu Thr Ala Lys Arg Arg Leu Phe Arg
115 120 125

Val Tyr Ala Ser Phe Thr Leu Ser Thr Phe Asn Lys Leu Gly Thr Asp
130 135 140

Leu His Phe Lys Ala Leu Gly Tyr Pro Gly Arg Glu Leu Arg Thr Gln
145 150 155 160

Ile Gln Asp Tyr Glu Val Asp Pro Phe Arg Tyr Ser Phe Met Glu Lys
165 170 175

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Leu Lys His Glu Gly His Glu Leu Phe Leu Pro Asp Ile Asp Val Leu
 180 185 190
 Ile Ile Gly Ser Gly Ser Gly Ala Gly Val Val Ala Gln Thr Leu Thr
 195 200 205
 Glu Ser Gly Leu Lys Ser Leu Val Leu Glu Lys Gly Lys Tyr Phe Ala
 210 215 220
 Ser Glu Glu Leu Cys Met Thr Asp Leu Asp Gly Asn Glu Ala Leu Phe
 225 230 235 240
 Glu Ser Gly Gly Thr Ile Pro Ser Thr Asn Gln Gln Leu Phe Met Ile
 245 250 255
 Ala Gly Ser Thr Phe Gly Gly Gly Ser Thr Val Asn Trp Ser Ala Cys
 260 265 270
 Leu Lys Thr Pro Phe Lys Val Arg Lys Glu Trp Tyr Asp Asp Phe Gly
 275 280 285
 Leu Asp Phe Val Ala Thr Gln Gln Tyr Asp Asp Cys Met Asp Tyr Val
 290 295 300
 Trp Lys Lys Met Gly Ala Ser Thr Glu His Ile Glu His Ser Ala Ala
 305 310 315 320
 Asn Ala Val Ile Met Asp Gly Ala Ala Lys Leu Gly Tyr Ala His Arg
 325 330 335
 Ala Leu Glu Gln Asn Thr Gly Gly His Val His Asp Cys Gly Met Cys
 340 345 350
 His Leu Gly Cys Arg Phe Gly Ile Lys Gln Gly Gly Val Asn Cys Trp
 355 360 365
 Phe Arg Glu Pro Ser Glu Lys Gly Ser Lys Phe Met Glu Gln Val Val
 370 375 380
 Val Glu Lys Ile Leu Gln His Lys Gly Lys Ala Thr Gly Ile Leu Cys
 385 390 395 400
 Arg Asp Thr Glu Ser Gly Ile Lys Phe Lys Ile Thr Gly Pro Lys Lys
 405 410 415
 Tyr Val Val Ser Gly Gly Ser Leu Gln Thr Pro Val Leu Leu Gln Lys
 420 425 430

ES 2 626 442 T3

Ser Gly Phe Lys Asn Lys His Ile Gly Ala Asn Leu Lys Leu His Pro
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 Val Ser Val Ala Leu Gly Asp Phe Gly Asn Glu Val Asp Phe Glu Ala
 450 455 460
 Tyr Lys Arg Pro Leu Met Thr Ala Val Cys Asn Ala Val Asp Asp Leu
 465 470 475 480
 Asp Gly Lys Ala His Gly Thr Arg Ile Glu Ala Ile Leu His Ala Pro
 485 490 495
 Tyr Val Thr Ala Pro Phe Tyr Pro Trp Gln Ser Gly Ala Gln Ala Arg
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 Lys Asn Leu Leu Lys Tyr Lys Gln Thr Val Pro Leu Leu Leu Ser
 515 520 525
 Arg Asp Thr Ser Ser Gly Thr Val Thr Tyr Asp Lys Gln Lys Pro Asp
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 Val Leu Val Val Asp Tyr Thr Val Asn Lys Phe Asp Arg Asn Ser Ile
 545 550 555 560
 Leu Gln Gly Phe Leu Val Ala Ser Asp Ile Leu Tyr Ile Glu Gly Ala
 565 570 575
 Lys Glu Ile Leu Ser Pro Gln Ala Trp Val Pro Thr Phe Lys Ser Asn
 580 585 590
 Lys Pro Lys His Ala Arg Ser Ile Lys Asp Glu Asp Tyr Val Lys Trp
 595 600 605
 Arg Glu Thr Val Ala Lys Ile Pro Phe Asp Ser Tyr Gly Ser Pro Tyr
 610 615 620
 Gly Ser Ala His Gln Met Ser Ser Cys Arg Met Ser Gly Lys Gly Pro
 625 630 635 640
 Gly Tyr Gly Ala Cys Asp Thr Lys Gly Arg Leu Phe Glu Cys Asn Asn
 645 650 655
 Val Tyr Val Ala Asp Ala Ser Val Met Pro Thr Ala Ser Gly Val Asn
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 Pro Met Ile Thr Thr Met Ala Phe Ala Arg His Val Ala Leu Cys Leu
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 Ala Lys Asp Leu Gln Pro Gln Thr Lys Leu
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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

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Pro	Gln	Gln	Asp	Gly	Gln	Glu	Leu	His	Phe	Pro	Asp	Ile	Asp	Val	Leu	
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Ile	Ile	Gly	Ser	Gly	Ser	Gly	Ala	Gly	Val	Val	Ala	Gln	Thr	Leu	Ser	
		195					200					205				
gaa	aac	gga	ctt	aaa	tca	ttg	gtg	ttg	gaa	aaa	ggt	aaa	tac	ttt	tcc	672
Glu	Asn	Gly	Leu	Lys	Ser	Leu	Val	Leu	Glu	Lys	Gly	Lys	Tyr	Phe	Ser	
	210					215					220					
aat	gat	gag	ttg	acc	atg	aat	gat	ttg	gaa	ggt	agt	gag	gca	tta	ttc	720
Asn	Asp	Glu	Leu	Thr	Met	Asn	Asp	Leu	Glu	Gly	Ser	Glu	Ala	Leu	Phe	
225					230					235					240	
gaa	aat	gga	ggt	gcc	ctc	agt	agt	acc	aac	caa	cag	ata	ttt	ata	att	768
Glu	Asn	Gly	Gly	Ala	Leu	Ser	Ser	Thr	Asn	Gln	Gln	Ile	Phe	Ile	Ile	
				245					250					255		
gca	ggt	tcg	act	ttt	ggg	ggt	ggt	tct	aca	gtt	aat	tgg	tct	gcc	tgt	816
Ala	Gly	Ser	Thr	Phe	Gly	Gly	Gly	Ser	Thr	Val	Asn	Trp	Ser	Ala	Cys	
			260					265						270		
tta	aaa	act	ccg	ttc	aaa	gta	aga	aaa	gag	tgg	tat	gac	aac	ttc	gga	864
Leu	Lys	Thr	Pro	Phe	Lys	Val	Arg	Lys	Glu	Trp	Tyr	Asp	Asn	Phe	Gly	
	275						280					285				
ctt	gat	ttc	gtc	gca	acc	caa	tac	tac	gaa	gat	tgt	atg	gat	tat	gtt	912
Leu	Asp	Phe	Val	Ala	Thr	Gln	Tyr	Tyr	Glu	Asp	Cys	Met	Asp	Tyr	Val	
	290					295					300					
tgg	aag	aaa	atg	ggt	gct	tcg	aac	gaa	aat	atc	gac	cat	tct	ggt	gct	960
Trp	Lys	Lys	Met	Gly	Ala	Ser	Asn	Glu	Asn	Ile	Asp	His	Ser	Gly	Ala	
305				310						315				320		
aat	agt	gtt	ata	ttg	gaa	ggg	tcc	aaa	aaa	ctt	ggc	tac	cct	cac	agg	1008
Asn	Ser	Val	Ile	Leu	Glu	Gly	Ser	Lys	Lys	Leu	Gly	Tyr	Pro	His	Arg	
			325						330					335		
gcc	gtt	gaa	caa	aat	aat	ggg	ggc	aaa	att	cat	gac	tgt	ggt	atg	tgt	1056
Ala	Val	Glu	Gln	Asn	Asn	Gly	Gly	Lys	Ile	His	Asp	Cys	Gly	Met	Cys	
			340					345					350			
cac	ttg	ggt	tgt	aga	ttt	ggt	att	aaa	cag	gga	agt	gta	aat	tgc	tgg	1104
His	Leu	Gly	Cys	Arg	Phe	Gly	Ile	Lys	Gln	Gly	Ser	Val	Asn	Cys	Trp	
		355				360						365				
ttc	cgt	ggt	cca	agt	gaa	aac	gga	tcc	aag	ttt	atg	caa	caa	gtt	ctc	1152
Phe	Arg	Gly	Pro	Ser	Glu	Asn	Gly	Ser	Lys	Phe	Met	Gln	Gln	Val	Leu	
	370					375					380					
gtg	gat	aag	ata	ttg	caa	cgt	gac	ggt	aaa	gca	gtc	ggt	gtt	ttg	tgt	1200
Val	Asp	Lys	Ile	Leu	Gln	Arg	Asp	Gly	Lys	Ala	Val	Gly	Val	Leu	Cys	
	385				390					395				400		
aga	gat	gtt	gta	acc	ggt	gtt	aag	ttc	aag	atc	act	gga	cca	aag	aaa	1248
Arg	Asp	Val	Val	Thr	Gly	Val	Lys	Phe	Lys	Ile	Thr	Gly	Pro	Lys	Lys	
				405				410					415			
att	gtt	gtt	ttc	tgg	tgg	ttc	ttt	gca	aac	tcc	ggt	ttt	gtt	aca	aaa	1296
Ile	Val	Val	Phe	Trp	Trp	Phe	Phe	Ala	Asn	Ser	Gly	Phe	Val	Thr	Lys	
			420					425					430			

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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 Gln Thr Val Pro Ile Leu Leu Leu Ser 515 520 525	1584
aga gat act act tca ggg tct gtc aca tat gat aaa caa aaa cca gat Arg Asp Thr Thr Ser Gly Ser Val Thr Tyr Asp Lys Gln Lys Pro Asp 530 535 540	1632
gca ttg gtg att gat tac ctg tta aac aag ttt gac aga aac tca att Ala Leu Val Ile Asp Tyr Leu Leu Asn Lys Phe Asp Arg Asn Ser Ile 545 550 555 560	1680
tta caa ggg ttt ttg ata gct tca gac ctt tta tat att gaa ggt gcc Leu Gln Gly Phe Leu Ile Ala Ser Asp Leu Leu Tyr Ile Glu Gly Ala 565 570 575	1728
agt aga gat cat gtc acc tac aag ctt ggg tac caa tgg ttc aag agt Ser Arg Asp His Val Thr Tyr Lys Leu Gly Tyr Gln Trp Phe Lys Ser 580 585 590	1776
tct aaa cct aaa cat gcc aga tcg att gaa gat gaa gac tac gta aac Ser Lys Pro Lys His Ala Arg Ser Ile Glu Asp Glu Asp Tyr Val Asn 595 600 605	1824
tgg aga gct aaa gtt gca aag att cca ttt gat tcc tac gga tca cca Trp Arg Ala Lys Val Ala Lys Ile Pro Phe Asp Ser Tyr Gly Ser Pro 610 615 620	1872
tac ggt tca gct cac caa atg agt aca tgc aga atg tca ggt aag gga Tyr Gly Ser Ala His Gln Met Ser Thr Cys Arg Met Ser Gly Lys Gly 625 630 635 640	1920
cca gga tat gga gct tgt gat acc aaa gga aaa tta ttt gaa tgt agc Pro Gly Tyr Gly Ala Cys Asp Thr Lys Gly Lys Leu Phe Glu Cys Ser 645 650 655	1968
aat gtt tat gtt gca gat gct tcc act ttg cct act gca tca ggg gct Asn Val Tyr Val Ala Asp Ala Ser Thr Leu Pro Thr Ala Ser Gly Ala 660 665 670	2016
aat cca atg gtt agt acc atg tca ttt gca agg cac gtg tcc tta gga Asn Pro Met Val Ser Thr Met Ser Phe Ala Arg His Val Ser Leu Gly 675 680 685	2064
att gtt aaa gaa ttg caa caa agt aaa ctt tag Ile Val Lys Glu Leu Gln Gln Ser Lys Leu 690 695	2097

<210> 56

<211> 698

<212> PRT

<213> Candida cloacae

ES 2 626 442 T3

<400> 56

Met Asn Pro Val Val Glu Asp Ser His Leu Asp Val Phe Cys Leu Leu
1 5 10 15

Ala Asp Ala Val Val His Glu Ile Pro Pro Ser Glu Ile Val Glu Tyr
20 25 30

Leu His Pro Asp Phe Pro Lys Asp Lys Val Glu Glu Tyr Leu Ala Glu
35 40 45

Phe Ser His Pro Ser Ala Ile Pro Glu Phe Arg Glu Val Ala Lys Arg
50 55 60

Ile Ile Asn Lys Gly Thr Val Leu Ser Ile Lys Leu Phe Leu Leu Leu
65 70 75 80

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

Thr Thr Leu Ile Arg Asp Met Asp Leu Ser Gln Arg Glu Glu Leu Leu
100 105 110

Arg Ser Trp Arg Asp Ser Pro Phe Thr Thr Lys Arg Lys Leu Phe Arg
115 120 125

Val Tyr Asn Ser Phe Thr Leu Asn Ala Phe Ser Lys Thr Ala Thr Asp
130 135 140

Leu His Phe Lys Ala Leu Gly Tyr Pro Gly Arg Glu Leu Arg Thr Gln
145 150 155 160

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

Pro Gln Gln Asp Gly Gln Glu Leu His Phe Pro Asp Ile Asp Val Leu
180 185 190

Ile Ile Gly Ser Gly Ser Gly Ala Gly Val Val Ala Gln Thr Leu Ser
195 200 205

ES 2 626 442 T3

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

ES 2 626 442 T3

450 455 460

Tyr Arg Lys Pro Ile Met Thr Ser Ile Cys Asn Lys Val Glu Asp Leu
465 470 475 480

Asp Gly Lys Ala His Gly Thr Arg Ile Glu Ala Met Leu Asn Ala Pro
485 490 495

Tyr Gly Val Ala Pro Phe Phe Pro Trp Lys Ser Gly Ala Glu Ser Arg
500 505 510

Lys Asp Leu Leu Arg Tyr Lys Gln Thr Val Pro Ile Leu Leu Leu Ser
515 520 525

Arg Asp Thr Thr Ser Gly Ser Val Thr Tyr Asp Lys Gln Lys Pro Asp
530 535 540

Ala Leu Val Ile Asp Tyr Leu Leu Asn Lys Phe Asp Arg Asn Ser Ile
545 550 555 560

Leu Gln Gly Phe Leu Ile Ala Ser Asp Leu Leu Tyr Ile Glu Gly Ala
565 570 575

Ser Arg Asp His Val Thr Tyr Lys Leu Gly Tyr Gln Trp Phe Lys Ser
580 585 590

Ser Lys Pro Lys His Ala Arg Ser Ile Glu Asp Glu Asp Tyr Val Asn
595 600 605

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

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

Pro Gly Tyr Gly Ala Cys Asp Thr Lys Gly Lys Leu Phe Glu Cys Ser
645 650 655

Asn Val Tyr Val Ala Asp Ala Ser Thr Leu Pro Thr Ala Ser Gly Ala
660 665 670

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

Ile Val Lys Glu Leu Gln Gln Ser Lys Leu
690 695

<210> 57

< 211> 948

< 212> DNA

5 < 213> Candida tropicalis

<220>

< 221> CDS

< 222> (1)..(948)

ES 2 626 442 T3

<400>	57
cga 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 ctg gtg cac gtg aaa tgc toc ggt gtt tgt cac tcg gat ata cac	96
Leu Leu Val His Val Lys Tyr Ser Gly Val Cys His Ser Asp Ile His	
20 25 30	
gtg tgg aag ggt gag tgg ttc cca gca tgc aaa ttg ccg 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 gtg 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 gag ttg gca ggt ata aag atg ttgaat gggtcc	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 tactgtcaa caagggtgct gaaccacaacctgtccc	288
Cys MetAsnCysGluTyrCysGlnGlnGlyAlaGluProAsnCysPro	
85 90 95	
cac gct gat gtg tgc ggt tac tgc cac ggt act ttc caa cag tac	336
His Ala Asp ValSerGlyTyrSerHisAspGlyThrPheGlnGlnTyr	
100 105 110	
gct acc gcc gat gct gtt caa gct gctaaa ttccaactgggttctgat	384
Ala ThrAlaAspAlaValGlnAlaAlaLysPheProAlaGlySerAsp	
115 120 125	
tta gct agc atc gca cct ata tgc tgc gcc ggt gtt act gtt tac aaa	432
Leu AlaSerIleAlaProIleSerCysAlaGlyValThrValTyrLys	
130 135 140	
gca ttg aaa act gca ggc ttg cag cca ggt caa tgg gtt gcc atc tot	480
Ala LeuLysThrAlaGlyLeuGlnProGlyGlnTrpValAlaIleSer	
145 150 155 160	
ggt gca gct ggt ggt ttg ggt tct ttg gct gtg caa tac gcc aag gcc	528
Gly AlaAlaGlyGlyLeuGlySerLeuAlaValGlnTyrAlaLysAla	
165 170 175	
atg ggt ttg aga gtc gtg gcc att gag ggt ggt gag gaa aga gga gtg	576
Met GlyLeuArgValValAlaIleAspGlyGlyAspGluArgGlyVal	
180 185 190	
ttt gtc aaa tgc ttg ggt gct gaa gtt ttc gtt gat ttc acc aaa gag	624
Phe ValLysSerLeuGlyAlaGluValPheValAspPheThrLysGlu	
195 200 205	

ES 2 626 442 T3

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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

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<210> 58

<211> 316

<212> PRT

5 <213> Candida tropicalis

<400> 58

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Pro Leu Gln Tyr Thr Asp Ile Pro Val Pro Val Pro Lys Pro Asn Glu
1                               5                               10                               15

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Leu Leu Val His Val Lys Tyr Ser Gly Val Cys His Ser Asp Ile His
20                               25                               30

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```

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

```

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Gly Trp Lys Val Gly Asp Leu Ala Gly Ile Lys Met Leu Asn Gly Ser
65                               70                               75                               80

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Cys Met Asn Cys Glu Tyr Cys Gln Gln Gly Ala Glu Pro Asn Cys Pro
85                               90                               95

```

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His Ala Asp Val Ser Gly Tyr Ser His Asp Gly Thr Phe Gln Gln Tyr
100                               105                               110

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ES 2 626 442 T3

Ala Thr Ala Asp Ala Val Gln Ala Ala Lys Phe Pro Ala Gly Ser Asp
115 120 125

Leu Ala Ser Ile Ala Pro Ile Ser Cys Ala Gly Val Thr Val Tyr Lys
130 135 140

Ala Leu Lys Thr Ala Gly Leu Gln Pro Gly Gln Trp Val Ala Ile Ser
145 150 155 160

Gly Ala Ala Gly Gly Leu Gly Ser Leu Ala Val Gln Tyr Ala Lys Ala
165 170 175

Met Gly Leu Arg Val Val Ala Ile Asp Gly Gly Asp Glu Arg Gly Val
180 185 190

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

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

Gly Val Ile Asn Val Ser Ile Ser Glu Lys Ala Ile Asn Gln Ser Val
225 230 235 240

Glu Tyr Val Arg Thr Leu Gly Thr Val Val Leu Val Gly Leu Pro Ala
245 250 255

Gly Ala Lys Leu Glu Ala Pro Ile Phe Asn Ala Val Ala Lys Ser Ile
260 265 270

Gln Ile Lys Gly Ser Tyr Val Gly Asn Arg Arg Asp Thr Ala Glu Ala
275 280 285

Val Asp Phe Phe Ala Arg Gly Leu Val Lys Cys Pro Ile Lys Val Val
290 295 300

Gly Leu Ser Glu Leu Pro Glu Ile Phe Lys Leu Leu
305 310 315

<210> 59

<211> 948

<212> DNA

5 <213> Candida tropicalis

<220>

<221> CDS

<222> (1)..(948)

<400> 59

ES 2 626 442 T3

aaa tta gaa tac aag gac atc cca gtt cca aag cca aag cca aac gaa Lys Leu Glu Tyr Lys Asp Ile Pro Val Pro Lys Pro Lys Pro Asn Glu 1 5 10 15	48
ttg ctc atc aac gtc aag tac tcc ggt gtc tgc cac act gat tta cac Leu Leu Ile Asn Val Lys Tyr Ser Gly Val Cys His Thr Asp Leu His 20 25 30	96
gcc tgg aag ggt gac tgg cca ttg gac acc aag ttg cca ttg gtg ggt Ala Trp Lys Gly Asp Trp Pro Leu Asp Thr Lys Leu Pro Leu Val Gly 35 40 45	144
ggt cac gaa ggt gct ggt gtt gtt gtt gcc att ggt gac aat gtc aag Gly His Glu Gly Ala Gly Val Val Val Ala Ile Gly Asp Asn Val Lys 50 55 60	192
gga tgg aag gtc ggt gat ttg gcc ggt gtc aag tgg ttg aac ggt tcc Gly Trp Lys Val Gly Asp Leu Ala Gly Val Lys Trp Leu Asn Gly Ser 65 70 75 80	240
tgt atg aac tgt gag tac tgt caa cag ggt gcc gaa cca aac tgt cca Cys Met Asn Cys Glu Tyr Cys Gln Gln Gly Ala Glu Pro Asn Cys Pro 85 90 95	288
cag gct gac ttg tct ggt tac acc cac gac ggt tct ttc cag caa tac Gln Ala Asp Leu Ser Gly Tyr Thr His Asp Gly Ser Phe Gln Gln Tyr 100 105 110	336
gcc act gca gat gcc gtg caa gcc gct aga att cca gct ggt act gat Ala Thr Ala Asp Ala Val Gln Ala Ala Arg Ile Pro Ala Gly Thr Asp 115 120 125	384
tta gcc aac gtt gcc ccc atc ttg tgt gct ggt gtc act gtt tac aag Leu Ala Asn Val Ala Pro Ile Leu Cys Ala Gly Val Thr Val Tyr Lys 130 135 140	432
gcc ttg aag acc gcc gac ttg cag cca ggt caa tgg gtc gcc att tcc Ala Leu Lys Thr Ala Asp Leu Gln Pro Gly Gln Trp Val Ala Ile Ser 145 150 155 160	480
ggt gcc gct ggt ggt ttg ggt tct ttg gcc gtt caa tac gcc aag gcc Gly Ala Ala Gly Gly Leu Gly Ser Leu Ala Val Gln Tyr Ala Lys Ala 165 170 175	528
atg ggc tac aga gtt gtc gcc atc gat ggt ggt gcc gac aag ggt gag Met Gly Tyr Arg Val Val Ala Ile Asp Gly Gly Ala Asp Lys Gly Glu 180 185 190	576
ttc gtc aag tct ttg ggc gct gag gtc ttt gtt gat ttc ctc aag gaa Phe Val Lys Ser Leu Gly Ala Glu Val Phe Val Asp Phe Leu Lys Glu 195 200 205	624
aag gac att gtt ggt gct gtc aag aag gca acc gat ggt ggc cca cac Lys Asp Ile Val Gly Ala Val Lys Lys Ala Thr Asp Gly Gly Pro His 210 215 220	672
ggt gcc gtt aac gtt tcc atc tcc gaa aag gcc atc aac caa tct gtc Gly Ala Val Asn Val Ser Ile Ser Glu Lys Ala Ile Asn Gln Ser Val 225 230 235 240	720
gac tac gtt aga acc ttg ggt aag gtt gtc ttg gtc ggt ttg cca gct Asp Tyr Val Arg Thr Leu Gly Lys Val Val Leu Val Gly Leu Pro Ala	768

ES 2 626 442 T3

	245	250	255	
	ggc tcc aag gtt tct gct cca gtc ttt gac tcc gtc gtc aag tcc atc			816
	Gly Ser Lys Val Ser Ala Pro Val Phe Asp Ser Val Val Lys Ser Ile			
	260	265	270	
	caa atc aag ggt tcc tat gtc ggt aac aga aag gac act gcc gaa gct			864
	Gln Ile Lys Gly Ser Tyr Val Gly Asn Arg Lys Asp Thr Ala Glu Ala			
	275	280	285	
	ggt gac ttt ttc tcc aga ggc ttg atc aag tgt cca atc aag gtt 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> 60			
	<211> 316			
	<212> PRT			
5	<213> Candida tropicalis			
	<400> 60			
	Lys Leu Glu Tyr Lys Asp Ile Pro Val Pro Lys Pro Lys Pro Asn Glu			
	1	5	10	15
	Leu Leu Ile Asn Val Lys Tyr Ser Gly Val Cys His Thr Asp Leu His			
	20	25	30	
	Ala Trp Lys Gly Asp Trp Pro Leu Asp Thr Lys Leu Pro Leu Val Gly			
	35	40	45	
	Gly His Glu Gly Ala Gly Val Val Val Ala Ile Gly Asp Asn Val Lys			
	50	55	60	
	Gly Trp Lys Val Gly Asp Leu Ala Gly Val Lys Trp Leu Asn Gly Ser			
	65	70	75	80
	Cys Met Asn Cys Glu Tyr Cys Gln Gln Gly Ala Glu Pro Asn Cys Pro			
	85	90	95	
	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			

ES 2 626 442 T3

145						150						155						160
Gly	Ala	Ala	Gly	Gly	Leu	Gly	Ser	Leu	Ala	Val	Gln	Tyr	Ala	Lys	Ala			
				165					170					175				
Met	Gly	Tyr	Arg	Val	Val	Ala	Ile	Asp	Gly	Gly	Ala	Asp	Lys	Gly	Glu			
			180					185					190					
Phe	Val	Lys	Ser	Leu	Gly	Ala	Glu	Val	Phe	Val	Asp	Phe	Leu	Lys	Glu			
		195					200					205						
Lys	Asp	Ile	Val	Gly	Ala	Val	Lys	Lys	Ala	Thr	Asp	Gly	Gly	Pro	His			
	210					215					220							
Gly	Ala	Val	Asn	Val	Ser	Ile	Ser	Glu	Lys	Ala	Ile	Asn	Gln	Ser	Val			
225					230					235					240			
Asp	Tyr	Val	Arg	Thr	Leu	Gly	Lys	Val	Val	Leu	Val	Gly	Leu	Pro	Ala			
				245					250					255				
Gly	Ser	Lys	Val	Ser	Ala	Pro	Val	Phe	Asp	Ser	Val	Val	Lys	Ser	Ile			
			260					265					270					
Gln	Ile	Lys	Gly	Ser	Tyr	Val	Gly	Asn	Arg	Lys	Asp	Thr	Ala	Glu	Ala			
		275					280					285						
Val	Asp	Phe	Phe	Ser	Arg	Gly	Leu	Ile	Lys	Cys	Pro	Ile	Lys	Val	Val			
	290					295					300							
Gly	Leu	Ser	Glu	Leu	Pro	Glu	Val	Tyr	Lys	Leu	Met							
305					310					315								

<210> 61
< 211> 456
< 212> DNA
< 213> *Candida tropicalis*

<220>
< 221> CDS
< 222> (1)..(456)

<400> 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

ES 2 626 442 T3

Ala Asp Ala Val Gln Ala Ala Lys Ile Pro Glu Gly Ala Asp Met Ala	
35 40 45	
agt atc gcc ccg atc ttg tgt gct ggt gtg acc gtg tac aag gct ttg	192
Ser Ile Ala Pro Ile Leu Cys Ala Gly Val Thr Val Tyr Lys Ala Leu	
50 55 60	
aag aac gcc gac ttg ttg gct ggc caa tgg gtg gct atc tct ggt gct	240
Lys Asn Ala Asp Leu Leu Ala Gly Gln Trp Val Ala Ile Ser Gly Ala	
65 70 75 80	
ggt ggt ggt ttg ggc tcc ttg ggt gtg cag tac gct aaa gcc atg ggt	288
Gly Gly Gly Leu Gly Ser Leu Gly Val Gln Tyr Ala Lys Ala Met Gly	
85 90 95	
tac aga gtg tta gcc atc gat ggt ggt gat gag aga gga gag ttt gtc	336
Tyr Arg Val Leu Ala Ile Asp Gly Gly Asp Glu Arg Gly Glu Phe Val	
100 105 110	
aag tca ttg ggc gcc gaa gtg tac att gac ttc ctt aag gaa cag gac	384
Lys Ser Leu Gly Ala Glu Val Tyr Ile Asp Phe Leu Lys Glu Gln Asp	
115 120 125	
att gtt agt gcc att aga aag gca act ggt ggt ggc cca cac ggt gtt	432
Ile Val Ser Ala Ile Arg Lys Ala Thr Gly Gly Gly Pro His Gly Val	
130 135 140	
att aac gtc tcg gtg tcc gaa aag	456
Ile Asn Val Ser Val Ser Glu Lys	
145 150	

<210> 62
 <211> 152
 <212> PRT
 5 <213> Candida tropicalis

<400> 62
Asn Cys Glu Phe Cys Gln Gln Gly Ala Glu Pro Asn Cys Pro Arg Ala
1 5 10 15
Asp Met Ser Gly Tyr Thr His Asp Gly Thr Phe Gln Gln Tyr Ala Thr
20 25 30
Ala Asp Ala Val Gln Ala Ala Lys Ile Pro Glu Gly Ala Asp Met Ala
35 40 45
Ser Ile Ala Pro Ile Leu Cys Ala Gly Val Thr Val Tyr Lys Ala Leu
50 55 60
Lys Asn Ala Asp Leu Leu Ala Gly Gln Trp Val Ala Ile Ser Gly Ala
65 70 75 80
Gly Gly Gly Leu Gly Ser Leu Gly Val Gln Tyr Ala Lys Ala Met Gly
85 90 95

ES 2 626 442 T3

Tyr Arg Val Leu Ala Ile Asp Gly Gly Asp Glu Arg Gly Glu Phe Val
100 105 110

Lys Ser Leu Gly Ala Glu Val Tyr Ile Asp Phe Leu Lys Glu Gln Asp
115 120 125

Ile Val Ser Ala Ile Arg Lys Ala Thr Gly Gly Gly Pro His Gly Val
130 135 140

Ile Asn Val Ser Val Ser Glu Lys
145 150

<210> 63
<211> 948
<212> DNA
5 <213> Candida tropicalis

<220>
<221> CDS
<222> (1)..(948)

<400> 63
aag tta gaa tac aaa gac gtg ccg gtc cct gtc cct aaa ccc aac gaa 48
Lys Leu Glu Tyr Lys Asp Val Pro Val Pro Lys Pro Asn Glu
1 5 10 15
ttg ctt gtc aac gtc aag tac tcg ggt gtg tgt cat tct gac ttg cat 96
Leu Leu Val Asn Val Lys Tyr Ser Gly Val Cys His Ser Leu His
20 25 30
gtc tgg aaa ggc gac tgg ccc att cct gcc aag ttg ccc ttg gtg gga 144
Val Trp Lys Gly Asp Trp Pro Ile Pro Ala Lys Leu Pro Leu Val Gly
35 40 45
ggt cac gaa ggt gct ggt gtc gtt gtc ggc atg ggt gac aac gtc aag 192
Gly His Glu Gly Ala Gly Val Val Val Gly Met Gly Asp Asn Val Lys
50 55 60
ggc tgg aag gtg ggg gac ttg gct ggt atc aag tgg ttg aat ggt tcg 240
Gly Trp Lys Val Gly Asp Leu Ala Gly Ile Lys Trp Leu Asn Gly Ser
65 70 75 80
tgt atg aac tgt gag ttt tgc caa cag ggc gca gaa cct aac tgt tca 288
Cys Met Asn Cys Glu Phe Cys Gln Gln Gly Ala Glu Pro Asn Cys Ser
85 90 95
aga gcc gac atg tct ggg tat acc cac gat gga act ttc caa caa tac 336
Arg Ala Asp Met Ser Gly Tyr Thr His Asp Gly Thr Phe Gln Gln Tyr
100 105 110
gcc act gct gat gct gtc caa gct gcc aag atc cca gaa ggc gcc gac 384
Ala Thr Ala Asp Ala Val Gln Ala Ala Lys Ile Pro Glu Gly Ala Asp
115 120 125
atg gct agt atc gcc ccg atc ttg tgc gct ggt 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

10

ES 2 626 442 T3

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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

ggt gct ggt ggt ggt ttg ggc tcc ttg ggt gtg cag tac gct aaa gcc      528
Gly Ala Gly Gly Gly Leu Gly Ser Leu Gly Val Gln Tyr Ala Lys Ala
                      165                      170                      175

atg ggt tac aga gtg ttg gct atc gac ggt ggt 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 ggt ggt ggt cca cac      672
Gln Asp Ile Val Ser Ala Ile Arg Lys Ala Thr Gly Gly Gly Pro His
                      210                      215                      220

ggt gtt att aac gtg tca gtg tcc gaa aag gca atc aac cag tcg gtg      720
Gly Val Ile Asn Val Ser Val Ser Glu Lys Ala Ile Asn Gln Ser Val
225                      230                      235                      240

gag tac gtc aga act ttg ggg aaa gtg gtt tta gtt agc ttg ccg gca      768
Glu Tyr Val Arg Thr Leu Gly Lys Val Val Leu Val Ser Leu Pro Ala
                      245                      250                      255

ggt ggt aaa ctc act gct cct ctt ttc gag tct gtt gct aga tca atc      816
Gly Gly Lys Leu Thr Ala Pro Leu Phe Glu Ser Val Ala Arg Ser Ile
                      260                      265                      270

cag att aga act acg tgt gtt ggc aac aga aag gat act act gaa gct      864
Gln Ile Arg Thr Thr Cys Val Gly Asn Arg Lys Asp Thr Thr Glu Ala
                      275                      280                      285

att gat ttc ttt gtt aga ggg ttg atc gat tgc cca att aaa gtc gct      912
Ile Asp Phe Phe Val Arg Gly Leu Ile Asp Cys Pro Ile Lys Val Ala
290                      295                      300

ggt tta agt gaa gtg cca gag att ttt gac ttg atg      948
Gly Leu Ser Glu Val Pro Glu Ile Phe Asp Leu Met
305                      310                      315

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<210> 64
 <211> 316
 <212> PRT
 5 <213> Candida tropicalis

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<400> 64
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

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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

<210> 65
 <211> 948
 <212> DNA
 <213> Candida tropicalis

<220>

< 221> CDS
< 222> (1)..(948)

<400> 65

gaa tta gaa tac aaa gat atc cca gtg cca acc cca aag gcc aac gaa	48
Glu Leu Glu Tyr Lys Asp Ile Pro Val Pro Thr Pro Lys Ala Asn Glu	
1 5 10 15	
ttg ctc atc aac gtc aaa tac tcg ggt gtc tgc cac act gat ttg cac	96
Leu Leu Ile Asn Val Lys Tyr Ser Gly Val Cys His Thr Asp Leu His	
20 25 30	
gcc tgg aag ggt gac tgg cca ttg gcc acc aag ttg cca ttg gtt ggt	144
Ala Trp Lys Gly Asp Trp Pro Leu Ala Thr Lys Leu Pro Leu Val Gly	
35 40 45	
ggt cac gaa ggt gct ggt gtc gtt gtc ggc atg ggt gaa aac gtc aag	192
Gly His Glu Gly Ala Gly Val Val Val Gly Met Gly Glu Asn Val Lys	
50 55 60	
ggc tgg aag att ggt gac ttc gcc ggt atc aaa tgg ttg aac ggt tcc	240
Gly Trp Lys Ile Gly Asp Phe Ala Gly Ile Lys Trp Leu Asn Gly Ser	
65 70 75 80	
tgt atg tcc tgt gag ttc tgt caa caa ggt gct gaa cca aac tgt ggt	288
Cys Met Ser Cys Glu Phe Cys Gln Gln Gly Ala Glu Pro Asn Cys Gly	
85 90 95	
gag gcc gac ttg tct ggt tac acc cac gat ggt tct ttc gaa caa tac	336
Glu Ala Asp Leu Ser Gly Tyr Thr His Asp Gly Ser Phe Glu Gln Tyr	
100 105 110	
gcc act gct gat gct gtt caa gcc gcc aga atc cca gct ggt act gat	384
Ala Thr Ala Asp Ala Val Gln Ala Ala Arg Ile Pro Ala Gly Thr Asp	
115 120 125	
ttg gcc gaa gtt gcc cca atc ttg tgt gcg ggt gtc acc gtc tac aaa	432
Leu Ala Glu Val Ala Pro Ile Leu Cys Ala Gly Val Thr Val Tyr Lys	
130 135 140	
gcc ttg aag act gcc gac ttg gcc gct ggt caa tgg gtc gct atc tcc	480
Ala Leu Lys Thr Ala Asp Leu Ala Ala Gly Gln Trp Val Ala Ile Ser	
145 150 155 160	
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	

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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	
ggg gct atc aat gtt tcc gtt tcc gaa aaa gcc att gac caa tcc gtc			720
Gly Ala Ile Asn Val Ser Val Ser Glu Lys Ala Ile Asp Gln Ser Val			
225	230	235	240
gag tac gtt aga cca ttg ggt aag gtt gtt ttg gtt ggt ttg cca gct			768
Glu Tyr Val Arg Pro Leu Gly Lys Val Val Leu Val Gly Leu Pro Ala			
245	250	255	
ggc tcc aag gtc act gct ggt gtt ttc gaa gcc gtt gtc aag tcc att			816
Gly Ser Lys Val Thr Ala Gly Val Phe Glu Ala Val Val Lys Ser Ile			
260	265	270	
gaa atc aag ggt tcc tat gtc ggt aac aga aag gat acc gcc gaa gcc			864
Glu Ile Lys Gly Ser Tyr Val Gly Asn Arg Lys Asp Thr Ala Glu Ala			
275	280	285	
gtt gac ttt ttc tcc aga ggc ttg atc aag tgt cca atc aag att gtt			912
Val Asp Phe Phe Ser Arg Gly Leu Ile Lys Cys Pro Ile Lys Ile Val			
290	295	300	
ggc ttg agt gaa ttg cca cag gtc ttc aag ttg atg			948
Gly Leu Ser Glu Leu Pro Gln Val Phe Lys Leu Met			
305	310	315	

<210> 66

<211> 316

<212> PRT

5 <213> Candida tropicalis

<400> 66

Glu Leu Glu Tyr Lys Asp Ile Pro Val Pro Thr Pro Lys Ala Asn Glu
1 5 10 15

Leu Leu Ile Asn Val Lys Tyr Ser Gly Val Cys His Thr Asp Leu His
20 25 30

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

Gly His Glu Gly Ala Gly Val Val Val Gly Met Gly Glu Asn Val Lys
50 55 60

Gly Trp Lys Ile Gly Asp Phe Ala Gly Ile Lys Trp Leu Asn Gly Ser
65 70 75 80

Cys Met Ser Cys Glu Phe Cys Gln Gln Gly Ala Glu Pro Asn Cys Gly

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	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> 67
 <211> 1992
 <212> DNA
 5 <213> Candida tropicalis

<220>
 <221> CDS
 <222> (1)..(1992)

<400> 67

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ctt atg tta tta tgt gac ggg atc atc cac gaa acc acc gtc gac caa Leu Met Leu Leu Cys Asp Gly Ile Ile His Glu Thr Thr Val Asp Gln 1 5 10 15	48
atc aaa gac gtt att gct cct gac ttc cct gct gac aag tac gaa gag Ile Lys Asp Val Ile Ala Pro Asp Phe Pro Ala Asp Lys Tyr Glu Glu 20 25 30	96
tac gtc agg aca ttc acc aaa ccc tcc gaa acc cca ggg ttc agg gaa Tyr Val Arg Thr Phe Thr Lys Pro Ser Glu Thr Pro Gly Phe Arg Glu 35 40 45	144
acc gtc tac aac aca gtc aac gca aac acc acg gac gca atc cac cag Thr Val Tyr Asn Thr Val Asn Ala Asn Thr Thr Asp Ala Ile His Gln 50 55 60	192
ttc att atc ttg acc aat gtt ttg gca tcc agg gtc ttg gct cca gct Phe Ile Ile Leu Thr Asn Val Leu Ala Ser Arg Val Leu Ala Pro Ala 65 70 75 80	240
ttg acc aac tcg ttg acg cct atc aag gac atg agc ttg gaa gac cgt Leu Thr Asn Ser Leu Thr Pro Ile Lys Asp Met Ser Leu Glu Asp Arg 85 90 95	288
gaa aaa ttg ttg gcc tcg tgg cgc gac tcc cca atc gct gcc aaa agg Glu Lys Leu Leu Ala Ser Trp Arg Asp Ser Pro Ile Ala Ala Lys Arg 100 105 110	336
aaa ttg ttc agg ttg gtt tcc acg ctt acc ttg gtt act ttc acg aga Lys Leu Phe Arg Leu Val Ser Thr Leu Thr Leu Val Thr Phe Thr Arg 115 120 125	384
ttg gcc aat gag ttg cat ttg aaa gcc att cac tat cca gga aga gaa Leu Ala Asn Glu Leu His Leu Lys Ala Ile His Tyr Pro Gly Arg Glu 130 135 140	432
gac cgt gaa aag gct tat gaa acc cag gag att gac cct ttc aag tac Asp Arg Glu Lys Ala Tyr Glu Thr Gln Glu Ile Asp Pro Phe Lys Tyr 145 150 155 160	480
cag ttt atg gaa aag cca aag ttt gac ggc gct gag ttg tac ttg cca Gln Phe Met Glu Lys Pro Lys Phe Asp Gly Ala Glu Leu Tyr Leu Pro 165 170 175	528
gat att gat gtt atc att att gga tct ggt gcc ggt gct ggt gtt gtg Asp Ile Asp Val Ile Ile Ile Gly Ser Gly Ala Gly Ala Gly Val Val 180 185 190	576
gcc cac act ttg gcc aac gat ggc ttc aag agt ttg gtt ttg gaa aag Ala His Thr Leu Ala Asn Asp Gly Phe Lys Ser Leu Val Leu Glu Lys 195 200 205	624
ggc aaa tac ttt agc aac tcc gag ttg aac ttt gat gac aag gac ggc Gly Lys Tyr Phe Ser Asn Ser Glu Leu Asn Phe Asp Asp Lys Asp Gly 210 215 220	672

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ggt caa gaa tta tac caa agt gga ggt act ttg act aca gtc aac caa Val Gln Glu Leu Tyr Gln Ser Gly Gly Thr Leu Thr Thr Val Asn Gln 225 230 235 240	720
cag ttg ttt gtt ctt gct ggt tcc act ttt ggt ggc ggt acc act gtc Gln Leu Phe Val Leu Ala Gly Ser Thr Phe Gly Gly Gly Thr Thr Val 245 250 255	768
aat tgg tca gcc tgt ctt aag acg cca ttc aag gtg cgt aag gaa tgg Asn Trp Ser Ala Cys Leu Lys Thr Pro Phe Lys Val Arg Lys Glu Trp 260 265 270	816
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
ggt 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 ggc 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
ggt 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 ggc 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	1488
Thr Ile Leu Asn Ala Pro Phe Ile Gln Ala Ser Phe Leu Pro Trp Arg	
485 490 495	
ggt agt aac gag gct aga cga gac ttg ttg cgt tac aac aac atg gtg	1536
Gly Ser Asn Glu Ala Arg Arg Asp Leu Leu Arg Tyr Asn Asn Met Val	
500 505 510	
gcg atg ttg ctc ctt agt cgt gac acc acc agt ggt tcc gtt tct gct	1584
Ala Met Leu Leu Leu Ser Arg Asp Thr Thr Ser Gly Ser Val Ser Ala	
515 520 525	
cat cca acc aaa cct gaa gct ttg gtt gtc gag tac gac gtg aac aag	1632
His Pro Thr Lys Pro Glu Ala Leu Val Val Glu Tyr Asp Val Asn Lys	
530 535 540	
ttt gac aga aac tcg atc ttg cag gca ttg ttg gtc act gct gac ttg	1680
Phe Asp Arg Asn Ser Ile Leu Gln Ala Leu Leu Val Thr Ala Asp Leu	
545 550 555 560	
ttg tat atc caa ggt gcc aag aga atc ctt agt cca cag gca tgg gtg	1728
Leu Tyr Ile Gln Gly Ala Lys Arg Ile Leu Ser Pro Gln Ala Trp Val	
565 570 575	
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	

<210> 68

<211> 664

<212> PRT

5 <213> Candida tropicalis

<400> 68

Leu Met Leu Leu Cys Asp Gly Ile Ile His Glu Thr Thr Val Asp Gln
1 5 10 15

Ile Lys Asp Val Ile Ala Pro Asp Phe Pro Ala Asp Lys Tyr Glu Glu
20 25 30

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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
 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

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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
Gly Tyr Lys Ala Lys Val Leu Asp Gln Asn Ser Gly Gly His Pro Gln				
		325		330
His Arg Cys Gly Phe Cys Tyr Leu Gly Cys Lys His Gly Ile Lys Gln				
		340		345
Gly Ser Val Asn Asn Trp Phe Arg Asp Ala Ala Ala His Gly Ser Gln				
		355		360
Phe Met Gln Gln Val Arg Val Leu Gln Ile Leu Asn Lys Lys Gly Ile				
		370		375
Ala Tyr Gly Ile Leu Cys Glu Asp Val Val Thr Gly Ala Lys Phe Thr				
		385		390
Ile Thr Gly Pro Lys Lys Phe Val Val Ala Ala Gly Ala Leu Asn Thr				
		405		410
Pro Ser Val Leu Val Asn Ser Gly Phe Lys Asn Lys Asn Ile Gly Lys				
		420		425
Asn Leu Thr Leu His Pro Val Ser Val Val Phe Gly Asp Phe Gly Lys				
		435		440
Asp Val Gln Ala Asp His Phe His Asn Ser Ile Met Thr Ala Leu Cys				
		450		455
Ser Glu Ala Ala Asp Leu Asp Gly Lys Gly His Gly Cys Arg Ile Glu				
		465		470
Thr Ile Leu Asn Ala Pro Phe Ile Gln Ala Ser Phe Leu Pro Trp Arg				
		485		490
Gly Ser Asn Glu Ala Arg Arg Asp Leu Leu Arg Tyr Asn Asn Met Val				
		500		505
Ala Met Leu Leu Leu Ser Arg Asp Thr Thr Ser Gly Ser Val Ser Ala				
		515		520

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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

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

REIVINDICACIONES

1.- Célula de *Candida tropicalis*, caracterizada porque la célula, en comparación con su tipo salvaje, presenta una actividad reducida de al menos uno de los enzimas, que se codifican a través de las secuencias de ácido nucleico exentas de intrón, seleccionadas a partir de ambos grupos

5 A) y B) constituidos por

A) Seq ID Nr. 63,

B) una secuencia que es idéntica a Seq ID Nr. 63 en al menos un 80 %,

10 debiéndose entender por la actividad del enzima la actividad enzimática que cataliza las reacciones de ácido 12-hidroxi-dodecanoico para dar diácido 1,12-dodecanoico a través de la célula total, además caracterizada por que la reducción de la actividad enzimática se obtiene mediante modificación de un gen que comprende una de las secuencias de ácido nucleico citadas anteriormente, seleccionándose la modificación a partir del grupo que comprende inserción de ADN ajeno en el gen, delección al menos de partes del gen, mutaciones puntuales en la secuencia génica, exposición del gen a la influencia de la interferencia de ARN e intercambio de partes del gen por ADN ajeno, en especial de la zona del promotor.

15 2.- Célula de *Candida tropicalis* según la reivindicación 1, caracterizada por que el ADN ajeno es un gen marcador de selección.

3.- Célula de *Candida tropicalis* según al menos una de las reivindicaciones precedentes, caracterizada por que la célula está bloqueada al menos parcialmente en su β -oxidación.

20 4.- Célula de *Candida tropicalis* según al menos una de las reivindicaciones precedentes, caracterizada por que la célula de *Candida tropicalis* se deriva de cepas seleccionadas a partir del grupo constituido por *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 y *Candida tropicalis* HDC100, en especial constituido por *Candida tropicalis* ATCC20962 y *Candida tropicalis* HDC100.

25 5.- Empleo de células según al menos una de las reivindicaciones precedentes para la producción de ácidos ω -hidroxi-carboxílicos y ω -hidroxi-carboxilatos.

6.- Procedimiento para la producción de una célula de *C. tropicalis* según al menos una de las reivindicaciones 1 a 4, que comprende los pasos de procedimiento:

I) puesta a disposición de una célula de *C. Tropicalis*, y

30 II) modificación de al menos un gen que comprende una de las secuencias seleccionadas a partir de los grupos de secuencias de ácido nucleico A) y B) citadas en la reivindicación 1, mediante inserción de ADN ajeno, en especial de ADN que codifica para un gen marcador de selección, en el gen, delección al menos de partes del gen, mutaciones puntuales en la secuencia génica, y exposición del gen a la influencia de la interferencia de ARN, e intercambio de partes del gen por ADN ajeno, en especial de la zona del promotor.

35 7.- Procedimiento para la producción de ácidos ω -hidroxi-carboxílicos o ω -hidroxi-carboxilatos, en especial de ácidos ω -hidroxi-carboxílicos o ω -hidroxi-carboxilatos con una longitud de cadena de ácido carboxílico de 6 a 24 átomos de carbono, y una longitud de cadena de componente alcohólico del éster de 1 a 4 átomos de carbono, en especial de ácido 12-hidroxi-dodecanoico o 12-hidroxi-dodecanoato de metilo, que comprende los pasos de procedimiento:

40 a) puesta en contacto de una célula según al menos una de las reivindicaciones 1 a 4 con un medio que contiene un ácido carboxílico, o bien un carboxilato,

b) cultivo de la célula bajo condiciones que posibiliten a la célula formar el correspondiente ácido ω -hidroxi-carboxílico o ω -hidroxi-carboxilato a partir del ácido carboxílico, o bien del carboxilato, y

c) en caso dado aislamiento del ácido ω -hidroxi-carboxílico o ω -hidroxicarboxilato formado.

8.- Procedimiento para la producción de un polímero que comprende el procedimiento para la producción de ácidos ω -hidroxi-carboxílicos o ω -hidroxi-carboxilatos según la reivindicación 7 y el paso de procedimiento

empleo de ácidos ω -hidroxi-carboxílicos o ω -hidroxi-carboxilatos para la producción de un polímero.

5 9.- Procedimiento para la producción de ácidos ω -amino-carboxílicos o ω -amino-carboxilatos que comprende los pasos de procedimiento:

a) puesta en contacto de una célula según al menos una de las reivindicaciones 1 a 4 con un medio que contiene un ácido carboxílico, o bien un carboxilato,

b) cultivo de la célula bajo condiciones que posibiliten a la célula formar el correspondiente ácido ω -hidroxi-carboxílico o ω -hidroxi-carboxilato a partir del ácido carboxílico, o bien del carboxilato, y

10 c) en caso dado aislamiento del ácido ω -hidroxi-carboxílico o ω -hidroxicarboxilato formado, y

un paso de reacción para la transformación de ácidos ω -hidroxi-carboxílicos o correspondientes ésteres en los ácidos ω -oxo-carboxílicos o los correspondientes ésteres, y a continuación puesta en práctica de la aminación del grupo oxo.

15 10.- Procedimiento según la reivindicación 9, caracterizado por que los ácidos ω -hidroxi-carboxílicos o los ω -hidroxi-carboxilatos presentan una longitud de cadena de ácido carboxílico de 6 a 24 átomos de carbono, y una longitud de cadena de componente alcohólico del éster de 1 a 4 átomos de carbono.

11.- Procedimiento según la reivindicación 9 o 10, caracterizado por que los ácidos ω -hidroxi-carboxílicos o los ω -hidroxi-carboxilatos representan ácido 12-hidroxi-dodecanoico o 12-hidroxi-dodecanoato de metilo.