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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. 57,

5 B) una secuencia que es idéntica a Seq ID Nr. 57 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).

15 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.

25 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:

30 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 NH₄Cl, 1,5 g de Na₂SO₄, 300 ml de un tampón fosfato potásico 1 mM (pH 7,0), 20 mg de ZnSO₄ x 7 H₂O, 20 mg de MnSO₄ x 4 H₂O, 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.

35 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 H₂SO₄ 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* bloqueadas 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 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.

40 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

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atg gcc aca caa gaa att att gat tct gca ctt ccg tac ttg aca aag	48
Met Ala Thr Gln Glu Ile Ile Asp Ser Ala Leu Pro Tyr Leu Thr Lys	
1 5 10 15	
tgg tat act gtt atc act tta gca gct ttg gtt ttc tta att tca tct	96
Trp Tyr Thr Val Ile Thr Leu Ala Ala Leu Val Phe Leu Ile Ser Ser	
20 25 30	
aat att aaa aat tac gtc aag gct aag aag ttg aaa tgc aga gat cct	144
Asn Ile Lys Asn Tyr Val Lys Ala Lys Lys Leu Lys Cys Arg Asp Pro	
35 40 45	
cca tat ttc aaa gga gcc ggt tgg aca ggt att agt cca tta att gaa	192
Pro Tyr Phe Lys Gly Ala Gly Trp Thr Gly Ile Ser Pro Leu Ile Glu	
50 55 60	
att att aaa gtt aaa ggt aat ggt aga ttg gca aga ttt tgg 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 tgg 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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ttt att cca aag ggt tcc act gtt gct tat att gtt tac aaa act cat 1296
 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
 500 505 510
 act atg agt cat gat gat ggt gtt ttc gtt aaa atg taa 1575
 Thr Met Ser His Asp Asp Gly Val Phe Val Lys Met
 515 520

<210> 2
 < 211> 524
 < 212> PRT
 5 < 213> Candida tropicalis

<400> 2
 Met Ala Thr Gln Glu Ile Ile Asp Ser Ala Leu Pro Tyr Leu Thr Lys
 1 5 10 15
 Trp Tyr Thr Val Ile Thr Leu Ala Ala Leu Val Phe Leu Ile Ser Ser
 20 25 30
 Asn Ile Lys Asn Tyr Val Lys Ala Lys Lys Leu Lys Cys Arg Asp Pro
 35 40 45
 Pro Tyr Phe Lys Gly Ala Gly Trp Thr Gly Ile Ser Pro Leu Ile Glu
 50 55 60
 Ile Ile Lys Val Lys Gly Asn Gly Arg Leu Ala Arg Phe Trp Pro Ile
 65 70 75 80
 Lys Thr Phe Asp Asp Tyr Pro Asn His Thr Phe Tyr Met Ser Ile Ile
 85 90 95
 Gly Ala Leu Lys Ile Val Leu Thr Val Ile Gln Glu Asn Ile Lys Ala
 100 105 110

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

His Phe Tyr Pro Leu Leu Gly Asp Gly Ile Phe Thr Leu Asp Gly Glu
 130 135 140

Gly Trp Lys His Ser Arg Ala Met Leu Arg Pro Gln Phe Ala Arg Asp
 145 150 155 160

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

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

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

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

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

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

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

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

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

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

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

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

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

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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
385 390 395 400

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

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

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

Arg Trp Phe Glu Pro Ser Thr Lys Lys Leu Gly Trp Ala Tyr Val Pro
450 455 460

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

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

Ser Ser Pro Pro Asp Val Glu Tyr Pro Pro Pro Lys Cys Ile His Leu
500 505 510

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

<210> 3
< 211> 1572
< 212> DNA
5 < 213> Candida tropicalis

<220>
< 221> CDS
< 222> (1)..(1572)

<400> 3
atg gcc aca caa gaa atc atc gat tct gta ctt ccg tac ttg acc aaa 48
Met Ala Thr Gln Glu Ile Ile Asp Ser Val Leu Pro Tyr Leu Thr Lys
1 5 10 15

tgg tac act gtg att act gca gca gta tta gtc ttc ott 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		
					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		
					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		
					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				

ES 2 631 987 T3

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

<210> 4
 <211> 523
 <212> PRT
 5 <213> Candida tropicalis

<400> 4

ES 2 631 987 T3

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

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

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

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

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

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

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

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

ES 2 631 987 T3

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

ES 2 631 987 T3

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

5 <220>
 < 221> CDS
 < 222> (1)..(1569)

<400> 5
 atg act gta cac gat att atc gcc aca tac ttc acc aaa tgg tac gtg 48
 Met Thr Val His Asp Ile Ile Ala Thr Tyr Phe Thr Lys Trp Tyr Val
 1 5 10 15
 ata gta cca ctc gct ttg att gct tat aga gtc ctc gac tac ttc tat 96
 Ile Val Pro Leu Ala Leu Ile Ala Tyr Arg Val Leu Asp Tyr Phe Tyr
 20 25 30
 ggc aga tac ttg atg tac aag ctt ggt gct aaa cca ttt ttc cag aaa 144
 Gly Arg Tyr Leu Met Tyr Lys Leu Gly Ala Lys Pro Phe Phe Gln Lys
 35 40 45
 cag aca gac ggc tgt ttc gga ttc aaa gct ccg ctt gaa ttg ttg aag 192
 Gln Thr Asp Gly Cys Phe Gly Phe Lys Ala Pro Leu Glu Leu Leu Lys
 50 55 60
 aag aag agc gac ggt acc ctc ata gac ttc aca ctc cag cgt atc cac 240
 Lys Lys Ser Asp Gly Thr Leu Ile Asp Phe Thr Leu Gln Arg Ile His
 65 70 75 80
 gat ctc gat cgt ccc gat atc cca act ttc aca ttc ccg gtc ttt tcc 288
 Asp Leu Asp Arg Pro Asp Ile Pro Thr Phe Thr Phe Pro Val Phe Ser
 85 90 95
 atc aac ctt gtc aat acc ctt gag ccg gag aac atc aag gcc atc ttg 336
 Ile Asn Leu Val Asn Thr Leu Glu Pro Glu Asn Ile Lys Ala Ile Leu
 100 105 110
 gcc act cag ttc aac gat ttc tcc ttg ggt acc aga cac tcg cac ttt 384
 Ala Thr Gln Phe Asn Asp Phe Ser Leu Gly Thr Arg His Ser His Phe
 115 120 125
 gct cct ttg ttg ggt gat ggt atc ttt acg ttg gat ggc gcc ggc tgg 432
 Ala Pro Leu Leu Gly Asp Gly Ile Phe Thr Leu Asp Gly Ala Gly Trp
 130 135 140
 aag cac agc aga tct atg ttg aga cca cag ttt gcc aga gaa cag att 480
 Lys His Ser Arg Ser Met Leu Arg Pro Gln Phe Ala Arg Glu Gln Ile
 145 150 155 160
 tcc cac gtc aag ttg ttg gag cca cac gtt cag gtg ttc ttc aaa cac 528

10

ES 2 631 987 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	ggt	gaa	tcc	ggt		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	ggt	atg	caa	caa	ttg	tac	tggt	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					
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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	ggt	aga		960
Lys	Gln	Val	Leu	Arg	Asp	Gln	Leu	Leu	Asn	Ile	Met	Val	Ala	Gly	Arg		
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Asp	Thr	Thr	Ala	Gly	Leu	Leu	Ser	Phe	Val	Phe	Phe	Glu	Leu	Ala	Arg		
			325					330						335			
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Asn	Pro	Glu	Val	Thr	Asn	Lys	Leu	Arg	Glu	Glu	Ile	Glu	Asp	Lys	Phe		
			340					345					350				
gga	ctc	ggt	gag	aat	gct	agt	ggt	gaa	gac	att	tcc	ttt	gag	tcg	ttg		1104
Gly	Leu	Gly	Glu	Asn	Ala	Ser	Val	Glu	Asp	Ile	Ser	Phe	Glu	Ser	Leu		
		355					360					365					
aag	tcc	tgt	gaa	tac	ttg	aag	gct	ggt	ctc	aac	gaa	acc	ttg	aga	ttg		1152
Lys	Ser	Cys	Glu	Tyr	Leu	Lys	Ala	Val	Leu	Asn	Glu	Thr	Leu	Arg	Leu		
	370					375					380						
tac	cca	tcc	gtg	cca	cag	aat	ttc	aga	ggt	gcc	acc	aag	aac	act	acc		1200
Tyr	Pro	Ser	Val	Pro	Gln	Asn	Phe	Arg	Val	Ala	Thr	Lys	Asn	Thr	Thr		
	385				390					395					400		
ctc	cca	aga	ggt	ggt	ggt	aag	gac	ggg	ttg	tct	cct	ggt	ttg	gtg	aga		1248
Leu	Pro	Arg	Gly	Gly	Gly	Lys	Asp	Gly	Leu	Ser	Pro	Val	Leu	Val	Arg		
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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
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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
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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
 145 150 155 160

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

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

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

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

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

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

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

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

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

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

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

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

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

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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
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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
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Pro Asp Thr Glu Tyr Pro Pro Lys Lys Met Ser His Leu Thr Met Ser
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 Ile Val Pro Leu Ala Leu Ile Ala Tyr Arg Val Leu Asp Tyr Phe Tyr
 20 25 30

10 ggc aga tac ttg atg tac aag ctt ggt gct aaa ccg ttt ttc cag aaa 144
 Gly Arg Tyr Leu Met Tyr Lys Leu Gly Ala Lys Pro Phe Phe Gln Lys

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

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Gln	Asp	Gly	Tyr	Val	Phe	Leu	Tyr	Glu	Leu	Val	Lys	Gln	Thr	Arg	Asp	
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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	
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Asn	Pro	Glu	Val	Thr	Asn	Lys	Leu	Arg	Glu	Glu	Ile	Glu	Asp	Lys	Phe	
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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	
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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	
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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
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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
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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 2 631 987 T3

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

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

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

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

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

gct tca tac gtc act gtc aga ttg ctc cag gag ttt gca cac ttg tct 1536
 Ala Ser Tyr Val Thr Val Arg Leu Leu Gln Glu Phe Ala His Leu Ser
 500 505 510

atg gac cca gac acc gaa tat cca cca aaa ttg cag aac acc ttg acc 1584
 Met Asp Pro Asp Thr Glu Tyr Pro Pro Lys Leu Gln Asn Thr Leu Thr
 515 520 525

ttg tcg ctc ttt gat ggt gct gat 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
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 1 5 10 15

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

Ile Pro Leu Val Leu Leu Ser Leu Asn Phe Ile Ser Leu Leu His Thr
 35 40 45

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

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

Lys Ser Lys Gly Thr Val Met Lys Phe Ala Trp Gly Leu Trp Asn Asn
 85 90 95

ES 2 631 987 T3

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

ES 2 631 987 T3

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
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 Met Ser Ser Ser Pro Ser Phe Ala Gln Glu Val Leu Ala Thr Thr Ser
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ES 2 631 987 T3

cct tac atc gag tac ttt ctt gac aac tac acc aga tgg tac tac ttc	96
Pro Tyr Ile Glu Tyr Phe Leu Asp Asn Tyr Thr Arg Trp Tyr Tyr Phe	
20 25 30	
atc cct ttg gtg ctt ctt tcg ttg aac ttc atc agc ttg ctc cac aca	144
Ile Pro Leu Val Leu Leu Ser Leu Asn Phe Ile Ser Leu Leu His Thr	
35 40 45	
aag tac ttg gaa cgc agg ttc cac gcc aag ccg ctc ggt aac gtc gtg	192
Lys Tyr Leu Glu Arg Arg Phe His Ala Lys Pro Leu Gly Asn Val Val	
50 55 60	
ttg gat cct acg ttt ggt atc gct act ccg ttg atc ttg atc tac tta	240
Leu Asp Pro Thr Phe Gly Ile Ala Thr Pro Leu Ile Leu Ile Tyr Leu	
65 70 75 80	
aag tcg aaa ggt aca gtc atg aag ttt gcc tgg agc ttc tgg aac aac	288
Lys Ser Lys Gly Thr Val Met Lys Phe Ala Trp Ser Phe Trp Asn Asn	
85 90 95	
aag tac att gtc aaa gac cca aag tac aag acc act ggc ctt aga att	336
Lys Tyr Ile Val Lys Asp Pro Lys Tyr Lys Thr Thr Gly Leu Arg Ile	
100 105 110	
gtc ggc ctc cca ttg att gaa acc ata gac cca gag aac atc aaa gct	384
Val Gly Leu Pro Leu Ile Glu Thr Ile Asp Pro Glu Asn Ile Lys Ala	
115 120 125	
gtg ttg gct act cag ttc aac gat ttc tcc ttg gga act aga cac gat	432
Val Leu Ala Thr Gln Phe Asn Asp Phe Ser Leu Gly Thr Arg His Asp	
130 135 140	
ttc ttg tac tcc ttg ttg ggc gat ggt att ttt acc ttg gac ggt gct	480
Phe Leu Tyr Ser Leu Leu Gly Asp Gly Ile Phe Thr Leu Asp Gly Ala	
145 150 155 160	
ggc tgg aaa cac agt aga act atg ttg aga cca cag ttt gct aga gaa	528
Gly Trp Lys His Ser Arg Thr Met Leu Arg Pro Gln Phe Ala Arg Glu	
165 170 175	
cag gtt tcc cac gtc aag ttg ttg gaa cca cac gtt cag gtg ttc ttc	576
Gln Val Ser His Val Lys Leu Leu Glu Pro His Val Gln Val Phe Phe	
180 185 190	
aag cac gtt aga aaa cac cgc ggt cag act ttt gac atc caa gaa ttg	624
Lys His Val Arg Lys His Arg Gly Gln Thr Phe Asp Ile Gln Glu Leu	
195 200 205	
ttc ttc aga ttg acc gtc gac tcc gcc acc gag ttc ttg ttt ggt gag	672
Phe Phe Arg Leu Thr Val Asp Ser Ala Thr Glu Phe Leu Phe Gly Glu	
210 215 220	
tct gct gaa tcc ttg aga gac gac tct gtt ggt ttg acc cca acc acc	720
Ser Ala Glu Ser Leu Arg Asp Asp Ser Val Gly Leu Thr Pro Thr Thr	
225 230 235 240	
aag gat ttc gaa ggc aga gga gat ttc gct gac gct ttc aac tac tcg	768
Lys Asp Phe Glu Gly Arg Gly Asp Phe Ala Asp Ala Phe Asn Tyr Ser	
245 250 255	
cag act tac cag gcc tac aga ttt ttg ttg caa caa atg tac tgg att	816
Gln Thr Tyr Gln Ala Tyr Arg Phe Leu Leu Gln Gln Met Tyr Trp Ile	

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

<210> 12
 <211> 540
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ES 2 631 987 T3

< 213> Candida tropicalis

<400> 12

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

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

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

ES 2 631 987 T3

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

ES 2 631 987 T3

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
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5 < 213> Candida tropicalis

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

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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

ES 2 631 987 T3

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

ES 2 631 987 T3

355	360	365	
ttg aaa gcg ttc ctt aat gaa acc ttg cgt att tac cca agt gtc cca			1152
Leu Lys Ala Phe Leu Asn Glu Thr Leu Arg Ile Tyr Pro Ser Val Pro			
370	375	380	
aga aac ttc aga atc gcc acc aag aac acg aca ttg cca agg ggc ggt			1200
Arg Asn Phe Arg Ile Ala Thr Lys Asn Thr Thr Leu Pro Arg Gly Gly			
385	390	395	400
ggt tca gac ggt acc tcg cca atc ttg atc caa aag gga gaa gct gtg			1248
Gly Ser Asp Gly Thr Ser Pro Ile Leu Ile Gln Lys Gly Glu Ala Val			
405	410	415	
tcg tat ggt atc aac tct act cat ttg gac cct gtc tat tac ggc cct			1296
Ser Tyr Gly Ile Asn Ser Thr His Leu Asp Pro Val Tyr Tyr Gly Pro			
420	425	430	
gat gct gct gag ttc aga cca gag aga tgg ttt gag cca tca acc aaa			1344
Asp Ala Ala Glu Phe Arg Pro Glu Arg Trp Phe Glu Pro Ser Thr Lys			
435	440	445	
aag ctc ggc tgg gct tac ttg cca ttc aac ggt ggt cca aga atc tgt			1392
Lys Leu Gly Trp Ala Tyr Leu Pro Phe Asn Gly Gly Pro Arg Ile Cys			
450	455	460	
ttg ggt cag cag ttt gcc ttg acg gaa gct ggc tat gtg ttg gtt aga			1440
Leu Gly Gln Gln Phe Ala Leu Thr Glu Ala Gly Tyr Val Leu Val Arg			
465	470	475	480
ttg gtg caa gag ttc tcc cac gtt agg ctg gac cca gac gag gtg tac			1488
Leu Val Gln Glu Phe Ser His Val Arg Leu Asp Pro Asp Glu Val Tyr			
485	490	495	
ccg cca aag agg ttg acc aac ttg acc atg tgt ttg cag gat ggt gct			1536
Pro Pro Lys Arg Leu Thr Asn Leu Thr Met Cys Leu Gln Asp Gly Ala			
500	505	510	
att gtc aag ttt gac tag			1554
Ile Val Lys Phe Asp			
515			

<210> 14
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 <212> PRT
 5 <213> Candida tropicalis

<400> 14
 Met Ile Glu Gln Leu Leu Glu Tyr Trp Tyr Val Val Val Pro Val Leu
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 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

ES 2 631 987 T3

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

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

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

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

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

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

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

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

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

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

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

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

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

Ile Val Lys Phe Asp
515

- <210> 15
- <211> 1554
- <212> DNA
- 5 <213> Candida tropicalis

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

<400> 15

ES 2 631 987 T3

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

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att ttg gtg cag acc ttc tac tgg ttg atc aac aac aag gag ttt aga Ile Leu Val Gln Thr Phe Tyr Trp Leu Ile Asn Asn Lys Glu Phe Arg 245 250 255	768
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
ttg aaa gcg ttc ctt aac gaa acc ttg cgt gtt tac cca agt gtc cca Leu Lys Ala Phe Leu Asn Glu Thr Leu Arg Val Tyr Pro Ser Val Pro 370 375 380	1152
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ggt cca gac ggt acc cag cca atc ttg atc caa aag gga gaa ggt gtg Gly Pro Asp Gly Thr Gln Pro Ile Leu Ile Gln Lys Gly Glu Gly Val 405 410 415	1248
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
gat gct gct gag ttc aga cca gag aga tgg ttt gag cca tca acc aga Asp Ala Ala Glu Phe Arg Pro Glu Arg Trp Phe Glu Pro Ser Thr Arg 435 440 445	1344
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
ttg ggt cag cag ttt gcc ttg acc gaa gct ggt tac gtt ttg gtc aga Leu Gly Gln Gln Phe Ala Leu Thr Glu Ala Gly Tyr Val Leu Val Arg 465 470 475 480	1440
ttg gtg caa gag ttc tcc cac att agg ctg gac cca gat gaa gtg tat Leu Val Gln Glu Phe Ser His Ile Arg Leu Asp Pro Asp Glu Val Tyr 485 490 495	1488
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 2 631 987 T3

<210> 16
 < 211> 517
 < 212> PRT
 < 213> Candida tropicalis

5 <400> 16
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 1 5 10 15
 Tyr Ile Ile Lys Gln Leu Ile Ala Tyr Ser Lys Thr Arg Val Leu Met
 20 25 30
 Lys Gln Leu Gly Ala Ala Pro Ile Thr Asn Gln Leu Tyr Asp Asn Val
 35 40 45
 Phe Gly Ile Val Asn Gly Trp Lys Ala Leu Gln Phe Lys Lys Glu Gly
 50 55 60
 Arg Ala Gln Glu Tyr Asn Asp His Lys Phe Asp Ser Ser Lys Asn Pro
 65 70 75 80
 Ser Val Gly Thr Tyr Val Ser Ile Leu Phe Gly Thr Lys Ile Val Val
 85 90 95
 Thr Lys Asp Pro Glu Asn Ile Lys Ala Ile Leu Ala Thr Gln Phe Gly
 100 105 110
 Asp Phe Ser Leu Gly Lys Arg His Ala Leu Phe Lys Pro Leu Leu Gly
 115 120 125
 Asp Gly Ile Phe Thr Leu Asp Gly Glu Gly Trp Lys His Ser Arg Ser
 130 135 140
 Met Leu Arg Pro Gln Phe Ala Arg Glu Gln Val Ala His Val Thr Ser
 145 150 155 160
 Leu Glu Pro His Phe Gln Leu Leu Lys Lys His Ile Leu Lys His Lys
 165 170 175
 Gly Glu Tyr Phe Asp Ile Gln Glu Leu Phe Phe Arg Phe Thr Val Asp

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

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

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

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

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

Ile Val Lys Phe Asp
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<210> 17

< 211> 1539

< 212> DNA

5 < 213> Candida tropicalis

<220>

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< 222> (1)..(1539)

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

aag aaa ttg ggt gct aag cca ttc aca cac gtc caa cgt gac ggg tgg 144
 Lys Lys Leu Gly Ala Lys Pro Phe Thr His Val Gln Arg Asp Gly Trp
 35 40 45

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

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

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

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

10

ES 2 631 987 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 tcg 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 tcg 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 tcg 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
ttg tac tgg ttg gtc aac aac aaa gag ttc aag gag tgc aat 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 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 2 631 987 T3

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

tag 1539

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 < 211> 512
 < 212> PRT
 5 < 213> Candida tropicalis

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

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

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

ES 2 631 987 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 2 631 987 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>
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 < 222> (1)..(1539)

<400> 19
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 Met Leu Asp Gln Ile Phe His Tyr Trp Tyr Ile Val Leu Pro Leu Leu
 10 1 5 10 15

ES 2 631 987 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
ttc tta ttt ggt gag tcc gtg cac tcc tta agg gac gag gaa att ggc Phe Leu Phe Gly Glu Ser Val His Ser Leu Arg Asp Glu Glu Ile Gly 195 200 205	624
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
ttc aac aag tcg caa gtc tat ttg tcc acc aga gtt gct tta cag aca Phe Asn Lys Ser Gln Val Tyr Leu Ser Thr Arg Val Ala Leu Gln Thr 225 230 235 240	720
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 2 631 987 T3

260	265	270	
cca gag gaa ctt gaa aaa caa ggc ggg tat gtg ttc ttg tac gag ctt Pro Glu Glu Leu Glu Lys Gln Gly Gly Tyr Val Phe Leu Tyr Glu Leu 275 280 285			864
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 Ala 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 His Arg 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 ggc ccc aac ggc aag Ala Ile Lys Asp Thr Thr Leu Pro Arg 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
aga ccg gaa aga tgg ttt gag cca tca act aga aac ttg gga tgg gct Arg Pro Glu Arg Trp Phe Glu Pro Ser Thr Arg Asn Leu Gly Trp Ala 435 440 445			1344
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
cct agc ttg tca cag gac ccc gaa act gag tac cca cca cct aga ttg Pro Ser Leu Ser Gln Asp Pro Glu Thr Glu Tyr Pro Pro Pro Arg Leu 485 490 495			1488
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

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< 211> 512

< 212> PRT

5 < 213> Candida tropicalis

<400> 20

ES 2 631 987 T3

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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

ES 2 631 987 T3

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

ES 2 631 987 T3

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 < 212> DNA
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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

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<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

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 atg gct cca ttt ttg ccc gac cag gtc gac tac aaa cac gtc gac acc 48
 Met Ala Pro Phe Leu Pro Asp Gln Val Asp Tyr Lys His Val Asp Thr
 1 5 10 15

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

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

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	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	ggt	gtc	gtg		624
Asp	Ile	Asp	Val	Ile	Ile	Ile	Gly	Ser	Gly	Ala	Gly	Ala	Gly	Val	Val		
		195					200					205					
gcc	cac	act	ttg	acc	aac	gac	ggc	ttc	aag	agt	ttg	ggt	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		
				230						235					240		
ggt	caa	gaa	tta	tac	caa	agt	gga	ggt	act	ttg	acc	acc	gtc	aac	cag		768
Val	Gln	Glu	Leu	Tyr	Gln	Ser	Gly	Gly	Thr	Leu	Thr	Thr	Val	Asn	Gln		
				245					250					255			
cag	ttg	ttt	ggt	ctt	gct	ggt	tcc	act	ttt	ggt	ggt	ggt	acc	act	gtc		816
Gln	Leu	Phe	Val	Leu	Ala	Gly	Ser	Thr	Phe	Gly	Gly	Gly	Thr	Thr	Val		
			260					265					270				
aat	tgg	tcg	gcc	tgt	ctt	aaa	acg	cca	ttc	aag	gtg	cgt	aag	gaa	tgg		864
Asn	Trp	Ser	Ala	Cys	Leu	Lys	Thr	Pro	Phe	Lys	Val	Arg	Lys	Glu	Trp		
			275					280					285				
tat	gat	gag	ttt	ggc	gtt	gac	ttt	gct	gcc	gat	gaa	gcc	tac	gac	aaa		912
Tyr	Asp	Glu	Phe	Gly	Val	Asp	Phe	Ala	Ala	Asp	Glu	Ala	Tyr	Asp	Lys		
		290				295					300						

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

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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

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 5 <213> Candida tropicalis

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 Met Ala Pro Phe Leu Pro Asp Gln Val Asp Tyr Lys His Val Asp Thr
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 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

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

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65	70	75	80	
tgt att gtc ttg acc acc gca ttg gac tcc aga atc ttg gcc ccc acg Cys Ile Val Leu Thr Thr Ala Leu Asp Ser Arg Ile Leu Ala Pro Thr	85	90	95	288
ttg acc aac tcg ttg acg cct atc aag gat atg acc ttg aag gag cgt Leu Thr Asn Ser Leu Thr Pro Ile Lys Asp Met Thr Leu Lys Glu Arg	100	105	110	336
gaa caa ttg ttg gcc tct tgg cgt gat tcc ccg att gcg gca aag aga Glu Gln Leu Leu Ala Ser Trp Arg Asp Ser Pro Ile Ala Ala Lys Arg	115	120	125	384
aga ttg ttc aga ttg att tcc tcg ctt acc ttg acg acg ttt acg aga Arg Leu Phe Arg Leu Ile Ser Ser Leu Thr Leu Thr Phe Thr Arg	130	135	140	432
ttg gcc agc gaa ttg cac ttg aaa gcc atc cac tac cct ggc aga gac Leu Ala Ser Glu Leu His Leu Lys Ala Ile His Tyr Pro Gly Arg Asp	145	150	155	480
ttg cgt gaa aag gcg tat gaa acc cag gtg gtt gac cct ttc agg tac Leu Arg Glu Lys Ala Tyr Glu Thr Gln Val Val Asp Pro Phe Arg Tyr	165	170	175	528
ctg ttt atg gag aaa cca aag ttt gac ggc gcc gaa ttg tac ttg cca Leu Phe Met Glu Lys Pro Lys Phe Asp Gly Ala Glu Leu Tyr Leu Pro	180	185	190	576
gat atc gac gtc atc atc att gga tca ggc gcc ggt gct ggt gtc atg Asp Ile Asp Val Ile Ile Ile gga Ser Gly Ala Gly Ala Gly Val Met	195	200	205	624
gcc cac act ctc gcc aac gac ggg ttc aag acc ttg gtt ttg gaa aag Ala His Thr Leu Ala Asn Asp Gly Phe Lys Thr Leu Val Leu Glu Lys	210	215	220	672
gga aag tat ttc agc aac tcc gag ttg aac ttt aat gac gct gat ggc Gly Lys Tyr Phe Ser Asn Ser Glu Leu Asn Phe Asn Asp Ala Asp Gly	225	230	235	720
gtg aaa gag ttg tac caa ggt aaa ggt gct ttg gcc acc acc aat cag Val Lys Glu Leu Tyr Gln Gly Lys Gly Ala Leu Ala Thr Thr Asn Gln	245	250	255	768
cag atg ttt att ctt gcc ggt tcc act ttg ggc ggt ggt acc act gtc Gln Met Phe Ile Leu Ala Gly Ser Thr Leu Gly Gly Gly Thr Thr Val	260	265	270	816
aac tgg tct gct tgc ctt aaa aca cca ttt aaa gtg cgt aag gag tgg Asn Trp Ser Ala Cys Leu Lys Thr Pro Phe Lys Val Arg Lys Glu Trp	275	280	285	864
tac gac gag ttt ggt ctt gaa ttt gct gcc gat gaa gcc tac gac aaa Tyr Asp Glu Phe Gly Leu Glu Phe Ala Ala Asp Glu Ala Tyr Asp Lys	290	295	300	912
gcg cag gat tat gtt tgg aaa caa atg ggt gct tca aca gat gga atc Ala Gln Asp Tyr Val Trp Lys Gln Met Gly Ala Ser Thr Asp Gly Ile	305	310	315	960
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	ggt	ggc	cac	cct	gac	1056
Gly	Tyr	Lys	Ser	Lys	Glu	Ile	Glu	Gln	Asn	Asn	Gly	Gly	His	Pro	Asp	
			340					345					350			
cac	cca	tgt	ggt	ttc	tgt	tac	ttg	ggc	tgt	aag	tac	ggt	att	aaa	cag	1104
His	Pro	Cys	Gly	Phe	Cys	Tyr	Leu	Gly	Cys	Lys	Tyr	Gly	Ile	Lys	Gln	
		355					360					365				
ggt	tct	gtg	aat	aac	tgg	ttt	aga	gac	gca	gct	gcc	cac	ggg	tcc	aag	1152
Gly	Ser	Val	Asn	Asn	Trp	Phe	Arg	Asp	Ala	Ala	Ala	His	Gly	Ser	Lys	
	370					375					380					
ttc	atg	caa	caa	gtc	aga	gtt	gtg	caa	atc	ctc	aac	aag	aat	ggc	gtc	1200
Phe	Met	Gln	Gln	Val	Arg	Val	Val	Gln	Ile	Leu	Asn	Lys	Asn	Gly	Val	
385					390					395					400	
gct	tat	ggt	atc	ttg	tgt	gag	gat	gtc	gaa	acc	gga	gtc	agg	ttc	act	1248
Ala	Tyr	Gly	Ile	Leu	Cys	Glu	Asp	Val	Glu	Thr	Gly	Val	Arg	Phe	Thr	
				405				410						415		
att	agt	ggc	ccc	aaa	aag	ttt	gtt	ggt	tct	gct	ggt	tct	ttg	aac	acg	1296
Ile	Ser	Gly	Pro	Lys	Lys	Phe	Val	Val	Ser	Ala	Gly	Ser	Leu	Asn	Thr	
			420					425					430			
cca	act	gtg	ttg	acc	aac	tcc	gga	ttc	aag	aac	aag	cac	att	ggt	aag	1344
Pro	Thr	Val	Leu	Thr	Asn	Ser	Gly	Phe	Lys	Asn	Lys	His	Ile	Gly	Lys	
		435					440					445				
aac	ttg	acg	ttg	cac	cca	ggt	tcc	acc	gtg	ttt	ggt	gac	ttt	ggc	aga	1392
Asn	Leu	Thr	Leu	His	Pro	Val	Ser	Thr	Val	Phe	Gly	Asp	Phe	Gly	Arg	
	450					455					460					
gac	gtg	caa	gcc	gac	cat	ttc	cac	aaa	tct	att	atg	act	tcg	ctt	tgt	1440
Asp	Val	Gln	Ala	Asp	His	Phe	His	Lys	Ser	Ile	Met	Thr	Ser	Leu	Cys	
465					470					475					480	
tac	gag	ggt	gct	gac	ttg	gac	ggc	aag	ggc	cac	gga	tgc	aga	atc	gaa	1488
Tyr	Glu	Val	Ala	Asp	Leu	Asp	Gly	Lys	Gly	His	Gly	Cys	Arg	Ile	Glu	
				485					490					495		
acc	atc	ttg	aac	gct	cca	ttc	atc	caa	gct	tct	ttg	ttg	cca	tgg	aga	1536
Thr	Ile	Leu	Asn	Ala	Pro	Phe	Ile	Gln	Ala	Ser	Leu	Leu	Pro	Trp	Arg	
			500					505					510			
gga	agt	gac	gag	gtc	aga	aga	gac	ttg	ttg	cgt	tac	aac	aac	atg	gtg	1584
Gly	Ser	Asp	Glu	Val	Arg	Arg	Asp	Leu	Leu	Arg	Tyr	Asn	Asn	Met	Val	
		515					520					525				
gcc	atg	ttg	ctt	atc	acg	cgt	gat	acc	acc	agt	ggt	tca	ggt	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		

ES 2 631 987 T3

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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 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

ES 2 631 987 T3

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

<220>
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 ctt ttg tta tta tgt gac ggg atc atc cac gaa acc aca gtc gac cag 96
 Leu Leu Leu Leu Cys Asp Gly Ile Ile His Glu Thr Thr Val Asp Gln
 20 25 30
 atc agg gac gcc att gct ccc gac ttc cct gaa gac cag tac gag gag 144
 Ile Arg Asp Ala Ile Ala Pro Asp Phe Pro Glu Asp Gln Tyr Glu Glu
 35 40 45
 tat ctc aag acc ttc acc aag cca tct gag acc cct ggg ttc aga gaa 192
 Tyr Leu Lys Thr Phe Thr Lys Pro Ser Glu Thr Pro Gly Phe Arg Glu
 50 55 60
 gcc gtc tac gac acg atc aac agc acc cca acc gag gct gtg cac atg 240
 Ala Val Tyr Asp Thr Ile Asn Ser Thr Pro Thr Glu Ala Val His Met
 65 70 75 80
 tgt att gta ttg acc acc gca ttg gac tcg aga atc ttg gcc ccc acg 288
 Cys Ile Val Leu Thr Thr Ala Leu Asp Ser Arg Ile Leu Ala Pro Thr
 85 90 95

10

ES 2 631 987 T3

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

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

ES 2 631 987 T3

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

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

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

tag 2115

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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
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 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

ES 2 631 987 T3

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

ES 2 631 987 T3

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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 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

ES 2 631 987 T3

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

ES 2 631 987 T3

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
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gca taa 1446
 Ala

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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
 Glu Thr Leu Arg Met Tyr Pro Pro Leu Gly Leu Ile Ile Asn Arg Tyr

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340 345 350

Thr Thr Arg Pro Thr Lys Leu Gly Asn Ile Val Ile Pro Lys Gly Val
355 360 365

Tyr Cys Gly Tyr Asn Asn Phe Gly Thr Gly Arg Asp Arg Asn Val Trp
370 375 380

Gly Pro Asp Ser Asp Glu Phe Lys Pro Glu Arg Trp Gly Arg Asp Asn
385 390 395 400

Ile Glu Glu Ile Asn Arg Asn Tyr Ala Asn Ala Lys Arg Ser Ala Glu
405 410 415

Leu Pro Ala Phe His Gly Arg Lys Arg Ala Cys Leu Gly Glu Lys Tyr
420 425 430

Ala Leu Tyr Glu Val Lys Glu Leu Leu Thr Ser Ile Leu Gly His Tyr
435 440 445

Lys Val Thr Leu Asp Ala Ser Trp Lys Glu Lys Ile Thr Pro Ala Gly
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Ala

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<400> 31

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Pro	Tyr	Val	Glu	Tyr	Cys	Gln	Glu	Asn	Tyr	Thr	Lys	Trp	Tyr	Tyr	Phe	
			20					25					30			
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Ile	Pro	Leu	Val	Ile	Leu	Ser	Leu	Asn	Leu	Ile	Ser	Met	Leu	His	Thr	
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Gln	Asp	Tyr	Thr	Phe	Gly	Leu	Ile	Thr	Pro	Leu	Val	Leu	Ile	Tyr	Tyr	
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aag	tct	aaa	ggt	acc	gtg	atg	caa	ttt	gcc	tgt	gat	tta	tgg	gac	aag	288
Lys	Ser	Lys	Gly	Thr	Val	Met	Gln	Phe	Ala	Cys	Asp	Leu	Trp	Asp	Lys	
				85					90					95		
aaa	ctc	att	gtc	agt	gat	cca	aag	gca	aag	act	att	ggt	ctt	aag	att	336
Lys	Leu	Ile	Val	Ser	Asp	Pro	Lys	Ala	Lys	Thr	Ile	Gly	Leu	Lys	Ile	
			100					105					110			
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Leu	Gly	Ile	Pro	Leu	Ile	Glu	Thr	Lys	Asp	Pro	Glu	Asn	Val	Lys	Ala	
		115				120						125				
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Ile	Leu	Ala	Thr	Gln	Phe	Asn	Asp	Phe	Ser	Leu	Gly	Thr	Arg	His	Asp	
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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	ggt	gaa	672
Phe	Phe	Arg	Leu	Thr	Val	Asp	Ser	Ala	Thr	Glu	Phe	Leu	Phe	Gly	Glu	
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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		
caa	act	tac	caa	gcg	tac	aga	ttc	ttg	ttg	caa	caa	atg	tat	tgg	att	816
Gln	Thr	Tyr	Gln	Ala	Tyr	Arg	Phe	Leu	Leu	Gln	Gln	Met	Tyr	Trp	Ile	
			260					265					270			
ttg	aat	ggt	tct	gaa	ttt	aga	aaa	tct	att	gct	att	gtc	cac	aag	ttt	864
Leu	Asn	Gly	Ser	Glu	Phe	Arg	Lys	Ser	Ile	Ala	Ile	Val	His	Lys	Phe	
		275					280					285				
gct	gac	cac	tat	gtt	caa	aag	gca	ttg	gaa	tta	act	gat	gaa	gat	ttg	912
Ala	Asp	His	Tyr	Val	Gln	Lys	Ala	Leu	Glu	Leu	Thr	Asp	Glu	Asp	Leu	
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gaa aag aaa gaa ggc tat gta ttt tta ttc gag tta gcc aaa caa acc 960
 Glu Lys Lys Glu Gly Tyr Val Phe Leu Phe Glu Leu Ala Lys Gln Thr
 305 310 315 320

aga gat cca aag gtt ttg aga gat caa ttg tta aat atc ttg gtt gct 1008
 Arg Asp Pro Lys Val Leu Arg Asp Gln Leu Leu Asn Ile Leu Val Ala
 325 330 335

ggt aga gat acc aca gct ggc ttg ttg tgc ttt ctt ttc ttt gaa ttg 1056
 Gly Arg Asp Thr Thr Ala Gly Leu Leu Ser Phe Leu Phe Phe Glu Leu
 340 345 350

tct aga aac cca gaa ata ttt gca aaa ttg aga gaa gaa atc gaa aac 1104
 Ser Arg Asn Pro Glu Ile Phe Ala Lys Leu Arg Glu Glu Ile Glu Asn
 355 360 365

aag ttt ggt ctt gga caa gat gct cgt gtt gaa gag att tct ttt gaa 1152
 Lys Phe Gly Leu Gly Gln Asp Ala Arg Val Glu Glu Ile Ser Phe Glu
 370 375 380

aca ttg aaa tct tgt gaa tac ttg aag gct gtt atc aat gaa act ttg 1200
 Thr Leu Lys Ser Cys Glu Tyr Leu Lys Ala Val Ile Asn Glu Thr Leu
 385 390 395 400

aga att tat cct tcc gtc cca cat aat ttt aga gtt gct act aga aac 1248
 Arg Ile Tyr Pro Ser Val Pro His Asn Phe Arg Val Ala Thr Arg Asn
 405 410 415

aca act tta cca aga ggt ggt ggt gaa ggt ggt tta tcc cca att gct 1296
 Thr Thr Leu Pro Arg Gly Gly Gly Glu Gly Gly Leu Ser Pro Ile Ala
 420 425 430

att aag aag ggc caa gtt gtt atg tac acg att ctt gct act cac aga 1344
 Ile Lys Lys Gly Gln Val Val Met Tyr Thr Ile Leu Ala Thr His Arg
 435 440 445

gat aaa gac att tat ggt gaa gat gct tat gtt ttc agg cca gaa aga 1392
 Asp Lys Asp Ile Tyr Gly Glu Asp Ala Tyr Val Phe Arg Pro Glu Arg
 450 455 460

tgg ttt gaa cct gaa acc aga aaa ttg ggc tgg gca tat gtt cca ttc 1440
 Trp Phe Glu Pro Glu Thr Arg Lys Leu Gly Trp Ala Tyr Val Pro Phe
 465 470 475 480

aat ggc ggt cca aga att tgt ttg ggt caa cag ttt gct tta act gaa 1488
 Asn Gly Gly Pro Arg Ile Cys Leu Gly Gln Gln Phe Ala Leu Thr Glu
 485 490 495

gca tca tat gtc act gtt aga ttg ctt caa gaa ttt ggt aac ttg aaa 1536
 Ala Ser Tyr Val Thr Val Arg Leu Leu Gln Glu Phe Gly Asn Leu Lys
 500 505 510

caa gat cca aat act gaa tat cca cca aaa tta caa aac aca ttg act 1584
 Gln Asp Pro Asn Thr Glu Tyr Pro Pro Lys Leu Gln Asn Thr Leu Thr
 515 520 525

ttg tct ctt ttt gaa ggt gct gaa gta caa atg tat taa 1623
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 530 535 540

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 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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	Ala	Ser	Tyr	Val	Thr	Val	Arg	Leu	Leu	Gln	Glu	Phe	Gly	Asn	Leu	Lys	
				500					505					510			
	Gln	Asp	Pro	Asn	Thr	Glu	Tyr	Pro	Pro	Lys	Leu	Gln	Asn	Thr	Leu	Thr	
			515					520					525				
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	1			5						10				15			
	ggt	gta	ctg	ggt	gct	ttg	att	gta	tac	aag	ggt	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	ggt	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		
	ggt	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					
10	aaa	cat	agt	aga	tct	atg	ttg	aga	cca	caa	ttt	gca	aga	gaa	cag	ggt	480

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Lys	His	Ser	Arg	Ser	Met	Leu	Arg	Pro	Gln	Phe	Ala	Arg	Glu	Gln	Val		
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tct	cac	ggt	aag	ttg	ttg	gaa	cca	cat	atg	caa	ggt	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	ggt	gat	tct	gcc	act	gag	ttt	ttg	ttt	ggt	gaa	tct	ggt		624
Arg	Leu	Thr	Val	Asp	Ser	Ala	Thr	Glu	Phe	Leu	Phe	Gly	Glu	Ser	Val		
		195					200					205					
gag	tct	tta	aga	gac	gag	tcc	atc	ggt	atg	tta	aac	gat	gct	ctt	gat		672
Glu	Ser	Leu	Arg	Asp	Glu	Ser	Ile	Gly	Met	Leu	Asn	Asp	Ala	Leu	Asp		
	210					215					220						
ttt	gat	ggt	aag	gct	gga	ttt	gct	gat	gcc	ttt	aac	tat	tct	caa	aac		720
Phe	Asp	Gly	Lys	Ala	Gly	Phe	Ala	Asp	Ala	Phe	Asn	Tyr	Ser	Gln	Asn		
	225				230					235					240		
tat	ttg	gct	tct	cga	gct	ctt	atg	caa	caa	atg	tac	tgg	att	ttg	aac		768
Tyr	Leu	Ala	Ser	Arg	Ala	Leu	Met	Gln	Gln	Met	Tyr	Trp	Ile	Leu	Asn		
				245					250					255			
gga	aaa	aag	ttt	aaa	gaa	tgt	aat	gcc	aag	ggt	cac	aag	ttt	gct	gat		816
Gly	Lys	Lys	Phe	Lys	Glu	Cys	Asn	Ala	Lys	Val	His	Lys	Phe	Ala	Asp		
			260					265					270				
tat	tat	ggt	gaa	aaa	gca	ttg	gaa	tta	act	ccg	gac	caa	ttg	gaa	aaa		864
Tyr	Tyr	Val	Glu	Lys	Ala	Leu	Glu	Leu	Thr	Pro	Asp	Gln	Leu	Glu	Lys		
		275					280					285					
caa	gat	ggg	tat	ggt	ttc	ttg	tat	gaa	ttg	gta	aaa	caa	acc	aga	gac		912
Gln	Asp	Gly	Tyr	Val	Phe	Leu	Tyr	Glu	Leu	Val	Lys	Gln	Thr	Arg	Asp		
	290					295					300						
aga	caa	gtc	ttg	aga	gat	cag	tta	ttg	aat	ata	tta	ggt	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	ggt	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	ggt	cca	caa	aac	ttt	aga	ggt	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
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 cta ttt gat ggt gcc aac att caa atg tat tag 1569
 Leu Phe Asp Gly Ala Asn Ile Gln Met Tyr
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 5 <213> Candida tropicalis

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 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
 145 150 155 160

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

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

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

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

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

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

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

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

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

Arg Gln Val Leu Arg Asp Gln Leu Leu Asn Ile Leu 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

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
 500 505 510

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

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 5 < 213> Candida tropicalis

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

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

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

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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	gtt	ttc	ttg	tat	gaa	ttg	gtt	aaa	caa	acc		912
Lys	Ser	Lys	Ser	Gly	Tyr	Val	Phe	Leu	Tyr	Glu	Leu	Val	Lys	Gln	Thr		
	290					295				300							
aga	gat	cca	aaa	ggt	tta	caa	gat	caa	tta	ttg	aac	att	atg	gtt	gcc		960
Arg	Asp	Pro	Lys	Val	Leu	Gln	Asp	Gln	Leu	Leu	Asn	Ile	Met	Val	Ala		
305					310					315					320		
ggt	aga	gat	acc	act	gct	ggt	tta	tta	tca	ttt	gca	atg	ttt	gaa	tta		1008
Gly	Arg	Asp	Thr	Thr	Ala	Gly	Leu	Leu	Ser	Phe	Ala	Met	Phe	Glu	Leu		
				325					330					335			
gct	aga	cat	cca	gaa	att	tgg	tct	aaa	tta	aga	gaa	gaa	att	gaa	gtt		1056
Ala	Arg	His	Pro	Glu	Ile	Trp	Ser	Lys	Leu	Arg	Glu	Glu	Ile	Glu	Val		
			340					345						350			
aac	ttt	ggt	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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5 < 213> Candida tropicalis

<400> 36

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

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

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

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

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

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

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

Phe Tyr Pro Leu Leu Gly Asp Gly Ile Phe Thr Leu Asp Gly Glu Gly
 130 135 140

Trp Lys His Ser Arg Ala Met Leu Arg Pro Gln Phe Ala Arg Asp Gln
 145 150 155 160

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

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

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

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

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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
 515 520

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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
 ggt 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

10

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

ES 2 631 987 T3

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
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 <211> 503
 <212> PRT

5 <213> Candida tropicalis

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 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

ES 2 631 987 T3

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

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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
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<220>
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 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

10

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

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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 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		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 Pro	Val Val Tyr		
	485		490		495		
cca cca aag aga tta aca aac ttg act atg tct tta cca 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
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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
- 5 <211> 1539
- <212> DNA
- <213> Candida tropicalis

<220>

ES 2 631 987 T3

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

<400> 41

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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	

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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
ggt 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
ggt 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	1344

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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 2 631 987 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

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 <211> 1572
 <212> DNA
 5 <213> Candida tropicalis

<220>
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 <222> (1)..(1572)

<400> 43
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 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

10

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

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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
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 < 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 2 631 987 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 2 631 987 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
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 < 212> DNA
 5 < 213> Candida tropicalis

<220>
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 < 222> (1)..(1728)

<400> 45

ES 2 631 987 T3

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

ES 2 631 987 T3

210	215	220	
caa gag att atc acc Gln Glu Ile Ile Thr 225	gtg gag aat aat atc Val Glu Asn Asn Ile 230	ata aga tta aga tca cca Ile Arg Leu Arg Ser Pro 235	720
ata tct aat ctt caa gat Ile Ser Asn Leu Gln Asp 245	tct gta cct ttc tta Ser Val Pro Phe Leu Arg 250	aga cta ata cca tgg Leu Ile Pro Trp 255	768
ttt aat aat cga gaa ttt Phe Asn Asn Arg Glu Phe 260	gcc ctt cgt tgt gga Ala Leu Arg Cys Gly Asn 265	aat aga agg aat aaa Arg Arg Asn Lys 270	816
tat atg gat caa tta tat Tyr Met Asp Gln Leu Tyr 275	aat agg tta caa aat Asn Arg Leu Gln Asn Gly 280	gga tta gct gaa aat Leu Ala Glu Asn 285	864
gat cca aat ata gct aat Asp Pro Asn Ile Ala Asn 290	agt att ctt gga caa tta Ser Ile Leu Gly Gln Leu 295	att ctt aat aat Ile Leu Asn Asn 300	912
gat aat aat aat tct aac Asp Asn Asn Asn Ser Ser 305	agc tta act agt caa gaa Ser Leu Thr Ser Gln Glu 310	ata caa agt att Ile Gln Ser Ile 320	960
tgt tta aca tta gta agt Cys Leu Thr Leu Val Ser 325	gct gga tta gat aat Ala Gly Leu Asp Asn Thr 330	acc cca ctt aat ttg Thr Pro Leu Asn Leu 335	1008
aat tat ctt att gga ata Asn Tyr Leu Ile Gly Ile 340	tta tca caa cca aga ata Leu Ser Pro Arg Ile Gly 345	ggg aag ata ttt Lys Ile Phe 350	1056
caa gat aaa gct ata aaa Gln Asp Lys Ala Ile Lys 355	gat att tta aat cat gca Asp Ile Leu Asn His Ala 360	aat gga gat att Asn Gly Asp Ile 365	1104
att caa gca tgg aat caa Ile Gln Ala Trp Asn Gln 370	ctg aat gaa gaa aat cga Leu Asn Glu Glu Asn Arg 375	gat tgt aaa tat Asp Cys Lys Tyr 380	1152
att caa gct tta att ctt Ile Gln Ala Leu Ile Leu 385	gaa act tta aga cat ttt Glu Thr Leu Arg His Phe 390	aca gta tta cca Thr Val Leu Pro 400	1200
tta agt tta cct aga tta Leu Ser Leu Pro Arg Leu 405	act aca aaa cca ata Thr Thr Lys Pro Ile Tyr 410	tat tat aaa aat ttt Tyr Tyr Lys Asn Phe 415	1248
atg att cct aaa aat act Met Ile Pro Lys Asn Thr 420	cat atg ttt atg aat gca His Met Phe Met Asn Ala 425	tat tct gca aat Tyr Ser Ala Asn 430	1296
cat gat gaa tta ata ttc His Asp Glu Leu Ile Phe 435	aaa aat cca ttt aaa ttt Asn Pro Phe Lys Phe Asp 440	gat cca gaa aga Pro Glu Arg 445	1344
tgg tta gat tca gaa act Trp Leu Asp Ser Glu Thr 450	aat gaa att aaa tca Asn Glu Ile Lys Ser Lys 455	ata ctt gct act Ile Leu Ala Thr 460	1392
act tct tcg tct tct tct tct tcg aca cat cat 465	ggg ggt gga aat gga 470	ata	1440

ES 2 631 987 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
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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 2 631 987 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 2 631 987 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 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 2 631 987 T3

atg tat caa tta ttt tgt ttt ctt gct ggt ata att gtt gta tat aaa Met Tyr Gln Leu Phe Cys Phe Leu Ala Gly Ile Ile Val Val Tyr Lys 1 5 10 15	48
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 2 631 987 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 Ile Asp Arg Val Val Gly Met	260	265	270	
tcc gaa gaa gaa ttg aac aat cat cca aag agc tat gtt ttg ttg tac				864
Ser Glu Glu Glu Leu Asn Asn His Pro Lys Ser Tyr Val Leu Leu Tyr	275	280	285	
caa tta gca aga caa act aag aat cgt gat ata tta caa gat gaa ttg				912
Gln Leu Ala Arg Gln Thr Lys Asn Arg Asp Ile Leu Gln Asp Glu Leu	290	295	300	
atg tcc att tta ctt gca ggt aga gac acc act gcc agt ttg ttg act				960
Met Ser Ile Leu Leu Leu Gly Arg Asp Thr Thr Ala Ser Leu Leu Thr	310	315	320	
ttt ttg ttt ttc gaa tta agt cac cat cca gaa gta ttt aac aaa tta				1008
Phe Leu Phe Phe Glu Leu Ser His His Pro Glu Val Phe Asn Lys Leu	325	330	335	
aaa gag gaa atc gaa aga cac ttt cct gat gtt gaa tcc gtt aca ttt				1056
Lys Glu Glu Ile Glu Arg His Phe Pro Asp Val Glu Ser Val Thr Phe	340	345	350	
gga act atc cag aga tgc gac tat ctt caa tgg tgt att aac gaa act				1104
Gly Thr Ile Gln Arg Cys Asp Tyr Leu Gln Trp Cys Ile Asn Glu Thr	355	360	365	
atg aga ctc cat cca tca gtt cct ttt aat ttc aga act gca gcc aat				1152
Met Arg Leu His Pro Ser Val Pro Phe Asn Phe Arg Thr Ala Ala Asn	370	375	380	
gac aca gta ata cca aga ggt gga ggt aaa tcc tgt aca gat cct att				1200
Asp Thr Val Ile Pro Arg Gly Gly Gly Lys Ser Cys Thr Asp Pro Ile	385	390	395	400
ctt gtc cat aag ggt gaa caa gta tta ttc agt ttc tat tct gta aac				1248
Leu Val His Lys Gly Glu Gln Val Leu Phe Ser Phe Tyr Ser Val Asn	405	410	415	
aga gaa gaa aag tat ttt ggt aca aat acc gac aag ttt gct cca gaa				1296
Arg Glu Glu Lys Tyr Phe Gly Thr Asn Thr Asp Lys Phe Ala Pro Glu	420	425	430	
aga tgg agt gaa tca tta agg aga act gag ttc ata cca ttt tct gct				1344
Arg Trp Ser Glu Ser Leu Arg Arg Thr Glu Phe Ile Pro Phe Ser Ala	435	440	445	
gga cct cgt gcc tgt ttg ggt caa cag tta gct aga gtt gaa gct tca				1392
Gly Pro Arg Ala Cys Leu Gly Gln Gln Leu Ala Arg Val Glu Ala Ser	450	455	460	
tat gtt act att aga ttg ctt caa acc ttt cat ggg ttg cat aat gcc				1440
Tyr Val Thr Ile Arg Leu Leu Gln Thr Phe His Gly Leu His Asn Ala	465	470	475	480
agt aaa caa tac cca cca aat aga gtg gtt gca gct aca atg aga ttg				1488
Ser Lys Gln Tyr Pro Pro Asn Arg Val Val Ala Ala Thr Met Arg Leu	485	490	495	
act gac ggt tgt aac gtt tgt ttt atc tag				1518
Thr Asp Gly Cys Asn Val Cys Phe Ile	500	505		

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

5

<400> 48

ES 2 631 987 T3

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

ES 2 631 987 T3

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

ES 2 631 987 T3

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

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

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<400> 49
atg agt gtc aat act act tct cca gtt gtg gat agt att agt gat aat      48
Met Ser Val Asn Thr Thr Ser Pro Val Val Asp Ser Ile Ser Asp Asn
1                               5                               10                               15

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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ES 2 631 987 T3

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

ES 2 631 987 T3

	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	
ggt tat gat gaa cca gat tct ttc att cca gaa aga tgg gcc act gct						1344
Val Tyr Asp Glu Pro Asp Ser Phe Ile Pro Glu Arg Trp Ala Thr Ala	435		440		445	
tct ggt gat atg tac aaa cgt aac tgg 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	465		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	
ggt att tta gaa tgg aaa aag aga gat ccg tta gct gct tct aat taa						1584
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 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

ES 2 631 987 T3

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

ES 2 631 987 T3

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
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 5 < 213> Candida tropicalis

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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

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ES 2 631 987 T3

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	144
35 40 45	
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	192
50 55 60	
ggg 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	240
65 70 75 80	
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	288
85 90 95	
ggg 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	336
100 105 110	
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	384
115 120 125	
ggg 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	432
130 135 140	
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	480
145 150 155 160	
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	528
165 170 175	
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	576
180 185 190	
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	624
195 200 205	
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	672
210 215 220	
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	720
225 230 235 240	
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	768
245 250 255	
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	816
260 265 270	
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	864
275 280 285	

ES 2 631 987 T3

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
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 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
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 515 520 525

tag 1587

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 <212> PRT
 <213> Candida tropicalis

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<400> 52

ES 2 631 987 T3

Met Ala Ile Val Asp Thr Ala Ile Asp Gly Ile Asn Tyr Phe Leu Ser
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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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 515 520 525

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ES 2 631 987 T3

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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	

ES 2 631 987 T3

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

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

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

gct aaa gac ttg caa cca caa act aaa ctt tag 2097
 Ala Lys Asp Leu Gln Pro Gln Thr Lys Leu
 690 695

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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

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

Val Ser Val Ala Leu Gly Asp Phe Gly Asn Glu Val Asp Phe Glu Ala
 450 455 460

Tyr Lys Arg Pro Leu Met Thr Ala Val Cys Asn Ala Val Asp Asp Leu
 465 470 475 480

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

Tyr Val Thr Ala Pro Phe Tyr Pro Trp Gln Ser Gly Ala Gln Ala Arg
 500 505 510

Lys Asn Leu Leu Lys Tyr Lys Gln Thr Val Pro Leu Leu Leu Ser
 515 520 525

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

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

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

Lys Glu Ile Leu Ser Pro Gln Ala Trp Val Pro Thr Phe Lys Ser Asn
 580 585 590

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

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

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

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

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

Pro Met Ile Thr Thr Met Ala Phe Ala Arg His Val Ala Leu Cys Leu
 675 680 685

Ala Lys Asp Leu Gln Pro Gln Thr Lys Leu
 690 695

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 <211> 2097
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ES 2 631 987 T3

< 213> Candida cloacae

<220>

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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	
			180					185					190			
att	atc	ggg	tct	ggt	tcg	gga	gca	gga	gtg	ggt	gct	caa	act	ctt	tcg	624
Ile	Ile	Gly	Ser	Gly	Ser	Gly	Ala	Gly	Val	Val	Ala	Gln	Thr	Leu	Ser	
		195					200					205				
gaa	aac	gga	ctt	aaa	tca	ttg	gtg	ttg	gaa	aaa	ggt	aaa	tac	ttt	tcc	672
Glu	Asn	Gly	Leu	Lys	Ser	Leu	Val	Leu	Glu	Lys	Gly	Lys	Tyr	Phe	Ser	
	210					215					220					
aat	gat	gag	ttg	acc	atg	aat	gat	ttg	gaa	ggt	agt	gag	gca	tta	ttc	720
Asn	Asp	Glu	Leu	Thr	Met	Asn	Asp	Leu	Glu	Gly	Ser	Glu	Ala	Leu	Phe	
225					230					235					240	
gaa	aat	gga	ggt	gcc	ctc	agt	agt	acc	aac	caa	cag	ata	ttt	ata	att	768
Glu	Asn	Gly	Gly	Ala	Leu	Ser	Ser	Thr	Asn	Gln	Gln	Ile	Phe	Ile	Ile	
				245					250						255	
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	Thr	Val	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	ggt	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	ggt	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	ggt	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	ggt	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	ggt	gta	acc	ggt	ggt	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	ggt	ggt	ttc	tgg	tgg	ttc	ttt	gca	aac	tcc	ggt	ttt	ggt	aca	aaa	1296
Ile	Val	Val	Phe	Trp	Trp	Phe	Phe	Ala	Asn	Ser	Gly	Phe	Val	Thr	Lys	
			420					425					430			

ES 2 631 987 T3

tca ggt ttc aag aat aaa cac att ggt gct aac ttg aag ctc cat cca 1344
 Ser Gly Phe Lys Asn Lys His Ile Gly Ala Asn Leu Lys Leu His Pro
 435 440 445

ggt tca ctt acg ctt gga gac ttc ggt aac aac gtg gat ttc gaa gct 1392
 Val Ser Leu Thr Leu Gly Asp Phe Gly Asn Asn Val Asp Phe Glu Ala
 450 455 460

tac agg aaa cca att atg aca tca att tgt aat aaa gtc gaa gat tta 1440
 Tyr Arg Lys Pro Ile Met Thr Ser Ile Cys Asn Lys Val Glu Asp Leu
 465 470 475 480

gat gga aag gcc cat ggt aca aga att gaa gct atg ttg aat gct cca 1488
 Asp Gly Lys Ala His Gly Thr Arg Ile Glu Ala Met Leu Asn Ala Pro
 485 490 495

tat ggt gtt gca cca ttt ttc ccc tgg aaa tca ggc gct gaa tca aga 1536
 Tyr Gly Val Ala Pro Phe Phe Pro Trp Lys Ser Gly Ala Glu Ser Arg
 500 505 510

aag gat ctc ttg aga tac aaa caa act gtg cct ata tta ctt ctt tcc 1584
 Lys Asp Leu Leu Arg Tyr Lys Gln Thr Val Pro Ile Leu Leu Leu Ser
 515 520 525

aga gat act act tca ggg tct gtc aca tat gat aaa caa aaa cca gat 1632
 Arg Asp Thr Thr Ser Gly Ser Val Thr Tyr Asp Lys Gln Lys Pro Asp
 530 535 540

gca ttg gtg att gat tac ctg tta aac aag ttt gac aga aac tca att 1680
 Ala Leu Val Ile Asp Tyr Leu Leu Asn Lys Phe Asp Arg Asn Ser Ile
 545 550 555 560

tta caa ggg ttt ttg ata gct tca gac ctt tta tat att gaa ggt gcc 1728
 Leu Gln Gly Phe Leu Ile Ala Ser Asp Leu Leu Tyr Ile Glu Gly Ala
 565 570 575

agt aga gat cat gtc acc tac aag ctt ggg tac caa tgg ttc aag agt 1776
 Ser Arg Asp His Val Thr Tyr Lys Leu Gly Tyr Gln Trp Phe Lys Ser
 580 585 590

tct aaa cct aaa cat gcc aga tcg att gaa gat gaa gac tac gta aac 1824
 Ser Lys Pro Lys His Ala Arg Ser Ile Glu Asp Glu Asp Tyr Val Asn
 595 600 605

tgg aga gct aaa gtt gca aag att cca ttt gat tcc tac gga tca cca 1872
 Trp Arg Ala Lys Val Ala Lys Ile Pro Phe Asp Ser Tyr Gly Ser Pro
 610 615 620

tac ggt tca gct cac caa atg agt aca tgc aga atg tca ggt aag gga 1920
 Tyr Gly Ser Ala His Gln Met Ser Thr Cys Arg Met Ser Gly Lys Gly
 625 630 635 640

cca gga tat gga gct tgt gat acc aaa gga aaa tta ttt gaa tgt agc 1968
 Pro Gly Tyr Gly Ala Cys Asp Thr Lys Gly Lys Leu Phe Glu Cys Ser
 645 650 655

aat gtt tat gtt gca gat gct tcc act ttg cct act gca tca ggg gct 2016
 Asn Val Tyr Val Ala Asp Ala Ser Thr Leu Pro Thr Ala Ser Gly Ala
 660 665 670

aat cca atg gtt agt acc atg tca ttt gca agg cac gtg tcc tta gga 2064
 Asn Pro Met Val Ser Thr Met Ser Phe Ala Arg His Val Ser Leu Gly
 675 680 685

att gtt aaa gaa ttg caa caa agt aaa ctt tag 2097
 Ile Val Lys Glu Leu Gln Gln Ser Lys Leu
 690 695

5 <210> 56
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ES 2 631 987 T3

<400> 56

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Ala Asp Ala Val Val His Glu Ile Pro Pro Ser Glu Ile Val Glu Tyr
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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 2 631 987 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
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Val Ser Leu Thr Leu Gly Asp Phe Gly Asn Asn Val Asp Phe Glu Ala

ES 2 631 987 T3

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ttg ctc gtc cac gtc aaa tac tcc ggt gtt tgt cac tca gat ata cac 96
Leu Leu Val His Val Lys Tyr Ser Gly Val Cys His Ser Asp Ile His
20 25 30

gtc tgg aag ggt gac tgg ttc cca gca tgc aaa ttg ccc gtt gtt ggt 144
Val Trp Lys Gly Asp Trp Phe Pro Ala Ser Lys Leu Pro Val Val Gly
35 40 45

ggc cac gaa ggt gcc ggt gtt gtc gtt gcc att ggt gaa aac gtc caa 192
Gly His Glu Gly Ala Gly Val Val Val Ala Ile Gly Glu Asn Val Gln
50 55 60

ggc tgg aaa gta ggt gac ttg gca ggt ata aag atg ttg aat ggt tcc 240
Gly Trp Lys Val Gly Asp Leu Ala Gly Ile Lys Met Leu Asn Gly Ser
65 70 75 80

tgt atg aac tgt gaa tac tgt caa caa ggt gct gaa cca aac tgt ccc 288
Cys Met Asn Cys Glu Tyr Cys Gln Gln Gly Ala Glu Pro Asn Cys Pro
85 90 95

cac gct gat gtc tgc ggt tac tcc cac gac ggt act ttc caa cag tac 336
His Ala Asp Val Ser Gly Tyr Ser His Asp Gly Thr Phe Gln Gln Tyr
100 105 110

gct acc gcc gat gct gtt caa gct gct aaa ttc cca gct ggt tct gat 384
Ala Thr Ala Asp Ala Val Gln Ala Ala Lys Phe Pro Ala Gly Ser Asp
115 120 125

tta gct agc atc gca cct ata tcc tgc gcc ggt gtt act gtt tac aaa 432
Leu Ala Ser Ile Ala Pro Ile Ser Cys Ala Gly Val Thr Val Tyr Lys
130 135 140

gca ttg aaa act gca gcc ttg cag cca ggt caa tgg gtt gcc atc tct 480
Ala Leu Lys Thr Ala Gly Leu Gln Pro Gly Gln Trp Val Ala Ile Ser
145 150 155 160

ggc gca gct ggt ggt ttg ggt tct ttg gct gtg caa tac gcc aag gcc 528
Gly Ala Ala Gly Gly Leu Gly Ser Leu Ala Val Gln Tyr Ala Lys Ala
165 170 175

atg ggt ttg aga gtc gtg gcc att gac ggt ggt gac gaa aga gga gtg 576
Met Gly Leu Arg Val Val Ala Ile Asp Gly Gly Asp Glu Arg Gly Val
180 185 190

ttt gtc aaa tgc ttg ggt gct gaa gtt ttc gtt gat ttc acc aaa gag 624
Phe Val Lys Ser Leu Gly Ala Glu Val Phe Val Asp Phe Thr Lys Glu
195 200 205

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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

<210> 58
 < 211> 316
 < 212> PRT
 5 < 213> Candida tropicalis

<400> 58
 Pro Leu Gln Tyr Thr Asp Ile Pro Val Pro Val Pro Lys Pro Asn Glu
 1 5 10 15
 Leu Leu Val His Val Lys Tyr Ser Gly Val Cys His Ser Asp Ile His
 20 25 30
 Val Trp Lys Gly Asp Trp Phe Pro Ala Ser Lys Leu Pro Val Val Gly
 35 40 45
 Gly His Glu Gly Ala Gly Val Val Val Ala Ile Gly Glu Asn Val Gln
 50 55 60
 Gly Trp Lys Val Gly Asp Leu Ala Gly Ile Lys Met Leu Asn Gly Ser
 65 70 75 80
 Cys Met Asn Cys Glu Tyr Cys Gln Gln Gly Ala Glu Pro Asn Cys Pro
 85 90 95
 His Ala Asp Val Ser Gly Tyr Ser His Asp Gly Thr Phe Gln Gln Tyr
 100 105 110

ES 2 631 987 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 2 631 987 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 245 250 255 260	768

ES 2 631 987 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
	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
	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 2 631 987 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
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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 2 631 987 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
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 < 212> DNA
 5 < 213> Candida tropicalis

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

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 1 5 10 15
 ttg ctt gtc aac gtc aag tac tcg ggt gtg tgt cat tct gac ttg cat 96
 Leu Leu Val Asn Val Lys Tyr Ser Gly Val Cys His Ser Asp Leu His
 20 25 30
 gtc tgg aaa ggc gac tgg ecc 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 gcc 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 2 631 987 T3

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

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

<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

ES 2 631 987 T3

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

5 <211> 948

<212> DNA

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<220>

ES 2 631 987 T3

< 221> CDS
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<400> 65

<p>gaa tta gaa tac aaa gat atc cca gtg cca acc cca aag gcc aac gaa Glu Leu Glu Tyr Lys Asp Ile Pro Val Pro Thr Pro Lys Ala Asn Glu 1 5 10 15</p>	<p>48</p>
<p>ttg ctc atc aac gtc aaa tac tcg ggt gtc tgc cac act gat ttg cac Leu Leu Ile Asn Val Lys Tyr Ser Gly Val Cys His Thr Asp Leu His 20 25 30</p>	<p>96</p>
<p>gcc tgg aag ggt gac tgg cca ttg gcc acc aag ttg cca ttg gtt ggt Ala Trp Lys Gly Asp Trp Pro Leu Ala Thr Lys Leu Pro Leu Val Gly 35 40 45</p>	<p>144</p>
<p>ggt cac gaa ggt gct ggt gtc gtt gtc ggc atg ggt gaa aac gtc aag Gly His Glu Gly Ala Gly Val Val Val Gly Met Gly Glu Asn Val Lys 50 55 60</p>	<p>192</p>
<p>ggc tgg aag att ggt gac ttc gcc ggt atc aaa tgg ttg aac ggt tcc Gly Trp Lys Ile Gly Asp Phe Ala Gly Ile Lys Trp Leu Asn Gly Ser 65 70 75 80</p>	<p>240</p>
<p>tgt atg tcc tgt gag ttc tgt caa caa ggt gct gaa cca aac tgt ggt Cys Met Ser Cys Glu Phe Cys Gln Gln Gly Ala Glu Pro Asn Cys Gly 85 90 95</p>	<p>288</p>
<p>gag gcc gac ttg tct ggt tac acc cac gat ggt tct ttc gaa caa tac Glu Ala Asp Leu Ser Gly Tyr Thr His Asp Gly Ser Phe Glu Gln Tyr 100 105 110</p>	<p>336</p>
<p>gcc act gct gat gct gtt caa gcc gcc aga atc cca gct ggt act gat Ala Thr Ala Asp Ala Val Gln Ala Ala Arg Ile Pro Ala Gly Thr Asp 115 120 125</p>	<p>384</p>
<p>ttg gcc gaa gtt gcc cca atc ttg tgt gcg ggt gtc acc gtc tac aaa Leu Ala Glu Val Ala Pro Ile Leu Cys Ala Gly Val Thr Val Tyr Lys 130 135 140</p>	<p>432</p>
<p>gcc ttg aag act gcc gac ttg gcc gct ggt caa tgg gtc gct atc tcc Ala Leu Lys Thr Ala Asp Leu Ala Ala Gly Gln Trp Val Ala Ile Ser 145 150 155 160</p>	<p>480</p>
<p>ggt gct ggt ggt ggt ttg ggt tcc ttg gct gtc caa tac gcc gtc gcc Gly Ala Gly Gly Gly Leu Gly Ser Leu Ala Val Gln Tyr Ala Val Ala 165 170 175</p>	<p>528</p>
<p>atg gcc ttg aga gtc gtt gcc att gac ggt ggt gac gaa aag ggt gcc Met Gly Leu Arg Val Val Ala Ile Asp Gly Gly Asp Glu Lys Gly Ala</p>	<p>576</p>

ES 2 631 987 T3

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	200	205	
	195		
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	215	220	
	210		
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	230	235	
	225		
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	
	240	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	280	285	
	275		
ggt 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	295	300	
	290		
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	310	315	
	305		

<210> 66
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 <212> PRT
 5 <213> Candida tropicalis

<400> 66
 Glu Leu Glu Tyr Lys Asp Ile Pro Val Pro Thr Pro Lys Ala Asn Glu
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 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

ES 2 631 987 T3

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

ES 2 631 987 T3

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
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ES 2 631 987 T3

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 565 570 575

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ES 2 631 987 T3

Tyr Val Arg Thr Phe Thr Lys Pro Ser Glu Thr Pro Gly Phe Arg Glu
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 50 55 60
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 Glu Lys Leu Leu Ala Ser Trp Arg Asp Ser Pro Ile Ala Ala Lys Arg
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 Leu Ala Asn Glu Leu His Leu Lys Ala Ile His Tyr Pro Gly Arg Glu
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 Asp Arg Glu Lys Ala Tyr Glu Thr Gln Glu Ile Asp Pro Phe Lys Tyr
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 Gln Phe Met Glu Lys Pro Lys Phe Asp Gly Ala Glu Leu Tyr Leu Pro
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 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
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 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

ES 2 631 987 T3

His Pro Thr Lys Pro Glu Ala Leu Val Val Glu Tyr Asp Val Asn Lys
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Phe Asp Arg Asn Ser Ile Leu Gln Ala Leu Leu Val Thr Ala Asp Leu
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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
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Glu Asp Tyr Val Glu Trp Arg Ala Lys Val Ala Lys Ile Pro Phe Asp
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Thr Tyr Gly Ser Pro Tyr Gly Ser Ala His Gln Met Ser Ser Cys Arg
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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. 57,
- B) una secuencia que es idéntica a Seq ID Nr. 57 en al menos un 80 %, 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
- 10 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.