República Federativa do Brasil
Ministério do Desenvolvimento, Indústria e do Comércio Exterior
Instituto Nacional da Propriedade Industrial.

(21) **PI0709896-0 A2**

BRPI0709896A2

(22) Data de Depósito: 02/04/2007
(43) Data da Publicação: 02/08/2011
(RPI 2117)

(51) Int.Cl.:
C07K 19/00 2006.01
C12N 15/62 2006.01
C12N 15/80 2006.01
C12N 9/16 2006.01
C12N 15/55 2006.01

(54) Título: **PROTEÍNAS DE FUSÃO ENTRE ENZIMAS DEGRADADORAS DA PAREDE DE CELULAR DE PLANTAS E UMA SWOLENINA, E SEUS USOS**

(30) Prioridade Unionista: 06/04/2006 EP 06290562.5

(73) Titular(es): Institut Français Du Petrole, Institut National De La Recherche Agronomique , Universite De Provence, VTT Technical Research Centre Of Filand

(72) Inventor(es): Anthony Levasseur, David Navarro, Eric Record, Frédéric Monot, Marcel Asther, Markku Soloheimo, Martina Andberg, Tiina Nakari-Setälä

(74) Procurador(es): Tavares Propriedade Intelectual LTDA

(86) Pedido Internacional: PCT EP2007002947 de 02/04/2007

(87) Publicação Internacional: WO 2007/115723de 18/10/2007

(57) Resumo: PROTEÍNAS DE FUSÃO ENTRE ENZIMAS DEGRADADORAS DA PAREDE DE CELULAR DE PLANTAS E UMA SWOLENINA, E SEUS USOS A invenção refere-se a proteínas de fusão compreendendo pelo menos uma swolenina e pelo menos uma enzima degradadora da parede celular de plantas, a referida swolenina e a enzima degradadora da parede celular de plantas sendo proteínas recombinantes correspondendo a proteínas nativas em fungos, ou suas formas mutadas. A invenção também se refere ao uso de proteínas de fusão conforme definidas acima, para realizar processos de degradação da parede celular de plantas no âmbito da preparação, a partir de plantas ou subprodutos vegetais, de compostos de interesse localizados na parede celular de plantas, ou no âmbito do branqueamento da polpa e do papel, para a produção de biocombustíveis ou nas indústrias alimentícias.

Relatório Descritivo da Patente de Invenção para **"PROTEÍNAS DE FUSÃO ENTRE ENZIMAS DEGRADADORAS DA PAREDE DE CELULAR DE PLANTAS E UMA SWOLENINA, E SEUS USOS"**.

A invenção refere-se à construção e superprodução de proteínas de fusão multifuncionais criadas por engenharia genética entre pelo menos uma swolenina e pelo menos uma enzima degradadora da parede celular de plantas, e a seus usos como ferramentas enzimáticas aperfeiçoadas para a valorização de subprodutos agrícolas.

ANTECEDENTES DA INVENÇÃO

A parede celular das plantas desenvolveu uma arquitetura complexa com uma composição intrínseca de diversos carboidratos para, dessa forma, proteger a célula de ataques microbianos. Como conseqüência, os microorganismos degradadores da parede celular de plantas desenvolveram diversos sistemas enzimáticos com o intuito de decompor a biomassa vegetal e, finalmente, assimilar os substratos de açúcares. Dentre os microorganismos bacterianos e fúngicos, são encontradas enzimas modulares contendo Módulos de Ligação a Carboidratos (CBMs) que auxiliam as enzimas no direcionamento aos substratos. Recentemente, foi identificado, no *Trichoderma reesei*, uma nova espécie de proteína, envolvida na dissolução da parede celular de plantas, a qual foi chamada de "swolenina" (Saloheimo M. e col. 2002). Essa proteína apresenta alta similaridade com as expansinas das plantas, que decompõe as

ligações de hidrogênio entre as microfibrilas de celulose, ou a celulose e outros polímeros da parede celular (Cosgrove 2000). De fato, imagina-se que as expansinas das plantas desempenham uma função da extensão da parede celular, sendo consideradas um regulador endógeno fundamental para o crescimento da parede celular da planta (Li Y e col. 2003). Ao contrário das expansinas de plantas, a swolenina tem uma estrutura bimodular composta de um CMB conectado por uma região de ligação ao domínio homólogo da expansina de plantas. Essa estrutura modular é típica das celulases fúngicas e de algumas hemicelulases que apresentam um CBM para direcionar o módulo enzimático. No caso específico da swolenina, não há atividade hidrolítica associada, mas sim um módulo de expansina com capacidade de dissolução da parede celular. Paralelamente, a célula dos microorganismos desenvolveu sistemas livres que não possuem um módulo CBM, sendo em vez disso segregados em grandes quantidades no meio extracelular. Esses tipos de enzimas podem ser encontrados nas celulases, hemicelulases e pectinases. Os estudos de engenharia genética têm se focado no aperfeiçoamento das enzimas livres por meio da associação de um módulo CBM para direcionar enzimas a um substrato específico da planta, tal como a celulose (Ito e col. 2004; Limón e col. 2004). No primeiro caso, Ito e col. demonstraram que a atividade hidrolítica de ume endoglucanase de T. reesei foi aumentada com o número de CBM adicionado à enzima. No segundo trabalho, um módulo CBM foi geneticamente fusionado a uma enzima sem ser de celulase, a

quitinase de *Trichoderma harzanium*, e os resultados mostraram que tanto as atividades antifúngicas como da quitinase aumentaram com o aumento da capacidade de ligação à celulose. Esse ganho de desempenho é de grande interesse para aplicações industriais em que a degradação da parede celular de plantas é um ponto essencial, por exemplo, nos setores de biocombustíveis e de polpa e papel.

Recentemente, os inventores passaram a se interessar em cinamoil esterases capazes de hidrolizar diferentes tipos de ácidos hidroxicinâmicos ligados a ésteres de açúcares. Essas enzimas foram classificadas com base na especificidade do substrato e na identidade de seqüência primária (Crepin e col. 2003). As primeiras cinamoil esterases a serem totalmente caracterizadas pertencem ao *Aspergillus niger*. A feruloil esterase (FAEIII, tipo A) foi descrita como sendo preferivelmente ativa contra o éster metílico de ácidos ferúlicos e sinápicos (Faulds e Williamson 1994), ao passo que a cinamoil esterase demonstrou ter preferência pelo éster metílico de ácidos caféicos e *p*-coumáticos (Kroon e col. 1996). Ambos os genes codificadores foram clonados e caracterizados. Eles foram superexpressos em *Pichia pastoris* e *A. niger* para produzir quantidades suficientes de proteínas recombinantes e permitir sua utilização em aplicações industriais (Juge e col. 2001 ; Record e col. 2003, Levasseur e col. 2003). A feruloil esterase foi avaliada quanto ao branqueamento da palha de trigo e da polpa de linho, em combinação com um tratamento com lacase, a redução do teor

final de lignina (Record e col. 2003; Sigoillot e col; 2005). De fato, a feruloil esterase é conhecida por hidrolizar oligossacarídeos feruloilados, mas também ligações cruzadas de diferulato encontradas na hemicelulose e na pectina (Williamson e col. 1998; Saulnier e Thibault 1999), facilitando o acesso de outros enzimas lignocelulolíticas.

O objetivo do presente trabalho é o de desenvolver novas ferramentas enzimáticas para degradar a biomassa vegetal ou biotransformar os componentes da parede celular de plantas. Duas estratégias foram desenvolvidas paralelamente. Em um trabalho anterior (Levasseur e col. 2004), o objetivo era o de desenvolver um novo tipo de enzima fúngica fusionada a uma doquerina bacteriana que posse, portanto, capaz de ser incorporada em celulossomas da *Clostridium thermocellum.* De fato, a celulosoma bacteriana é um sistema muito eficaz no aumento do efeito sinérgico das enzimas (Ciruela e col. 1998, Fierobe e col. 2002). De forma alternativa, demonstrou-se que enzimas quiméricas associando duas enzimas possuem grande eficácia na degradação da biomassa vegetal, especialmente se um módulo CBM tiver sido integrado no complexo enzimático (Levasseur e col 2005). Em outros trabalhos, a fusão dos módulos CBM aos parceiros enzimáticos demonstrou ser uma boa maneira de melhorar a eficiência do parceiro enzimático pelo auxílio do direcionamento enzimático ao substrato e pelo aumento da concentração local das enzimas (Pages et al. 1997, Boraston et al. 2004). Além disso, foi

verificado que apenas alguns CBMs mediam o efeito de dissolução não-catalítica da estrutura cristalina da celulose (Din e col. 1994, Gao e col. 2001).

Na presente invenção, os inventores descrevem pela primeira vez a associação de uma swolenina a uma enzima degradadora da parede celular de plantas, tal como a feruloil esterase utilizada como modelo enzimático, utilizando-se uma fusão genética de ambos os genes correspondentes.

SUMÁRIO DA INVENÇÃO

A presente invenção se baseia na demonstração do efeito da eficiência enzimática, relacionado à associação física em uma única proteína quimérica, de enzimas degradadoras da parede celular de plantas e da swolenina, quando comparado ao uso das enzimas livres degradadoras da parede celular de plantas.

Assim, o principal objetivo da presente invenção é obter novas proteínas de fusão entre a swolenina e enzimas de degradação da parede celular de plantas.

Outro objetivo da presente invenção é o de propor um novo processo para a preparação dos compostos de interesse ligados às paredes das células vegetais, por meio da aplicação das referidas proteínas de fusão às plantas, e vantajosamente aos subprodutos agrícolas, como substratos.

BREVE DESCRIÇÃO DOS DESENHOS

A Figura 1 representa a produção da Feruloil esterase (FAEA) em *Trichoderma reesei*. A atividade da feruloil esterase foi medida no meio extracelular obtido a partir dos

melhores transformantes FAEA de *T. reesei* Rut-C (●) e CL847 (■). Utilizou-se ferulato de metila como substrato para testes de atividade.

A Figura 2 ilustra a análise Western blot e o número de cópia dos cassetes integrados no genoma de *T. reesei.* Utilizaram-se anticorpos contra FAEA para a imunodetecção da FAEA e transformantes SWOI-FAEA a partir do meio extracelular total. Pista 1 e 2: transformantes Rut-C30 produzindo FAEA e SWOI-FAEA, respectivamente. Pista 3 e 4: transformantes CL847 produzindo FAEA e SWOI-FAEA, respectivamente. O número de cópia dos cassetes de expressão foi estimado pela análise Southern blot. Utilizou-se o BRFM da linhagem de *Aspergillus niger* do tipo selvagem como controle contendo a cópia do gene *fae*A. Sd: padrões de peso molecular.

A Figura 3 representa um gel SDS-PAGE de proteínas extracelulares e purificadas de *Trichoderma reesei.* Pista 1: linhagem CL847 de *T. reesei* não-transformada. Pista 2 e 3: Meio extracelular total da linhagem CL847 de *T. reesei* transformado pelos cassetes de expressão para produção de FAEA ou SWOI-FAEA, respectivamente. Pistas 4 e 5: FAEA é SWOI-FAEA purificados. Sd: padrões de peso molecular.

A Figura 4 mostra a estabilidade de temperatura da FAEA e SWOI-FAEA obtidas da linhagem 847 de *Trichoderma reesei.* A atividade da proteína purificada (♦) e SWOI-FAEA (■) após 60 min de incubação à temperatura

indicada é representada. Utilizou-se ferulato de metila como substrato para testes de atividade.

A Figura 5 ilustra a liberação de ácido ferúlico utilizando-se a FAWA ou SWOI-FAEA de *Trichoderma reesei* CL847. Utilizou-se farelo de trigo como substrato, sendo a liberação de ácido ferúlico determinada por HPLC após 4 h (barras brancas), 16 h (barras cinzas) e 24 h (barras pretas) de hidrólise. As atividades foram expressas como a porcentagem da concentração total de ácido ferúlico no farelo de trigo. R: referência contendo apenas o tampão; S: meio extracelular da linhagem não transformada; C: controle como a feruloil esterase de *Aspergillus niger*; F: feruloil esterase (FAEA) de *T. reesei*, S: Swolenina (SWOI) de *T. reesei*; proteína de fusão S-F (SWOI-FAEA) de *T. reesei*.

DESCRIÇÃO DETALHADA DA INVENÇÃO

A invenção refere-se a proteínas de fusão, compreendendo:

- pelo menos uma swolenina, isto é, uma proteína contendo um domínio de molécula de ligação a carboidratos (CBM) que direciona para a celulose das plantas, e um domínio de expansina que decompõe as ligações de hidrogênio entre as microfibrilas da celulose,

- e pelo menos uma enzima degradadora da parede celular de plantas,

a referida enzima sendo de tal forma que ela contém um domínio CBM ou não, contanto que contenha um

CBM, o último pode ser excluído, se necessário, a referida swolenina e a enzima degradadora da parede celular de plantas sendo proteínas recombinantes correspondendo a proteínas nativas em fungos, ou formas mutadas destes.

A expressão "enzimas degradadoras da parede celular de plantas" refere-se a enzimas que são capazes de efetuar a digestão dos componentes de parede celular, como a celulose, hemicelulose e lignina. As enzimas degradadoras da parede celular de plantas nas referidas proteínas de fusão são idênticas, ou diferentes uma da outra.

A expressão "molécula de ligação a carboidratos" refere-se a uma molécula com afinidade por celulose, que direciona sua enzima associada à celulose.

A invenção refere-se mais especificamente a proteínas de fusão conforme definidas acima, em que a swolenina corresponde a proteínas nativas, ou suas formas mutadas, de fungos escolhidos dentre ascomicetes, como por exemplo:

- Linhagens de *Trichoderma*, e mais particularmente *Trichoderma reesei*, ou
- linhagens de *Aspergillus*, e mais particularmente *Aspergillus fumigatus*. A invenção refere-se mais especificamente a proteínas de fusão conforme definidas acima, em que a swolenina corresponde a enzimas nativas, ou suas formas mutadas, de linhagens de *Trichoderma*, tal como *Trichoderma reesei*.

A invenção refere-se mais especificamente a proteínas de fusão conforme definidas acima, em que a swolenina é a proteína da *Trichoderma reesei*, representada pela:

- SEQ ID NO: 2 em seu estado pré-proteína, ou seja, contendo o peptídeo de sinal SEQ ID NO : 102 dos seguintes 18 aminoácidos: MAGKLILVALASLVSLSI,

- ou pela SEQ ID NO : 4 em seu estado maduro, ou seja, sem o peptídeo de sinal supramencionado.

A invenção refere-se mais especificamente a proteínas de fusão conforme definidas acima, em que a swolenina corresponde a enzimas nativas, ou suas formas mutadas, de linhagens de *Aspergillus*, tal como *Aspergillus fumigatus*.

A invenção refere-se mais especificamente a proteínas de fusão conforme definidas acima, em que a swolenina é a proteína de *Aspergillus fumigatus*, representada pela:

- SEQ ID NO: 6 em seu estado pré-proteína, ou seja, contendo o peptídeo de sinal SEQ ID NO : 104 dos seguintes 17 aminoácidos: MTLLFGIFLARLAVAAA,

- ou pela SEQ ID NO : 8 em seu estado maduro, ou seja, sem o peptídeo de sinal supramencionado.

A invenção refere-se, mais particularmente, a proteínas de fusão conforme definidas acima, em que as enzimas degradadoras da parede celular de plantas são escolhidas dentre enzimas capazes de hidrolizar a celulose, a hemicelulose e degradar a lignina.

A invenção refere-se mais particularmente a proteínas de fusão conforme definidas acima, em que as enzimas degradadoras da parede celular de plantas são hidrolases escolhidas dentre:

- celulases, tais como endoglucanases, exoglucanases, tais como celobiohidrolases, ou β-glucosidases,
- hemicelulases, tais como xilanases,
- ligninases capazes de degradar ligninas, tais como lacases, manganês peroxidases, lignina peroxidases, peroxidases versáteis ou enzimas suplementares, tais como celobiose deidrogenases, e aril álcool oxidases,
- cinamoil éster hidrolases capazes de liberar ácidos cinâmicos, tais como ácidos ferúlicos e de hidrolizar ligações cruzadas de ácido diferúlico entre cadeias de hemicelulose, tais como feruloil esterases, cinamoil esterases e ácido clorogênico hidrolases.

A invenção refere-se, mais especificamente, a proteínas de fusão conforme definidas acima, em que as enzimas degradadoras da parede celular de plantas são escolhidas entre feruloil esterases, celobiohidrolases com ou sem seus domínios CBM, endoglucanases com ou sem seus domínios CBM, xilanases e lacases.

A invenção refere-se, mais particularmente, a proteínas de fusão conforme definidas acima, em que as enzimas degradadoras da parede celular de plantas correspondem a

enzimas nativas, ou a suas formas mutadas, de fungos selecionados entre:

* ascomicetes, tal como:

- linhagens de *Aspergillus*, e mais particularmente *Aspergillus niger*,

- linhagens de *Trichoderma*, e mais particularmente *Trichoderma reesei*,

- linhagens de *Magnaporthe*, e mais particularmente *Magnaporthe grisea*,

* basidiomicetes, como linhagens de *Pycnoporus*, *Halociphina* ou *Phanerochaete*, e mais particularmente, *Pycnoporus cinnabarinus, Pycnoporus sanguineus* ou *Halocyphina villosa*, ou *Phanerochaete chrysosporium*.

A invenção refere-se mais especificamente a proteínas de fusão conforme definidas acima, em que as enzimas degradadoras da parede celular de plantas correspondem a enzimas nativas, ou suas formas mutadas, de linhagens de *Aspergillus*, tal como *Aspergillus fumigatus*.

A invenção refere-se mais especificamente a proteínas de fusão conforme definidas acima, em que pelo menos uma das enzimas degradadoras da parede celular de plantas é uma feruloil esterase, tal como a selecionada dentre:

- a feruloil esterase A de *A. niger*, representada pela SEQ ID NO : 10,

- ou a feruloil esterase B de *A. niger*, representada pelo SEQ ID NO : 12.

A invenção refere-se mais particularmente a proteínas de fusão conforme definidas acima, em que pelo menos uma das enzimas degradadoras da parede celular de plantas é uma xilanase, tal como a xilanase B de *A. niger*, representada pela SEQ ID NO : 14.

A invenção refere-se mais especificamente a proteínas de fusão conforme definidas acima, em que as enzimas degradadoras da parede celular de plantas correspondem a enzimas nativas, ou suas formas mutadas, de linhagens de *Trichoderma*, tal como *Trichoderma reesei*.

A invenção refere-se mais especificamente a proteínas de fusão conforme definidas acima, em que pelo menos uma das enzimas degradadoras da parede celular de plantas é uma celobiohidrolase, tal como a selecionada dentre:

- A celobiohidrolase I de *T. reesei*, e representada pela SEQ ID NO : 16,

- a celobiohidrolase I de *T. reesei*, em que o domínio CBM foi deletado, e representada pela SEQ ID NO : 18,

- a celobiohidrolase II de *T. reesei*, e representada pela SEQ ID NO : 20,

- a celobiohidrolase II de *T. reesei*, em que o domínio CBM foi deletado, e representada pela SEQ ID NO : 22.

A invenção refere-se mais especificamente a proteínas de fusão conforme definidas acima, em que pelo menos

uma das enzimas degradadoras da parede celular de plantas é uma endoglucanase, tal como a selecionada dentre:

- a endoglucanase I de *T. reesei*, e representada pela SEQ ID NO : 24,

- a endoglucanase I de *T. reesei*, em que o domínio CBM foi deletado, e representada pela SEQ ID NO : 26.

A invenção refere-se mais particularmente a proteínas de fusão conforme definidas acima, compreendendo peptídeos de ligação entre pelo menos duas das proteínas compreendidas nas referidas proteínas de fusão, os referidos peptídeos de ligação sendo polipeptídeos de 10 a 100 aminoácidos, de preferência de cerca de 50 aminoácidos.

A invenção refere-se mais especificamente a proteínas de fusão conforme definidas acima, em que um peptídeo de ligação está incluído entre cada proteína compreendida nas referidas proteínas de fusão.

A invenção também se refere mais especificamente a proteínas de fusão conforme definidas acima, em que o peptídeo de ligação é um polipeptídeo hiperglicosilado, tal como a seqüência representada pela SEQ ID NO : 28, presente na celobiohidrolase B de *A. niger*.

A invenção refere-se mais particularmente a proteínas de fusão conforme descritas acima, escolhidas dentre as proteínas de fusão da swolenina de *Trichoderma reesei* representada pela SEQ ID NO : 4, com:

- a feruloil esterase A de *A. niger*, representada pela SEQ ID NO : 10, a referida proteína de fusão sendo representada pela SEQ ID NO : 30,

- a feruloil esterase A de *A. niger*, representada pela SEQ ID NO : 10, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 4 e a SEQ ID NO : 10, e sendo representada pela SEQ ID NO : 32,

- a feruloil esterase B de *A. niger*, representada pela SEQ ID NO : 12, a referida proteína de fusão sendo representada pela SEQ ID NO : 34,

- a feruloil esterase B de *A. niger*, representada pela SEQ ID NO : 12, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 4 e a SEQ ID NO : 12, e sendo representada pela SEQ ID NO : 36,

- a xilanase B de *A. niger*, representada pela SEQ ID NO : 14, a referida proteína de fusão sendo representada pela SEQ ID NO : 38,

- a xilanase B de *A. niger*, representada pela SEQ ID NO : 14, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 4 e a SEQ ID NO : 14, e sendo representada pela SEQ ID NO : 40,

- a celobiohidrolase I de *T. reesei* representada pela SEQ ID NO : 16, a referida proteína de fusão sendo representada pela SEQ ID NO : 42,

- a celobiohidrolase I de *T. reesei*, representada pela SEQ ID NO : 16, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 4 e a SEQ ID NO : 16, e sendo representada pela SEQ ID NO : 44,

- a celobiohidrolase I de *T. reesei* sem sua CBM endógena representada pela SEQ ID NO : 18, a referida proteína de fusão sendo representada pela SEQ ID NO : 46,

- a celobiohidrolase I de *T. reesei*, sem sua CBM endógena representada pela SEQ ID NO : 18, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 4 e a SEQ ID NO : 18, e sendo representada pela SEQ ID NO : 48,

- a celobiohidrolase II de *T. reesei* pela SEQ ID NO : 20, a referida proteína de fusão sendo representada pela SEQ ID NO : 50,

- a celobiohidrolase II de *T. reesei*, representada pela SEQ ID NO : 20, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO

: 4 e a SEQ ID NO : 20, e sendo representada pela SEQ ID NO : 52,

- a celobiohidrolase II de *T. reesei* sem sua CBM endógena representada pela SEQ ID NO : 22, a referida proteína de fusão sendo representada pela SEQ ID NO : 54,

- a celobiohidrolase II de *T. reesei*, sem sua CBM endógena representada pela SEQ ID NO : 22, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 4 e a SEQ ID NO : 22, e sendo representada pela SEQ ID NO : 56,

- a endoglucanase I de *T. reesei* representada pela SEQ ID NO : 24, a referida proteína de fusão sendo representada pela SEQ ID NO : 58,

- a endoglucanase I de *T. reesei*, representada pela SEQ ID NO : 24, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 4 e a SEQ ID NO : 24, e sendo representada pela SEQ ID NO : 60,

- a endoglucanase I de *T. reesei* sem sua CBM endógena representada pela SEQ ID NO : 26, a referida proteína de fusão sendo representada pela SEQ ID NO : 62,

- a endoglucanase I de *T. reesei*, sem sua CBM endógena representada pela SEQ ID NO : 26, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID

NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 4 e a SEQ ID NO : 26, e sendo representada pela SEQ ID NO : 64.

A invenção refere-se mais especificamente a proteínas de fusão conforme descritas acima, escolhidas dentre as proteínas de fusão da swolenina de *Aspergillus fumigatus* representada pela SEQ ID NO : 8, com:

- a feruloil esterase A de *A. niger*, representada pelo SEQ ID NO : 10, a referida proteína de fusão sendo representada pela SEQ ID NO : 66,

- a feruloil esterase A de *A. niger*, representada pela SEQ ID NO : 10, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 8 e a SEQ ID NO : 10, e sendo representada pela SEQ ID NO : 68,

- a feruloil esterase B de *A. niger*, representada pela SEQ ID NO : 12, a referida proteína de fusão sendo representada pela SEQ ID NO : 70,

- a feruloil esterase B de *A. niger*, representada pela SEQ ID NO : 12, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 8 e a SEQ ID NO : 12, e sendo representada pela SEQ ID NO : 72,

- a xilanase B de *A. niger*, representada pela SEQ ID NO : 14, a referida proteína de fusão sendo representada pela SEQ ID NO : 74,

- a xilanase B de *A. niger*, representada pela SEQ ID NO : 14, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 8 e a SEQ ID NO : 14, e sendo representada pela SEQ ID NO : 76,

- a celobiohidrolase I de *T. reesei* representada pela SEQ ID NO : 16, a referida proteína de fusão sendo representada pela SEQ ID NO : 78,

- a celobiohidrolase I de *T. reesei*, representada pela SEQ ID NO : 16, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 8 e a SEQ ID NO : 16, e sendo representada pela SEQ ID NO : 80,

- a celobiohidrolase I de *T. reesei* sem sua CBM endógena representada pela SEQ ID NO : 18, a referida proteína de fusão sendo representada pela SEQ ID NO : 82,

- a celobiohidrolase I de *T. reesei*, sem sua CBM endógena representada pela SEQ ID NO : 18, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 8 e a SEQ ID NO : 18, e sendo representada pela SEQ ID NO : 84,

- a celobiohidrolase II de *T. reesei* pela SEQ ID NO : 20, a referida proteína de fusão sendo representada pela SEQ ID NO : 86,

- a celobiohidrolase II de *T. reesei*, representada pela SEQ ID NO : 20, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 8 e a SEQ ID NO : 20, e sendo representada pela SEQ ID NO : 88,

- a celobiohidrolase II de *T. reesei* sem sua CBM endógena representada pela SEQ ID NO : 22, a referida proteína de fusão sendo representada pela SEQ ID NO : 90,

- a celobiohidrolase II de *T. reesei*, sem sua CBM endógena representada pela SEQ ID NO : 22, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 8 e a SEQ ID NO : 22, e sendo representada pela SEQ ID NO : 92,

- a endoglucanase I de *T. reesei* representada pela SEQ ID NO : 24, a referida proteína de fusão sendo representada pela SEQ ID NO : 94,

- a endoglucanase I de *T. reesei*, representada pela SEQ ID NO : 24, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO

: 8 e a SEQ ID NO : 24, e sendo representada pela SEQ ID NO : 96,

- a endoglucanase I de *T. reesei* sem sua CBM endógena representada pela SEQ ID NO : 26, a referida proteína de fusão sendo representada pela SEQ ID NO : 98,

- a endoglucanase I de *T. reesei*, sem sua CBM endógena representada pela SEQ ID NO : 26, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 4 e a SEQ ID NO : 26, e sendo representada pela SEQ ID NO : 100.

A invenção também se refere a ácidos nucléicos codificando uma proteína de fusão conforme definida acima, e mais particularmente ácidos nucléicos escolhidos entre a SEQ ID NO : 29 a 99 codificando a SEQ ID NO : 30 a 100, os referidos ácidos nucléicos opcionalmente começando com a seqüência SEQ ID NO : 101 ou 103 codificando, respectivamente, os peptídeos de sinal SEQ ID NO : 102 ou 104 mencionados acima, localizados a montante dos aminoácidos da SEQ ID NO : 30 a 100.

A invenção também se refere a vetores transformados com um ácido nucléico conforme definido acima.

A invenção também se refere a células hospedeiras transformadas com um ácido nucléico conforme definido acima, usando um vetor conforme definido acima.

A invenção também se refere a células hospedeiras transformadas conforme definido acima, escolhidas entre células de fungos, tais como os fungos conforme definidos acima, e mais especificamente *A. niger*, *A. fumigatus*, *Trichoderma reesei* ou *Pycnoporus cinnabarinus*.

A invenção também se refere mais especificamente a um processo para a preparação de proteínas de fusão conforme definidas acima, compreendendo a cultura *in vitro* de células hospedeiras conforme definidas acima, a recuperação, e, se necessária, a purificação das proteínas de fusão produzidas pelas referidas células hospedeiras na cultura. A invenção refere-se, mais especificamente, ao uso de proteínas de fusão conforme definidas acima, para realizar processos de degradação da parede celular de plantas no âmbito da preparação a partir de plantas ou subprodutos vegetais, de compostos de interesse localizados na parede celular da planta, ou no âmbito do branqueamento da polpa e do papel, para a produção de biocombustíveis ou nas indústrias alimentícias.

A invenção também se refere, mais particularmente, ao uso, conforme definido acima, para realizar processos de degradação de parede celular de plantas no âmbito da preparação dos seguintes compostos de interesse:

- bioetanol,

- antioxidantes, como ácido ferúlico ou ácido caféico, que são ácidos cinâmicos, e hidroxitirosol, ou ácido gálico,

- aromas, como vanilina ou *p*-hidroxibenzaldeído, obtidos da biotransformação do ácido ferúlico ou do ácido *p*-coumárico, respectivamente.

A invenção também se refere ao uso, conforme definido acima, em que as referidas proteínas de fusão são adicionadas diretamente às plantas ou subprodutos vegetais como substratos para sua hidrólise.

A invenção também se refere ao uso, conforme definido acima, em que células hospedeiras transformadas com ácidos nucléicos codificando as referidas proteínas de fusão, tais como os fungos mencionados acima, mais especificamente *A. niger* e *Pycnoporus cinnabarinus*, são colocadas em contato com as referidas plantas ou subprodutos vegetais como substratos para sua hidrólise.

A invenção se refere mais especificamente a um processo de degradação da parede celular de plantas no âmbito da preparação, a partir de plantas ou subprodutos vegetais, de compostos de interesse localizados na parede celular de plantas, caracterizado por compreender as seguintes etapas:

- o tratamento enzimático de plantas ou subprodutos vegetais ou resíduos industriais, com proteínas de fusão conforme definidas acima, ou com células transformadas conforme definido acima,

- opcionalmente, o tratamento físico de plantas ou subprodutos vegetais por explosão a vapor em combinação com a ação das proteínas de fusão,

- opcionalmente a biotransformação com microorganismos ou enzimas apropriados dos compostos contidos nas paredes celulares e liberados destas durante o tratamento enzimático anterior,

- a recuperação, e se necessária, a purificação do composto de interesse liberado pelas paredes celulares durante o tratamento enzimático anterior ou obtido durante a etapa de biotransformação anterior.

De preferência, as plantas tratadas com proteínas de fusão no processo de acordo com a invenção são selecionadas entre beterraba, trigo, milho, arroz, ou todas as árvores usadas nas indústrias papeleiras.

De preferência, os subprodutos vegetais ou resíduos industriais tratados com proteínas de fusão no processo de acordo com a invenção são selecionados entre palha de trigo, farelo de milho, farelo de trigo, farelo de arroz, bagaço de maçã, bagaço de café, subprodutos do café e água residual de usinas de oliva.

A invenção refere-se, mais particularmente, a um processo, conforme definido acima, para a preparação de antioxidantes, tais como ácidos cinâmicos, e mais especificamente ácido ferúlico, como compostos de interesse, o referido processo compreendendo: o tratamento das plantas ou subprodutos vegetais com proteínas de fusão conforme definido acima compreendendo uma da swolenina mencionada acima e pelo menos uma das enzimas degradadoras da parede celular: feruloil esterases, como

a feruloil esterase A e a feruloil esterase B, xinalanases, como a xilanase B, tal como definida acima, a recuperação, e, se necessária, a purificação, dos antioxidantes liberados das paredes celulares das referidas plantas ou subprodutos vegetais. De forma vantajosa, no âmbito da preparação de antioxidantes, tal como ácido ferúlico, as plantas tratadas com as proteínas de fusão definidas acima são escolhidas entre as seguintes: beterraba, trigo, trigo, arroz, subprodutos vegetais ou resíduos industriais tratados com proteínas de fusão definidas acima, sendo selecionados dentre o seguinte: palha de trigo, farelo de milho, farelo de trigo, farelo de arroz, bagaço de maçã, bagaço de café, subprodutos do café, água residual de usinas de oliva.

A invenção refere-se ainda a um processo, conforme definido acima, para a preparação de aromas como compostos de interesse, o referido processo compreendendo:

- o tratamento de plantas ou subprodutos vegetais com as proteínas de fusão conforme definidas acima, usadas no âmbito da preparação dos antioxidantes, conforme definido acima,

- a biotransformação dos compostos liberados pelas paredes celulares durante a etapa anterior, pela colocação dos referidas compostos em contato com enzimas não definidas produzidas por microorganismos selecionados entre ascomicetes ou basidiomicetes, tal como *A. niger ou P. cinnabarinus,* respectivamente,

- a recuperação, e, se necessária, a purificação, dos aromas obtidos na etapa de biotransformação anterior.

A invenção refere-se, mais particularmente, a um processo conforme definido acima, para a preparação de vanilina como o aroma de interesse, em que a proteína de fusão usada é selecionada entre as usadas para a preparação de ácido ferúlico conforme definido acima, e a etapa de biotransformação é realizada colocando o ácido ferúlico liberado pelas paredes celulares em contato com enzimas não definidas produzidas por ascomicetes ou basidiomicetes, tal como *A. niger* ou *P. cinnabarinus*, respectivamente.

De forma vantajosa, as plantas e subprodutos vegetais, ou resíduos industriais usados no âmbito da preparação dos aromas, tal como vanilina, são selecionados entre os mencionados acima para a preparação dos antioxidantes.

A invenção refere-se ainda a um processo, conforme definido acima, para a preparação de bioetanol como o composto de interesse, o referido processo compreendendo:

- o tratamento das plantas ou subprodutos vegetais com proteínas de fusão conforme definido acima compreendendo uma da swolenina mencionada acima e pelo menos uma das enzimas degradadoras da parede celular: Feruloil esterases, como a feruloil esterase A e a feruloil esterase B, xilanases, como a xilanase B, celulases, como a endoglucanase I, celobiohidrolase I e celobiohidrolase II, tal como definido acima,

o referido tratamento sendo preferivelmente combinado com um tratamento físico das referidas plantas ou subprodutos vegetais,

- a biotransformação das plantas ou subprodutos vegetais tratados obtidos pela etapa anterior em açúcares fermentáveis, pelo uso das proteínas de fusão descritas acima ou com um fungo transformado segregando as referidas proteínas de fusão, em combinação com enzimas selecionadas entre celulases, hemicelulases ou esterases, ou microorganismos selecionados entre ascomicetes, tal como *A. niger* ou *Trichoderma reesei,*

- a biotransformação dos açúcares fermentáveis em bioetanol por levedura;

De maneira vantajosa, as plantas e subprodutos vegetais ou resíduos industriais usados no âmbito da preparação do bioetanol são selecionados entre os seguintes: madeira, plantas anuais ou subprodutos agrícolas.

A invenção também se refere a um processo para o branqueamento da polpa e do papel, o referido processo compreendendo:

- o tratamento químico e físico das plantas ou subprodutos vegetais em combinação com proteínas de fusão conforme definidas acima compreendendo uma da swolenina mencionada acima e pelo menos uma das seguintes enzimas degradadoras da parede celular: Feruloil esterases, como a feruloil esterase A e a feruloil esterase B, xilanases, como a xilanase B, ligninases, como as lacases, manganês peroxidases, lignina peroxidases, peroxidases versáteis, ou enzimas suplementares

como celobiose deidrogenases, e álcool arílico oxidases, tal como definido acima,

- opcionalmente, a biopolpação das plantas ou subprodutos vegetais tratados obtidos na etapa anterior, com um fungo transformado, tal como *P. cinnabarinus*, *T. reesei* ou *A. niger*, segregando proteínas de fusão conforme definidas acima, compreendendo uma da swolenina mencionada acima e pelo menos uma das seguintes enzimas degradadoras da parede celular de plantas: feruloil esterases, como a feruloil esterase A e a feruloil esterase B, xilanases, como a xilanase B, ligninases capazes de degradar ligninas, como as lacases, manganês peroxidases, lignina peroxidases, peroxidases versáteis, ou enzimas suplementares como celobiose deidrogenases, e álcool arílico oxidases, como definido acima,

- o biobranqueamento das plantas ou subprodutos vegetais tratados obtidos na etapa anterior com proteínas de fusão conforme definidas acima compreendendo uma da swolenina mencionada acima e pelo menos uma das seguintes enzimas degradadoras da parede celular: feruloil esterases, como a feruloil esterase A e a feruloil esterase B, xilanases, como a xilanase B, ligninases capazes de degradar ligninas, como as lacases, manganês peroxidases, lignina peroxidases, peroxidases versáteis, ou enzimas suplementares como celobiose deidrogenases, e álcool arílico oxidases, tal como definido acima.

A invenção é ilustrada adicionalmente na descrição detalhada seguinte da preparação e das propriedades da

proteína de fusão entre uma swolenina e uma enzima degradadora da parede celular de plantas, tal como a esterase feruloil.

Resumidamente, a ação de uma proteína do tipo expansina foi avaliada, em combinação física com a feruloil esterase, para a liberação de ácidos ferúlicos, que são compostos de alto valor derivados de produtos agrícolas. Esse ácido hidroxicinâmico é um ácido aromático atrativo, conhecido como antioxidante e precursor aromático, nos setores alimentício e farmacêutico. A enzima recombinante foi produzida em *T. reesei*, conhecido por ser um hospedeiro muito eficaz, para segregar uma grande quantidade de proteínas extracelulares de interesse industrial. A nova enzima recombinante foi caracterizada e purificada para ser testada em um substrato natural. Finalmente, a linhagem recombinante produzindo a enzima multimodular foi comparada com a linhagem parental para avaliar a capacidade da linhagem quanto à liberação de ácido ferúlico.

O objetivo do presente trabalho era estudar o efeito da associação de uma nova categoria de proteína, a swolenina de *T. reesei* (Saloheimo e col. 2002), que está envolvida na dissolução da estrutura da parede celular, a um domínio catalítico. Para o parceiro enzimático, uma enzima suplementar livre, a feruloil esterase de *A. niger*, foi selecionada como modelo. Ao contrário dos módulos CBM convencionais, a swolenina fúngica é composta de dois domínios diferentes, um sendo responsável pelo direcionamento aos substratos e identificado como um CBM. O segundo domínio apresenta forte

similaridade com as expansinas de plantas que foram propostas para dissolver a ligação de hidrogênio entre as microfibrilas da celulose sem ter atividade hidrolítica (Cosgrove 2000, Li e col. E col. 2003). O gene da swolenina foi expresso em levedura e em *A. niger* (Saloheimo e col. 2002) e ensaios de atividade foram analisados em fibras de algodão, papéis-filtro e nas paredes celulares da alga *Valonia*. A swolenina de *T. reesei* demonstrou modificar a estrutura das fibras de celulose sem quantidades detectáveis de açúcares redutores. Além disso, o efeito da swolenina foi atribuído principalmente ao domínio da expansina, e especialmente à celulose das fibras de algodão e papéis-filtro. Como conclusão, imagina-se que a swolenina seja um bom candidato para representar o "fator de intumescimento", C1, como um componente não hidrolítico necessário para tornar o substrato mais acessível aos componentes hidrolíticos, Cx (Reese *et al.* 1950).

O potencial biotecnológico de tal proteína é muito atrativo no contexto da valorização da biomassa vegetal e o efeito do enxerto físico da swolenina na esterase feruloil para a liberação de ácido ferúlico foi estudado. Assim, esse trabalho representa o primeiro trabalho da associação de três domínios diferentes e complementares em uma única ferramenta enzimática para uma ação integrante de direcionamento, dissolução e hidrólise. A produção da proteína quimérica foi obtida em duas linhagens industriais de *T. reesei*, RutC30 e CL847, com o objetivo de comparar a capacidade de produção das duas

linhagens. O *T. reesei* é um fungo filamentoso bem conhecido, utilizado pelo setor industrial pela sua incrível capacidade de produzir celulases (Montenecourt e Eveleigh 1979, Durand e col. 1988), sendo uma linhagem de referência para a produção de novas enzimas a nível industrial. Paralelamente, a produção heteróloga da FAEA separadamente foi realizada para ser utilizada como controle em nossos ensaios de aplicação.

Com o objetivo de avaliar o efeito gerado pela proximidade física de ambos os parceiros, a SWO (SEQ ID NO : 4) foi fusionada a montante da FAEA (SEQ ID NO : 10) sem peptídeo de ligação. Portanto, a SWOI foi utilizada como proteína transportadora para facilitar a secreção da FAEA heteróloga. Para a produção da FAEA, o peptídeo de sinal da FAEA foi mantido para direcionar a secreção da proteína. As proteínas recombinantes, FAEA e SWOI-FAEA (SEQ ID NO : 30) foram produzidas com êxito por ambas as linhagens de *T. reesei*. Com respeito à FAEA, a linhagem CL 847 demonstrou produzir rendimentos maiores se comparado à linhagem Rut-C30, isto é, 70 contra 30 mg l^{-1}, enquanto que para a proteína SWOI-FAEA, a produção atingiu o mesmo nível de 25 mg l^{-1} para ambas as linhagens.

A eficiência da proteína SWOI-FAEA quimérica foi testada quanto à liberação de ácido ferúlico usando farelo de trigo desamidado como substrato. Nesses ensaios de aplicação, o substrato não foi pré-tratado pela temperatura, uma vez que as propriedades de dissolução e intumescimento da

swolenina devem ser um indicador específico da ação da proteína sobre o substrato. O ácido ferúlico foi liberado com concentrações similares usando a FAEA obtida de *A. niger* (Record e col. 2003) ou *T. reesei*. Esse resultado confirma que ambas as proteínas têm as mesmas propriedades, mesmo se forem produzidas por duas linhagens de hospedeiros diferentes. Se a swolenina livre fosse adicionada à FAEA, nenhuma liberação adicional foi observada. Por outro lado, foi observado um aumento de 50% na liberação de ácido ferúlico com a SWOI-FAEA se comparado à ação dos módulos livres correspondentes. Além disso, a linhagem de *T. reesei* produzindo a proteína SWOI-FAEA quimérica foi avaliada para estimar a capacidade da linhagem transformada quanto à liberação do ácido ferúlico. Usando o meio extracelular concentrado de *T. reesei* CL847 por um curto período de incubação de 4 h, 45% do ácido ferúlico total foram obtidos, correspondendo a 1,8 g de ácido ferúlico por kg de farelo de trigo. Como conclusão, nossos testes de aplicação demonstraram que a SWOI-FAEA é mais eficiente para a liberação de ácido ferúlico se comparada ao módulo livre SWOI e FAEA. O efeito positivo poderia ser o resultado do direcionamento ao substrato da proteína devido ao CBM endógeno da SWOI. Assim, o CBM da SWOI poderia aumentar a concentração local da enzima para a proximidade do substrato e aumentar os rendimentos finais da hidrólise. Além disso, a eficiência da proteína quimérica poderia ser aperfeiçoada pela mobilidade específica do módulo de expansina da SWOI (Cosgrove e col. 2000). De fato, supõe-se que

o módulo de expansina facilite a difusão lateral da FAEA ao longo da superfície das microfibrilas da celulose, e ao mesmo tempo dissolva a estrutura da parede celular, ambas as ações sendo sinérgicas para a liberação final do ácido ferúlico. Na verdade, o parceiro de swolenina da enzima quimérica deverá facilitar o acesso do módulo catalítico aumentando o espectro de ação da enzima para a área menos acessível.

Esse estudo demonstra pela primeira vez o efeito positivo da proximidade física de uma enzima complementar a uma proteína envolvida na dissolução da parede celular. Portanto, essas ferramentas enzimáticas representam uma alternativa não poluente e um processo de custo reduzido para o processo biotecnológico existente de biotransformação de produtos agrícolas. Por exemplo, tais enzimas quiméricas podem ser usadas na produção de polpa e papel, e bioetanol, com outras combinações de parceiros, dependendo das aplicações biotecnológicas.

EXEMPLOS

Materiais e métodos

Linhagens

Utilizou-se *Echerichia coli* JM 109 (Promega, Charbonnieres, França) para a construção e propagação dos vetores. A linhagem Rut-C30 (Montenecourt a Eveleigh 1979) e CL847 (Durand e col. 1998) de *Trichoderma reesei* foi utilizada para expressão heteróloga usando os diferentes cassetes de expressão.

Meios e condições de cultura

As linhagens de *T. reesei* foram mantidas em tubos inclinados contendo ágar-batata-dextrose (Difco, Sparks, MD). Os transformantes foram regenerados em meio sólido mínimo contendo, por litro: $(NH_4)_2SO_4$ 5,0 g, KH_2PO_4 15,0 g, $CaCl_2$ 0,45 g, $MgSO_4$ 0,6 g, $CoCl_2$ 3,7 mg, $FeSO_4$-H_2O 5 mg, $ZnSO_4$-H_2O 1,4 mg; $MnSO_4$-H_2O 1,6 mg, glicose como fonte de carbono, sorbitol 182 g como estabilizante osmótico e hidgromicina 125 mg para a seleção. As placas foram solidificadas e o crescimento das colônias foi restrito adicionando-se 2% de ágar 0,1% de Triton X-100 ao meio. Os protoplastos transformados foram distribuídos em placas em ágar de superfície seletivo a 3% contendo 1M sorbitol.

De modo a examinar a atividade da FAEA de diferentes transformantes, os fungos foram cultivados em meio mínimo contendo, por litro: $(NH_4)_2SO_4$ 5,0 g, KH_2PO_4 15,0 g, $CaCl_2$ 0,6 g, $MgSO_4$ 0,6 g, $CoCl_2$ 3,7 mg, $FeSO_4$-H_2O 5 mg, $ZnSO_4$-H_2O 1,4 mg; $MnSO_4.H_2O$ 1,6 mg, peptona 5 g e lactose 40 g e celulose Solka floe (International Fiber Corporation, North Tonawanda, NY) 20 g como fontes de carbono e indutores, Pipes 33 g para ajustar o pH para 5.2 com KOH. O meio de cultura foi inoculado com $1x10^7$ esporos por 50 ml e cultivado em frascos cônicos a 30°C com agitação a 200 rpm.

Vetores de expressão e transformação fúngica

A FAEA e SWOI de codificação do cDNA foram amplificadas por PCR a partir do plasmídeo pF (Record e

col. 2003) e, pMS89, incluindo o peptídeo de sinal, foi amplificado utilizando-se

- tanto o iniciador direto F1 5'-GATACCGCGGATGAAGCAATTCTCTGC -3 '(com o sítio SacII sublinhado)

- quanto o iniciador F2 5'-GTGCAGTTTAGCAATGCCTCCACGCAAGGCATC -3 ' e o iniciador reverso R1 5'-AATACATATGTTAGTGGTGGTGGTGGTGGTGCCAAGTA CAAGCTCCGCTCG-3' (com o sítio NdeI sublinhado, His-tag sublinhado com pontos).

O primeiro par de iniciadores (F1/R1) foi usado para obter um fragmento de DNA amplificado que será usado no cassete de expressão pFaeA para a expressão do gene de codificação da faeA (SEQ ID NO : 9) (Y09330) em *T. reesei*. A segunda construção foi obtida fusionando o gene *faeA* ao gene (AK245918) codificando a SWO1 (SEQ ID NO : 1) utilizando-se uma PCR de extensão por sobreposição (Ho e col. 1989). No primeiro experimento PCR, o gene *faeA* foi amplificado usando o par de iniciadores F2/R1 e o iniciador direto F3 5'-ATATCCGCGGATGGCTGGTAAGCTTATC-3 ' (com o sítio *SacII* sublinhado) e o iniciador reverso R2 5'-GATGCCTTGCGTGGAGGCATTCTGGCTAAACTGCAC-3' .

Ambos os fragmentos sobrepostos resultantes foram misturados e um fragmento fusionado foi sintetizado usando apenas iniciadores externos. Esse fragmento recém-obtido

foi clonado no cassete de expressão para expressar o gene de fusão *Swo1-FaeA* (pSwo-Faea).

Ambos os fragmentos amplificados foram verificados por sequenciamento, e então ligados no vetor de expressão pAMH110 (sítios de clonagem, *SacII* e *NdeI*) após digestão com as enzimas de restrição *SacII* e *NdeI*. Neste vetor, o promotor do gene de codificação (cbhI) da celobiohidrolase I de *T. reesei* foi utilizado para conduzir a expressão de ambos os insertos. No primeiro (pFaeA) e no segundo (pSwo-FaeA) cassetes de expressão, o peptídeo de sinal da FAEA e SWO1, respectivamente, foram usados para iniciar a secreção das proteínas recombinantes.

A transformação fúngica foi realizada como descrito anteriormente (Penttila e col. 1987) utilizando-se os vetores de expressão. Os transformantes foram purificados pela seleção de conídios no meio seletivo.

Separação da atividade da feruloil esterase

As culturas foram monitoradas por 10 dias a 30°C em uma incubadora agitadora e o pH foi ajustado para 5.5 diariamente com um 1 M KOH. Cada condição de cultura foi realizada em duplicata. A partir do meio de cultura líquido, alíquotas (de 1 mL) foram coletadas diariamente, removendo os micélios por filtração. A atividade da esterase foi analisada, conforme descrito anteriormente, usando ferulato de metila (MFA) como substrato (Ralet e col. 1994). As atividades foram expressas em nkatal (nkat), com 1 nkat sendo definido como a

quantidade de enzima que catalisa a liberação de 1 nmol de ácidos ferúlicos por segundo sob condições estabelecidas. Cada experimento foi realizado em duplicata, e as medições em triplicata. O desvio padrão foi registrado como menos de 2% para a média.

Análise Protéica e Western blot

A concentração protéica foi determinada de acordo com Lowry et al. (1951) com soroalbumina bovina como padrão. A purificação protéica foi seguida de eletroforese em gel de poliacrilamida-SDS em géis em placa de poliacrilamida a 10% (Laemli 1970). Em seguida, as proteínas foram coradas com azul Coomassie. A seqüência N-terminal foi determinada a partir de uma amostra de FAEA analisada por eletroblotting (40 μg) sobre uma membrana de poli(difluoreto de vinilidina) (Millipore, Saint-Quentin-Yvelines, França) segundo a degradação de Edman. As análises foram realizadas em um Applied Biosystem 470A.

Para a análise Western blot, as proteínas totais e purificadas foram submetidas à eletroforese em gel de poliacrilamida/SDS a 11% analisadas por "electroblotting" em membranas de nitrocelulose BA85 (Schleicher e Schuell, Dassel, Alemanha) à temperatura ambiente durante 45 minutos. As membranas foram incubadas em solução de bloqueio (50 mM de Tris, 150 mM de NaCl e 2% (v/v) de leite, pH 7,5) durante a noite a 4°C. Em seguida, as membranas foram lavadas com TBS a 0,2% Tween e tratadas com solução de bloqueio contendo soro anti-FAEA a uma diluição de 1/6000. Para anticorpos anti-FAEA, as

membranas foram subseqüentemente incubadas com anti-imunoglobina G de coelho produzido em cabra, conjugado com peroxidase alcalina (1/2500) (Promega). A fosfatase alcalina foi revelada a cores usando o ensaio do fosfato de 5-bromo-4-cloro-3-indoilo-azul de nitrotetrazólio (Roche Applied Science, Meylan, France) segundo o procedimento do fabricante.

Purificação e caracterização das proteínas

Para purificar ambas as proteínas recombinantes, o melhor isolado para cada construção foi inoculado nas mesmas condições que o procedimento de separação. A cultura foi coletada após 8 dias de crescimento, filtrada (0,7 μm) e concentrada por ultrafiltração por meio de uma membrana de polietersulfona (corte de massa molecular de 30 kDa) (Millipore). As frações concentradas foram dialisadas em um tampão de ligação de 30 mM de Tris-HCl, pH 7,0, e a purificação das proteínas marcadas com His foi realizada em uma coluna de Fluxo Rápido de Sefarose Quelante (13x15 cm) (Amersham Biosciences) (Porath e col. 1975).

As principais características enzimáticas foram determinadas para ambas as proteínas recombinantes. A termoestabilidade das proteínas purificadas (100% refere-se a 4,3 e 0,2 nanokatals ml^{-1} de FAEA e SWOI-FAEA, respectivamente) foi testada na faixa de 30 a 70°C. As alíquotas foram pré-incubadas na temperatura designada por 60 min e, após resfriamento a 0°C, as atividades da esterase foram então analisadas conforme indicado anteriormente, em condições

padrão. As amostras foram analisadas por SDS-PAGE após a incubação com o objetivo de verificar a integridade das proteínas recombinantes. O efeito do pH sobre a estabilidade protéica foi também estudado pela incubação, durante 60 minutos, das proteínas recombinantes purificadas em tampão citrato-fosfato (pH 2,5 a 7,0) e fosfato de sódio (pH 7,0 a 8,0). Todas as incubações foram realizadas durante 90 minutos, e então as alíquotas foram transferidas em mistura reacional convencional para determinar a quantidade de atividade restante. A atividade determinada antes das pré-incubações foi de 100% (4,3 e 0,2 nanokatals ml^{-1} de FAEA e FAES-SWO, respectivamente).

Para determinar a temperatura ideal sob as condições utilizadas, alíquotas das proteínas recombinantes purificadas (100% refere-se a 4,3 e 0,2 nanokatals ml^{-1} de FAEA e SWEOI-FAEA, respectivamente) foram incubadas a várias temperaturas (de 30 a 70°C) e as atividades da esterase foram analisadas. O pH ideal foi determinado usando tampão citrato-fosfato (pH 2,5 a 7,0) e tampão fosfato de sódio (pH 7,0 a 8,0) usando condições padrão.

Análise Southern blot

O DNA genômico de cada um dos transformantes (10 μg) foi digerido durante a noite com várias enzimas de restrição e submetido à eletroforese em um gel de agarose-TAE a 0,5%. O DNA foi então submetido ao "blotting" sobre uma membrana Hybond N+ e sondado com uma sonda marcada com ^{32}P consistindo da seqüência amplificada por PCR

faeA. A hibridização foi realizada em um tampão contendo fosfato de sódio a 0,5M pH7,2, EDTA a 0,01M, SDS a 7% (p/v), agente de bloqueio a 2% (p/v) (Roche Applied Science) durante a noite a 65°C. As lavagens pós-hibridização consistiram de 2 x 15 min em SSC a 0,2 (1 x SSC é NaCl a 0,15 M mais tampão citrato de sódio 0,015 M pH 7,0), contendo SDS a 1% a 65°C e 1 x 5 min em 0,2 X SSC à temperatura ambiente. Os blots foram expostos a um filme radiográfico (Biomax MR, Eastman Kodak Company, Nova Iorque, EUA). A linhagem BRFM 281 de *A. niger* tipo selvagem (Banque de Ressources Fongique de Marseille) foi utilizada como controle contendo uma cópia do gene *fae*A.

Testes de aplicação

O farelo de trigo (WB) foi desamidado e fornecido pela AED (Agro-industrie Recherche et Développement, Pomacle, França). A hidrólise enzimática foi realizada em tampão ácido 3-(N-morfolino)propanosulfônico (MOPS) a 0,1 M contendo azida de sódio a 0,01% ao pH 6,0, em uma incubadora com agitação controlada termostaticamente (120 rpm) a 37°C. O WB (180 mg) foi incubado com a FAEA, SWOI + FAEA e SWOI-FAEA purificadas, de forma independente, em um volume final de 5 mL. Com respeito às aplicações de teste com meio de cultura dos transformantes, o volume final foi aumentado para 9 mL. As concentrações enzimáticas foram de 1,8 nkatal de atividade da esterase por 180 mg de farelo seco para cada ensaio. Cada ensaio foi realizado em duplicata, e o desvio padrão foi menor do que 5% da média do valor para WB.

Para estimarmos o teor de ácido hidroxicinâmico, o total extraível de álcali dos compostos fenólicos foi determinado pela adição de 20 mg de WB ou MB em NaOH a 2 N e incubada durante 30 minutos a 35 °C em escuridão. O pH foi ajustado para 2 com HCl a 2N. Os ácidos fenólicos foram extraídos três vezes com 3 ml de éter. A fase orgânica foi transferida para um tubo de ensaio e seca a 40°C. Um mililitro de metanol/H_2O (50:50) (v/v) foi adicionado ao extrato seco e as amostras foram injetadas em um sistema HPLC, conforme descrito na próxima seção. O teor total de ácido ferúlico extraível de álcali foi considerado como 100% para a hidrólise enzimática.

Finalmente, para determinarmos o teor de ácido ferúlico, os hidrolisatos enzimáticos foram diluídos a ½ com ácido acético a 5%, centrifugados a 12.000 × g durante 5 minutos, e os sobrenadantes foram filtrados através de um filtro de náilon de 0,2 μm (Gelman Sciences, Acrodisc 13, Ann Arbor, MI). Os líquidos filtrados foram analisados por HPLC (25 μL injetados). As análises HPLC foram efetuadas a 280 nm e 30°C em um modelo HP1100 (Hewlett-Packard Rockville, MD) equipado com um detector UV/VIS variável, um autoamostrador-autoinjetor de 100 posições. As separações foram obtidas em uma coluna de fase invertida Merck RP18 (Chromolith 3,5 μm, 4,6×100 mm, Merck). A vazão foi de 1,4 mL/min. A fase móvel usada foi ácido acético a 1% e acetonitrilo a 10% em água (A) versus acetonitrilo a 100% (B) durante um tempo de execução total de 20 minutos, e o

gradiente se modificou como segue: o solvente B começou em 0% durante 2 minutos, aumentando então para 50% em 10 minutos, para 100% em 3 minutos até o final da execução. Os dados foram processados por uma HP 3365 ChemStation e a quantificação foi realizada por calibração externa padrão.

Exemplo 1: Transformação fúngica e produção das enzimas recombinantes.

Duas linhagens de *T. reesei*, Rut-C30 e CL847, utilizadas por companhias industriais para produzir, em processos de fermentação controlada, uma grande quantidade de enzimas, foram transformadas pelos vetores de expressão contendo os genes de interesse. Na primeira construção, o gene *faeA* de *A. niger* foi colocado sob controle do promotor do gene *cbhI* usando o peptídeo de sinal da FAEA para direcionar a secreção. A FAEA recombinante foi utilizada nos seguintes testes de aplicação como controle. Na segunda construção, o gene *faeA* foi fusionado ao gene de codificação de *SwoI* para produzir uma proteína quimérica associando a FAEA de *A. niger* à proteina SWOI de *T. reesei*. Nesta construção, o peptídeo de sinal da SWOI foi utilizado para a secreção da proteína recombinante. Protoplastos obtidos de ambas as linhagens foram transformados de forma independente por ambos os cassetes genéricos clonados no vetor de expressão pAMH110. Os transformantes foram então selecionados pela sua capacidade de crescer em meio mínimo contendo higromicina. Aproximadamente trezentos transformantes foram adicionalmente purificados pela seleção de

conídios em meio seletivo, e mais ou menos 150 colônias resistentes à higromicina foram separadas detectando-se a atividade da feruloil esterase produzida no meio de cultura e realizando-se uma análise western blot. Considerando todos os transformantes, somente uma atividade da feruloil foi detectável para aqueles transformados por pFaeA (transformantes FaeA). Além disso, a produção da FAEA foi confirmada pela análise western blot. Com respeito às colônias de *T. reesei* transformadas por pSwo-FaeA (transformantes Swo-FaeA), uma produção de FAEA só foi detectada pela análise western blot, pois a atividade da feruloil esterase teve pouquíssima produção. No entanto, para os transformantes FaeA, 1,3 e 23,3% das colônias demonstraram produzir uma atividade da feruloil esterase, respectivamente, para as linhagens Rut-C30 e CL847. No segundo evento de transformação usando pSwo-FaeA, a porcentagem foi maior, com 23,3 e 51,7% das colônias, respectivamente. Para cada construção e linhagem de *T. reesei*, os transformantes que apresentaram melhor produção foram então cultivados para estudarmos o curso de tempo da atividade da feruloil esterase.

A atividade da esterase foi estimada tanto em Rut-C30 como em CL847 transformadas, que foram transformadas por pFAEA, e relatada em função do tempo (Fig. 1). Em ambos os casos, a atividade da esterase já era detectável no segundo dia e aumentou progressivamente a 0,45 e 1,15 nkatal, respectivamente. Com respeito à *T. reesei* transformada por pSwo-FaeA, uma pequena atividade foi medida no oitavo dia, de

aproximadamente 0,06 nkatal mL^{-1}, para ambas as linhagens, análises Western blot foram realizadas a partir do meio de cultura dos transformantes FaeA (Fig. 2) e uma banda de aproximadamente 40 kDa correspondendo à FAEA recombinante foi apresentada (Fig. 2, pistas 1 e 3). Além desse primeiro conjunto de transformantes fúngicos, os transformantes Swo-FaeA produziram uma banda principal de aproximadamente 120 kDa correspondendo à fusão da FAEA (36 kDa) e da proteína SWOI (75 kDa) (Fig. 2, pistas 2 e 4). Além disso, apareceu uma banda fraca de 40 kDa, a qual corresponde ao tamanho da FAEA. Finalmente, o número de cópia dos cassetes de expressão integrados no genoma fúngico foi estimado pela análise Southern blot e revelou que os transformantes FaeA contêm de 4 a 5 e 9 a 10 cópias, respectivamente, para as linhagens Rut-C30 e CL847. Com respeito ao conjunto de transformantes Swo-FaeA, foram estimadas 6 a 7 e 14 a 15 cópias para as duas linhagens, respectivamente. Uma vez que o *T. reesei* CL847 produz a mesma quantidade de SWOI-FAEA que a linhagem Rut-C30, mas um rendimento maior de FAEA, os seguintes experimentos foram realizados com as proteínas obtidas dessa linhagem.

Exemplo 2: Caracterização das enzimas recombinantes

A FAEA purificada e a SWOI-FAEA quimérica foram purificadas em uma coluna de Sefarose Quelante e a homogeneidade das proteínas foi verificada em um gel de SDS/poliacrilamida (Fig. 3). A massa molecular da FAEA

recombinante foi ligeiramente maior que a esperada, se comparado à FAEA produzida em *A. niger*. Ambas as seqüências N-terminais da FAEA (ASTQF) e da SWOI-FAEA (QQNCA) foram seqüenciadas, e foi constatado que elas são 100% idênticas àquelas das proteínas nativas correspondentes, demonstrando que o processamento foi correto. Todas as propriedades físico-químicas e cinéticas principais foram adicionalmente determinadas e comparadas com a FAEA de *A. niger* (Record e col. 2003) (Tabela I e Fig. 4). Considerando o efeito da temperatura e do pH, bem como a estabilidade do pH, não foi encontrada nenhuma diferença significativa. A estabilidade de temperatura de ambas as proteínas também foi estimada e nossos resultados demonstraram que a FAEA recombinante foi estável até 45°C e que a atividade diminuiu em 60% após uma incubação de 60 min a 55°C. Nenhuma atividade restante foi encontrada a 60°C. Por outro lado, com respeito à proteína SWOI-FAEA, a atividade permaneceu estável até 40°C e nenhuma atividade restante foi detectada após 60 minutos de incubação a 50°C. Não foi encontrada nenhuma diferença grande para o valor de Km. Entretanto, embora o Vm e as atividades específicas estivessem na mesma faixa para a FAEA produzida por *A. niger* e *T. reesei*, um claro desvio foi observado para a proteína SWOI-FAEA, que demonstrou ser menos eficiente para hidrolisar o ferulato de metila do que a FAEA correspondente.

Exemplo 3: Liberação enzimática de ácido ferúlico a partir de farelo de trigo

O efeito sinérgico gerado pela proximidade física da FAEA e da SWOI foi estudada para a liberação de ácido ferúlico a partir de farelo de trigo. O farelo de trigo foi incubado com enzimas purificadas (Fig. 5), e os resultados mostraram que a FAEA produzida em *A. niger* e *T. reesei* foi capaz de liberara a mesma quantidade de ácido ferúlico, isto é, de 6 a 9%, dependendo do tempo de incubação. Considerando a SWOI, a proteína nativa sozinha, ou em adição com a FAEA (S ou F+S) não foi eficiente se comparada com a referência ou experimento com a FAEA, respectivamente. Por outro lado, um valor significativamente maior de liberação de ácido ferúlico, isto é, de 7 a 13,5%, foi obtido com a proteína SWOI-FAEA correspondendo a um fator de aperfeiçoamento de 1,5 após 24 horas de hidrólise.

A linhagem CL847 recombinante produzindo a SWOI-FAEA recombinante foi avaliada quanto à liberação de ácido ferúlico usando o coquetel extracelular total das enzimas segregadas. Embora o meio extracelular obtido da linhagem parenteral não transformada fosse capaz de liberar 0,5 a 1,8% de ácido ferúlico de 4 a 24 horas de incubação, A linhagem CL847 transformada segregou um coquetel enzimático incluindo a SWOI-FAEA que liberou até 45% até 4 horas, isto é, 1,8 g de ácido ferúlico por kg de farelo de trigo. Esse rendimento não aumentou mesmo após 24 horas de incubação.

Tabela 1: Características físico-químicas e cinéticas da feruloil esterase recombinante e da enzima quimérica de *Trichoderma reesei*.

	FAEA[a]	FAEA	SWOI-FAEA
MM (kDa)	36	40	120
Tp ideal (oC)	55	50-55	50
Estabilidade de Tp (oC)	--	45	40
pH ideal	5	5	5
Estabilidade do pH	5-6	5-6	5-6
Km[b]	0,75	0,83	0,81
Vm[c]	382	291	52
Atividade específica[d]	20	16,4	2,6

[a]estimado a partir da esterase feruloil de *Aspergillus niger* (Record e col. 2003)

[b]Km foram expressos em milimols

[c]Vm foram expressos em nanokatal por mg de proteína

[d] as atividades específicas foram expressas em nanokatal por mg de proteína

As atividades foram analisadas utilizando-se ferulato de metila como substrato.

Referências

Boraston AB, Bolam DN, Gilbert HJ, Davies GJ (2004) Carbohydrate-binding modules: fine-tuning polysaccharide recognition. Biochem J, 382: 769-781.

Ciruela AHJ, Gilbert BR Ali, Hazlewood GP (1998) Synergistic interaction of the cellulosome integrating

protein (CipA) from *Clostridium thermocellum* with a cellulosomal endoglucanase. FEBS Lett 422:221-224.

Cosgrove DJ (2000) Expansive growth of plant cell walls. Plant Physiol Biochem. 38:109-24

Crepin VF, Faulds CB, Connerton IF (2003) Functional classification of the microbial feruloyl esterases. Appl Microbiol Biotechnol 63:647-52.

Cosgrove DJ (2000) Loosening of plant cell wall by expansin. Nature 407:321-326.

de Vries R P, Michelsen B, Poulsen CH., Kroon PA, van den Heuvel RHH, Faulds CB, Williamson G, van den Hombergh JPTW, Visser J (1997). The *faeA* genes from *Aspergillus niger* and *Aspergillus tubingensis* encode ferulic acid esterases involved in degradation of complex cell wall polysaccharides. Appl Environ Microbiol 63:4638-4644.

de Vries RP, VanKuyk PA, Kester HCM, Visser. J. (2002) The *Aspergillus niger faeB* gene encodes a second feruloyl esterase involved in pectin and xylan degradation and is specifically induced in the presence of aromatic compounds. Biochem J 363, 377-386.

Din N, Gilkes NR, Tekan B, Miller RC Jr, Warren RAJ, Kilburn DG (1991) Non- hydrolytic disruption of cellulose fibres by the binding domain of a bacterial cellulose. Bio/technol 9-1096-1099.

Durand H, Baron M, Calmels T, Tiraby G (1988) Classical and molecular genetics applied to *Trichoderma*

reesei for the selection of improved cellulolytic industrial strains. FEMS Symp 43: 135-152.

Faulds CB, Williamson G (1994) Purification and characterization of a ferulic acid esterase (FAEIII) from *Aspergillus niger*. specificity for the phenolic moiety and binding to microcrystalline cellulose. Microbiology 140:779-787.

Fierobe, H. P., E. A Bayer, C. Tardif, M. Czjzek, A. Mechaly, A. Belaich, R. Lamed, Y. Shoham, and J. P. Belaich. 2002. Degradation of cellulose substrates by cellulosome chimeras. Substrate targeting versus proximity of enzyme components. J. Biol. Chem. 277:49621-49630.

Gao PJ, Chen GJ, Wang TH, Zhang YS, Liu J (2001) Non-hydrolytic disruption of crystalline structure of cellulose by cellulose binding domain and linker sequence of cellobiohydrolase I from *Penicillium janthinellum*. Shengwu Huaxue Yu Shengwu Wuli Xuebao 33, 13-18.

Ho, S. N., H. D. Hunt, R. M. Horton, J. K. Pullen, L. R. Pease. 1989. Site-directed mutagenesis by overlap extension using the polymerase chain reaction. Gene. 77:51-59.

Ito J, Fujita Y, Ueda M, Fukuda H, Kondo A (2004) Improvement of cellulose-degrading ability of a yeast strain displaying *Trichoderma reesei* endoglucanase II by recombination of cellulose-binding domains. Biotechnol Prog 20:688-91.

Juge N, Wiliamson G, Puigserver A, Cummings NJ, Connerton IF, Faulds CB (2001) High-level production of

recombinant *Aspergillus niger* cinnamoyl esterase (FAEA) in the methylotrophic yeast Fichia pastor is. FEMS Yeast Research 1:127-132.

Kroon, P. A., Faulds C. B., Williamson G (1996) Purification and characterization of a novel esterase induced by growth of *Aspergillus niger* on sugar beet pulp. Biotechnol. Appl. Biochem. 23, 255-262.

Laemli UK (1970) Cleavage of structural proteins during the assembly of the head of bacteriophage T4. Nature 227:680-685.

Levasseur A, Benoit I, Asther M, Asther M, Record E (2004) Homologous expression of the feruloyl esterase B gene from *Aspergillus niger* and characterization of the recombinant enzyme. Protein Expr Purif 37:126-33.

Levasseur A., Navarro D., Punt P.J., Belaïch J-P., Asther M., Record E. (2005) Improvement of ferulic acid release by action of engineered bifunctional enzymes associating the feruloyl esterase A, the xylanase B and a carbohydrate-binding module from *Aspergillus niger*. Appl and Envir Microbiol, 71 :8132-8140.

Li Y, Jones L, McQueen-Mason, (2003) Expansins and cell growth. Curr Opinion Plant Biol 6:603-610.

Limon MC, Chacon MR, Mejias R, Delgado-Jarana J, Rincon AM, Codon AC, Benitez T (2004) Increased antifungal and chitinase specific activities of *Trichoderma*

harzianum CECT 2413 by addition of a cellulose binding domain. Appl Microbiol Biotechnol 64:675-85.

Lowry OH, Rosebrough NJ, Farr AL, Randall RJ (1951) Protéin measurement with the Folin phenol reagent. J Biol Chem 193:265-275.

Montenecourt BS, Eveleigh DE (1977) Selective screening methods for the isolation of high yielding cellulase mutants of *Trichoderma reesei* on various carbon sources. Adv Chem Ser 181 :289-301.

Penttila M, Nevalainen H, Ratto M, Salminen E, Knowles J. (1987) A versatile transformation system for the cellulolytic filamentous fungus *Trichoderma reesei*. Gene 61:155-64.

Porath, J, Carlsson J, Olsson I, Belfrage G (1975). Metal chelate affinity chromatography, a new approach to protein fractionation. Nature. 258:598-599.

Record, E., Asther M., Sigoillot C, Pages S., Punt P. J., Delattre M., Haon M., van den Hondel C. A., Sigoillot J. C, Lesage-Meessen L., Asther M. (2003) Overproduction of the *Aspergillus niger* feruloyl esterase for pulp bleaching application. Appl. Microbiol. Biotechnol. 62:349-355.

Ralet M.C, Faulds CB, Williamson G, Thibault JF (1994) Degradation of feruloylated oligosaccharides from sugar-beet pulp and wheat bran by ferulic acid esterases from *Aspergillus niger*. Carbohydr Res 263:257-269.

Reese ET, Siu RGH, Levinson HS (1950) The biological degradation of soluble cellulose derivatives and its relationship to the mechanism of cellulose hydrolysis. J Bacteriol 59, 485- 497.

Saloheimo M., Paloheimo M., Hakola S., Pere J., Swanson B., Nyyssonen E., Bhatia A., Ward M., Penttila M. (2002). Swollenin, a *Trichoderma reesei* protein with sequence similarity to the plant expansins, exhibits disruption activity on cellulosic materials. Eur J Biochem 269:4202-4211.

Saulnier L, Thibault JF (1999) Ferulic acid and diferulic acids as components of sugar- beet pectins and maize bran heteroxylans. J Sci Food Agric 79:396-402.

Sigoillot C, Camarero S, Vidal T, Record E, Asther M, Perez-Boada M, Martinez MJ, Sigoillot JC, Asther M, Colom JF, Martinez AT (2005) Comparison of different fungal enzymes for bleaching high-quality paper pulps. J Biotechnol 115:333-43.

Williamson G, Kroon PA, Faulds GB (1998) Hairy plant polysaccharides : a close shave with microbial esterases. Microbiol 144:2011-2023.

(Folha papel)

Petn° - 020080155748/RJ
(18/12/2008)
PI0709896-0

LISTAGEM DE SEQUENCIA

<110> INSTITUT FRANCAIS DU PETROLE
VTT TECHNICAL RESEARCH CENTRE OF FINLAND
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE

<120> PROTEÍNAS DE FUSÃO ENTRE ENZIMAS DEGRADADORAS DA PAREDE DE CELULAR DE PLANTAS E UMA SWOLENINA, E SEUS USOS

<130> IOB 06 AF IFP SWOL

<140> EP 06 290 562.5
<141> 2006-04-06

<160> 109

<170> PatentIn version 3.3

<210> 1
<211> 1479
<212> DNA
<213> Trichoderma reesei

<220>
<221> CDS
<222> (1)..(1479)

<400> 1

```
atg gct ggt aag ctt atc ctc gtg gct cta gca agc ctt gta tca ctc      48
Met Ala Gly Lys Leu Ile Leu Val Ala Leu Ala Ser Leu Val Ser Leu
1               5                  10                  15

tct att cag cag aat tgc gca gca tta ttt ggc caa tgt gga ggc ata      96
Ser Ile Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile
            20                  25                  30

ggg tgg tcc ggc acc aca tgt tgc gtt gct ggc gcc cag tgc agt ttt     144
Gly Trp Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe
        35                  40                  45

gtc aat gac tgg tac tcc cag tgc ctt gcg tca acc ggc gga aac ccc     192
Val Asn Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro
    50                  55                  60

cca aac gga aca act tcc tct agc ttg gtt tca cgg acg tcg tca gca     240
Pro Asn Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala
65                  70                  75                  80

tcc tca tcc gtc ggc tcg tct tca ccc ggc ggc aac tca cca act ggc     288
Ser Ser Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly
                85                  90                  95

agt gct tcc acc tac aca acc aca gat aca gct acc gtg gct cct cat     336
Ser Ala Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His
            100                 105                 110

tcg cag tct cct tac ccc agc att gcc gca tcc agt tgc gga tcg tgg     384
Ser Gln Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp
        115                 120                 125
```

```
acc ctc gtg gat aat gtt tgc tgc cca tca tat tgt gct aat gat gac      432
Thr Leu Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp
    130                 135                 140

aca tcc gag tca tgc tca ggc tgc ggt acc tgc act acg ccg ccc tcg      480
Thr Ser Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser
145                 150                 155                 160

gcg gac tgc aaa tcc gga acc atg tat cca gag gtc cat cac gta tcc      528
Ala Asp Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser
                165                 170                 175

agc aac gag agc tgg cac tac agt aga tca acc cac ttt ggc cta acg      576
Ser Asn Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
            180                 185                 190

agc ggc ggg gcc tgt ggc ttt ggc ctg tac ggt ctc tgc aca aag ggc      624
Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly
        195                 200                 205

agt gtt aca gcc agc tgg acg gat ccc atg ctt ggc gcg acg tgt gac      672
Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp
    210                 215                 220

gct ttt tgt aca gcg tat ccc ctg ctt tgc aaa gac cct acc ggc act      720
Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr
225                 230                 235                 240

acc ctt cgt ggc aac ttc gca gct cca aac ggc gat tac tac acc caa      768
Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
                245                 250                 255

ttc tgg tcc tcg ttg cca gga gcc ctc gat aac tac ctg tcc tgc ggc      816
Phe Trp Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly
            260                 265                 270

gag tgc att gag ctg ata caa aca aag ccc gat ggg acc gat tat gct      864
Glu Cys Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala
        275                 280                 285

gtc gga gaa gcc ggc tac acg gat cca att act ctc gag att gtg gac      912
Val Gly Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp
    290                 295                 300

agc tgc ccg tgc agc gcg aac tcc aag tgg tgc tgt ggt ccg ggc gcc      960
Ser Cys Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala
305                 310                 315                 320

gat cat tgc gga gag atc gac ttc aaa tac ggc tgt cct ctt cct gct     1008
Asp His Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala
                325                 330                 335

gac agc att cat ctc gac ctg tca gac att gcc atg ggc cgt ttg cag     1056
Asp Ser Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln
            340                 345                 350

ggc aat gga tca cta acc aat ggc gtc atc ccg act cga tat aga aga     1104
Gly Asn Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg
        355                 360                 365

gtc caa tgc ccc aaa gtt ggg aac gcc tac att tgg ctt cga aat ggc     1152
```

```
Val Gln Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly
    370                 375                 380

gga ggg cct tac tat ttt gct ctc acg gca gtc aac acc aac gga ccg    1200
Gly Gly Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro
385                 390                 395                 400

ggc tca gtc acc aaa atc gag atc aag ggc gca gac acc gac aac tgg    1248
Gly Ser Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp
                405                 410                 415

gtt gcc ttg gtc cat gac cca aac tat acg agt agc cgc cca caa gaa    1296
Val Ala Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu
            420                 425                 430

cgc tat ggc agt tgg gta atc cca cag gga tca ggg ccc ttt aac ttg    1344
Arg Tyr Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu
        435                 440                 445

cct gtt gga att cgt ctg act agc cca acg ggg gaa cag att gtg aat    1392
Pro Val Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn
    450                 455                 460

gaa cag gcc atc aag aca ttc act cct ccg gcc aca ggt gac ccc aat    1440
Glu Gln Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn
465                 470                 475                 480

ttt tac tac att gac att ggt gtg cag ttt agc cag aat                1479
Phe Tyr Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn
                485                 490
```

<210> 2
<211> 493
<212> PRT
<213> Trichoderma reesei

<400> 2

```
Met Ala Gly Lys Leu Ile Leu Val Ala Leu Ala Ser Leu Val Ser Leu
1               5                  10                  15

Ser Ile Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile
            20                  25                  30

Gly Trp Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe
        35                  40                  45

Val Asn Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro
    50                  55                  60

Pro Asn Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala
65                  70                  75                  80

Ser Ser Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly
                85                  90                  95
```

Ser Ala Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His
100 105 110

Ser Gln Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp
115 120 125

Thr Leu Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp
130 135 140

Thr Ser Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser
145 150 155 160

Ala Asp Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser
165 170 175

Ser Asn Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
180 185 190

Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly
195 200 205

Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp
210 215 220

Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr
225 230 235 240

Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
245 250 255

Phe Trp Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly
260 265 270

Glu Cys Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala
275 280 285

Val Gly Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp
290 295 300

Ser Cys Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala
305 310 315 320

Asp His Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala
325 330 335

Asp Ser Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln
340 345 350

Gly Asn Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg
355 360 365

Val Gln Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly
370 375 380

Gly Gly Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro
385 390 395 400

Gly Ser Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp
405 410 415

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

Arg Tyr Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu
435 440 445

Pro Val Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn
450 455 460

Glu Gln Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn
465 470 475 480

Phe Tyr Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn
485 490

<210> 3
<211> 1425
<212> DNA
<213> Trichoderma reesei

<220>
<221> CDS
<222> (1)..(1425)

<400> 3
cag cag aat tgc gca gca tta ttt ggc caa tgt gga ggc ata ggg tgg 48
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1 5 10 15

tcc ggc acc aca tgt tgc gtt gct ggc gcc cag tgc agt ttt gtc aat 96
Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
20 25 30

gac tgg tac tcc cag tgc ctt gcg tca acc ggc gga aac ccc cca aac 144

```
Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
        35                  40                  45

gga aca act tcc tct agc ttg gtt tca cgg acg tcg tca gca tcc tca      192
Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
    50                  55                  60

tcc gtc ggc tcg tct tca ccc ggc ggc aac tca cca act ggc agt gct      240
Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65                  70                  75                  80

tcc acc tac aca acc aca gat aca gct acc gtg gct cct cat tcg cag      288
Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
                85                  90                  95

tct cct tac ccc agc att gcc gca tcc agt tgc gga tcg tgg acc ctc      336
Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
            100                 105                 110

gtg gat aat gtt tgc tgc cca tca tat tgt gct aat gat gac aca tcc      384
Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
        115                 120                 125

gag tca tgc tca ggc tgc ggt acc tgc act acg ccg ccc tcg gcg gac      432
Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
    130                 135                 140

tgc aaa tcc gga acc atg tat cca gag gtc cat cac gta tcc agc aac      480
Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145                 150                 155                 160

gag agc tgg cac tac agt aga tca acc cac ttt ggc cta acg agc ggc      528
Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
                165                 170                 175

ggg gcc tgt ggc ttt ggc ctg tac ggt ctc tgc aca aag ggc agt gtt      576
Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
            180                 185                 190

aca gcc agc tgg acg gat ccc atg ctt ggc gcg acg tgt gac gct ttt      624
Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
        195                 200                 205

tgt aca gcg tat ccc ctg ctt tgc aaa gac cct acc ggc act acc ctt      672
Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
    210                 215                 220

cgt ggc aac ttc gca gct cca aac ggc gat tac tac acc caa ttc tgg      720
Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225                 230                 235                 240

tcc tcg ttg cca gga gcc ctc gat aac tac ctg tcc tgc ggc gag tgc      768
Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
                245                 250                 255

att gag ctg ata caa aca aag ccc gat ggg acc gat tat gct gtc gga      816
Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
            260                 265                 270

gaa gcc ggc tac acg gat cca att act ctc gag att gtg gac agc tgc      864
Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
```

```
        275                 280                 285

ccg tgc agc gcg aac tcc aag tgg tgc tgt ggt ccg ggc gcc gat cat      912
Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
    290                 295                 300

tgc gga gag atc gac ttc aaa tac ggc tgt cct ctt cct gct gac agc      960
Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305                 310                 315                 320

att cat ctc gac ctg tca gac att gcc atg ggc cgt ttg cag ggc aat     1008
Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
                325                 330                 335

gga tca cta acc aat ggc gtc atc ccg act cga tat aga aga gtc caa     1056
Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
            340                 345                 350

tgc ccc aaa gtt ggg aac gcc tac att tgg ctt cga aat ggc gga ggg     1104
Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
        355                 360                 365

cct tac tat ttt gct ctc acg gca gtc aac acc aac gga ccg ggc tca     1152
Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
    370                 375                 380

gtc acc aaa atc gag atc aag ggc gca gac acc gac aac tgg gtt gcc     1200
Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385                 390                 395                 400

ttg gtc cat gac cca aac tat acg agt agc cgc cca caa gaa cgc tat     1248
Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
                405                 410                 415

ggc agt tgg gta atc cca cag gga tca ggg ccc ttt aac ttg cct gtt     1296
Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
            420                 425                 430

gga att cgt ctg act agc cca acg ggg gaa cag att gtg aat gaa cag     1344
Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
        435                 440                 445

gcc atc aag aca ttc act cct ccg gcc aca ggt gac ccc aat ttt tac     1392
Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
    450                 455                 460

tac att gac att ggt gtg cag ttt agc cag aat                        1425
Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn
465                 470                 475
```

<210> 4
<211> 475
<212> PRT
<213> Trichoderma reesei

<400> 4

```
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1               5                  10                  15
```

```
Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
            20                  25                  30

Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
        35                  40                  45

Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
    50                  55                  60

Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65                  70                  75                  80

Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
                85                  90                  95

Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
            100                 105                 110

Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
        115                 120                 125

Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
    130                 135                 140

Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145                 150                 155                 160

Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
                165                 170                 175

Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
            180                 185                 190

Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
        195                 200                 205

Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
    210                 215                 220

Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225                 230                 235                 240

Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
                245                 250                 255
```

104

Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
260 265 270

Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
275 280 285

Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
290 295 300

Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305 310 315 320

Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
325 330 335

Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
340 345 350

Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
355 360 365

Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
370 375 380

Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385 390 395 400

Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
405 410 415

Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
420 425 430

Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
435 440 445

Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
450 455 460

Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn
465 470 475

<210> 5
<211> 1503
<212> DNA
<213> Aspergillus fumigatus

<220>
<221> CDS
<222> (1)..(1503)

<400> 5

```
atg act ctt cta ttt ggt ata ttt ctt gcc cgg ctt gcg gtg gct gcc       48
Met Thr Leu Leu Phe Gly Ile Phe Leu Ala Arg Leu Ala Val Ala Ala
1               5                   10                  15

gcc cag agc agc tgc gtc tcg gct tgg ggt caa tgt ggc ggt att tct       96
Ala Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser
            20                  25                  30

tat acc ggg tct acc tgc tgt cag agt ggg aat acc tgc gcc gag att      144
Tyr Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile
        35                  40                  45

aac tcg tac tac tac cag tgc ata cca gca aca gct gtg agt act tca      192
Asn Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser
    50                  55                  60

act acc aca gtg aca tct ccc tct agc tct ggt tcg tct tct gcc aac      240
Thr Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn
65                  70                  75                  80

acg tca ggt tat aca acg acg act gtc ttg ccc agt ccc acg gca aca      288
Thr Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr
                85                  90                  95

cag aac cct tat cct ccg gcc aat gcc agc tca tgt gga tcg tgg gct      336
Gln Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala
            100                 105                 110

ctc gtt gat aac gtt tgc tgc cca tac tac tgt ctc tcg gat aat gaa      384
Leu Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu
        115                 120                 125

tcc gag tcc tgc acg agc agc tgt acc ggc ggc tgc ggc agt cct gat      432
Ser Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp
    130                 135                 140

tcc tcc atg tgc aag tcc ggg acg atg tgg gga gag caa cac acc gta      480
Ser Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val
145                 150                 155                 160

act tcc aac gag gac tgg cat tac agc cgc tca aca cac ttt ggt ctg      528
Thr Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu
                165                 170                 175

acc agc ggt ggc gcc tgc ggg ttc ggt ctg tac ggc ctc tgc acc aag      576
Thr Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys
            180                 185                 190

aac agt gtc acc gcg agc tgg aca gac cca atg ctg ggc tct acc tgc      624
Asn Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys
        195                 200                 205

gac gcc ttc tgc acc gcg tat ccg ctc ctc tgc aaa gac ccc gct aac      672
Asp Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn
    210                 215                 220
```

```
gtc act ctc cgc ggg aac ttt gct gcc ccg aac gga gac tac tac act      720
Val Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr
225                 230                 235                 240

cag ttc tgg cct tcc ctg gct gca tcc ggc aat ccc gac aac tac ctc      768
Gln Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu
                245                 250                 255

tct tgc ggg gag tgt ttc gag gtc atc cgc acc aag ccc gac ggg aca      816
Ser Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr
            260                 265                 270

gac tac gcc gtc ggc gag agc gga tat acc gac ccc ata gtc ctc gag      864
Asp Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu
        275                 280                 285

gta gta gac agc tgt ccc tgc aat gcc aat tca aaa tgg tgc tgt aag      912
Val Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys
    290                 295                 300

cgg ccc ccc ccc ccc ccc ttt ttt tcc ccg cct tcc aac gga caa aat      960
Arg Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn
305                 310                 315                 320

ctc aca aga cca ggc ggc agc ggc gca gac cac tgc ggc gaa atc gac     1008
Leu Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp
                325                 330                 335

ttc aag tac ggc tgt cct ctg ccg gaa gga tcc cat cac atg gac ctc     1056
Phe Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu
            340                 345                 350

tcc gat att gcc atg ggc cga ctc cag gga aac ggc agt ctc gcc gac     1104
Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp
        355                 360                 365

ggt gtg att ccc atc cgc tac cgg cgt gtc ccc tgt ccc aag ccg ggg     1152
Gly Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly
    370                 375                 380

aac atc tac atc tgg ctt cat gat ggg gcg gga ccg tat tat ttt gcg     1200
Asn Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala
385                 390                 395                 400

ctg agc gcg gtc aat acc aac ggc ccc ggc tcc gta atc agt atc gaa     1248
Leu Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu
                405                 410                 415

gtc cag gct ggt ggc tcc ggg cca tgg gtt gcc ctc gag cac gat ccg     1296
Val Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro
            420                 425                 430

aac tac acc agt agc cgg ccg cag gag cgg tat ggc tct tgg gtc ctc     1344
Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu
        435                 440                 445

ccg cag ggc aag gga ccc att act gtg cct gtt tcg atg agg ctg acg     1392
Pro Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr
    450                 455                 460
```

```
gcg ccc aat ggg cag cag gtg gtt aag gag ggc gcc att acc agc tat      1440
Ala Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr
465                 470                 475                 480

acc ccg ccg gcg act gcg gtc gag ggc ttt tgg tat att gat ctg gga      1488
Thr Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly
                485                 490                 495

gtg cag ttc acc tag                                                  1503
Val Gln Phe Thr
            500
```

<210> 6
<211> 500
<212> PRT
<213> Aspergillus fumigatus

<400> 6

```
Met Thr Leu Leu Phe Gly Ile Phe Leu Ala Arg Leu Ala Val Ala Ala
1               5                   10                  15

Ala Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser
            20                  25                  30

Tyr Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile
        35                  40                  45

Asn Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser
    50                  55                  60

Thr Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn
65                  70                  75                  80

Thr Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr
                85                  90                  95

Gln Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala
            100                 105                 110

Leu Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu
        115                 120                 125

Ser Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp
    130                 135                 140

Ser Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val
145                 150                 155                 160

Thr Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu
```

165 170 175

Thr Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys
180 185 190

Asn Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys
195 200 205

Asp Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn
210 215 220

Val Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr
225 230 235 240

Gln Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu
245 250 255

Ser Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr
260 265 270

Asp Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu
275 280 285

Val Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys
290 295 300

Arg Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn
305 310 315 320

Leu Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp
325 330 335

Phe Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu
340 345 350

Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp
355 360 365

Gly Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly
370 375 380

Asn Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala
385 390 395 400

Leu Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu
405 410 415

```
Val Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro
            420                 425                 430

Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu
        435                 440                 445

Pro Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr
    450                 455                 460

Ala Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr
465                 470                 475                 480

Thr Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly
                485                 490                 495

Val Gln Phe Thr
            500
```

<210> 7
<211> 1449
<212> DNA
<213> Aspergillus fumigatus

<220>
<221> CDS
<222> (1)..(1449)

<400> 7

```
cag agc agc tgc gtc tcg gct tgg ggt caa tgt ggc ggt att tct tat      48
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1               5                   10                  15

acc ggg tct acc tgc tgt cag agt ggg aat acc tgc gcc gag att aac      96
Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
            20                  25                  30

tcg tac tac tac cag tgc ata cca gca aca gct gtg agt act tca act     144
Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
        35                  40                  45

acc aca gtg aca tct ccc tct agc tct ggt tcg tct tct gcc aac acg     192
Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
    50                  55                  60

tca ggt tat aca acg acg act gtc ttg ccc agt ccc acg gca aca cag     240
Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65                  70                  75                  80

aac cct tat cct ccg gcc aat gcc agc tca tgt gga tcg tgg gct ctc     288
Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
                85                  90                  95
```

```
gtt gat aac gtt tgc tgc cca tac tac tgt ctc tcg gat aat gaa tcc      336
Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
            100                 105                 110

gag tcc tgc acg agc agc tgt acc ggc ggc tgc ggc agt cct gat tcc      384
Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
        115                 120                 125

tcc atg tgc aag tcc ggg acg atg tgg gga gag caa cac acc gta act      432
Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
    130                 135                 140

tcc aac gag gac tgg cat tac agc cgc tca aca cac ttt ggt ctg acc      480
Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145                 150                 155                 160

agc ggt ggc gcc tgc ggg ttc ggt ctg tac ggc ctc tgc acc aag aac      528
Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
                165                 170                 175

agt gtc acc gcg agc tgg aca gac cca atg ctg ggc tct acc tgc gac      576
Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
            180                 185                 190

gcc ttc tgc acc gcg tat ccg ctc ctc tgc aaa gac ccc gct aac gtc      624
Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
        195                 200                 205

act ctc cgc ggg aac ttt gct gcc ccg aac gga gac tac tac act cag      672
Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
    210                 215                 220

ttc tgg cct tcc ctg gct gca tcc ggc aat ccc gac aac tac ctc tct      720
Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225                 230                 235                 240

tgc ggg gag tgt ttc gag gtc atc cgc acc aag ccc gac ggg aca gac      768
Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
                245                 250                 255

tac gcc gtc ggc gag agc gga tat acc gac ccc ata gtc ctc gag gta      816
Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
            260                 265                 270

gta gac agc tgt ccc tgc aat gcc aat tca aaa tgg tgc tgt aag cgg      864
Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
        275                 280                 285

ccc ccc ccc ccc ccc ttt ttt tcc ccg cct tcc aac gga caa aat ctc      912
Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
    290                 295                 300

aca aga cca ggc ggc agc ggc gca gac cac tgc ggc gaa atc gac ttc      960
Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305                 310                 315                 320

aag tac ggc tgt cct ctg ccg gaa gga tcc cat cac atg gac ctc tcc     1008
Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
                325                 330                 335

gat att gcc atg ggc cga ctc cag gga aac ggc agt ctc gcc gac ggt     1056
```

```
Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
            340                 345                 350

gtg att ccc atc cgc tac cgg cgt gtc ccc tgt ccc aag ccg ggg aac     1104
Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
        355                 360                 365

atc tac atc tgg ctt cat gat ggg gcg gga ccg tat tat ttt gcg ctg     1152
Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
    370                 375                 380

agc gcg gtc aat acc aac ggc ccc ggc tcc gta atc agt atc gaa gtc     1200
Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385                 390                 395                 400

cag gct ggt ggc tcc ggg cca tgg gtt gcc ctc gag cac gat ccg aac     1248
Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
                405                 410                 415

tac acc agt agc cgg ccg cag gag cgg tat ggc tct tgg gtc ctc ccg     1296
Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
            420                 425                 430

cag ggc aag gga ccc att act gtg cct gtt tcg atg agg ctg acg gcg     1344
Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
        435                 440                 445

ccc aat ggg cag cag gtg gtt aag gag ggc gcc att acc agc tat acc     1392
Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
    450                 455                 460

ccg ccg gcg act gcg gtc gag ggc ttt tgg tat att gat ctg gga gtg     1440
Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465                 470                 475                 480

cag ttc acc                                                        1449
Gln Phe Thr
```

<210> 8
<211> 483
<212> PRT
<213> Aspergillus fumigatus

<400> 8

```
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1               5                   10                  15

Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
            20                  25                  30

Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
        35                  40                  45

Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
    50                  55                  60
```

Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65 70 75 80

Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
85 90 95

Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
100 105 110

Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
115 120 125

Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
130 135 140

Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145 150 155 160

Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
165 170 175

Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
180 185 190

Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
195 200 205

Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
210 215 220

Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225 230 235 240

Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
245 250 255

Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
260 265 270

Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
275 280 285

Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
290 295 300

Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305 310 315 320

Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
325 330 335

Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
340 345 350

Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
355 360 365

Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
370 375 380

Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385 390 395 400

Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
405 410 415

Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
420 425 430

Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
435 440 445

Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
450 455 460

Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465 470 475 480

Gln Phe Thr

<210> 9
<211> 780
<212> DNA
<213> Aspergillus niger

<220>
<221> CDS
<222> (1)..(780)

<400> 9
gcc tcc acg caa ggc atc tcc gaa gac ctc tac aat cgc ttg gta gag 48

```
Ala Ser Thr Gln Gly Ile Ser Glu Asp Leu Tyr Asn Arg Leu Val Glu
1               5                  10                  15

atg gcc act atc tcc caa gcc gcc tac gcc gac cta tgc aat att cca      96
Met Ala Thr Ile Ser Gln Ala Ala Tyr Ala Asp Leu Cys Asn Ile Pro
            20                  25                  30

tcg act att atc aaa gga gag aaa att tac aac gct caa act gat atc     144
Ser Thr Ile Ile Lys Gly Glu Lys Ile Tyr Asn Ala Gln Thr Asp Ile
        35                  40                  45

aac gga tgg atc ctc cgc gac gac acc agc aaa gaa att atc acc gtc     192
Asn Gly Trp Ile Leu Arg Asp Asp Thr Ser Lys Glu Ile Ile Thr Val
    50                  55                  60

ttc cgt ggc act ggc agt gac aca aac cta cag ctc gat act aac tac     240
Phe Arg Gly Thr Gly Ser Asp Thr Asn Leu Gln Leu Asp Thr Asn Tyr
65                  70                  75                  80

acg ctc acg cca ttc gac act cta cct caa tgc aac gat tgc gag gta     288
Thr Leu Thr Pro Phe Asp Thr Leu Pro Gln Cys Asn Asp Cys Glu Val
                85                  90                  95

cac ggt gga tac tat att gga tgg atc tca gtc caa gac caa gtc gag     336
His Gly Gly Tyr Tyr Ile Gly Trp Ile Ser Val Gln Asp Gln Val Glu
            100                 105                 110

tcg ctt gtc aaa caa cag gct agc cag tat ccg gac tat gcg ctt acc     384
Ser Leu Val Lys Gln Gln Ala Ser Gln Tyr Pro Asp Tyr Ala Leu Thr
        115                 120                 125

gtg aca ggc cat agt ctg gga gcg tcg atg gca gca ctc act gcc gcc     432
Val Thr Gly His Ser Leu Gly Ala Ser Met Ala Ala Leu Thr Ala Ala
    130                 135                 140

cag ctg tcc gcg aca tac gac aac gtc cgt ctg tac aca ttc ggc gaa     480
Gln Leu Ser Ala Thr Tyr Asp Asn Val Arg Leu Tyr Thr Phe Gly Glu
145                 150                 155                 160

ccg cgc agc ggc aac cag gcc ttc gcg tcg tac atg aac gat gcg ttc     528
Pro Arg Ser Gly Asn Gln Ala Phe Ala Ser Tyr Met Asn Asp Ala Phe
                165                 170                 175

cag gtc tcg agc ccg gag acg acc cag tac ttc cgg gtc act cat tcc     576
Gln Val Ser Ser Pro Glu Thr Thr Gln Tyr Phe Arg Val Thr His Ser
            180                 185                 190

aac gac ggc atc cca aac ttg ccc ccg gcg gac gag ggt tac gcc cat     624
Asn Asp Gly Ile Pro Asn Leu Pro Pro Ala Asp Glu Gly Tyr Ala His
        195                 200                 205

ggt ggt gta gag tac tgg agc gtt gat cct tac agc gcc cag aac acg     672
Gly Gly Val Glu Tyr Trp Ser Val Asp Pro Tyr Ser Ala Gln Asn Thr
    210                 215                 220

ttt gtc tgt act ggg gat gaa gta cag tgc tgt gag gca cag ggc gga     720
Phe Val Cys Thr Gly Asp Glu Val Gln Cys Cys Glu Ala Gln Gly Gly
225                 230                 235                 240

cag ggg gtg aat gat gcg cat act act tat ttt ggg atg acg agc gga     768
Gln Gly Val Asn Asp Ala His Thr Thr Tyr Phe Gly Met Thr Ser Gly
```

245 250 255

780

gct tgt act tgg
Ala Cys Thr Trp
260

<210> 10
<211> 260
<212> PRT
<213> Aspergillus niger

<400> 10

Ala Ser Thr Gln Gly Ile Ser Glu Asp Leu Tyr Asn Arg Leu Val Glu
1 5 10 15

Met Ala Thr Ile Ser Gln Ala Ala Tyr Ala Asp Leu Cys Asn Ile Pro
20 25 30

Ser Thr Ile Ile Lys Gly Glu Lys Ile Tyr Asn Ala Gln Thr Asp Ile
35 40 45

Asn Gly Trp Ile Leu Arg Asp Asp Thr Ser Lys Glu Ile Ile Thr Val
50 55 60

Phe Arg Gly Thr Gly Ser Asp Thr Asn Leu Gln Leu Asp Thr Asn Tyr
65 70 75 80

Thr Leu Thr Pro Phe Asp Thr Leu Pro Gln Cys Asn Asp Cys Glu Val
85 90 95

His Gly Gly Tyr Tyr Ile Gly Trp Ile Ser Val Gln Asp Gln Val Glu
100 105 110

Ser Leu Val Lys Gln Gln Ala Ser Gln Tyr Pro Asp Tyr Ala Leu Thr
115 120 125

Val Thr Gly His Ser Leu Gly Ala Ser Met Ala Ala Leu Thr Ala Ala
130 135 140

Gln Leu Ser Ala Thr Tyr Asp Asn Val Arg Leu Tyr Thr Phe Gly Glu
145 150 155 160

Pro Arg Ser Gly Asn Gln Ala Phe Ala Ser Tyr Met Asn Asp Ala Phe
165 170 175

Gln Val Ser Ser Pro Glu Thr Thr Gln Tyr Phe Arg Val Thr His Ser
180 185 190

```
Asn Asp Gly Ile Pro Asn Leu Pro Pro Ala Asp Glu Gly Tyr Ala His
        195                 200                 205

Gly Gly Val Glu Tyr Trp Ser Val Asp Pro Tyr Ser Ala Gln Asn Thr
    210                 215                 220

Phe Val Cys Thr Gly Asp Glu Val Gln Cys Cys Glu Ala Gln Gly Gly
225                 230                 235                 240

Gln Gly Val Asn Asp Ala His Thr Thr Tyr Phe Gly Met Thr Ser Gly
                245                 250                 255

Ala Cys Thr Trp
            260
```

<210> 11
<211> 1512
<212> DNA
<213> Aspergillus niger

<220>
<221> CDS
<222> (1)..(1512)

<400> 11

```
gcg acc gac ccc ttc cag tcg cgg tgc aat gaa ttc cag aac aag atc      48
Ala Thr Asp Pro Phe Gln Ser Arg Cys Asn Glu Phe Gln Asn Lys Ile
1               5                   10                  15

gac atc gcc aat gtc acc gtc aga tcg gtc gca tac gtt gct gct gga      96
Asp Ile Ala Asn Val Thr Val Arg Ser Val Ala Tyr Val Ala Ala Gly
            20                  25                  30

cag aac atc tcc caa gcg gag gtc gcc tcc gtg tgt aaa gca tcg gtt     144
Gln Asn Ile Ser Gln Ala Glu Val Ala Ser Val Cys Lys Ala Ser Val
        35                  40                  45

caa gcc agt gtc gac ctg tgc cgg gta acc atg aac atc tcg acg tcg     192
Gln Ala Ser Val Asp Leu Cys Arg Val Thr Met Asn Ile Ser Thr Ser
    50                  55                  60

gat cgc agc cat ctg tgg gct gag gcc tgg ctc cca aga aat tat acc     240
Asp Arg Ser His Leu Trp Ala Glu Ala Trp Leu Pro Arg Asn Tyr Thr
65                  70                  75                  80

ggt cgc ttc gtg agc acg ggg aat gga ggt cta gcc ggc tgt gtc caa     288
Gly Arg Phe Val Ser Thr Gly Asn Gly Gly Leu Ala Gly Cys Val Gln
                85                  90                  95

gaa acg gac ctc aac ttt gca gcc aac ttt ggt ttc gct acc gtg ggc     336
Glu Thr Asp Leu Asn Phe Ala Ala Asn Phe Gly Phe Ala Thr Val Gly
            100                 105                 110

acc aac ggt gga cat gac ggg gac acg gcc aaa tac ttc ctc aac aac     384
```

```
Thr Asn Gly Gly His Asp Gly Asp Thr Ala Lys Tyr Phe Leu Asn Asn
        115                 120                 125

tcg gag gtt ctg gcc gat ttt gcc tat cgc tca gtg cac gaa ggg acc      432
Ser Glu Val Leu Ala Asp Phe Ala Tyr Arg Ser Val His Glu Gly Thr
    130                 135                 140

gtg gtg ggt aag caa cta act caa ttg ttt tat gac gag gga tac aac      480
Val Val Gly Lys Gln Leu Thr Gln Leu Phe Tyr Asp Glu Gly Tyr Asn
145                 150                 155                 160

tac tcc tac tat ttg ggt tgc tcc acc gga ggc cgc caa ggc tac cag      528
Tyr Ser Tyr Tyr Leu Gly Cys Ser Thr Gly Gly Arg Gln Gly Tyr Gln
                165                 170                 175

caa gtc caa cgg ttt ccc gac gac tat gac gga gtg att gcg ggc tcc      576
Gln Val Gln Arg Phe Pro Asp Asp Tyr Asp Gly Val Ile Ala Gly Ser
            180                 185                 190

gca gcg atg aac ttt atc aac ctg atc tcc tgg ggg gcc ttc ttg tgg      624
Ala Ala Met Asn Phe Ile Asn Leu Ile Ser Trp Gly Ala Phe Leu Trp
        195                 200                 205

aag gcg acg ggg tta gcg gat gat cca gac ttt atc tct gca aac ctg      672
Lys Ala Thr Gly Leu Ala Asp Asp Pro Asp Phe Ile Ser Ala Asn Leu
    210                 215                 220

tgg tcc gta atc cac cag gag att gtt cgt cag tgc gac ctg gtc gat      720
Trp Ser Val Ile His Gln Glu Ile Val Arg Gln Cys Asp Leu Val Asp
225                 230                 235                 240

ggg gct ctg gat gga atc atc gaa gac cct gat ttc tgt gct cca gtc      768
Gly Ala Leu Asp Gly Ile Ile Glu Asp Pro Asp Phe Cys Ala Pro Val
                245                 250                 255

atc gag cgc ttg atc tgc gac ggg act acc aac ggc acc tct tgt atc      816
Ile Glu Arg Leu Ile Cys Asp Gly Thr Thr Asn Gly Thr Ser Cys Ile
            260                 265                 270

acg gga gcc cag gca gca aag gtc aac cgg gcc ttg agt gac ttc tat      864
Thr Gly Ala Gln Ala Ala Lys Val Asn Arg Ala Leu Ser Asp Phe Tyr
        275                 280                 285

ggc ccc gac ggg aca gtg tac tac ccg cgc ctg aac tat ggg ggt gag      912
Gly Pro Asp Gly Thr Val Tyr Tyr Pro Arg Leu Asn Tyr Gly Gly Glu
    290                 295                 300

gcc gac tcg gct tcc ctg tac ttc acg ggg tcg atg tac agc cgt acg      960
Ala Asp Ser Ala Ser Leu Tyr Phe Thr Gly Ser Met Tyr Ser Arg Thr
305                 310                 315                 320

gag gaa tgg tac aaa tat gtg gtc tat aac gac acc aac tgg aac tcc     1008
Glu Glu Trp Tyr Lys Tyr Val Val Tyr Asn Asp Thr Asn Trp Asn Ser
                325                 330                 335

agc cag tgg acg ctg gag agt gcc aag ctg gcc ctg gag cag aat ccg     1056
Ser Gln Trp Thr Leu Glu Ser Ala Lys Leu Ala Leu Glu Gln Asn Pro
            340                 345                 350

ttc aat atc cag gcg ttt gat ccc aac atc acg gcc ttc cgg gac cgg     1104
Phe Asn Ile Gln Ala Phe Asp Pro Asn Ile Thr Ala Phe Arg Asp Arg
```

```
        355                 360                 365

ggt ggc aag ctg ctg tcc tac cac ggc acg cag gat ccc att atc agc     1152
Gly Gly Lys Leu Leu Ser Tyr His Gly Thr Gln Asp Pro Ile Ile Ser
    370                 375                 380

tcc acg gat agc aag ctc tac tac cga cgg gta gcg aat gcc ctg aat     1200
Ser Thr Asp Ser Lys Leu Tyr Tyr Arg Arg Val Ala Asn Ala Leu Asn
385                 390                 395                 400

gcc gcg ccg tcc gag cta gat gag ttc tat cgg ttc ttc cag atc tcc     1248
Ala Ala Pro Ser Glu Leu Asp Glu Phe Tyr Arg Phe Phe Gln Ile Ser
                405                 410                 415

ggc atg ggc cac tgt ggc gat ggc acg gga gca tcg tac atc ggc cag     1296
Gly Met Gly His Cys Gly Asp Gly Thr Gly Ala Ser Tyr Ile Gly Gln
            420                 425                 430

gga tat ggc acg tac acc tcc aag gcg ccc caa gtc aac ctg ctg cgc     1344
Gly Tyr Gly Thr Tyr Thr Ser Lys Ala Pro Gln Val Asn Leu Leu Arg
        435                 440                 445

acg atg gtg gac tgg gtg gaa aac gga aag gcg ccc gag tat atg ccg     1392
Thr Met Val Asp Trp Val Glu Asn Gly Lys Ala Pro Glu Tyr Met Pro
    450                 455                 460

ggc aac aag ctc aac gcg aac ggg tca att gag tac atg cgc aag cac     1440
Gly Asn Lys Leu Asn Ala Asn Gly Ser Ile Glu Tyr Met Arg Lys His
465                 470                 475                 480

tgc cgg tat ccg aag cat aac att cac acg ggg ccg ggt aac tac acc     1488
Cys Arg Tyr Pro Lys His Asn Ile His Thr Gly Pro Gly Asn Tyr Thr
                485                 490                 495

gat cct aac tcc tgg act tgc gta                                    1512
Asp Pro Asn Ser Trp Thr Cys Val
            500
```

<210> 12
<211> 504
<212> PRT
<213> Aspergillus niger

<400> 12

```
Ala Thr Asp Pro Phe Gln Ser Arg Cys Asn Glu Phe Gln Asn Lys Ile
1               5                   10                  15

Asp Ile Ala Asn Val Thr Val Arg Ser Val Ala Tyr Val Ala Ala Gly
            20                  25                  30

Gln Asn Ile Ser Gln Ala Glu Val Ala Ser Val Cys Lys Ala Ser Val
        35                  40                  45

Gln Ala Ser Val Asp Leu Cys Arg Val Thr Met Asn Ile Ser Thr Ser
    50                  55                  60
```

Asp Arg Ser His Leu Trp Ala Glu Ala Trp Leu Pro Arg Asn Tyr Thr
65 70 75 80

Gly Arg Phe Val Ser Thr Gly Asn Gly Gly Leu Ala Gly Cys Val Gln
85 90 95

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

Thr Asn Gly Gly His Asp Gly Asp Thr Ala Lys Tyr Phe Leu Asn Asn
115 120 125

Ser Glu Val Leu Ala Asp Phe Ala Tyr Arg Ser Val His Glu Gly Thr
130 135 140

Val Val Gly Lys Gln Leu Thr Gln Leu Phe Tyr Asp Glu Gly Tyr Asn
145 150 155 160

Tyr Ser Tyr Tyr Leu Gly Cys Ser Thr Gly Gly Arg Gln Gly Tyr Gln
165 170 175

Gln Val Gln Arg Phe Pro Asp Asp Tyr Asp Gly Val Ile Ala Gly Ser
180 185 190

Ala Ala Met Asn Phe Ile Asn Leu Ile Ser Trp Gly Ala Phe Leu Trp
195 200 205

Lys Ala Thr Gly Leu Ala Asp Asp Pro Asp Phe Ile Ser Ala Asn Leu
210 215 220

Trp Ser Val Ile His Gln Glu Ile Val Arg Gln Cys Asp Leu Val Asp
225 230 235 240

Gly Ala Leu Asp Gly Ile Ile Glu Asp Pro Asp Phe Cys Ala Pro Val
245 250 255

Ile Glu Arg Leu Ile Cys Asp Gly Thr Thr Asn Gly Thr Ser Cys Ile
260 265 270

Thr Gly Ala Gln Ala Ala Lys Val Asn Arg Ala Leu Ser Asp Phe Tyr
275 280 285

Gly Pro Asp Gly Thr Val Tyr Tyr Pro Arg Leu Asn Tyr Gly Gly Glu
290 295 300

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

Glu Glu Trp Tyr Lys Tyr Val Val Tyr Asn Asp Thr Asn Trp Asn Ser
325 330 335

Ser Gln Trp Thr Leu Glu Ser Ala Lys Leu Ala Leu Glu Gln Asn Pro
340 345 350

Phe Asn Ile Gln Ala Phe Asp Pro Asn Ile Thr Ala Phe Arg Asp Arg
355 360 365

Gly Gly Lys Leu Leu Ser Tyr His Gly Thr Gln Asp Pro Ile Ile Ser
370 375 380

Ser Thr Asp Ser Lys Leu Tyr Tyr Arg Arg Val Ala Asn Ala Leu Asn
385 390 395 400

Ala Ala Pro Ser Glu Leu Asp Glu Phe Tyr Arg Phe Phe Gln Ile Ser
405 410 415

Gly Met Gly His Cys Gly Asp Gly Thr Gly Ala Ser Tyr Ile Gly Gln
420 425 430

Gly Tyr Gly Thr Tyr Thr Ser Lys Ala Pro Gln Val Asn Leu Leu Arg
435 440 445

Thr Met Val Asp Trp Val Glu Asn Gly Lys Ala Pro Glu Tyr Met Pro
450 455 460

Gly Asn Lys Leu Asn Ala Asn Gly Ser Ile Glu Tyr Met Arg Lys His
465 470 475 480

Cys Arg Tyr Pro Lys His Asn Ile His Thr Gly Pro Gly Asn Tyr Thr
485 490 495

Asp Pro Asn Ser Trp Thr Cys Val
500

<210> 13
<211> 564
<212> DNA
<213> Aspergillus niger

<220>
<221> CDS
<222> (1)..(564)

<400> 13

```
tcg acc ccg agc tcg acc ggc gag aac aac ggc ttc tac tac tcc ttc      48
Ser Thr Pro Ser Ser Thr Gly Glu Asn Asn Gly Phe Tyr Tyr Ser Phe
1               5                  10                  15

tgg acc gac ggc ggt gga gac gtg acc tac acc aac gga gat gct ggt      96
Trp Thr Asp Gly Gly Gly Asp Val Thr Tyr Thr Asn Gly Asp Ala Gly
            20                  25                  30

gcc tac act gtt gag tgg tcc aac gtg ggc aac ttt gtc ggt gga aag     144
Ala Tyr Thr Val Glu Trp Ser Asn Val Gly Asn Phe Val Gly Gly Lys
        35                  40                  45

ggc tgg aac ccc gga agt gcg cag gac atc acc tac agc ggc acc ttc     192
Gly Trp Asn Pro Gly Ser Ala Gln Asp Ile Thr Tyr Ser Gly Thr Phe
    50                  55                  60

acc cct agc ggc aac ggc tac ctc tcc gtc tat ggc tgg acc act gac     240
Thr Pro Ser Gly Asn Gly Tyr Leu Ser Val Tyr Gly Trp Thr Thr Asp
65                  70                  75                  80

cct ctg atc gag tac tac atc gtc gag tct tac ggc gac tac aac ccc     288
Pro Leu Ile Glu Tyr Tyr Ile Val Glu Ser Tyr Gly Asp Tyr Asn Pro
                85                  90                  95

ggc agt gga ggc acg tac aag ggc acc gtc acc tcg gac gga tcc gtt     336
Gly Ser Gly Gly Thr Tyr Lys Gly Thr Val Thr Ser Asp Gly Ser Val
            100                 105                 110

tac gat atc tac acg gct acc cgt acc aat gct gct tcc att cag gga     384
Tyr Asp Ile Tyr Thr Ala Thr Arg Thr Asn Ala Ala Ser Ile Gln Gly
        115                 120                 125

acc gct acc ttc act cag tac tgg tcc gtt cgc cag aac aag aga gtt     432
Thr Ala Thr Phe Thr Gln Tyr Trp Ser Val Arg Gln Asn Lys Arg Val
    130                 135                 140

ggc gga acc gtt acc acc tcc aac cac ttc aat gct tgg gct aag ctg     480
Gly Gly Thr Val Thr Thr Ser Asn His Phe Asn Ala Trp Ala Lys Leu
145                 150                 155                 160

gga atg aac ctg ggt act cac aac tac cag atc gtg gct acc gag ggt     528
Gly Met Asn Leu Gly Thr His Asn Tyr Gln Ile Val Ala Thr Glu Gly
                165                 170                 175

tac cag agc agt gga tct tcg tcc atc act gtt cag                     564
Tyr Gln Ser Ser Gly Ser Ser Ser Ile Thr Val Gln
            180                 185
```

<210> 14
<211> 188
<212> PRT
<213> Aspergillus niger

<400> 14

```
Ser Thr Pro Ser Ser Thr Gly Glu Asn Asn Gly Phe Tyr Tyr Ser Phe
1               5                  10                  15
```

Trp Thr Asp Gly Gly Gly Asp Val Thr Tyr Thr Asn Gly Asp Ala Gly
20 25 30

Ala Tyr Thr Val Glu Trp Ser Asn Val Gly Asn Phe Val Gly Gly Lys
35 40 45

Gly Trp Asn Pro Gly Ser Ala Gln Asp Ile Thr Tyr Ser Gly Thr Phe
50 55 60

Thr Pro Ser Gly Asn Gly Tyr Leu Ser Val Tyr Gly Trp Thr Thr Asp
65 70 75 80

Pro Leu Ile Glu Tyr Tyr Ile Val Glu Ser Tyr Gly Asp Tyr Asn Pro
85 90 95

Gly Ser Gly Gly Thr Tyr Lys Gly Thr Val Thr Ser Asp Gly Ser Val
100 105 110

Tyr Asp Ile Tyr Thr Ala Thr Arg Thr Asn Ala Ala Ser Ile Gln Gly
115 120 125

Thr Ala Thr Phe Thr Gln Tyr Trp Ser Val Arg Gln Asn Lys Arg Val
130 135 140

Gly Gly Thr Val Thr Thr Ser Asn His Phe Asn Ala Trp Ala Lys Leu
145 150 155 160

Gly Met Asn Leu Gly Thr His Asn Tyr Gln Ile Val Ala Thr Glu Gly
165 170 175

Tyr Gln Ser Ser Gly Ser Ser Ser Ile Thr Val Gln
180 185

<210> 15
<211> 1494
<212> DNA
<213> Trichoderma reesei

<220>
<221> CDS
<222> (1)..(1494)

<400> 15
cag tcg gcc tgc act ctc caa tcg gag act cac ccg cct ctg aca tgg 48
Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
1 5 10 15

cag aaa tgc tcg tct ggt ggc acg tgc act caa cag aca ggc tcc gtg 96

```
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
            20                  25                  30

gtc atc gac gcc aac tgg cgc tgg act cac gct acg aac agc agc acg      144
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
        35                  40                  45

aac tgc tac gat ggc aac act tgg agc tcg acc cta tgt cct gac aac      192
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
    50                  55                  60

gag acc tgc gcg aag aac tgc tgt ctg gac ggt gcc gcc tac gcg tcc      240
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65                  70                  75                  80

acg tac gga gtt acc acg agc ggt aac agc ctc tcc att ggc ttt gtc      288
Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe Val
                85                  90                  95

acc cag tct gcg cag aag aac gtt ggc gct cgc ctt tac ctt atg gcg      336
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
            100                 105                 110

agc gac acg acc tac cag gaa ttc acc ctg ctt ggc aac gag ttc tct      384
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
        115                 120                 125

ttc gat gtt gat gtt tcg cag ctg ccg tgc ggc ttg aac gga gct ctc      432
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
    130                 135                 140

tac ttc gtg tcc atg gac gcg gat ggt ggc gtg agc aag tat ccc acc      480
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
145                 150                 155                 160

aac acc gct ggc gcc aag tac ggc acg ggg tac tgt gac agc cag tgt      528
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
                165                 170                 175

ccc cgc gat ctg aag ttc atc aat ggc cag gcc aac gtt gag ggc tgg      576
Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp
            180                 185                 190

gag ccg tca tcc aac aac gcg aac acg ggc att gga gga cac gga agc      624
Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
        195                 200                 205

tgc tgc tct gag atg gat atc tgg gag gcc aac tcc atc tcc gag gct      672
Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala
    210                 215                 220

ctt acc ccc cac cct tgc acg act gtc ggc cag gag atc tgc gag ggt      720
Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly
225                 230                 235                 240

gat ggg tgc ggc gga act tac tcc gat aac aga tat ggc ggc act tgc      768
Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr Cys
                245                 250                 255

gat ccc gat ggc tgc gac tgg aac cca tac cgc ctg ggc aac acc agc      816
Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser
```

```
                260                 265                 270

ttc tac ggc cct ggc tca agc ttt acc ctc gat acc acc aag aaa ttg      864
Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu
        275                 280                 285

acc gtt gtc acc cag ttc gag acg tcg ggt gcc atc aac cga tac tat      912
Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr
    290                 295                 300

gtc cag aat ggc gtc act ttc cag cag ccc aac gcc gag ctt ggt agt      960
Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser
305                 310                 315                 320

tac tct ggc aac gag ctc aac gat gat tac tgc aca gct gag gag gca     1008
Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu Ala
                325                 330                 335

gaa ttc ggc gga tcc tct ttc tca gac aag ggc ggc ctg act cag ttc     1056
Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe
            340                 345                 350

aag aag gct acc tct ggc ggc atg gtt ctg gtc atg agt ctg tgg gat     1104
Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp Asp
        355                 360                 365

gat tac tac gcc aac atg ctg tgg ctg gac tcc acc tac ccg aca aac     1152
Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr Asn
    370                 375                 380

gag acc tcc tcc aca ccc ggt gcc gtg cgc gga agc tgc tcc acc agc     1200
Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr Ser
385                 390                 395                 400

tcc ggt gtc cct gct cag gtc gaa tct cag tct ccc aac gcc aag gtc     1248
Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys Val
                405                 410                 415

acc ttc tcc aac atc aag ttc gga ccc att ggc agc acc ggc aac cct     1296
Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn Pro
            420                 425                 430

agc ggc ggc aac cct ccc ggc gga aac ccg cct ggc acc acc acc acc     1344
Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr Thr
        435                 440                 445

cgc cgc cca gcc act acc act gga agc tct ccc gga cct acc cag tct     1392
Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln Ser
    450                 455                 460

cac tac ggc cag tgc ggc ggt att ggc tac agc ggc ccc acg gtc tgc     1440
His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val Cys
465                 470                 475                 480

gcc agc ggc aca act tgc cag gtc ctg aac cct tac tac tct cag tgc     1488
Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln Cys
                485                 490                 495

                                                                    1494
ctg taa
Leu
```

<210> 16
<211> 497
<212> PRT
<213> Trichoderma reesei

<400> 16

Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
1 5 10 15

Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
20 25 30

Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
35 40 45

Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
50 55 60

Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65 70 75 80

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

Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
100 105 110

Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
115 120 125

Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
130 135 140

Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
145 150 155 160

Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
165 170 175

Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp
180 185 190

Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
195 200 205

Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala
210 215 220

Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly
225 230 235 240

Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr Cys
245 250 255

Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser
260 265 270

Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu
275 280 285

Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr
290 295 300

Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser
305 310 315 320

Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu Ala
325 330 335

Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe
340 345 350

Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp Asp
355 360 365

Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr Asn
370 375 380

Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr Ser
385 390 395 400

Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys Val
405 410 415

Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn Pro
420 425 430

Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr Thr
435 440 445

Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln Ser

```
    450                 455                 460

His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val Cys
465                 470                 475                 480

Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln Cys
                485                 490                 495

Leu
```

<210> 17
<211> 1494
<212> DNA
<213> Trichoderma reesei

<220>
<221> CDS
<222> (1)..(1494)

<400> 17

```
cag tcg gcc tgc act ctc caa tcg gag act cac ccg cct ctg aca tgg      48
Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
1               5                   10                  15

cag aaa tgc tcg tct ggt ggc acg tgc act caa cag aca ggc tcc gtg      96
Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
            20                  25                  30

gtc atc gac gcc aac tgg cgc tgg act cac gct acg aac agc agc acg     144
Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
        35                  40                  45

aac tgc tac gat ggc aac act tgg agc tcg acc cta tgt cct gac aac     192
Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
    50                  55                  60

gag acc tgc gcg aag aac tgc tgt ctg gac ggt gcc gcc tac gcg tcc     240
Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65                  70                  75                  80

acg tac gga gtt acc acg agc ggt aac agc ctc tcc att ggc ttt gtc     288
Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe Val
                85                  90                  95

acc cag tct gcg cag aag aac gtt ggc gct cgc ctt tac ctt atg gcg     336
Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
            100                 105                 110

agc gac acg acc tac cag gaa ttc acc ctg ctt ggc aac gag ttc tct     384
Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
        115                 120                 125

ttc gat gtt gat gtt tcg cag ctg ccg tgc ggc ttg aac gga gct ctc     432
Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
    130                 135                 140
```

```
tac ttc gtg tcc atg gac gcg gat ggt ggc gtg agc aag tat ccc acc      480
Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
145                 150                 155                 160

aac acc gct ggc gcc aag tac ggc acg ggg tac tgt gac agc cag tgt      528
Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
                165                 170                 175

ccc cgc gat ctg aag ttc atc aat ggc cag gcc aac gtt gag ggc tgg      576
Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp
            180                 185                 190

gag ccg tca tcc aac aac gcg aac acg ggc att gga gga cac gga agc      624
Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
        195                 200                 205

tgc tgc tct gag atg gat atc tgg gag gcc aac tcc atc tcc gag gct      672
Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala
    210                 215                 220

ctt acc ccc cac cct tgc acg act gtc ggc cag gag atc tgc gag ggt      720
Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly
225                 230                 235                 240

gat ggg tgc ggc gga act tac tcc gat aac aga tat ggc ggc act tgc      768
Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr Cys
                245                 250                 255

gat ccc gat ggc tgc gac tgg aac cca tac cgc ctg ggc aac acc agc      816
Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser
            260                 265                 270

ttc tac ggc cct ggc tca agc ttt acc ctc gat acc acc aag aaa ttg      864
Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu
        275                 280                 285

acc gtt gtc acc cag ttc gag acg tcg ggt gcc atc aac cga tac tat      912
Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr
    290                 295                 300

gtc cag aat ggc gtc act ttc cag cag ccc aac gcc gag ctt ggt agt      960
Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser
305                 310                 315                 320

tac tct ggc aac gag ctc aac gat gat tac tgc aca gct gag gag gca     1008
Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu Ala
                325                 330                 335

gaa ttc ggc gga tcc tct ttc tca gac aag ggc ggc ctg act cag ttc     1056
Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe
            340                 345                 350

aag aag gct acc tct ggc ggc atg gtt ctg gtc atg agt ctg tgg gat     1104
Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp Asp
        355                 360                 365

gat tac tac gcc aac atg ctg tgg ctg gac tcc acc tac ccg aca aac     1152
Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr Asn
    370                 375                 380
```

```
gag acc tcc tcc aca ccc ggt gcc gtg cgc gga agc tgc tcc acc agc      1200
Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr Ser
385                 390                 395                 400

tcc ggt gtc cct gct cag gtc gaa tct cag tct ccc aac gcc aag gtc      1248
Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys Val
                405                 410                 415

acc ttc tcc aac atc aag ttc gga ccc att ggc agc acc ggc aac cct      1296
Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn Pro
            420                 425                 430

agc ggc ggc aac cct ccc ggc gga aac ccg cct ggc acc acc acc acc      1344
Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr Thr
        435                 440                 445

cgc cgc cca gcc act acc act gga agc tct ccc gga cct acc cag tct      1392
Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln Ser
    450                 455                 460

cac tac ggc cag tgc ggc ggt att ggc tac agc ggc ccc acg gtc tgc      1440
His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val Cys
465                 470                 475                 480

gcc agc ggc aca act tgc cag gtc ctg aac cct tac tac tct cag tgc      1488
Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln Cys
                485                 490                 495

ctg taa                                                             1494
Leu
```

<210> 18
<211> 497
<212> PRT
<213> Trichoderma reesei

<400> 18

```
Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp
1               5                   10                  15

Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val
            20                  25                  30

Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr
        35                  40                  45

Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn
    50                  55                  60

Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser
65                  70                  75                  80

Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe Val
```

85 90 95

Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala
100 105 110

Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser
115 120 125

Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu
130 135 140

Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr
145 150 155 160

Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys
165 170 175

Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp
180 185 190

Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser
195 200 205

Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala
210 215 220

Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly
225 230 235 240

Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr Cys
245 250 255

Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser
260 265 270

Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu
275 280 285

Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr
290 295 300

Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser
305 310 315 320

Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu Ala
325 330 335

Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe
340 345 350

Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp Asp
355 360 365

Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr Asn
370 375 380

Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr Ser
385 390 395 400

Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys Val
405 410 415

Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn Pro
420 425 430

Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr Thr
435 440 445

Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln Ser
450 455 460

His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val Cys
465 470 475 480

Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln Cys
485 490 495

Leu

<210> 19
<211> 1344
<212> DNA
<213> Trichoderma reesei

<220>
<221> CDS
<222> (1)..(1344)

<400> 19
caa gct tgc tca agc gtc tgg ggc caa tgt ggt ggc cag aat tgg tcg 48
Gln Ala Cys Ser Ser Val Trp Gly Gln Cys Gly Gly Gln Asn Trp Ser
1 5 10 15

132

```
ggt ccg act tgc tgt gct tcc gga agc aca tgc gtc tac tcc aac gac      96
Gly Pro Thr Cys Cys Ala Ser Gly Ser Thr Cys Val Tyr Ser Asn Asp
            20                  25                  30

tat tac tcc cag tgt ctt ccc ggc gct gca agc tca agc tcg tcc acg     144
Tyr Tyr Ser Gln Cys Leu Pro Gly Ala Ala Ser Ser Ser Ser Ser Thr
        35                  40                  45

cgc gcc gcg tcg acg act tct cga gta tcc ccc aca aca tcc cgg tcg     192
Arg Ala Ala Ser Thr Thr Ser Arg Val Ser Pro Thr Thr Ser Arg Ser
    50                  55                  60

agc tcc gcg acg cct cca cct ggt tct act act acc aga gta cct cca     240
Ser Ser Ala Thr Pro Pro Pro Gly Ser Thr Thr Thr Arg Val Pro Pro
65                  70                  75                  80

gtc gga tcg gga acc gct acg tat tca ggc aac cct ttt gtt ggg gtc     288
Val Gly Ser Gly Thr Ala Thr Tyr Ser Gly Asn Pro Phe Val Gly Val
                85                  90                  95

act cct tgg gcc aat gca tat tac gcc tct gaa gtt agc agc ctc gct     336
Thr Pro Trp Ala Asn Ala Tyr Tyr Ala Ser Glu Val Ser Ser Leu Ala
            100                 105                 110

att cct agc ttg act gga gcc atg gcc act gct gca gca gct gtc gca     384
Ile Pro Ser Leu Thr Gly Ala Met Ala Thr Ala Ala Ala Ala Val Ala
        115                 120                 125

aag gtt ccc tct ttt atg tgg cta gat act ctt gac aag acc cct ctc     432
Lys Val Pro Ser Phe Met Trp Leu Asp Thr Leu Asp Lys Thr Pro Leu
    130                 135                 140

atg gag caa acc ttg gcc gac atc cgc acc gcc aac aag aat ggc ggt     480
Met Glu Gln Thr Leu Ala Asp Ile Arg Thr Ala Asn Lys Asn Gly Gly
145                 150                 155                 160

aac tat gcg gga cag ttt gtg gtg tat gac ttg ccg gat cgc gat tgc     528
Asn Tyr Ala Gly Gln Phe Val Val Tyr Asp Leu Pro Asp Arg Asp Cys
                165                 170                 175

gct gcc ctt gcc tcg aat ggc gaa tac tct att gcc gat ggt ggc gtc     576
Ala Ala Leu Ala Ser Asn Gly Glu Tyr Ser Ile Ala Asp Gly Gly Val
            180                 185                 190

gcc aaa tat aag aac tat atc gac acc att cgt caa att gtc gtg gaa     624
Ala Lys Tyr Lys Asn Tyr Ile Asp Thr Ile Arg Gln Ile Val Val Glu
        195                 200                 205

tat tcc gat atc cgg acc ctc ctg gtt att gag cct gac tct ctt gcc     672
Tyr Ser Asp Ile Arg Thr Leu Leu Val Ile Glu Pro Asp Ser Leu Ala
    210                 215                 220

aac ctg gtg acc aac ctc ggt act cca aag tgt gcc aat gct cag tca     720
Asn Leu Val Thr Asn Leu Gly Thr Pro Lys Cys Ala Asn Ala Gln Ser
225                 230                 235                 240

gcc tac ctt gag tgc atc aac tac gcc gtc aca cag ctg aac ctt cca     768
Ala Tyr Leu Glu Cys Ile Asn Tyr Ala Val Thr Gln Leu Asn Leu Pro
                245                 250                 255

aat gtt gcg atg tat ttg gac gct ggc cat gca gga tgg ctt ggc tgg     816
```

```
Asn Val Ala Met Tyr Leu Asp Ala Gly His Ala Gly Trp Leu Gly Trp
            260                 265                 270

ccg gca aac caa gac ccg gcc gct cag cta ttt gca aat gtt tac aag      864
Pro Ala Asn Gln Asp Pro Ala Ala Gln Leu Phe Ala Asn Val Tyr Lys
        275                 280                 285

aat gca tcg tct ccg aga gct ctt cgc gga ttg gca acc aat gtc gcc      912
Asn Ala Ser Ser Pro Arg Ala Leu Arg Gly Leu Ala Thr Asn Val Ala
    290                 295                 300

aac tac aac ggg tgg aac att acc agc ccc cca tcg tac acg caa ggc      960
Asn Tyr Asn Gly Trp Asn Ile Thr Ser Pro Pro Ser Tyr Thr Gln Gly
305                 310                 315                 320

aac gct gtc tac aac gag aag ctg tac atc cac gct att gga cgt ctt     1008
Asn Ala Val Tyr Asn Glu Lys Leu Tyr Ile His Ala Ile Gly Arg Leu
                325                 330                 335

ctt gcc aat cac ggc tgg tcc aac gcc ttc ttc atc act gat caa ggt     1056
Leu Ala Asn His Gly Trp Ser Asn Ala Phe Phe Ile Thr Asp Gln Gly
            340                 345                 350

cga tcg gga aag cag cct acc gga cag caa cag tgg gga gac tgg tgc     1104
Arg Ser Gly Lys Gln Pro Thr Gly Gln Gln Gln Trp Gly Asp Trp Cys
        355                 360                 365

aat gtg atc ggc acc gga ttt ggt att cgc cca tcc gca aac act ggg     1152
Asn Val Ile Gly Thr Gly Phe Gly Ile Arg Pro Ser Ala Asn Thr Gly
    370                 375                 380

gac tcg ttg ctg gat tcg ttt gtc tgg gtc aag cca ggc ggc gag tgt     1200
Asp Ser Leu Leu Asp Ser Phe Val Trp Val Lys Pro Gly Gly Glu Cys
385                 390                 395                 400

gac ggc acc agc gac agc agt gcg cca cga ttt gac tcc cac tgt gcg     1248
Asp Gly Thr Ser Asp Ser Ser Ala Pro Arg Phe Asp Ser His Cys Ala
                405                 410                 415

ctc cca gat gcc ttg caa ccg gcg gct caa gct ggt gct tgg ttc caa     1296
Leu Pro Asp Ala Leu Gln Pro Ala Ala Gln Ala Gly Ala Trp Phe Gln
            420                 425                 430

gcc tac ttt gtg cag ctt ctc aca aac gca aac cca tcg ttc ctg taa     1344
Ala Tyr Phe Val Gln Leu Leu Thr Asn Ala Asn Pro Ser Phe Leu
        435                 440                 445
```

<210> 20
<211> 447
<212> PRT
<213> Trichoderma reesei

<400> 20

```
Gln Ala Cys Ser Ser Val Trp Gly Gln Cys Gly Gly Gln Asn Trp Ser
1               5                   10                  15

Gly Pro Thr Cys Cys Ala Ser Gly Ser Thr Cys Val Tyr Ser Asn Asp
            20                  25                  30
```

Tyr Tyr Ser Gln Cys Leu Pro Gly Ala Ala Ser Ser Ser Ser Ser Thr
35 40 45

Arg Ala Ala Ser Thr Thr Ser Arg Val Ser Pro Thr Thr Ser Arg Ser
50 55 60

Ser Ser Ala Thr Pro Pro Pro Gly Ser Thr Thr Thr Arg Val Pro Pro
65 70 75 80

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

Thr Pro Trp Ala Asn Ala Tyr Tyr Ala Ser Glu Val Ser Ser Leu Ala
100 105 110

Ile Pro Ser Leu Thr Gly Ala Met Ala Thr Ala Ala Ala Ala Val Ala
115 120 125

Lys Val Pro Ser Phe Met Trp Leu Asp Thr Leu Asp Lys Thr Pro Leu
130 135 140

Met Glu Gln Thr Leu Ala Asp Ile Arg Thr Ala Asn Lys Asn Gly Gly
145 150 155 160

Asn Tyr Ala Gly Gln Phe Val Val Tyr Asp Leu Pro Asp Arg Asp Cys
165 170 175

Ala Ala Leu Ala Ser Asn Gly Glu Tyr Ser Ile Ala Asp Gly Gly Val
180 185 190

Ala Lys Tyr Lys Asn Tyr Ile Asp Thr Ile Arg Gln Ile Val Val Glu
195 200 205

Tyr Ser Asp Ile Arg Thr Leu Leu Val Ile Glu Pro Asp Ser Leu Ala
210 215 220

Asn Leu Val Thr Asn Leu Gly Thr Pro Lys Cys Ala Asn Ala Gln Ser
225 230 235 240

Ala Tyr Leu Glu Cys Ile Asn Tyr Ala Val Thr Gln Leu Asn Leu Pro
245 250 255

Asn Val Ala Met Tyr Leu Asp Ala Gly His Ala Gly Trp Leu Gly Trp
260 265 270

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

Asn Ala Ser Ser Pro Arg Ala Leu Arg Gly Leu Ala Thr Asn Val Ala
290 295 300

Asn Tyr Asn Gly Trp Asn Ile Thr Ser Pro Pro Ser Tyr Thr Gln Gly
305 310 315 320

Asn Ala Val Tyr Asn Glu Lys Leu Tyr Ile His Ala Ile Gly Arg Leu
325 330 335

Leu Ala Asn His Gly Trp Ser Asn Ala Phe Phe Ile Thr Asp Gln Gly
340 345 350

Arg Ser Gly Lys Gln Pro Thr Gly Gln Gln Gln Trp Gly Asp Trp Cys
355 360 365

Asn Val Ile Gly Thr Gly Phe Gly Ile Arg Pro Ser Ala Asn Thr Gly
370 375 380

Asp Ser Leu Leu Asp Ser Phe Val Trp Val Lys Pro Gly Gly Glu Cys
385 390 395 400

Asp Gly Thr Ser Asp Ser Ser Ala Pro Arg Phe Asp Ser His Cys Ala
405 410 415

Leu Pro Asp Ala Leu Gln Pro Ala Ala Gln Ala Gly Ala Trp Phe Gln
420 425 430

Ala Tyr Phe Val Gln Leu Leu Thr Asn Ala Asn Pro Ser Phe Leu
435 440 445

<210> 21
<211> 1230
<212> DNA
<213> Trichoderma reesei

<220>
<221> CDS
<222> (1)..(1230)

<400> 21
ccc ggc gct gca agc tca agc tcg tcc acg cgc gcc gcg tcg acg act 48
Pro Gly Ala Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr Thr
1 5 10 15

tct cga gta tcc ccc aca aca tcc cgg tcg agc tcc gcg acg cct cca 96

```
Ser Arg Val Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro Pro
            20                  25                  30

cct ggt tct act act acc aga gta cct cca gtc gga tcg gga acc gct      144
Pro Gly Ser Thr Thr Thr Arg Val Pro Pro Val Gly Ser Gly Thr Ala
        35                  40                  45

acg tat tca ggc aac cct ttt gtt ggg gtc act cct tgg gcc aat gca      192
Thr Tyr Ser Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala Asn Ala
    50                  55                  60

tat tac gcc tct gaa gtt agc agc ctc gct att cct agc ttg act gga      240
Tyr Tyr Ala Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu Thr Gly
65                  70                  75                  80

gcc atg gcc act gct gca gca gct gtc gca aag gtt ccc tct ttt atg      288
Ala Met Ala Thr Ala Ala Ala Ala Val Ala Lys Val Pro Ser Phe Met
                85                  90                  95

tgg cta gat act ctt gac aag acc cct ctc atg gag caa acc ttg gcc      336
Trp Leu Asp Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr Leu Ala
            100                 105                 110

gac atc cgc acc gcc aac aag aat ggc ggt aac tat gcg gga cag ttt      384
Asp Ile Arg Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln Phe
        115                 120                 125

gtg gtg tat gac ttg ccg gat cgc gat tgc gct gcc ctt gcc tcg aat      432
Val Val Tyr Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser Asn
    130                 135                 140

ggc gaa tac tct att gcc gat ggt ggc gtc gcc aaa tat aag aac tat      480
Gly Glu Tyr Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn Tyr
145                 150                 155                 160

atc gac acc att cgt caa att gtc gtg gaa tat tcc gat atc cgg acc      528
Ile Asp Thr Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile Arg Thr
                165                 170                 175

ctc ctg gtt att gag cct gac tct ctt gcc aac ctg gtg acc aac ctc      576
Leu Leu Val Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu
            180                 185                 190

ggt act cca aag tgt gcc aat gct cag tca gcc tac ctt gag tgc atc      624
Gly Thr Pro Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Ile
        195                 200                 205

aac tac gcc gtc aca cag ctg aac ctt cca aat gtt gcg atg tat ttg      672
Asn Tyr Ala Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu
    210                 215                 220

gac gct ggc cat gca gga tgg ctt ggc tgg ccg gca aac caa gac ccg      720
Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro
225                 230                 235                 240

gcc gct cag cta ttt gca aat gtt tac aag aat gca tcg tct ccg aga      768
Ala Ala Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg
                245                 250                 255

gct ctt cgc gga ttg gca acc aat gtc gcc aac tac aac ggg tgg aac      816
Ala Leu Arg Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp Asn
```

```
            260                 265                 270

att acc agc ccc cca tcg tac acg caa ggc aac gct gtc tac aac gag      864
Ile Thr Ser Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu
        275                 280                 285

aag ctg tac atc cac gct att gga cgt ctt ctt gcc aat cac ggc tgg      912
Lys Leu Tyr Ile His Ala Ile Gly Arg Leu Leu Ala Asn His Gly Trp
    290                 295                 300

tcc aac gcc ttc ttc atc act gat caa ggt cga tcg gga aag cag cct      960
Ser Asn Ala Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln Pro
305                 310                 315                 320

acc gga cag caa cag tgg gga gac tgg tgc aat gtg atc ggc acc gga     1008
Thr Gly Gln Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly
                325                 330                 335

ttt ggt att cgc cca tcc gca aac act ggg gac tcg ttg ctg gat tcg     1056
Phe Gly Ile Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp Ser
            340                 345                 350

ttt gtc tgg gtc aag cca ggc ggc gag tgt gac ggc acc agc gac agc     1104
Phe Val Trp Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp Ser
        355                 360                 365

agt gcg cca cga ttt gac tcc cac tgt gcg ctc cca gat gcc ttg caa     1152
Ser Ala Pro Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu Gln
    370                 375                 380

ccg gcg gct caa gct ggt gct tgg ttc caa gcc tac ttt gtg cag ctt     1200
Pro Ala Ala Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln Leu
385                 390                 395                 400

ctc aca aac gca aac cca tcg ttc ctg taa                            1230
Leu Thr Asn Ala Asn Pro Ser Phe Leu
                405
```

<210> 22
<211> 409
<212> PRT
<213> Trichoderma reesei

<400> 22

```
Pro Gly Ala Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr Thr
1               5                   10                  15

Ser Arg Val Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro Pro
            20                  25                  30

Pro Gly Ser Thr Thr Thr Arg Val Pro Pro Val Gly Ser Gly Thr Ala
        35                  40                  45

Thr Tyr Ser Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala Asn Ala
    50                  55                  60
```

Tyr Tyr Ala Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu Thr Gly
65 70 75 80

Ala Met Ala Thr Ala Ala Ala Ala Val Ala Lys Val Pro Ser Phe Met
85 90 95

Trp Leu Asp Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr Leu Ala
100 105 110

Asp Ile Arg Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln Phe
115 120 125

Val Val Tyr Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser Asn
130 135 140

Gly Glu Tyr Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn Tyr
145 150 155 160

Ile Asp Thr Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile Arg Thr
165 170 175

Leu Leu Val Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu
180 185 190

Gly Thr Pro Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Ile
195 200 205

Asn Tyr Ala Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu
210 215 220

Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro
225 230 235 240

Ala Ala Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg
245 250 255

Ala Leu Arg Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp Asn
260 265 270

Ile Thr Ser Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu
275 280 285

Lys Leu Tyr Ile His Ala Ile Gly Arg Leu Leu Ala Asn His Gly Trp
290 295 300

Ser Asn Ala Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln Pro
305 310 315 320

Thr Gly Gln Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly
325 330 335

Phe Gly Ile Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp Ser
340 345 350

Phe Val Trp Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp Ser
355 360 365

Ser Ala Pro Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu Gln
370 375 380

Pro Ala Ala Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln Leu
385 390 395 400

Leu Thr Asn Ala Asn Pro Ser Phe Leu
405

<210> 23
<211> 1314
<212> DNA
<213> Trichoderma reesei

<220>
<221> CDS
<222> (1)..(1314)

<400> 23
cag caa ccg ggt acc agc acc ccc gag gtc cat ccc aag ttg aca acc 48
Gln Gln Pro Gly Thr Ser Thr Pro Glu Val His Pro Lys Leu Thr Thr
1 5 10 15

tac aag tgt aca aag tcc ggg ggg tgc gtg gcc cag gac acc tcg gtg 96
Tyr Lys Cys Thr Lys Ser Gly Gly Cys Val Ala Gln Asp Thr Ser Val
20 25 30

gtc ctt gac tgg aac tac cgc tgg atg cac gac gca aac tac aac tcg 144
Val Leu Asp Trp Asn Tyr Arg Trp Met His Asp Ala Asn Tyr Asn Ser
35 40 45

tgc acc gtc aac ggc ggc gtc aac acc acg ctc tgc cct gac gag gcg 192
Cys Thr Val Asn Gly Gly Val Asn Thr Thr Leu Cys Pro Asp Glu Ala
50 55 60

acc tgt ggc aag aac tgc ttc atc gag ggc gtc gac tac gcc gcc tcg 240
Thr Cys Gly Lys Asn Cys Phe Ile Glu Gly Val Asp Tyr Ala Ala Ser
65 70 75 80

ggc gtc acg acc tcg ggc agc agc ctc acc atg aac cag tac atg ccc 288
Gly Val Thr Thr Ser Gly Ser Ser Leu Thr Met Asn Gln Tyr Met Pro

140 C

```
                85                  90                  95

agc agc tct ggc ggc tac agc agc gtc tct cct cgg ctg tat ctc ctg      336
Ser Ser Ser Gly Gly Tyr Ser Ser Val Ser Pro Arg Leu Tyr Leu Leu
            100                 105                 110

gac tct gac ggt gag tac gtg atg ctg aag ctc aac ggc cag gag ctg      384
Asp Ser Asp Gly Glu Tyr Val Met Leu Lys Leu Asn Gly Gln Glu Leu
        115                 120                 125

agc ttc gac gtc gac ctc tct gct ctg ccg tgt gga gag aac ggc tcg      432
Ser Phe Asp Val Asp Leu Ser Ala Leu Pro Cys Gly Glu Asn Gly Ser
    130                 135                 140

ctc tac ctg tct cag atg gac gag aac ggg ggc gcc aac cag tat aac      480
Leu Tyr Leu Ser Gln Met Asp Glu Asn Gly Gly Ala Asn Gln Tyr Asn
145                 150                 155                 160

acg gcc ggt gcc aac tac ggg agc ggc tac tgc gat gct cag tgc ccc      528
Thr Ala Gly Ala Asn Tyr Gly Ser Gly Tyr Cys Asp Ala Gln Cys Pro
                165                 170                 175

gtc cag aca tgg agg aac ggc acc ctc aac act agc cac cag ggc ttc      576
Val Gln Thr Trp Arg Asn Gly Thr Leu Asn Thr Ser His Gln Gly Phe
            180                 185                 190

tgc tgc aac gag atg gat atc ctg gag ggc aac tcg agg gcg aat gcc      624
Cys Cys Asn Glu Met Asp Ile Leu Glu Gly Asn Ser Arg Ala Asn Ala
        195                 200                 205

ttg acc cct cac tct tgc acg gcc acg gcc tgc gac tct gcc ggt tgc      672
Leu Thr Pro His Ser Cys Thr Ala Thr Ala Cys Asp Ser Ala Gly Cys
    210                 215                 220

ggc ttc aac ccc tat ggc agc ggc tac aaa agc tac tac ggc ccc gga      720
Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys Ser Tyr Tyr Gly Pro Gly
225                 230                 235                 240

gat acc gtt gac acc tcc aag acc ttc acc atc atc acc cag ttc aac      768
Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe Asn
                245                 250                 255

acg gac aac ggc tcg ccc tcg ggc aac ctt gtg agc atc acc cgc aag      816
Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile Thr Arg Lys
            260                 265                 270

tac cag caa aac ggc gtc gac atc ccc agc gcc cag ccc ggc ggc gac      864
Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro Gly Gly Asp
        275                 280                 285

acc atc tcg tcc tgc ccg tcc gcc tca gcc tac ggc ggc ctc gcc acc      912
Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala Thr
    290                 295                 300

atg ggc aag gcc ctg agc agc ggc atg gtg ctc gtg ttc agc att tgg      960
Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe Ser Ile Trp
305                 310                 315                 320

aac gac aac agc cag tac atg aac tgg ctc gac agc ggc aac gcc ggc     1008
Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala Gly
                325                 330                 335
```

```
ccc tgc agc agc acc gag ggc aac cca tcc aac atc ctg gcc aac aac      1056
Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Ile Leu Ala Asn Asn
            340                 345                 350

ccc aac acg cac gtc gtc ttc tcc aac atc cgc tgg gga gac att ggg      1104
Pro Asn Thr His Val Val Phe Ser Asn Ile Arg Trp Gly Asp Ile Gly
        355                 360                 365

tct act acg aac tcg act gcg ccc ccg ccc ccg cct gcg tcc agc acg      1152
Ser Thr Thr Asn Ser Thr Ala Pro Pro Pro Pro Pro Ala Ser Ser Thr
    370                 375                 380

acg ttt tcg act aca cgg agg agc tcg acg act tcg agc agc ccg agc      1200
Thr Phe Ser Thr Thr Arg Arg Ser Ser Thr Thr Ser Ser Ser Pro Ser
385                 390                 395                 400

tgc acg cag act cac tgg ggg cag tgc ggt ggc att ggg tac agc ggg      1248
Cys Thr Gln Thr His Trp Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly
                405                 410                 415

tgc aag acg tgc acg tcg ggc act acg tgc cag tat agc aac gac tac      1296
Cys Lys Thr Cys Thr Ser Gly Thr Thr Cys Gln Tyr Ser Asn Asp Tyr
            420                 425                 430

tac tcg caa tgc ctt tag                                             1314
Tyr Ser Gln Cys Leu
        435
```

<210> 24
<211> 437
<212> PRT
<213> Trichoderma reesei

<400> 24

```
Gln Gln Pro Gly Thr Ser Thr Pro Glu Val His Pro Lys Leu Thr Thr
1               5                   10                  15

Tyr Lys Cys Thr Lys Ser Gly Gly Cys Val Ala Gln Asp Thr Ser Val
            20                  25                  30

Val Leu Asp Trp Asn Tyr Arg Trp Met His Asp Ala Asn Tyr Asn Ser
        35                  40                  45

Cys Thr Val Asn Gly Gly Val Asn Thr Thr Leu Cys Pro Asp Glu Ala
    50                  55                  60

Thr Cys Gly Lys Asn Cys Phe Ile Glu Gly Val Asp Tyr Ala Ala Ser
65                  70                  75                  80

Gly Val Thr Thr Ser Gly Ser Ser Leu Thr Met Asn Gln Tyr Met Pro
                85                  90                  95
```

Ser Ser Ser Gly Gly Tyr Ser Ser Val Ser Pro Arg Leu Tyr Leu Leu
100 105 110

Asp Ser Asp Gly Glu Tyr Val Met Leu Lys Leu Asn Gly Gln Glu Leu
115 120 125

Ser Phe Asp Val Asp Leu Ser Ala Leu Pro Cys Gly Glu Asn Gly Ser
130 135 140

Leu Tyr Leu Ser Gln Met Asp Glu Asn Gly Gly Ala Asn Gln Tyr Asn
145 150 155 160

Thr Ala Gly Ala Asn Tyr Gly Ser Gly Tyr Cys Asp Ala Gln Cys Pro
165 170 175

Val Gln Thr Trp Arg Asn Gly Thr Leu Asn Thr Ser His Gln Gly Phe
180 185 190

Cys Cys Asn Glu Met Asp Ile Leu Glu Gly Asn Ser Arg Ala Asn Ala
195 200 205

Leu Thr Pro His Ser Cys Thr Ala Thr Ala Cys Asp Ser Ala Gly Cys
210 215 220

Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys Ser Tyr Tyr Gly Pro Gly
225 230 235 240

Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe Asn
245 250 255

Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile Thr Arg Lys
260 265 270

Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro Gly Gly Asp
275 280 285

Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala Thr
290 295 300

Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe Ser Ile Trp
305 310 315 320

Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala Gly
325 330 335

Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Ile Leu Ala Asn Asn

340 345 350

Pro Asn Thr His Val Val Phe Ser Asn Ile Arg Trp Gly Asp Ile Gly
355 360 365

Ser Thr Thr Asn Ser Thr Ala Pro Pro Pro Pro Pro Ala Ser Ser Thr
370 375 380

Thr Phe Ser Thr Thr Arg Arg Ser Ser Thr Thr Ser Ser Ser Pro Ser
385 390 395 400

Cys Thr Gln Thr His Trp Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly
405 410 415

Cys Lys Thr Cys Thr Ser Gly Thr Thr Cys Gln Tyr Ser Asn Asp Tyr
420 425 430

Tyr Ser Gln Cys Leu
435

<210> 25
<211> 1200
<212> DNA
<213> Trichoderma reesei

<220>
<221> CDS
<222> (1)..(1200)

<400> 25

cag caa ccg ggt acc agc acc ccc gag gtc cat ccc aag ttg aca acc 48
Gln Gln Pro Gly Thr Ser Thr Pro Glu Val His Pro Lys Leu Thr Thr
1 5 10 15

tac aag tgt aca aag tcc ggg ggg tgc gtg gcc cag gac acc tcg gtg 96
Tyr Lys Cys Thr Lys Ser Gly Gly Cys Val Ala Gln Asp Thr Ser Val
20 25 30

gtc ctt gac tgg aac tac cgc tgg atg cac gac gca aac tac aac tcg 144
Val Leu Asp Trp Asn Tyr Arg Trp Met His Asp Ala Asn Tyr Asn Ser
35 40 45

tgc acc gtc aac ggc ggc gtc aac acc acg ctc tgc cct gac gag gcg 192
Cys Thr Val Asn Gly Gly Val Asn Thr Thr Leu Cys Pro Asp Glu Ala
50 55 60

acc tgt ggc aag aac tgc ttc atc gag ggc gtc gac tac gcc gcc tcg 240
Thr Cys Gly Lys Asn Cys Phe Ile Glu Gly Val Asp Tyr Ala Ala Ser
65 70 75 80

ggc gtc acg acc tcg ggc agc agc ctc acc atg aac cag tac atg ccc 288
Gly Val Thr Thr Ser Gly Ser Ser Leu Thr Met Asn Gln Tyr Met Pro
85 90 95

```
agc agc tct ggc ggc tac agc agc gtc tct cct cgg ctg tat ctc ctg      336
Ser Ser Ser Gly Gly Tyr Ser Ser Val Ser Pro Arg Leu Tyr Leu Leu
            100                 105                 110

gac tct gac ggt gag tac gtg atg ctg aag ctc aac ggc cag gag ctg      384
Asp Ser Asp Gly Glu Tyr Val Met Leu Lys Leu Asn Gly Gln Glu Leu
        115                 120                 125

agc ttc gac gtc gac ctc tct gct ctg ccg tgt gga gag aac ggc tcg      432
Ser Phe Asp Val Asp Leu Ser Ala Leu Pro Cys Gly Glu Asn Gly Ser
    130                 135                 140

ctc tac ctg tct cag atg gac gag aac ggg ggc gcc aac cag tat aac      480
Leu Tyr Leu Ser Gln Met Asp Glu Asn Gly Gly Ala Asn Gln Tyr Asn
145                 150                 155                 160

acg gcc ggt gcc aac tac ggg agc ggc tac tgc gat gct cag tgc ccc      528
Thr Ala Gly Ala Asn Tyr Gly Ser Gly Tyr Cys Asp Ala Gln Cys Pro
                165                 170                 175

gtc cag aca tgg agg aac ggc acc ctc aac act agc cac cag ggc ttc      576
Val Gln Thr Trp Arg Asn Gly Thr Leu Asn Thr Ser His Gln Gly Phe
            180                 185                 190

tgc tgc aac gag atg gat atc ctg gag ggc aac tcg agg gcg aat gcc      624
Cys Cys Asn Glu Met Asp Ile Leu Glu Gly Asn Ser Arg Ala Asn Ala
        195                 200                 205

ttg acc cct cac tct tgc acg gcc acg gcc tgc gac tct gcc ggt tgc      672
Leu Thr Pro His Ser Cys Thr Ala Thr Ala Cys Asp Ser Ala Gly Cys
    210                 215                 220

ggc ttc aac ccc tat ggc agc ggc tac aaa agc tac tac ggc ccc gga      720
Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys Ser Tyr Tyr Gly Pro Gly
225                 230                 235                 240

gat acc gtt gac acc tcc aag acc ttc acc atc atc acc cag ttc aac      768
Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe Asn
                245                 250                 255

acg gac aac ggc tcg ccc tcg ggc aac ctt gtg agc atc acc cgc aag      816
Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile Thr Arg Lys
            260                 265                 270

tac cag caa aac ggc gtc gac atc ccc agc gcc cag ccc ggc ggc gac      864
Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro Gly Gly Asp
        275                 280                 285

acc atc tcg tcc tgc ccg tcc gcc tca gcc tac ggc ggc ctc gcc acc      912
Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala Thr
    290                 295                 300

atg ggc aag gcc ctg agc agc ggc atg gtg ctc gtg ttc agc att tgg      960
Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe Ser Ile Trp
305                 310                 315                 320

aac gac aac agc cag tac atg aac tgg ctc gac agc ggc aac gcc ggc     1008
Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala Gly
                325                 330                 335
```

```
ccc tgc agc agc acc gag ggc aac cca tcc aac atc ctg gcc aac aac   1056
Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Ile Leu Ala Asn Asn
            340                 345                 350

ccc aac acg cac gtc gtc ttc tcc aac atc cgc tgg gga gac att ggg   1104
Pro Asn Thr His Val Val Phe Ser Asn Ile Arg Trp Gly Asp Ile Gly
        355                 360                 365

tct act acg aac tcg act gcg ccc ccg ccc ccg cct gcg tcc agc acg   1152
Ser Thr Thr Asn Ser Thr Ala Pro Pro Pro Pro Pro Ala Ser Ser Thr
    370                 375                 380

acg ttt tcg act aca cgg agg agc tcg acg act tcg agc agc ccg agc   1200
Thr Phe Ser Thr Thr Arg Arg Ser Ser Thr Thr Ser Ser Ser Pro Ser
385                 390                 395                 400
```

<210> 26
<211> 400
<212> PRT
<213> Trichoderma reesei

<400> 26

```
Gln Gln Pro Gly Thr Ser Thr Pro Glu Val His Pro Lys Leu Thr Thr
1               5                   10                  15

Tyr Lys Cys Thr Lys Ser Gly Gly Cys Val Ala Gln Asp Thr Ser Val
            20                  25                  30

Val Leu Asp Trp Asn Tyr Arg Trp Met His Asp Ala Asn Tyr Asn Ser
        35                  40                  45

Cys Thr Val Asn Gly Gly Val Asn Thr Thr Leu Cys Pro Asp Glu Ala
    50                  55                  60

Thr Cys Gly Lys Asn Cys Phe Ile Glu Gly Val Asp Tyr Ala Ala Ser
65                  70                  75                  80

Gly Val Thr Thr Ser Gly Ser Ser Leu Thr Met Asn Gln Tyr Met Pro
                85                  90                  95

Ser Ser Ser Gly Gly Tyr Ser Ser Val Ser Pro Arg Leu Tyr Leu Leu
            100                 105                 110

Asp Ser Asp Gly Glu Tyr Val Met Leu Lys Leu Asn Gly Gln Glu Leu
        115                 120                 125

Ser Phe Asp Val Asp Leu Ser Ala Leu Pro Cys Gly Glu Asn Gly Ser
    130                 135                 140

Leu Tyr Leu Ser Gln Met Asp Glu Asn Gly Gly Ala Asn Gln Tyr Asn
```

145 150 155 160

Thr Ala Gly Ala Asn Tyr Gly Ser Gly Tyr Cys Asp Ala Gln Cys Pro
165 170 175

Val Gln Thr Trp Arg Asn Gly Thr Leu Asn Thr Ser His Gln Gly Phe
180 185 190

Cys Cys Asn Glu Met Asp Ile Leu Glu Gly Asn Ser Arg Ala Asn Ala
195 200 205

Leu Thr Pro His Ser Cys Thr Ala Thr Ala Cys Asp Ser Ala Gly Cys
210 215 220

Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys Ser Tyr Tyr Gly Pro Gly
225 230 235 240

Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe Asn
245 250 255

Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile Thr Arg Lys
260 265 270

Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro Gly Gly Asp
275 280 285

Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala Thr
290 295 300

Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe Ser Ile Trp
305 310 315 320

Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala Gly
325 330 335

Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Ile Leu Ala Asn Asn
340 345 350

Pro Asn Thr His Val Val Phe Ser Asn Ile Arg Trp Gly Asp Ile Gly
355 360 365

Ser Thr Thr Asn Ser Thr Ala Pro Pro Pro Pro Pro Ala Ser Ser Thr
370 375 380

Thr Phe Ser Thr Thr Arg Arg Ser Ser Thr Thr Ser Ser Ser Pro Ser
385 390 395 400

<210> 27
<211> 138
<212> DNA
<213> Trichoderma reesei

<220>
<221> CDS
<222> (1)..(138)

<400> 27
ggc tcg act tac tcc agt gga tct tct tcg ggg tcg ggg tct agc tcc 48
Gly Ser Thr Tyr Ser Ser Gly Ser Ser Ser Gly Ser Gly Ser Ser Ser
1 5 10 15

agc tcg agt tcg act acc act aag gcc act tcg acg acc ttg aag act 96
Ser Ser Ser Ser Thr Thr Thr Lys Ala Thr Ser Thr Thr Leu Lys Thr
20 25 30

acc tcg acc acc agc agt gga agc agt tcg aca tcg gcg gcg 138
Thr Ser Thr Thr Ser Ser Gly Ser Ser Ser Thr Ser Ala Ala
35 40 45

<210> 28
<211> 46
<212> PRT
<213> Trichoderma reesei

<400> 28

Gly Ser Thr Tyr Ser Ser Gly Ser Ser Ser Gly Ser Gly Ser Ser Ser
1 5 10 15

Ser Ser Ser Ser Thr Thr Thr Lys Ala Thr Ser Thr Thr Leu Lys Thr
20 25 30

Thr Ser Thr Thr Ser Ser Gly Ser Ser Ser Thr Ser Ala Ala
35 40 45

<210> 29
<211> 2205
<212> DNA
<213> Seqüência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2205)

<400> 29
cag cag aat tgc gca gca tta ttt ggc caa tgt gga ggc ata ggg tgg 48
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp

```
1               5                   10                  15

tcc ggc acc aca tgt tgc gtt gct ggc gcc cag tgc agt ttt gtc aat      96
Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
            20                  25                  30

gac tgg tac tcc cag tgc ctt gcg tca acc ggc gga aac ccc cca aac     144
Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
        35                  40                  45

gga aca act tcc tct agc ttg gtt tca cgg acg tcg tca gca tcc tca     192
Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
    50                  55                  60

tcc gtc ggc tcg tct tca ccc ggc ggc aac tca cca act ggc agt gct     240
Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65                  70                  75                  80

tcc acc tac aca acc aca gat aca gct acc gtg gct cct cat tcg cag     288
Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
                85                  90                  95

tct cct tac ccc agc att gcc gca tcc agt tgc gga tcg tgg acc ctc     336
Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
            100                 105                 110

gtg gat aat gtt tgc tgc cca tca tat tgt gct aat gat gac aca tcc     384
Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
        115                 120                 125

gag tca tgc tca ggc tgc ggt acc tgc act acg ccg ccc tcg gcg gac     432
Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
    130                 135                 140

tgc aaa tcc gga acc atg tat cca gag gtc cat cac gta tcc agc aac     480
Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145                 150                 155                 160

gag agc tgg cac tac agt aga tca acc cac ttt ggc cta acg agc ggc     528
Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
                165                 170                 175

ggg gcc tgt ggc ttt ggc ctg tac ggt ctc tgc aca aag ggc agt gtt     576
Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
            180                 185                 190

aca gcc agc tgg acg gat ccc atg ctt ggc gcg acg tgt gac gct ttt     624
Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
        195                 200                 205

tgt aca gcg tat ccc ctg ctt tgc aaa gac cct acc ggc act acc ctt     672
Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
    210                 215                 220

cgt ggc aac ttc gca gct cca aac ggc gat tac tac acc caa ttc tgg     720
Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225                 230                 235                 240

tcc tcg ttg cca gga gcc ctc gat aac tac ctg tcc tgc ggc gag tgc     768
Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
                245                 250                 255
```

```
att gag ctg ata caa aca aag ccc gat ggg acc gat tat gct gtc gga      816
Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
            260                 265                 270

gaa gcc ggc tac acg gat cca att act ctc gag att gtg gac agc tgc      864
Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
        275                 280                 285

ccg tgc agc gcg aac tcc aag tgg tgc tgt ggt ccg ggc gcc gat cat      912
Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
    290                 295                 300

tgc gga gag atc gac ttc aaa tac ggc tgt cct ctt cct gct gac agc      960
Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305                 310                 315                 320

att cat ctc gac ctg tca gac att gcc atg ggc cgt ttg cag ggc aat     1008
Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
                325                 330                 335

gga tca cta acc aat ggc gtc atc ccg act cga tat aga aga gtc caa     1056
Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
            340                 345                 350

tgc ccc aaa gtt ggg aac gcc tac att tgg ctt cga aat ggc gga ggg     1104
Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
        355                 360                 365

cct tac tat ttt gct ctc acg gca gtc aac acc aac gga ccg ggc tca     1152
Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
    370                 375                 380

gtc acc aaa atc gag atc aag ggc gca gac acc gac aac tgg gtt gcc     1200
Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385                 390                 395                 400

ttg gtc cat gac cca aac tat acg agt agc cgc cca caa gaa cgc tat     1248
Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
                405                 410                 415

ggc agt tgg gta atc cca cag gga tca ggg ccc ttt aac ttg cct gtt     1296
Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
            420                 425                 430

gga att cgt ctg act agc cca acg ggg gaa cag att gtg aat gaa cag     1344
Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
        435                 440                 445

gcc atc aag aca ttc act cct ccg gcc aca ggt gac ccc aat ttt tac     1392
Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
    450                 455                 460

tac att gac att ggt gtg cag ttt agc cag aat gcc tcc acg caa ggc     1440
Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Ala Ser Thr Gln Gly
465                 470                 475                 480

atc tcc gaa gac ctc tac aat cgc ttg gta gag atg gcc act atc tcc     1488
Ile Ser Glu Asp Leu Tyr Asn Arg Leu Val Glu Met Ala Thr Ile Ser
                485                 490                 495
```

```
caa gcc gcc tac gcc gac cta tgc aat att cca tcg act att atc aaa      1536
Gln Ala Ala Tyr Ala Asp Leu Cys Asn Ile Pro Ser Thr Ile Ile Lys
            500                 505                 510

gga gag aaa att tac aac gct caa act gat atc aac gga tgg atc ctc      1584
Gly Glu Lys Ile Tyr Asn Ala Gln Thr Asp Ile Asn Gly Trp Ile Leu
        515                 520                 525

cgc gac gac acc agc aaa gaa att atc acc gtc ttc cgt ggc act ggc      1632
Arg Asp Asp Thr Ser Lys Glu Ile Ile Thr Val Phe Arg Gly Thr Gly
    530                 535                 540

agt gac aca aac cta cag ctc gat act aac tac acg ctc acg cca ttc      1680
Ser Asp Thr Asn Leu Gln Leu Asp Thr Asn Tyr Thr Leu Thr Pro Phe
545                 550                 555                 560

gac act cta cct caa tgc aac gat tgc gag gta cac ggt gga tac tat      1728
Asp Thr Leu Pro Gln Cys Asn Asp Cys Glu Val His Gly Gly Tyr Tyr
                565                 570                 575

att gga tgg atc tca gtc caa gac caa gtc gag tcg ctt gtc aaa caa      1776
Ile Gly Trp Ile Ser Val Gln Asp Gln Val Glu Ser Leu Val Lys Gln
            580                 585                 590

cag gct agc cag tat ccg gac tat gcg ctt acc gtg aca ggc cat agt      1824
Gln Ala Ser Gln Tyr Pro Asp Tyr Ala Leu Thr Val Thr Gly His Ser
        595                 600                 605

ctg gga gcg tcg atg gca gca ctc act gcc gcc cag ctg tcc gcg aca      1872
Leu Gly Ala Ser Met Ala Ala Leu Thr Ala Ala Gln Leu Ser Ala Thr
    610                 615                 620

tac gac aac gtc cgt ctg tac aca ttc ggc gaa ccg cgc agc ggc aac      1920
Tyr Asp Asn Val Arg Leu Tyr Thr Phe Gly Glu Pro Arg Ser Gly Asn
625                 630                 635                 640

cag gcc ttc gcg tcg tac atg aac gat gcg ttc cag gtc tcg agc ccg      1968
Gln Ala Phe Ala Ser Tyr Met Asn Asp Ala Phe Gln Val Ser Ser Pro
                645                 650                 655

gag acg acc cag tac ttc cgg gtc act cat tcc aac gac ggc atc cca      2016
Glu Thr Thr Gln Tyr Phe Arg Val Thr His Ser Asn Asp Gly Ile Pro
            660                 665                 670

aac ttg ccc ccg gcg gac gag ggt tac gcc cat ggt ggt gta gag tac      2064
Asn Leu Pro Pro Ala Asp Glu Gly Tyr Ala His Gly Gly Val Glu Tyr
        675                 680                 685

tgg agc gtt gat cct tac agc gcc cag aac acg ttt gtc tgt act ggg      2112
Trp Ser Val Asp Pro Tyr Ser Ala Gln Asn Thr Phe Val Cys Thr Gly
    690                 695                 700

gat gaa gta cag tgc tgt gag gca cag ggc gga cag ggg gtg aat gat      2160
Asp Glu Val Gln Cys Cys Glu Ala Gln Gly Gly Gln Gly Val Asn Asp
705                 710                 715                 720

gcg cat act act tat ttt ggg atg acg agc gga gct tgt act tgg          2205
Ala His Thr Thr Tyr Phe Gly Met Thr Ser Gly Ala Cys Thr Trp
                725                 730                 735
```

<210> 30
<211> 735
<212> PRT
<213> Seqüência artificial

<220>
<223> Construção Sintética

<400> 30

Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1 5 10 15

Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
20 25 30

Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
35 40 45

Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
50 55 60

Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65 70 75 80

Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
85 90 95

Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
100 105 110

Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
115 120 125

Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
130 135 140

Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145 150 155 160

Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
165 170 175

Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
180 185 190

Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
195 200 205

Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
210 215 220

Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225 230 235 240

Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
245 250 255

Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
260 265 270

Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
275 280 285

Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
290 295 300

Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305 310 315 320

Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
325 330 335

Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
340 345 350

Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
355 360 365

Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
370 375 380

Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385 390 395 400

Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
405 410 415

Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
420 425 430

Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
435 440 445

Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
450 455 460

Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Ala Ser Thr Gln Gly
465 470 475 480

Ile Ser Glu Asp Leu Tyr Asn Arg Leu Val Glu Met Ala Thr Ile Ser
485 490 495

Gln Ala Ala Tyr Ala Asp Leu Cys Asn Ile Pro Ser Thr Ile Ile Lys
500 505 510

Gly Glu Lys Ile Tyr Asn Ala Gln Thr Asp Ile Asn Gly Trp Ile Leu
515 520 525

Arg Asp Asp Thr Ser Lys Glu Ile Ile Thr Val Phe Arg Gly Thr Gly
530 535 540

Ser Asp Thr Asn Leu Gln Leu Asp Thr Asn Tyr Thr Leu Thr Pro Phe
545 550 555 560

Asp Thr Leu Pro Gln Cys Asn Asp Cys Glu Val His Gly Gly Tyr Tyr
565 570 575

Ile Gly Trp Ile Ser Val Gln Asp Gln Val Glu Ser Leu Val Lys Gln
580 585 590

Gln Ala Ser Gln Tyr Pro Asp Tyr Ala Leu Thr Val Thr Gly His Ser
595 600 605

Leu Gly Ala Ser Met Ala Ala Leu Thr Ala Ala Gln Leu Ser Ala Thr
610 615 620

Tyr Asp Asn Val Arg Leu Tyr Thr Phe Gly Glu Pro Arg Ser Gly Asn
625 630 635 640

Gln Ala Phe Ala Ser Tyr Met Asn Asp Ala Phe Gln Val Ser Ser Pro
645 650 655

Glu Thr Thr Gln Tyr Phe Arg Val Thr His Ser Asn Asp Gly Ile Pro
660 665 670

Asn Leu Pro Pro Ala Asp Glu Gly Tyr Ala His Gly Gly Val Glu Tyr
675 680 685

Trp Ser Val Asp Pro Tyr Ser Ala Gln Asn Thr Phe Val Cys Thr Gly

690 695 700

Asp Glu Val Gln Cys Cys Glu Ala Gln Gly Gly Gln Gly Val Asn Asp
705 710 715 720

Ala His Thr Thr Tyr Phe Gly Met Thr Ser Gly Ala Cys Thr Trp
725 730 735

<210> 31
<211> 2343
<212> DNA
<213> Sequência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2343)

<400> 31
cag cag aat tgc gca gca tta ttt ggc caa tgt gga ggc ata ggg tgg 48
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1 5 10 15

tcc ggc acc aca tgt tgc gtt gct ggc gcc cag tgc agt ttt gtc aat 96
Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
20 25 30

gac tgg tac tcc cag tgc ctt gcg tca acc ggc gga aac ccc cca aac 144
Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
35 40 45

gga aca act tcc tct agc ttg gtt tca cgg acg tcg tca gca tcc tca 192
Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
50 55 60

tcc gtc ggc tcg tct tca ccc ggc ggc aac tca cca act ggc agt gct 240
Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65 70 75 80

tcc acc tac aca acc aca gat aca gct acc gtg gct cct cat tcg cag 288
Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
85 90 95

tct cct tac ccc agc att gcc gca tcc agt tgc gga tcg tgg acc ctc 336
Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
100 105 110

gtg gat aat gtt tgc tgc cca tca tat tgt gct aat gat gac aca tcc 384
Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
115 120 125

gag tca tgc tca ggc tgc ggt acc tgc act acg ccg ccc tcg gcg gac 432
Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
130 135 140

```
tgc aaa tcc gga acc atg tat cca gag gtc cat cac gta tcc agc aac      480
Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145                 150                 155                 160

gag agc tgg cac tac agt aga tca acc cac ttt ggc cta acg agc ggc      528
Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
                165                 170                 175

ggg gcc tgt ggc ttt ggc ctg tac ggt ctc tgc aca aag ggc agt gtt      576
Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
            180                 185                 190

aca gcc agc tgg acg gat ccc atg ctt ggc gcg acg tgt gac gct ttt      624
Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
        195                 200                 205

tgt aca gcg tat ccc ctg ctt tgc aaa gac cct acc ggc act acc ctt      672
Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
    210                 215                 220

cgt ggc aac ttc gca gct cca aac ggc gat tac tac acc caa ttc tgg      720
Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225                 230                 235                 240

tcc tcg ttg cca gga gcc ctc gat aac tac ctg tcc tgc ggc gag tgc      768
Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
                245                 250                 255

att gag ctg ata caa aca aag ccc gat ggg acc gat tat gct gtc gga      816
Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
            260                 265                 270

gaa gcc ggc tac acg gat cca att act ctc gag att gtg gac agc tgc      864
Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
        275                 280                 285

ccg tgc agc gcg aac tcc aag tgg tgc tgt ggt ccg ggc gcc gat cat      912
Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
    290                 295                 300

tgc gga gag atc gac ttc aaa tac ggc tgt cct ctt cct gct gac agc      960
Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305                 310                 315                 320

att cat ctc gac ctg tca gac att gcc atg ggc cgt ttg cag ggc aat     1008
Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
                325                 330                 335

gga tca cta acc aat ggc gtc atc ccg act cga tat aga aga gtc caa     1056
Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
            340                 345                 350

tgc ccc aaa gtt ggg aac gcc tac att tgg ctt cga aat ggc gga ggg     1104
Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
        355                 360                 365

cct tac tat ttt gct ctc acg gca gtc aac acc aac gga ccg ggc tca     1152
Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
    370                 375                 380

gtc acc aaa atc gag atc aag ggc gca gac acc gac aac tgg gtt gcc     1200
```

```
Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385                 390                 395                 400

ttg gtc cat gac cca aac tat acg agt agc cgc cca caa gaa cgc tat    1248
Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
                405                 410                 415

ggc agt tgg gta atc cca cag gga tca ggg ccc ttt aac ttg cct gtt    1296
Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
            420                 425                 430

gga att cgt ctg act agc cca acg ggg gaa cag att gtg aat gaa cag    1344
Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
        435                 440                 445

gcc atc aag aca ttc act cct ccg gcc aca ggt gac ccc aat ttt tac    1392
Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
    450                 455                 460

tac att gac att ggt gtg cag ttt agc cag aat ggc tcg act tac tcc    1440
Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gly Ser Thr Tyr Ser
465                 470                 475                 480

agt gga tct tct tcg ggg tcg ggg tct agc tcc agc tcg agt tcg act    1488
Ser Gly Ser Ser Ser Gly Ser Gly Ser Ser Ser Ser Ser Ser Ser Thr
                485                 490                 495

acc act aag gcc act tcg acg acc ttg aag act acc tcg acc acc agc    1536
Thr Thr Lys Ala Thr Ser Thr Thr Leu Lys Thr Thr Ser Thr Thr Ser
            500                 505                 510

agt gga agc agt tcg aca tcg gcg gcg gcc tcc acg caa ggc atc tcc    1584
Ser Gly Ser Ser Ser Thr Ser Ala Ala Ala Ser Thr Gln Gly Ile Ser
        515                 520                 525

gaa gac ctc tac aat cgc ttg gta gag atg gcc act atc tcc caa gcc    1632
Glu Asp Leu Tyr Asn Arg Leu Val Glu Met Ala Thr Ile Ser Gln Ala
    530                 535                 540

gcc tac gcc gac cta tgc aat att cca tcg act att atc aaa gga gag    1680
Ala Tyr Ala Asp Leu Cys Asn Ile Pro Ser Thr Ile Ile Lys Gly Glu
545                 550                 555                 560

aaa att tac aac gct caa act gat atc aac gga tgg atc ctc cgc gac    1728
Lys Ile Tyr Asn Ala Gln Thr Asp Ile Asn Gly Trp Ile Leu Arg Asp
                565                 570                 575

gac acc agc aaa gaa att atc acc gtc ttc cgt ggc act ggc agt gac    1776
Asp Thr Ser Lys Glu Ile Ile Thr Val Phe Arg Gly Thr Gly Ser Asp
            580                 585                 590

aca aac cta cag ctc gat act aac tac acg ctc acg cca ttc gac act    1824
Thr Asn Leu Gln Leu Asp Thr Asn Tyr Thr Leu Thr Pro Phe Asp Thr
        595                 600                 605

cta cct caa tgc aac gat tgc gag gta cac ggt gga tac tat att gga    1872
Leu Pro Gln Cys Asn Asp Cys Glu Val His Gly Gly Tyr Tyr Ile Gly
    610                 615                 620

tgg atc tca gtc caa gac caa gtc gag tcg ctt gtc aaa caa cag gct    1920
Trp Ile Ser Val Gln Asp Gln Val Glu Ser Leu Val Lys Gln Gln Ala
```

```
625                 630                 635                 640

agc cag tat ccg gac tat gcg ctt acc gtg aca ggc cat agt ctg gga   1968
Ser Gln Tyr Pro Asp Tyr Ala Leu Thr Val Thr Gly His Ser Leu Gly
                645                 650                 655

gcg tcg atg gca gca ctc act gcc gcc cag ctg tcc gcg aca tac gac   2016
Ala Ser Met Ala Ala Leu Thr Ala Ala Gln Leu Ser Ala Thr Tyr Asp
            660                 665                 670

aac gtc cgt ctg tac aca ttc ggc gaa ccg cgc agc ggc aac cag gcc   2064
Asn Val Arg Leu Tyr Thr Phe Gly Glu Pro Arg Ser Gly Asn Gln Ala
        675                 680                 685

ttc gcg tcg tac atg aac gat gcg ttc cag gtc tcg agc ccg gag acg   2112
Phe Ala Ser Tyr Met Asn Asp Ala Phe Gln Val Ser Ser Pro Glu Thr
    690                 695                 700

acc cag tac ttc cgg gtc act cat tcc aac gac ggc atc cca aac ttg   2160
Thr Gln Tyr Phe Arg Val Thr His Ser Asn Asp Gly Ile Pro Asn Leu
705                 710                 715                 720

ccc ccg gcg gac gag ggt tac gcc cat ggt ggt gta gag tac tgg agc   2208
Pro Pro Ala Asp Glu Gly Tyr Ala His Gly Gly Val Glu Tyr Trp Ser
                725                 730                 735

gtt gat cct tac agc gcc cag aac acg ttt gtc tgt act ggg gat gaa   2256
Val Asp Pro Tyr Ser Ala Gln Asn Thr Phe Val Cys Thr Gly Asp Glu
            740                 745                 750

gta cag tgc tgt gag gca cag ggc gga cag ggg gtg aat gat gcg cat   2304
Val Gln Cys Cys Glu Ala Gln Gly Gly Gln Gly Val Asn Asp Ala His
        755                 760                 765

act act tat ttt ggg atg acg agc gga gct tgt act tgg               2343
Thr Thr Tyr Phe Gly Met Thr Ser Gly Ala Cys Thr Trp
    770                 775                 780
```

<210> 32
<211> 781
<212> PRT
<213> Seqüência artificial

<220>
<223> Construção Sintética

<400> 32

```
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1               5                   10                  15

Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
            20                  25                  30

Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
        35                  40                  45
```

Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
50 55 60

Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65 70 75 80

Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
85 90 95

Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
100 105 110

Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
115 120 125

Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
130 135 140

Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145 150 155 160

Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
165 170 175

Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
180 185 190

Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
195 200 205

Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
210 215 220

Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225 230 235 240

Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
245 250 255

Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
260 265 270

Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
275 280 285

Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His

290 295 300

Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305 310 315 320

Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
325 330 335

Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
340 345 350

Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
355 360 365

Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
370 375 380

Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385 390 395 400

Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
405 410 415

Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
420 425 430

Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
435 440 445

Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
450 455 460

Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gly Ser Thr Tyr Ser
465 470 475 480

Ser Gly Ser Ser Ser Gly Ser Gly Ser Ser Ser Ser Ser Ser Ser Thr
485 490 495

Thr Thr Lys Ala Thr Ser Thr Thr Leu Lys Thr Thr Ser Thr Thr Ser
500 505 510

Ser Gly Ser Ser Ser Thr Ser Ala Ala Ala Ser Thr Gln Gly Ile Ser
515 520 525

Glu Asp Leu Tyr Asn Arg Leu Val Glu Met Ala Thr Ile Ser Gln Ala
530 535 540

Ala Tyr Ala Asp Leu Cys Asn Ile Pro Ser Thr Ile Ile Lys Gly Glu
545 550 555 560

Lys Ile Tyr Asn Ala Gln Thr Asp Ile Asn Gly Trp Ile Leu Arg Asp
565 570 575

Asp Thr Ser Lys Glu Ile Ile Thr Val Phe Arg Gly Thr Gly Ser Asp
580 585 590

Thr Asn Leu Gln Leu Asp Thr Asn Tyr Thr Leu Thr Pro Phe Asp Thr
595 600 605

Leu Pro Gln Cys Asn Asp Cys Glu Val His Gly Gly Tyr Tyr Ile Gly
610 615 620

Trp Ile Ser Val Gln Asp Gln Val Glu Ser Leu Val Lys Gln Gln Ala
625 630 635 640

Ser Gln Tyr Pro Asp Tyr Ala Leu Thr Val Thr Gly His Ser Leu Gly
645 650 655

Ala Ser Met Ala Ala Leu Thr Ala Ala Gln Leu Ser Ala Thr Tyr Asp
660 665 670

Asn Val Arg Leu Tyr Thr Phe Gly Glu Pro Arg Ser Gly Asn Gln Ala
675 680 685

Phe Ala Ser Tyr Met Asn Asp Ala Phe Gln Val Ser Ser Pro Glu Thr
690 695 700

Thr Gln Tyr Phe Arg Val Thr His Ser Asn Asp Gly Ile Pro Asn Leu
705 710 715 720

Pro Pro Ala Asp Glu Gly Tyr Ala His Gly Gly Val Glu Tyr Trp Ser
725 730 735

Val Asp Pro Tyr Ser Ala Gln Asn Thr Phe Val Cys Thr Gly Asp Glu
740 745 750

Val Gln Cys Cys Glu Ala Gln Gly Gly Gln Gly Val Asn Asp Ala His
755 760 765

Thr Thr Tyr Phe Gly Met Thr Ser Gly Ala Cys Thr Trp
770 775 780

<210> 33
<211> 2937
<212> DNA
<213> Seqüência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2937)

<400> 33

```
cag cag aat tgc gca gca tta ttt ggc caa tgt gga ggc ata ggg tgg      48
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1               5                  10                  15

tcc ggc acc aca tgt tgc gtt gct ggc gcc cag tgc agt ttt gtc aat      96
Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
            20                  25                  30

gac tgg tac tcc cag tgc ctt gcg tca acc ggc gga aac ccc cca aac     144
Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
        35                  40                  45

gga aca act tcc tct agc ttg gtt tca cgg acg tcg tca gca tcc tca     192
Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
    50                  55                  60

tcc gtc ggc tcg tct tca ccc ggc ggc aac tca cca act ggc agt gct     240
Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65                  70                  75                  80

tcc acc tac aca acc aca gat aca gct acc gtg gct cct cat tcg cag     288
Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
                85                  90                  95

tct cct tac ccc agc att gcc gca tcc agt tgc gga tcg tgg acc ctc     336
Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
            100                 105                 110

gtg gat aat gtt tgc tgc cca tca tat tgt gct aat gat gac aca tcc     384
Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
        115                 120                 125

gag tca tgc tca ggc tgc ggt acc tgc act acg ccg ccc tcg gcg gac     432
Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
    130                 135                 140

tgc aaa tcc gga acc atg tat cca gag gtc cat cac gta tcc agc aac     480
Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145                 150                 155                 160

gag agc tgg cac tac agt aga tca acc cac ttt ggc cta acg agc ggc     528
Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
                165                 170                 175

ggg gcc tgt ggc ttt ggc ctg tac ggt ctc tgc aca aag ggc agt gtt     576
Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
```

```
                180                 185                 190

aca gcc agc tgg acg gat ccc atg ctt ggc gcg acg tgt gac gct ttt      624
Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
        195                 200                 205

tgt aca gcg tat ccc ctg ctt tgc aaa gac cct acc ggc act acc ctt      672
Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
    210                 215                 220

cgt ggc aac ttc gca gct cca aac ggc gat tac tac acc caa ttc tgg      720
Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225                 230                 235                 240

tcc tcg ttg cca gga gcc ctc gat aac tac ctg tcc tgc ggc gag tgc      768
Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
                245                 250                 255

att gag ctg ata caa aca aag ccc gat ggg acc gat tat gct gtc gga      816
Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
            260                 265                 270

gaa gcc ggc tac acg gat cca att act ctc gag att gtg gac agc tgc      864
Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
        275                 280                 285

ccg tgc agc gcg aac tcc aag tgg tgc tgt ggt ccg ggc gcc gat cat      912
Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
    290                 295                 300

tgc gga gag atc gac ttc aaa tac ggc tgt cct ctt cct gct gac agc      960
Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305                 310                 315                 320

att cat ctc gac ctg tca gac att gcc atg ggc cgt ttg cag ggc aat     1008
Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
                325                 330                 335

gga tca cta acc aat ggc gtc atc ccg act cga tat aga aga gtc caa     1056
Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
            340                 345                 350

tgc ccc aaa gtt ggg aac gcc tac att tgg ctt cga aat ggc gga ggg     1104
Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
        355                 360                 365

cct tac tat ttt gct ctc acg gca gtc aac acc aac gga ccg ggc tca     1152
Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
    370                 375                 380

gtc acc aaa atc gag atc aag ggc gca gac acc gac aac tgg gtt gcc     1200
Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385                 390                 395                 400

ttg gtc cat gac cca aac tat acg agt agc cgc cca caa gaa cgc tat     1248
Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
                405                 410                 415

ggc agt tgg gta atc cca cag gga tca ggg ccc ttt aac ttg cct gtt     1296
Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
            420                 425                 430
```

```
gga att cgt ctg act agc cca acg ggg gaa cag att gtg aat gaa cag     1344
Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
        435                 440                 445

gcc atc aag aca ttc act cct ccg gcc aca ggt gac ccc aat ttt tac     1392
Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
    450                 455                 460

tac att gac att ggt gtg cag ttt agc cag aat gcg acc gac ccc ttc     1440
Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Ala Thr Asp Pro Phe
465                 470                 475                 480

cag tcg cgg tgc aat gaa ttc cag aac aag atc gac atc gcc aat gtc     1488
Gln Ser Arg Cys Asn Glu Phe Gln Asn Lys Ile Asp Ile Ala Asn Val
                485                 490                 495

acc gtc aga tcg gtc gca tac gtt gct gct gga cag aac atc tcc caa     1536
Thr Val Arg Ser Val Ala Tyr Val Ala Ala Gly Gln Asn Ile Ser Gln
            500                 505                 510

gcg gag gtc gcc tcc gtg tgt aaa gca tcg gtt caa gcc agt gtc gac     1584
Ala Glu Val Ala Ser Val Cys Lys Ala Ser Val Gln Ala Ser Val Asp
        515                 520                 525

ctg tgc cgg gta acc atg aac atc tcg acg tcg gat cgc agc cat ctg     1632
Leu Cys Arg Val Thr Met Asn Ile Ser Thr Ser Asp Arg Ser His Leu
    530                 535                 540

tgg gct gag gcc tgg ctc cca aga aat tat acc ggt cgc ttc gtg agc     1680
Trp Ala Glu Ala Trp Leu Pro Arg Asn Tyr Thr Gly Arg Phe Val Ser
545                 550                 555                 560

acg ggg aat gga ggt cta gcc ggc tgt gtc caa gaa acg gac ctc aac     1728
Thr Gly Asn Gly Gly Leu Ala Gly Cys Val Gln Glu Thr Asp Leu Asn
                565                 570                 575

ttt gca gcc aac ttt ggt ttc gct acc gtg ggc acc aac ggt gga cat     1776
Phe Ala Ala Asn Phe Gly Phe Ala Thr Val Gly Thr Asn Gly Gly His
            580                 585                 590

gac ggg gac acg gcc aaa tac ttc ctc aac aac tcg gag gtt ctg gcc     1824
Asp Gly Asp Thr Ala Lys Tyr Phe Leu Asn Asn Ser Glu Val Leu Ala
        595                 600                 605

gat ttt gcc tat cgc tca gtg cac gaa ggg acc gtg gtg ggt aag caa     1872
Asp Phe Ala Tyr Arg Ser Val His Glu Gly Thr Val Val Gly Lys Gln
    610                 615                 620

cta act caa ttg ttt tat gac gag gga tac aac tac tcc tac tat ttg     1920
Leu Thr Gln Leu Phe Tyr Asp Glu Gly Tyr Asn Tyr Ser Tyr Tyr Leu
625                 630                 635                 640

ggt tgc tcc acc gga ggc cgc caa ggc tac cag caa gtc caa cgg ttt     1968
Gly Cys Ser Thr Gly Gly Arg Gln Gly Tyr Gln Gln Val Gln Arg Phe
                645                 650                 655

ccc gac gac tat gac gga gtg att gcg ggc tcc gca gcg atg aac ttt     2016
Pro Asp Asp Tyr Asp Gly Val Ile Ala Gly Ser Ala Ala Met Asn Phe
            660                 665                 670
```

```
atc aac ctg atc tcc tgg ggg gcc ttc ttg tgg aag gcg acg ggg tta   2064
Ile Asn Leu Ile Ser Trp Gly Ala Phe Leu Trp Lys Ala Thr Gly Leu
        675                 680                 685

gcg gat gat cca gac ttt atc tct gca aac ctg tgg tcc gta atc cac   2112
Ala Asp Asp Pro Asp Phe Ile Ser Ala Asn Leu Trp Ser Val Ile His
    690                 695                 700

cag gag att gtt cgt cag tgc gac ctg gtc gat ggg gct ctg gat gga   2160
Gln Glu Ile Val Arg Gln Cys Asp Leu Val Asp Gly Ala Leu Asp Gly
705                 710                 715                 720

atc atc gaa gac cct gat ttc tgt gct cca gtc atc gag cgc ttg atc   2208
Ile Ile Glu Asp Pro Asp Phe Cys Ala Pro Val Ile Glu Arg Leu Ile
                725                 730                 735

tgc gac ggg act acc aac ggc acc tct tgt atc acg gga gcc cag gca   2256
Cys Asp Gly Thr Thr Asn Gly Thr Ser Cys Ile Thr Gly Ala Gln Ala
            740                 745                 750

gca aag gtc aac cgg gcc ttg agt gac ttc tat ggc ccc gac ggg aca   2304
Ala Lys Val Asn Arg Ala Leu Ser Asp Phe Tyr Gly Pro Asp Gly Thr
        755                 760                 765

gtg tac tac ccg cgc ctg aac tat ggg ggt gag gcc gac tcg gct tcc   2352
Val Tyr Tyr Pro Arg Leu Asn Tyr Gly Gly Glu Ala Asp Ser Ala Ser
    770                 775                 780

ctg tac ttc acg ggg tcg atg tac agc cgt acg gag gaa tgg tac aaa   2400
Leu Tyr Phe Thr Gly Ser Met Tyr Ser Arg Thr Glu Glu Trp Tyr Lys
785                 790                 795                 800

tat gtg gtc tat aac gac acc aac tgg aac tcc agc cag tgg acg ctg   2448
Tyr Val Val Tyr Asn Asp Thr Asn Trp Asn Ser Ser Gln Trp Thr Leu
                805                 810                 815

gag agt gcc aag ctg gcc ctg gag cag aat ccg ttc aat atc cag gcg   2496
Glu Ser Ala Lys Leu Ala Leu Glu Gln Asn Pro Phe Asn Ile Gln Ala
            820                 825                 830

ttt gat ccc aac atc acg gcc ttc cgg gac cgg ggt ggc aag ctg ctg   2544
Phe Asp Pro Asn Ile Thr Ala Phe Arg Asp Arg Gly Gly Lys Leu Leu
        835                 840                 845

tcc tac cac ggc acg cag gat ccc att atc agc tcc acg gat agc aag   2592
Ser Tyr His Gly Thr Gln Asp Pro Ile Ile Ser Ser Thr Asp Ser Lys
    850                 855                 860

ctc tac tac cga cgg gta gcg aat gcc ctg aat gcc gcg ccg tcc gag   2640
Leu Tyr Tyr Arg Arg Val Ala Asn Ala Leu Asn Ala Ala Pro Ser Glu
865                 870                 875                 880

cta gat gag ttc tat cgg ttc ttc cag atc tcc ggc atg ggc cac tgt   2688
Leu Asp Glu Phe Tyr Arg Phe Phe Gln Ile Ser Gly Met Gly His Cys
                885                 890                 895

ggc gat ggc acg gga gca tcg tac atc ggc cag gga tat ggc acg tac   2736
Gly Asp Gly Thr Gly Ala Ser Tyr Ile Gly Gln Gly Tyr Gly Thr Tyr
            900                 905                 910

acc tcc aag gcg ccc caa gtc aac ctg ctg cgc acg atg gtg gac tgg   2784
```

```
Thr Ser Lys Ala Pro Gln Val Asn Leu Leu Arg Thr Met Val Asp Trp
        915                 920                 925

gtg gaa aac gga aag gcg ccc gag tat atg ccg ggc aac aag ctc aac     2832
Val Glu Asn Gly Lys Ala Pro Glu Tyr Met Pro Gly Asn Lys Leu Asn
    930                 935                 940

gcg aac ggg tca att gag tac atg cgc aag cac tgc cgg tat ccg aag     2880
Ala Asn Gly Ser Ile Glu Tyr Met Arg Lys His Cys Arg Tyr Pro Lys
945                 950                 955                 960

cat aac att cac acg ggg ccg ggt aac tac acc gat cct aac tcc tgg     2928
His Asn Ile His Thr Gly Pro Gly Asn Tyr Thr Asp Pro Asn Ser Trp
                965                 970                 975

act tgc gta                                                        2937
Thr Cys Val
```

<210> 34
<211> 979
<212> PRT
<213> Sequência artificial
<220>
<223> Construção Sintética

<400> 34

```
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1               5                   10                  15

Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
            20                  25                  30

Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
        35                  40                  45

Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
    50                  55                  60

Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65                  70                  75                  80

Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
                85                  90                  95

Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
            100                 105                 110

Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
        115                 120                 125
```

Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
130 135 140

Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145 150 155 160

Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
165 170 175

Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
180 185 190

Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
195 200 205

Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
210 215 220

Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225 230 235 240

Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
245 250 255

Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
260 265 270

Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
275 280 285

Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
290 295 300

Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305 310 315 320

Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
325 330 335

Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
340 345 350

Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
355 360 365

Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
370 375 380

Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385 390 395 400

Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
405 410 415

Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
420 425 430

Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
435 440 445

Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
450 455 460

Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Ala Thr Asp Pro Phe
465 470 475 480

Gln Ser Arg Cys Asn Glu Phe Gln Asn Lys Ile Asp Ile Ala Asn Val
485 490 495

Thr Val Arg Ser Val Ala Tyr Val Ala Ala Gly Gln Asn Ile Ser Gln
500 505 510

Ala Glu Val Ala Ser Val Cys Lys Ala Ser Val Gln Ala Ser Val Asp
515 520 525

Leu Cys Arg Val Thr Met Asn Ile Ser Thr Ser Asp Arg Ser His Leu
530 535 540

Trp Ala Glu Ala Trp Leu Pro Arg Asn Tyr Thr Gly Arg Phe Val Ser
545 550 555 560

Thr Gly Asn Gly Gly Leu Ala Gly Cys Val Gln Glu Thr Asp Leu Asn
565 570 575

Phe Ala Ala Asn Phe Gly Phe Ala Thr Val Gly Thr Asn Gly Gly His
580 585 590

Asp Gly Asp Thr Ala Lys Tyr Phe Leu Asn Asn Ser Glu Val Leu Ala
595 600 605

Asp Phe Ala Tyr Arg Ser Val His Glu Gly Thr Val Val Gly Lys Gln

610 615 620

Leu Thr Gln Leu Phe Tyr Asp Glu Gly Tyr Asn Tyr Ser Tyr Tyr Leu
625 630 635 640

Gly Cys Ser Thr Gly Gly Arg Gln Gly Tyr Gln Gln Val Gln Arg Phe
645 650 655

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

Ile Asn Leu Ile Ser Trp Gly Ala Phe Leu Trp Lys Ala Thr Gly Leu
675 680 685

Ala Asp Asp Pro Asp Phe Ile Ser Ala Asn Leu Trp Ser Val Ile His
690 695 700

Gln Glu Ile Val Arg Gln Cys Asp Leu Val Asp Gly Ala Leu Asp Gly
705 710 715 720

Ile Ile Glu Asp Pro Asp Phe Cys Ala Pro Val Ile Glu Arg Leu Ile
725 730 735

Cys Asp Gly Thr Thr Asn Gly Thr Ser Cys Ile Thr Gly Ala Gln Ala
740 745 750

Ala Lys Val Asn Arg Ala Leu Ser Asp Phe Tyr Gly Pro Asp Gly Thr
755 760 765

Val Tyr Tyr Pro Arg Leu Asn Tyr Gly Gly Glu Ala Asp Ser Ala Ser
770 775 780

Leu Tyr Phe Thr Gly Ser Met Tyr Ser Arg Thr Glu Glu Trp Tyr Lys
785 790 795 800

Tyr Val Val Tyr Asn Asp Thr Asn Trp Asn Ser Ser Gln Trp Thr Leu
805 810 815

Glu Ser Ala Lys Leu Ala Leu Glu Gln Asn Pro Phe Asn Ile Gln Ala
820 825 830

Phe Asp Pro Asn Ile Thr Ala Phe Arg Asp Arg Gly Gly Lys Leu Leu
835 840 845

Ser Tyr His Gly Thr Gln Asp Pro Ile Ile Ser Ser Thr Asp Ser Lys
850 855 860

Leu Tyr Tyr Arg Arg Val Ala Asn Ala Leu Asn Ala Ala Pro Ser Glu
865 870 875 880

Leu Asp Glu Phe Tyr Arg Phe Phe Gln Ile Ser Gly Met Gly His Cys
885 890 895

Gly Asp Gly Thr Gly Ala Ser Tyr Ile Gly Gln Gly Tyr Gly Thr Tyr
900 905 910

Thr Ser Lys Ala Pro Gln Val Asn Leu Leu Arg Thr Met Val Asp Trp
915 920 925

Val Glu Asn Gly Lys Ala Pro Glu Tyr Met Pro Gly Asn Lys Leu Asn
930 935 940

Ala Asn Gly Ser Ile Glu Tyr Met Arg Lys His Cys Arg Tyr Pro Lys
945 950 955 960

His Asn Ile His Thr Gly Pro Gly Asn Tyr Thr Asp Pro Asn Ser Trp
965 970 975

Thr Cys Val

<210> 35
<211> 3075
<212> DNA
<213> Seqüência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(3075)

<400> 35
cag cag aat tgc gca gca tta ttt ggc caa tgt gga ggc ata ggg tgg 48
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1 5 10 15

tcc ggc acc aca tgt tgc gtt gct ggc gcc cag tgc agt ttt gtc aat 96
Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
20 25 30

gac tgg tac tcc cag tgc ctt gcg tca acc ggc gga aac ccc cca aac 144
Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
35 40 45

gga aca act tcc tct agc ttg gtt tca cgg acg tcg tca gca tcc tca 192

```
Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
    50                  55                  60

tcc gtc ggc tcg tct tca ccc ggc ggc aac tca cca act ggc agt gct      240
Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65                  70                  75                  80

tcc acc tac aca acc aca gat aca gct acc gtg gct cct cat tcg cag      288
Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
                85                  90                  95

tct cct tac ccc agc att gcc gca tcc agt tgc gga tcg tgg acc ctc      336
Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
            100                 105                 110

gtg gat aat gtt tgc tgc cca tca tat tgt gct aat gat gac aca tcc      384
Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
        115                 120                 125

gag tca tgc tca ggc tgc ggt acc tgc act acg ccg ccc tcg gcg gac      432
Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
    130                 135                 140

tgc aaa tcc gga acc atg tat cca gag gtc cat cac gta tcc agc aac      480
Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145                 150                 155                 160

gag agc tgg cac tac agt aga tca acc cac ttt ggc cta acg agc ggc      528
Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
                165                 170                 175

ggg gcc tgt ggc ttt ggc ctg tac ggt ctc tgc aca aag ggc agt gtt      576
Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
            180                 185                 190

aca gcc agc tgg acg gat ccc atg ctt ggc gcg acg tgt gac gct ttt      624
Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
        195                 200                 205

tgt aca gcg tat ccc ctg ctt tgc aaa gac cct acc ggc act acc ctt      672
Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
    210                 215                 220

cgt ggc aac ttc gca gct cca aac ggc gat tac tac acc caa ttc tgg      720
Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225                 230                 235                 240

tcc tcg ttg cca gga gcc ctc gat aac tac ctg tcc tgc ggc gag tgc      768
Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
                245                 250                 255

att gag ctg ata caa aca aag ccc gat ggg acc gat tat gct gtc gga      816
Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
            260                 265                 270

gaa gcc ggc tac acg gat cca att act ctc gag att gtg gac agc tgc      864
Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
        275                 280                 285

ccg tgc agc gcg aac tcc aag tgg tgc tgt ggt ccg ggc gcc gat cat      912
Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
```

```
    290                 295                 300

tgc gga gag atc gac ttc aaa tac ggc tgt cct ctt cct gct gac agc      960
Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305                 310                 315                 320

att cat ctc gac ctg tca gac att gcc atg ggc cgt ttg cag ggc aat     1008
Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
                325                 330                 335

gga tca cta acc aat ggc gtc atc ccg act cga tat aga aga gtc caa     1056
Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
            340                 345                 350

tgc ccc aaa gtt ggg aac gcc tac att tgg ctt cga aat ggc gga ggg     1104
Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
        355                 360                 365

cct tac tat ttt gct ctc acg gca gtc aac acc aac gga ccg ggc tca     1152
Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
    370                 375                 380

gtc acc aaa atc gag atc aag ggc gca gac acc gac aac tgg gtt gcc     1200
Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385                 390                 395                 400

ttg gtc cat gac cca aac tat acg agt agc cgc cca caa gaa cgc tat     1248
Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
                405                 410                 415

ggc agt tgg gta atc cca cag gga tca ggg ccc ttt aac ttg cct gtt     1296
Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
            420                 425                 430

gga att cgt ctg act agc cca acg ggg gaa cag att gtg aat gaa cag     1344
Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
        435                 440                 445

gcc atc aag aca ttc act cct ccg gcc aca ggt gac ccc aat ttt tac     1392
Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
    450                 455                 460

tac att gac att ggt gtg cag ttt agc cag aat ggc tcg act tac tcc     1440
Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gly Ser Thr Tyr Ser
465                 470                 475                 480

agt gga tct tct tcg ggg tcg ggg tct agc tcc agc tcg agt tcg act     1488
Ser Gly Ser Ser Ser Gly Ser Gly Ser Ser Ser Ser Ser Ser Ser Thr
                485                 490                 495

acc act aag gcc act tcg acg acc ttg aag act acc tcg acc acc agc     1536
Thr Thr Lys Ala Thr Ser Thr Thr Leu Lys Thr Thr Ser Thr Thr Ser
            500                 505                 510

agt gga agc agt tcg aca tcg gcg gcg gcg acc gac ccc ttc cag tcg     1584
Ser Gly Ser Ser Ser Thr Ser Ala Ala Ala Thr Asp Pro Phe Gln Ser
        515                 520                 525

cgg tgc aat gaa ttc cag aac aag atc gac atc gcc aat gtc acc gtc     1632
Arg Cys Asn Glu Phe Gln Asn Lys Ile Asp Ile Ala Asn Val Thr Val
    530                 535                 540
```

```
aga tcg gtc gca tac gtt gct gct gga cag aac atc tcc caa gcg gag    1680
Arg Ser Val Ala Tyr Val Ala Ala Gly Gln Asn Ile Ser Gln Ala Glu
545                 550                 555                 560

gtc gcc tcc gtg tgt aaa gca tcg gtt caa gcc agt gtc gac ctg tgc    1728
Val Ala Ser Val Cys Lys Ala Ser Val Gln Ala Ser Val Asp Leu Cys
                565                 570                 575

cgg gta acc atg aac atc tcg acg tcg gat cgc agc cat ctg tgg gct    1776
Arg Val Thr Met Asn Ile Ser Thr Ser Asp Arg Ser His Leu Trp Ala
            580                 585                 590

gag gcc tgg ctc cca aga aat tat acc ggt cgc ttc gtg agc acg ggg    1824
Glu Ala Trp Leu Pro Arg Asn Tyr Thr Gly Arg Phe Val Ser Thr Gly
        595                 600                 605

aat gga ggt cta gcc ggc tgt gtc caa gaa acg gac ctc aac ttt gca    1872
Asn Gly Gly Leu Ala Gly Cys Val Gln Glu Thr Asp Leu Asn Phe Ala
    610                 615                 620

gcc aac ttt ggt ttc gct acc gtg ggc acc aac ggt gga cat gac ggg    1920
Ala Asn Phe Gly Phe Ala Thr Val Gly Thr Asn Gly Gly His Asp Gly
625                 630                 635                 640

gac acg gcc aaa tac ttc ctc aac aac tcg gag gtt ctg gcc gat ttt    1968
Asp Thr Ala Lys Tyr Phe Leu Asn Asn Ser Glu Val Leu Ala Asp Phe
                645                 650                 655

gcc tat cgc tca gtg cac gaa ggg acc gtg gtg ggt aag caa cta act    2016
Ala Tyr Arg Ser Val His Glu Gly Thr Val Val Gly Lys Gln Leu Thr
            660                 665                 670

caa ttg ttt tat gac gag gga tac aac tac tcc tac tat ttg ggt tgc    2064
Gln Leu Phe Tyr Asp Glu Gly Tyr Asn Tyr Ser Tyr Tyr Leu Gly Cys
        675                 680                 685

tcc acc gga ggc cgc caa ggc tac cag caa gtc caa cgg ttt ccc gac    2112
Ser Thr Gly Gly Arg Gln Gly Tyr Gln Gln Val Gln Arg Phe Pro Asp
    690                 695                 700

gac tat gac gga gtg att gcg ggc tcc gca gcg atg aac ttt atc aac    2160
Asp Tyr Asp Gly Val Ile Ala Gly Ser Ala Ala Met Asn Phe Ile Asn
705                 710                 715                 720

ctg atc tcc tgg ggg gcc ttc ttg tgg aag gcg acg ggg tta gcg gat    2208
Leu Ile Ser Trp Gly Ala Phe Leu Trp Lys Ala Thr Gly Leu Ala Asp
                725                 730                 735

gat cca gac ttt atc tct gca aac ctg tgg tcc gta atc cac cag gag    2256
Asp Pro Asp Phe Ile Ser Ala Asn Leu Trp Ser Val Ile His Gln Glu
            740                 745                 750

att gtt cgt cag tgc gac ctg gtc gat ggg gct ctg gat gga atc atc    2304
Ile Val Arg Gln Cys Asp Leu Val Asp Gly Ala Leu Asp Gly Ile Ile
        755                 760                 765

gaa gac cct gat ttc tgt gct cca gtc atc gag cgc ttg atc tgc gac    2352
Glu Asp Pro Asp Phe Cys Ala Pro Val Ile Glu Arg Leu Ile Cys Asp
    770                 775                 780
```

```
ggg act acc aac ggc acc tct tgt atc acg gga gcc cag gca gca aag      2400
Gly Thr Thr Asn Gly Thr Ser Cys Ile Thr Gly Ala Gln Ala Ala Lys
785                 790                 795                 800

gtc aac cgg gcc ttg agt gac ttc tat ggc ccc gac ggg aca gtg tac      2448
Val Asn Arg Ala Leu Ser Asp Phe Tyr Gly Pro Asp Gly Thr Val Tyr
                805                 810                 815

tac ccg cgc ctg aac tat ggg ggt gag gcc gac tcg gct tcc ctg tac      2496
Tyr Pro Arg Leu Asn Tyr Gly Gly Glu Ala Asp Ser Ala Ser Leu Tyr
            820                 825                 830

ttc acg ggg tcg atg tac agc cgt acg gag gaa tgg tac aaa tat gtg      2544
Phe Thr Gly Ser Met Tyr Ser Arg Thr Glu Glu Trp Tyr Lys Tyr Val
        835                 840                 845

gtc tat aac gac acc aac tgg aac tcc agc cag tgg acg ctg gag agt      2592
Val Tyr Asn Asp Thr Asn Trp Asn Ser Ser Gln Trp Thr Leu Glu Ser
    850                 855                 860

gcc aag ctg gcc ctg gag cag aat ccg ttc aat atc cag gcg ttt gat      2640
Ala Lys Leu Ala Leu Glu Gln Asn Pro Phe Asn Ile Gln Ala Phe Asp
865                 870                 875                 880

ccc aac atc acg gcc ttc cgg gac cgg ggt ggc aag ctg ctg tcc tac      2688
Pro Asn Ile Thr Ala Phe Arg Asp Arg Gly Gly Lys Leu Leu Ser Tyr
                885                 890                 895

cac ggc acg cag gat ccc att atc agc tcc acg gat agc aag ctc tac      2736
His Gly Thr Gln Asp Pro Ile Ile Ser Ser Thr Asp Ser Lys Leu Tyr
            900                 905                 910

tac cga cgg gta gcg aat gcc ctg aat gcc gcg ccg tcc gag cta gat      2784
Tyr Arg Arg Val Ala Asn Ala Leu Asn Ala Ala Pro Ser Glu Leu Asp
        915                 920                 925

gag ttc tat cgg ttc ttc cag atc tcc ggc atg ggc cac tgt ggc gat      2832
Glu Phe Tyr Arg Phe Phe Gln Ile Ser Gly Met Gly His Cys Gly Asp
    930                 935                 940

ggc acg gga gca tcg tac atc ggc cag gga tat ggc acg tac acc tcc      2880
Gly Thr Gly Ala Ser Tyr Ile Gly Gln Gly Tyr Gly Thr Tyr Thr Ser
945                 950                 955                 960

aag gcg ccc caa gtc aac ctg ctg cgc acg atg gtg gac tgg gtg gaa      2928
Lys Ala Pro Gln Val Asn Leu Leu Arg Thr Met Val Asp Trp Val Glu
                965                 970                 975

aac gga aag gcg ccc gag tat atg ccg ggc aac aag ctc aac gcg aac      2976
Asn Gly Lys Ala Pro Glu Tyr Met Pro Gly Asn Lys Leu Asn Ala Asn
            980                 985                 990

ggg tca att gag tac atg cgc aag  cac tgc cgg tat ccg  aag cat aac    3024
Gly Ser Ile Glu Tyr Met Arg Lys  His Cys Arg Tyr Pro  Lys His Asn
        995                 1000                1005

att cac  acg ggg ccg ggt aac  tac acc gat cct aac  tcc tgg act       3069
Ile His  Thr Gly Pro Gly Asn  Tyr Thr Asp Pro Asn  Ser Trp Thr
    1010                1015                1020

tgc gta                                                             3075
```

Cys Val
1025

<210> 36
<211> 1025
<212> PRT
<213> Seqüência artificial

<220>
<223> Construção Sintética

<400> 36

Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1 5 10 15

Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
20 25 30

Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
35 40 45

Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
50 55 60

Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65 70 75 80

Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
85 90 95

Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
100 105 110

Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
115 120 125

Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
130 135 140

Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145 150 155 160

Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
165 170 175

Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
180 185 190

Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
195 200 205

Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
210 215 220

Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225 230 235 240

Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
245 250 255

Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
260 265 270

Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
275 280 285

Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
290 295 300

Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305 310 315 320

Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
325 330 335

Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
340 345 350

Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
355 360 365

Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
370 375 380

Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385 390 395 400

Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
405 410 415

Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
420 425 430

Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
435 440 445

Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
450 455 460

Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gly Ser Thr Tyr Ser
465 470 475 480

Ser Gly Ser Ser Ser Gly Ser Gly Ser Ser Ser Ser Ser Ser Ser Thr
485 490 495

Thr Thr Lys Ala Thr Ser Thr Thr Leu Lys Thr Thr Ser Thr Thr Ser
500 505 510

Ser Gly Ser Ser Ser Thr Ser Ala Ala Ala Thr Asp Pro Phe Gln Ser
515 520 525

Arg Cys Asn Glu Phe Gln Asn Lys Ile Asp Ile Ala Asn Val Thr Val
530 535 540

Arg Ser Val Ala Tyr Val Ala Ala Gly Gln Asn Ile Ser Gln Ala Glu
545 550 555 560

Val Ala Ser Val Cys Lys Ala Ser Val Gln Ala Ser Val Asp Leu Cys
565 570 575

Arg Val Thr Met Asn Ile Ser Thr Ser Asp Arg Ser His Leu Trp Ala
580 585 590

Glu Ala Trp Leu Pro Arg Asn Tyr Thr Gly Arg Phe Val Ser Thr Gly
595 600 605

Asn Gly Gly Leu Ala Gly Cys Val Gln Glu Thr Asp Leu Asn Phe Ala
610 615 620

Ala Asn Phe Gly Phe Ala Thr Val Gly Thr Asn Gly Gly His Asp Gly
625 630 635 640

Asp Thr Ala Lys Tyr Phe Leu Asn Asn Ser Glu Val Leu Ala Asp Phe
645 650 655

Ala Tyr Arg Ser Val His Glu Gly Thr Val Val Gly Lys Gln Leu Thr
660 665 670

Gln Leu Phe Tyr Asp Glu Gly Tyr Asn Tyr Ser Tyr Tyr Leu Gly Cys

675 680 685

Ser Thr Gly Gly Arg Gln Gly Tyr Gln Gln Val Gln Arg Phe Pro Asp
690 695 700

Asp Tyr Asp Gly Val Ile Ala Gly Ser Ala Ala Met Asn Phe Ile Asn
705 710 715 720

Leu Ile Ser Trp Gly Ala Phe Leu Trp Lys Ala Thr Gly Leu Ala Asp
725 730 735

Asp Pro Asp Phe Ile Ser Ala Asn Leu Trp Ser Val Ile His Gln Glu
740 745 750

Ile Val Arg Gln Cys Asp Leu Val Asp Gly Ala Leu Asp Gly Ile Ile
755 760 765

Glu Asp Pro Asp Phe Cys Ala Pro Val Ile Glu Arg Leu Ile Cys Asp
770 775 780

Gly Thr Thr Asn Gly Thr Ser Cys Ile Thr Gly Ala Gln Ala Ala Lys
785 790 795 800

Val Asn Arg Ala Leu Ser Asp Phe Tyr Gly Pro Asp Gly Thr Val Tyr
805 810 815

Tyr Pro Arg Leu Asn Tyr Gly Gly Glu Ala Asp Ser Ala Ser Leu Tyr
820 825 830

Phe Thr Gly Ser Met Tyr Ser Arg Thr Glu Glu Trp Tyr Lys Tyr Val
835 840 845

Val Tyr Asn Asp Thr Asn Trp Asn Ser Ser Gln Trp Thr Leu Glu Ser
850 855 860

Ala Lys Leu Ala Leu Glu Gln Asn Pro Phe Asn Ile Gln Ala Phe Asp
865 870 875 880

Pro Asn Ile Thr Ala Phe Arg Asp Arg Gly Gly Lys Leu Leu Ser Tyr
885 890 895

His Gly Thr Gln Asp Pro Ile Ile Ser Ser Thr Asp Ser Lys Leu Tyr
900 905 910

Tyr Arg Arg Val Ala Asn Ala Leu Asn Ala Ala Pro Ser Glu Leu Asp
915 920 925

Glu Phe Tyr Arg Phe Phe Gln Ile Ser Gly Met Gly His Cys Gly Asp
930 935 940

Gly Thr Gly Ala Ser Tyr Ile Gly Gln Gly Tyr Gly Thr Tyr Thr Ser
945 950 955 960

Lys Ala Pro Gln Val Asn Leu Leu Arg Thr Met Val Asp Trp Val Glu
965 970 975

Asn Gly Lys Ala Pro Glu Tyr Met Pro Gly Asn Lys Leu Asn Ala Asn
980 985 990

Gly Ser Ile Glu Tyr Met Arg Lys His Cys Arg Tyr Pro Lys His Asn
995 1000 1005

Ile His Thr Gly Pro Gly Asn Tyr Thr Asp Pro Asn Ser Trp Thr
1010 1015 1020

Cys Val
1025

<210> 37
<211> 1989
<212> DNA
<213> Sequência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(1989)

<400> 37
cag cag aat tgc gca gca tta ttt ggc caa tgt gga ggc ata ggg tgg 48
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1 5 10 15

tcc ggc acc aca tgt tgc gtt gct ggc gcc cag tgc agt ttt gtc aat 96
Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
20 25 30

gac tgg tac tcc cag tgc ctt gcg tca acc ggc gga aac ccc cca aac 144
Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
35 40 45

gga aca act tcc tct agc ttg gtt tca cgg acg tcg tca gca tcc tca 192
Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
50 55 60

tcc gtc ggc tcg tct tca ccc ggc ggc aac tca cca act ggc agt gct 240

```
Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65                  70                  75                  80

tcc acc tac aca acc aca gat aca gct acc gtg gct cct cat tcg cag      288
Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
                85                  90                  95

tct cct tac ccc agc att gcc gca tcc agt tgc gga tcg tgg acc ctc      336
Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
            100                 105                 110

gtg gat aat gtt tgc tgc cca tca tat tgt gct aat gat gac aca tcc      384
Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
        115                 120                 125

gag tca tgc tca ggc tgc ggt acc tgc act acg ccg ccc tcg gcg gac      432
Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
    130                 135                 140

tgc aaa tcc gga acc atg tat cca gag gtc cat cac gta tcc agc aac      480
Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145                 150                 155                 160

gag agc tgg cac tac agt aga tca acc cac ttt ggc cta acg agc ggc      528
Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
                165                 170                 175

ggg gcc tgt ggc ttt ggc ctg tac ggt ctc tgc aca aag ggc agt gtt      576
Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
            180                 185                 190

aca gcc agc tgg acg gat ccc atg ctt ggc gcg acg tgt gac gct ttt      624
Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
        195                 200                 205

tgt aca gcg tat ccc ctg ctt tgc aaa gac cct acc ggc act acc ctt      672
Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
    210                 215                 220

cgt ggc aac ttc gca gct cca aac ggc gat tac tac acc caa ttc tgg      720
Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225                 230                 235                 240

tcc tcg ttg cca gga gcc ctc gat aac tac ctg tcc tgc ggc gag tgc      768
Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
                245                 250                 255

att gag ctg ata caa aca aag ccc gat ggg acc gat tat gct gtc gga      816
Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
            260                 265                 270

gaa gcc ggc tac acg gat cca att act ctc gag att gtg gac agc tgc      864
Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
        275                 280                 285

ccg tgc agc gcg aac tcc aag tgg tgc tgt ggt ccg ggc gcc gat cat      912
Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
    290                 295                 300

tgc gga gag atc gac ttc aaa tac ggc tgt cct ctt cct gct gac agc      960
Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
```

```
305                 310                 315                 320

att cat ctc gac ctg tca gac att gcc atg ggc cgt ttg cag ggc aat     1008
Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
                325                 330                 335

gga tca cta acc aat ggc gtc atc ccg act cga tat aga aga gtc caa     1056
Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
            340                 345                 350

tgc ccc aaa gtt ggg aac gcc tac att tgg ctt cga aat ggc gga ggg     1104
Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
        355                 360                 365

cct tac tat ttt gct ctc acg gca gtc aac acc aac gga ccg ggc tca     1152
Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
    370                 375                 380

gtc acc aaa atc gag atc aag ggc gca gac acc gac aac tgg gtt gcc     1200
Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385                 390                 395                 400

ttg gtc cat gac cca aac tat acg agt agc cgc cca caa gaa cgc tat     1248
Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
                405                 410                 415

ggc agt tgg gta atc cca cag gga tca ggg ccc ttt aac ttg cct gtt     1296
Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
            420                 425                 430

gga att cgt ctg act agc cca acg ggg gaa cag att gtg aat gaa cag     1344
Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
        435                 440                 445

gcc atc aag aca ttc act cct ccg gcc aca ggt gac ccc aat ttt tac     1392
Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
    450                 455                 460

tac att gac att ggt gtg cag ttt agc cag aat tcg acc ccg agc tcg     1440
Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Ser Thr Pro Ser Ser
465                 470                 475                 480

acc ggc gag aac aac ggc ttc tac tac tcc ttc tgg acc gac ggc ggt     1488
Thr Gly Glu Asn Asn Gly Phe Tyr Tyr Ser Phe Trp Thr Asp Gly Gly
                485                 490                 495

gga gac gtg acc tac acc aac gga gat gct ggt gcc tac act gtt gag     1536
Gly Asp Val Thr Tyr Thr Asn Gly Asp Ala Gly Ala Tyr Thr Val Glu
            500                 505                 510

tgg tcc aac gtg ggc aac ttt gtc ggt gga aag ggc tgg aac ccc gga     1584
Trp Ser Asn Val Gly Asn Phe Val Gly Gly Lys Gly Trp Asn Pro Gly
        515                 520                 525

agt gcg cag gac atc acc tac agc ggc acc ttc acc cct agc ggc aac     1632
Ser Ala Gln Asp Ile Thr Tyr Ser Gly Thr Phe Thr Pro Ser Gly Asn
    530                 535                 540

ggc tac ctc tcc gtc tat ggc tgg acc act gac cct ctg atc gag tac     1680
Gly Tyr Leu Ser Val Tyr Gly Trp Thr Thr Asp Pro Leu Ile Glu Tyr
545                 550                 555                 560
```

```
tac atc gtc gag tct tac ggc gac tac aac ccc ggc agt gga ggc acg     1728
Tyr Ile Val Glu Ser Tyr Gly Asp Tyr Asn Pro Gly Ser Gly Gly Thr
                565                 570                 575

tac aag ggc acc gtc acc tcg gac gga tcc gtt tac gat atc tac acg     1776
Tyr Lys Gly Thr Val Thr Ser Asp Gly Ser Val Tyr Asp Ile Tyr Thr
            580                 585                 590

gct acc cgt acc aat gct gct tcc att cag gga acc gct acc ttc act     1824
Ala Thr Arg Thr Asn Ala Ala Ser Ile Gln Gly Thr Ala Thr Phe Thr
        595                 600                 605

cag tac tgg tcc gtt cgc cag aac aag aga gtt ggc gga acc gtt acc     1872
Gln Tyr Trp Ser Val Arg Gln Asn Lys Arg Val Gly Gly Thr Val Thr
    610                 615                 620

acc tcc aac cac ttc aat gct tgg gct aag ctg gga atg aac ctg ggt     1920
Thr Ser Asn His Phe Asn Ala Trp Ala Lys Leu Gly Met Asn Leu Gly
625                 630                 635                 640

act cac aac tac cag atc gtg gct acc gag ggt tac cag agc agt gga     1968
Thr His Asn Tyr Gln Ile Val Ala Thr Glu Gly Tyr Gln Ser Ser Gly
                645                 650                 655

tct tcg tcc atc act gtt cag                                        1989
Ser Ser Ser Ile Thr Val Gln
            660
```

<210> 38
<211> 663
<212> PRT
<213> Sequência artificial

<220>
<223> Construção Sintética

<400> 38

```
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1               5                   10                  15

Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
            20                  25                  30

Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
        35                  40                  45

Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
    50                  55                  60

Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65                  70                  75                  80

Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
```

85 90 95

Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
100 105 110

Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
115 120 125

Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
130 135 140

Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145 150 155 160

Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
165 170 175

Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
180 185 190

Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
195 200 205

Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
210 215 220

Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225 230 235 240

Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
245 250 255

Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
260 265 270

Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
275 280 285

Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
290 295 300

Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305 310 315 320

Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
325 330 335

Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
340 345 350

Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
355 360 365

Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
370 375 380

Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385 390 395 400

Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
405 410 415

Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
420 425 430

Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
435 440 445

Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
450 455 460

Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Ser Thr Pro Ser Ser
465 470 475 480

Thr Gly Glu Asn Asn Gly Phe Tyr Tyr Ser Phe Trp Thr Asp Gly Gly
485 490 495

Gly Asp Val Thr Tyr Thr Asn Gly Asp Ala Gly Ala Tyr Thr Val Glu
500 505 510

Trp Ser Asn Val Gly Asn Phe Val Gly Gly Lys Gly Trp Asn Pro Gly
515 520 525

Ser Ala Gln Asp Ile Thr Tyr Ser Gly Thr Phe Thr Pro Ser Gly Asn
530 535 540

Gly Tyr Leu Ser Val Tyr Gly Trp Thr Thr Asp Pro Leu Ile Glu Tyr
545 550 555 560

Tyr Ile Val Glu Ser Tyr Gly Asp Tyr Asn Pro Gly Ser Gly Gly Thr
565 570 575

Tyr Lys Gly Thr Val Thr Ser Asp Gly Ser Val Tyr Asp Ile Tyr Thr
580 585 590

Ala Thr Arg Thr Asn Ala Ala Ser Ile Gln Gly Thr Ala Thr Phe Thr
595 600 605

Gln Tyr Trp Ser Val Arg Gln Asn Lys Arg Val Gly Gly Thr Val Thr
610 615 620

Thr Ser Asn His Phe Asn Ala Trp Ala Lys Leu Gly Met Asn Leu Gly
625 630 635 640

Thr His Asn Tyr Gln Ile Val Ala Thr Glu Gly Tyr Gln Ser Ser Gly
645 650 655

Ser Ser Ser Ile Thr Val Gln
660

<210> 39
<211> 2127
<212> DNA
<213> Sequência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2127)

<400> 39
cag cag aat tgc gca gca tta ttt ggc caa tgt gga ggc ata ggg tgg 48
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1 5 10 15

tcc ggc acc aca tgt tgc gtt gct ggc gcc cag tgc agt ttt gtc aat 96
Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
20 25 30

gac tgg tac tcc cag tgc ctt gcg tca acc ggc gga aac ccc cca aac 144
Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
35 40 45

gga aca act tcc tct agc ttg gtt tca cgg acg tcg tca gca tcc tca 192
Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
50 55 60

tcc gtc ggc tcg tct tca ccc ggc ggc aac tca cca act ggc agt gct 240
Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65 70 75 80

tcc acc tac aca acc aca gat aca gct acc gtg gct cct cat tcg cag 288
Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln

```
                85                  90                  95

tct cct tac ccc agc att gcc gca tcc agt tgc gga tcg tgg acc ctc      336
Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
            100                 105                 110

gtg gat aat gtt tgc tgc cca tca tat tgt gct aat gat gac aca tcc      384
Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
        115                 120                 125

gag tca tgc tca ggc tgc ggt acc tgc act acg ccg ccc tcg gcg gac      432
Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
    130                 135                 140

tgc aaa tcc gga acc atg tat cca gag gtc cat cac gta tcc agc aac      480
Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145                 150                 155                 160

gag agc tgg cac tac agt aga tca acc cac ttt ggc cta acg agc ggc      528
Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
                165                 170                 175

ggg gcc tgt ggc ttt ggc ctg tac ggt ctc tgc aca aag ggc agt gtt      576
Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
            180                 185                 190

aca gcc agc tgg acg gat ccc atg ctt ggc gcg acg tgt gac gct ttt      624
Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
        195                 200                 205

tgt aca gcg tat ccc ctg ctt tgc aaa gac cct acc ggc act acc ctt      672
Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
    210                 215                 220

cgt ggc aac ttc gca gct cca aac ggc gat tac tac acc caa ttc tgg      720
Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225                 230                 235                 240

tcc tcg ttg cca gga gcc ctc gat aac tac ctg tcc tgc ggc gag tgc      768
Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
                245                 250                 255

att gag ctg ata caa aca aag ccc gat ggg acc gat tat gct gtc gga      816
Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
            260                 265                 270

gaa gcc ggc tac acg gat cca att act ctc gag att gtg gac agc tgc      864
Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
        275                 280                 285

ccg tgc agc gcg aac tcc aag tgg tgc tgt ggt ccg ggc gcc gat cat      912
Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
    290                 295                 300

tgc gga gag atc gac ttc aaa tac ggc tgt cct ctt cct gct gac agc      960
Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305                 310                 315                 320

att cat ctc gac ctg tca gac att gcc atg ggc cgt ttg cag ggc aat     1008
Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
                325                 330                 335
```

```
gga tca cta acc aat ggc gtc atc ccg act cga tat aga aga gtc caa      1056
Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
            340                 345                 350

tgc ccc aaa gtt ggg aac gcc tac att tgg ctt cga aat ggc gga ggg      1104
Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
        355                 360                 365

cct tac tat ttt gct ctc acg gca gtc aac acc aac gga ccg ggc tca      1152
Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
    370                 375                 380

gtc acc aaa atc gag atc aag ggc gca gac acc gac aac tgg gtt gcc      1200
Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385                 390                 395                 400

ttg gtc cat gac cca aac tat acg agt agc cgc cca caa gaa cgc tat      1248
Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
                405                 410                 415

ggc agt tgg gta atc cca cag gga tca ggg ccc ttt aac ttg cct gtt      1296
Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
            420                 425                 430

gga att cgt ctg act agc cca acg ggg gaa cag att gtg aat gaa cag      1344
Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
        435                 440                 445

gcc atc aag aca ttc act cct ccg gcc aca ggt gac ccc aat ttt tac      1392
Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
    450                 455                 460

tac att gac att ggt gtg cag ttt agc cag aat ggc tcg act tac tcc      1440
Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gly Ser Thr Tyr Ser
465                 470                 475                 480

agt gga tct tct tcg ggg tcg ggg tct agc tcc agc tcg agt tcg act      1488
Ser Gly Ser Ser Ser Gly Ser Gly Ser Ser Ser Ser Ser Ser Ser Thr
                485                 490                 495

acc act aag gcc act tcg acg acc ttg aag act acc tcg acc acc agc      1536
Thr Thr Lys Ala Thr Ser Thr Thr Leu Lys Thr Thr Ser Thr Thr Ser
            500                 505                 510

agt gga agc agt tcg aca tcg gcg gcg tcg acc ccg agc tcg acc ggc      1584
Ser Gly Ser Ser Ser Thr Ser Ala Ala Ser Thr Pro Ser Ser Thr Gly
        515                 520                 525

gag aac aac ggc ttc tac tac tcc ttc tgg acc gac ggc ggt gga gac      1632
Glu Asn Asn Gly Phe Tyr Tyr Ser Phe Trp Thr Asp Gly Gly Gly Asp
    530                 535                 540

gtg acc tac acc aac gga gat gct ggt gcc tac act gtt gag tgg tcc      1680
Val Thr Tyr Thr Asn Gly Asp Ala Gly Ala Tyr Thr Val Glu Trp Ser
545                 550                 555                 560

aac gtg ggc aac ttt gtc ggt gga aag ggc tgg aac ccc gga agt gcg      1728
Asn Val Gly Asn Phe Val Gly Gly Lys Gly Trp Asn Pro Gly Ser Ala
                565                 570                 575
```

```
cag gac atc acc tac agc ggc acc ttc acc cct agc ggc aac ggc tac    1776
Gln Asp Ile Thr Tyr Ser Gly Thr Phe Thr Pro Ser Gly Asn Gly Tyr
            580                 585                 590

ctc tcc gtc tat ggc tgg acc act gac cct ctg atc gag tac tac atc    1824
Leu Ser Val Tyr Gly Trp Thr Thr Asp Pro Leu Ile Glu Tyr Tyr Ile
        595                 600                 605

gtc gag tct tac ggc gac tac aac ccc ggc agt gga ggc acg tac aag    1872
Val Glu Ser Tyr Gly Asp Tyr Asn Pro Gly Ser Gly Gly Thr Tyr Lys
    610                 615                 620

ggc acc gtc acc tcg gac gga tcc gtt tac gat atc tac acg gct acc    1920
Gly Thr Val Thr Ser Asp Gly Ser Val Tyr Asp Ile Tyr Thr Ala Thr
625                 630                 635                 640

cgt acc aat gct gct tcc att cag gga acc gct acc ttc act cag tac    1968
Arg Thr Asn Ala Ala Ser Ile Gln Gly Thr Ala Thr Phe Thr Gln Tyr
                645                 650                 655

tgg tcc gtt cgc cag aac aag aga gtt ggc gga acc gtt acc acc tcc    2016
Trp Ser Val Arg Gln Asn Lys Arg Val Gly Gly Thr Val Thr Thr Ser
            660                 665                 670

aac cac ttc aat gct tgg gct aag ctg gga atg aac ctg ggt act cac    2064
Asn His Phe Asn Ala Trp Ala Lys Leu Gly Met Asn Leu Gly Thr His
        675                 680                 685

aac tac cag atc gtg gct acc gag ggt tac cag agc agt gga tct tcg    2112
Asn Tyr Gln Ile Val Ala Thr Glu Gly Tyr Gln Ser Ser Gly Ser Ser
    690                 695                 700

tcc atc act gtt cag                                             2127
Ser Ile Thr Val Gln
705
```

<210> 40
<211> 709
<212> PRT
<213> Sequência artificial

<220>
<223> Construção Sintética

<400> 40

```
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1               5                   10                  15

Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
            20                  25                  30

Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
        35                  40                  45

Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
    50                  55                  60
```

Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65 70 75 80

Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
85 90 95

Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
100 105 110

Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
115 120 125

Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
130 135 140

Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145 150 155 160

Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
165 170 175

Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
180 185 190

Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
195 200 205

Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
210 215 220

Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225 230 235 240

Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
245 250 255

Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
260 265 270

Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
275 280 285

Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
290 295 300

Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305 310 315 320

Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
325 330 335

Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
340 345 350

Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
355 360 365

Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
370 375 380

Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385 390 395 400

Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
405 410 415

Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
420 425 430

Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
435 440 445

Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
450 455 460

Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gly Ser Thr Tyr Ser
465 470 475 480

Ser Gly Ser Ser Ser Gly Ser Gly Ser Ser Ser Ser Ser Ser Ser Thr
485 490 495

Thr Thr Lys Ala Thr Ser Thr Thr Leu Lys Thr Thr Ser Thr Thr Ser
500 505 510

Ser Gly Ser Ser Ser Thr Ser Ala Ala Ser Thr Pro Ser Ser Thr Gly
515 520 525

Glu Asn Asn Gly Phe Tyr Tyr Ser Phe Trp Thr Asp Gly Gly Gly Asp
530 535 540

Val Thr Tyr Thr Asn Gly Asp Ala Gly Ala Tyr Thr Val Glu Trp Ser
545 550 555 560

Asn Val Gly Asn Phe Val Gly Gly Lys Gly Trp Asn Pro Gly Ser Ala
565 570 575

Gln Asp Ile Thr Tyr Ser Gly Thr Phe Thr Pro Ser Gly Asn Gly Tyr
580 585 590

Leu Ser Val Tyr Gly Trp Thr Thr Asp Pro Leu Ile Glu Tyr Tyr Ile
595 600 605

Val Glu Ser Tyr Gly Asp Tyr Asn Pro Gly Ser Gly Gly Thr Tyr Lys
610 615 620

Gly Thr Val Thr Ser Asp Gly Ser Val Tyr Asp Ile Tyr Thr Ala Thr
625 630 635 640

Arg Thr Asn Ala Ala Ser Ile Gln Gly Thr Ala Thr Phe Thr Gln Tyr
645 650 655

Trp Ser Val Arg Gln Asn Lys Arg Val Gly Gly Thr Val Thr Thr Ser
660 665 670

Asn His Phe Asn Ala Trp Ala Lys Leu Gly Met Asn Leu Gly Thr His
675 680 685

Asn Tyr Gln Ile Val Ala Thr Glu Gly Tyr Gln Ser Ser Gly Ser Ser
690 695 700

Ser Ile Thr Val Gln
705

<210> 41
<211> 2919
<212> DNA
<213> Seqüência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2919)

<400> 41
cag cag aat tgc gca gca tta ttt ggc caa tgt gga ggc ata ggg tgg 48
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1 5 10 15

```
tcc ggc acc aca tgt tgc gtt gct ggc gcc cag tgc agt ttt gtc aat      96
Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
            20                  25                  30

gac tgg tac tcc cag tgc ctt gcg tca acc ggc gga aac ccc cca aac     144
Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
        35                  40                  45

gga aca act tcc tct agc ttg gtt tca cgg acg tcg tca gca tcc tca     192
Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
    50                  55                  60

tcc gtc ggc tcg tct tca ccc ggc ggc aac tca cca act ggc agt gct     240
Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65                  70                  75                  80

tcc acc tac aca acc aca gat aca gct acc gtg gct cct cat tcg cag     288
Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
                85                  90                  95

tct cct tac ccc agc att gcc gca tcc agt tgc gga tcg tgg acc ctc     336
Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
            100                 105                 110

gtg gat aat gtt tgc tgc cca tca tat tgt gct aat gat gac aca tcc     384
Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
        115                 120                 125

gag tca tgc tca ggc tgc ggt acc tgc act acg ccg ccc tcg gcg gac     432
Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
    130                 135                 140

tgc aaa tcc gga acc atg tat cca gag gtc cat cac gta tcc agc aac     480
Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145                 150                 155                 160

gag agc tgg cac tac agt aga tca acc cac ttt ggc cta acg agc ggc     528
Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
                165                 170                 175

ggg gcc tgt ggc ttt ggc ctg tac ggt ctc tgc aca aag ggc agt gtt     576
Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
            180                 185                 190

aca gcc agc tgg acg gat ccc atg ctt ggc gcg acg tgt gac gct ttt     624
Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
        195                 200                 205

tgt aca gcg tat ccc ctg ctt tgc aaa gac cct acc ggc act acc ctt     672
Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
    210                 215                 220

cgt ggc aac ttc gca gct cca aac ggc gat tac tac acc caa ttc tgg     720
Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225                 230                 235                 240

tcc tcg ttg cca gga gcc ctc gat aac tac ctg tcc tgc ggc gag tgc     768
Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
                245                 250                 255
```

```
att gag ctg ata caa aca aag ccc gat ggg acc gat tat gct gtc gga      816
Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
            260                 265                 270

gaa gcc ggc tac acg gat cca att act ctc gag att gtg gac agc tgc      864
Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
        275                 280                 285

ccg tgc agc gcg aac tcc aag tgg tgc tgt ggt ccg ggc gcc gat cat      912
Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
    290                 295                 300

tgc gga gag atc gac ttc aaa tac ggc tgt cct ctt cct gct gac agc      960
Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305                 310                 315                 320

att cat ctc gac ctg tca gac att gcc atg ggc cgt ttg cag ggc aat     1008
Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
                325                 330                 335

gga tca cta acc aat ggc gtc atc ccg act cga tat aga aga gtc caa     1056
Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
            340                 345                 350

tgc ccc aaa gtt ggg aac gcc tac att tgg ctt cga aat ggc gga ggg     1104
Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
        355                 360                 365

cct tac tat ttt gct ctc acg gca gtc aac acc aac gga ccg ggc tca     1152
Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
    370                 375                 380

gtc acc aaa atc gag atc aag ggc gca gac acc gac aac tgg gtt gcc     1200
Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385                 390                 395                 400

ttg gtc cat gac cca aac tat acg agt agc cgc cca caa gaa cgc tat     1248
Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
                405                 410                 415

ggc agt tgg gta atc cca cag gga tca ggg ccc ttt aac ttg cct gtt     1296
Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
            420                 425                 430

gga att cgt ctg act agc cca acg ggg gaa cag att gtg aat gaa cag     1344
Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
        435                 440                 445

gcc atc aag aca ttc act cct ccg gcc aca ggt gac ccc aat ttt tac     1392
Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
    450                 455                 460

tac att gac att ggt gtg cag ttt agc cag aat cag tcg gcc tgc act     1440
Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gln Ser Ala Cys Thr
465                 470                 475                 480

ctc caa tcg gag act cac ccg cct ctg aca tgg cag aaa tgc tcg tct     1488
Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp Gln Lys Cys Ser Ser
                485                 490                 495

ggt ggc acg tgc act caa cag aca ggc tcc gtg gtc atc gac gcc aac     1536
```

```
Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val Val Ile Asp Ala Asn
            500                 505                 510

tgg cgc tgg act cac gct acg aac agc agc acg aac tgc tac gat ggc     1584
Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr Asn Cys Tyr Asp Gly
        515                 520                 525

aac act tgg agc tcg acc cta tgt cct gac aac gag acc tgc gcg aag     1632
Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn Glu Thr Cys Ala Lys
    530                 535                 540

aac tgc tgt ctg gac ggt gcc gcc tac gcg tcc acg tac gga gtt acc     1680
Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser Thr Tyr Gly Val Thr
545                 550                 555                 560

acg agc ggt aac agc ctc tcc att ggc ttt gtc acc cag tct gcg cag     1728
Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe Val Thr Gln Ser Ala Gln
                565                 570                 575

aag aac gtt ggc gct cgc ctt tac ctt atg gcg agc gac acg acc tac     1776
Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala Ser Asp Thr Thr Tyr
            580                 585                 590

cag gaa ttc acc ctg ctt ggc aac gag ttc tct ttc gat gtt gat gtt     1824
Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser Phe Asp Val Asp Val
        595                 600                 605

tcg cag ctg ccg tgc ggc ttg aac gga gct ctc tac ttc gtg tcc atg     1872
Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu Tyr Phe Val Ser Met
    610                 615                 620

gac gcg gat ggt ggc gtg agc aag tat ccc acc aac acc gct ggc gcc     1920
Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr Asn Thr Ala Gly Ala
625                 630                 635                 640

aag tac ggc acg ggg tac tgt gac agc cag tgt ccc cgc gat ctg aag     1968
Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys Pro Arg Asp Leu Lys
                645                 650                 655

ttc atc aat ggc cag gcc aac gtt gag ggc tgg gag ccg tca tcc aac     2016
Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp Glu Pro Ser Ser Asn
            660                 665                 670

aac gcg aac acg ggc att gga gga cac gga agc tgc tgc tct gag atg     2064
Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser Cys Cys Ser Glu Met
        675                 680                 685

gat atc tgg gag gcc aac tcc atc tcc gag gct ctt acc ccc cac cct     2112
Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala Leu Thr Pro His Pro
    690                 695                 700

tgc acg act gtc ggc cag gag atc tgc gag ggt gat ggg tgc ggc gga     2160
Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly Asp Gly Cys Gly Gly
705                 710                 715                 720

act tac tcc gat aac aga tat ggc ggc act tgc gat ccc gat ggc tgc     2208
Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr Cys Asp Pro Asp Gly Cys
                725                 730                 735

gac tgg aac cca tac cgc ctg ggc aac acc agc ttc tac ggc cct ggc     2256
Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser Phe Tyr Gly Pro Gly
```

```
                740                 745                 750

tca agc ttt acc ctc gat acc acc aag aaa ttg acc gtt gtc acc cag     2304
Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu Thr Val Val Thr Gln
        755                 760                 765

ttc gag acg tcg ggt gcc atc aac cga tac tat gtc cag aat ggc gtc     2352
Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr Val Gln Asn Gly Val
    770                 775                 780

act ttc cag cag ccc aac gcc gag ctt ggt agt tac tct ggc aac gag     2400
Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser Tyr Ser Gly Asn Glu
785                 790                 795                 800

ctc aac gat gat tac tgc aca gct gag gag gca gaa ttc ggc gga tcc     2448
Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu Ala Glu Phe Gly Gly Ser
                805                 810                 815

tct ttc tca gac aag ggc ggc ctg act cag ttc aag aag gct acc tct     2496
Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe Lys Lys Ala Thr Ser
            820                 825                 830

ggc ggc atg gtt ctg gtc atg agt ctg tgg gat gat tac tac gcc aac     2544
Gly Gly Met Val Leu Val Met Ser Leu Trp Asp Asp Tyr Tyr Ala Asn
        835                 840                 845

atg ctg tgg ctg gac tcc acc tac ccg aca aac gag acc tcc tcc aca     2592
Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr Asn Glu Thr Ser Ser Thr
    850                 855                 860

ccc ggt gcc gtg cgc gga agc tgc tcc acc agc tcc ggt gtc cct gct     2640
Pro Gly Ala Val Arg Gly Ser Cys Ser Thr Ser Ser Gly Val Pro Ala
865                 870                 875                 880

cag gtc gaa tct cag tct ccc aac gcc aag gtc acc ttc tcc aac atc     2688
Gln Val Glu Ser Gln Ser Pro Asn Ala Lys Val Thr Phe Ser Asn Ile
                885                 890                 895

aag ttc gga ccc att ggc agc acc ggc aac cct agc ggc ggc aac cct     2736
Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn Pro Ser Gly Gly Asn Pro
            900                 905                 910

ccc ggc gga aac ccg cct ggc acc acc acc acc cgc cgc cca gcc act     2784
Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr Thr Arg Arg Pro Ala Thr
        915                 920                 925

acc act gga agc tct ccc gga cct acc cag tct cac tac ggc cag tgc     2832
Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln Ser His Tyr Gly Gln Cys
    930                 935                 940

ggc ggt att ggc tac agc ggc ccc acg gtc tgc gcc agc ggc aca act     2880
Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val Cys Ala Ser Gly Thr Thr
945                 950                 955                 960

tgc cag gtc ctg aac cct tac tac tct cag tgc ctg taa                 2919
Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln Cys Leu
                965                 970
```

<210> 42
<211> 972

195

<212> PRT
<213> Seqüência artificial

<220>
<223> Construção Sintética

<400> 42

```
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1               5                  10                  15

Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
            20                  25                  30

Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
        35                  40                  45

Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
    50                  55                  60

Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65                  70                  75                  80

Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
                85                  90                  95

Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
            100                 105                 110

Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
        115                 120                 125

Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
    130                 135                 140

Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145                 150                 155                 160

Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
                165                 170                 175

Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
            180                 185                 190

Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
        195                 200                 205

Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
```

210 215 220

Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225 230 235 240

Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
245 250 255

Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
260 265 270

Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
275 280 285

Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
290 295 300

Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305 310 315 320

Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
325 330 335

Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
340 345 350

Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
355 360 365

Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
370 375 380

Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385 390 395 400

Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
405 410 415

Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
420 425 430

Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
435 440 445

Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
450 455 460

Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gln Ser Ala Cys Thr
465 470 475 480

Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp Gln Lys Cys Ser Ser
485 490 495

Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val Val Ile Asp Ala Asn
500 505 510

Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr Asn Cys Tyr Asp Gly
515 520 525

Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn Glu Thr Cys Ala Lys
530 535 540

Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser Thr Tyr Gly Val Thr
545 550 555 560

Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe Val Thr Gln Ser Ala Gln
565 570 575

Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala Ser Asp Thr Thr Tyr
580 585 590

Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser Phe Asp Val Asp Val
595 600 605

Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu Tyr Phe Val Ser Met
610 615 620

Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr Asn Thr Ala Gly Ala
625 630 635 640

Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys Pro Arg Asp Leu Lys
645 650 655

Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp Glu Pro Ser Ser Asn
660 665 670

Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser Cys Cys Ser Glu Met
675 680 685

Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala Leu Thr Pro His Pro
690 695 700

```
Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly Asp Gly Cys Gly Gly
705                 710                 715                 720

Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr Cys Asp Pro Asp Gly Cys
                725                 730                 735

Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser Phe Tyr Gly Pro Gly
            740                 745                 750

Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu Thr Val Val Thr Gln
        755                 760                 765

Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr Val Gln Asn Gly Val
    770                 775                 780

Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser Tyr Ser Gly Asn Glu
785                 790                 795                 800

Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu Ala Glu Phe Gly Gly Ser
                805                 810                 815

Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe Lys Lys Ala Thr Ser
            820                 825                 830

Gly Gly Met Val Leu Val Met Ser Leu Trp Asp Asp Tyr Tyr Ala Asn
        835                 840                 845

Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr Asn Glu Thr Ser Ser Thr
    850                 855                 860

Pro Gly Ala Val Arg Gly Ser Cys Ser Thr Ser Ser Gly Val Pro Ala
865                 870                 875                 880

Gln Val Glu Ser Gln Ser Pro Asn Ala Lys Val Thr Phe Ser Asn Ile
                885                 890                 895

Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn Pro Ser Gly Gly Asn Pro
            900                 905                 910

Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr Thr Arg Arg Pro Ala Thr
        915                 920                 925

Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln Ser His Tyr Gly Gln Cys
    930                 935                 940
```

Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val Cys Ala Ser Gly Thr Thr
945 950 955 960

Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln Cys Leu
965 970

<210> 43
<211> 3057
<212> DNA
<213> Sequência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(3057)

<400> 43

```
cag cag aat tgc gca gca tta ttt ggc caa tgt gga ggc ata ggg tgg      48
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1               5                  10                  15

tcc ggc acc aca tgt tgc gtt gct ggc gcc cag tgc agt ttt gtc aat      96
Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
            20                  25                  30

gac tgg tac tcc cag tgc ctt gcg tca acc ggc gga aac ccc cca aac     144
Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
        35                  40                  45

gga aca act tcc tct agc ttg gtt tca cgg acg tcg tca gca tcc tca     192
Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
    50                  55                  60

tcc gtc ggc tcg tct tca ccc ggc ggc aac tca cca act ggc agt gct     240
Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65                  70                  75                  80

tcc acc tac aca acc aca gat aca gct acc gtg gct cct cat tcg cag     288
Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
                85                  90                  95

tct cct tac ccc agc att gcc gca tcc agt tgc gga tcg tgg acc ctc     336
Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
            100                 105                 110

gtg gat aat gtt tgc tgc cca tca tat tgt gct aat gat gac aca tcc     384
Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
        115                 120                 125

gag tca tgc tca ggc tgc ggt acc tgc act acg ccg ccc tcg gcg gac     432
Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
    130                 135                 140

tgc aaa tcc gga acc atg tat cca gag gtc cat cac gta tcc agc aac     480
Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145                 150                 155                 160
```

```
gag agc tgg cac tac agt aga tca acc cac ttt ggc cta acg agc ggc      528
Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
                165                 170                 175

ggg gcc tgt ggc ttt ggc ctg tac ggt ctc tgc aca aag ggc agt gtt      576
Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
            180                 185                 190

aca gcc agc tgg acg gat ccc atg ctt ggc gcg acg tgt gac gct ttt      624
Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
        195                 200                 205

tgt aca gcg tat ccc ctg ctt tgc aaa gac cct acc ggc act acc ctt      672
Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
    210                 215                 220

cgt ggc aac ttc gca gct cca aac ggc gat tac tac acc caa ttc tgg      720
Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225                 230                 235                 240

tcc tcg ttg cca gga gcc ctc gat aac tac ctg tcc tgc ggc gag tgc      768
Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
                245                 250                 255

att gag ctg ata caa aca aag ccc gat ggg acc gat tat gct gtc gga      816
Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
            260                 265                 270

gaa gcc ggc tac acg gat cca att act ctc gag att gtg gac agc tgc      864
Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
        275                 280                 285

ccg tgc agc gcg aac tcc aag tgg tgc tgt ggt ccg ggc gcc gat cat      912
Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
    290                 295                 300

tgc gga gag atc gac ttc aaa tac ggc tgt cct ctt cct gct gac agc      960
Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305                 310                 315                 320

att cat ctc gac ctg tca gac att gcc atg ggc cgt ttg cag ggc aat     1008
Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
                325                 330                 335

gga tca cta acc aat ggc gtc atc ccg act cga tat aga aga gtc caa     1056
Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
            340                 345                 350

tgc ccc aaa gtt ggg aac gcc tac att tgg ctt cga aat ggc gga ggg     1104
Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
        355                 360                 365

cct tac tat ttt gct ctc acg gca gtc aac acc aac gga ccg ggc tca     1152
Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
    370                 375                 380

gtc acc aaa atc gag atc aag ggc gca gac acc gac aac tgg gtt gcc     1200
Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385                 390                 395                 400
```

```
ttg gtc cat gac cca aac tat acg agt agc cgc cca caa gaa cgc tat      1248
Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
                405                 410                 415

ggc agt tgg gta atc cca cag gga tca ggg ccc ttt aac ttg cct gtt      1296
Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
            420                 425                 430

gga att cgt ctg act agc cca acg ggg gaa cag att gtg aat gaa cag      1344
Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
        435                 440                 445

gcc atc aag aca ttc act cct ccg gcc aca ggt gac ccc aat ttt tac      1392
Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
    450                 455                 460

tac att gac att ggt gtg cag ttt agc cag aat ggc tcg act tac tcc      1440
Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gly Ser Thr Tyr Ser
465                 470                 475                 480

agt gga tct tct tcg ggg tcg ggg tct agc tcc agc tcg agt tcg act      1488
Ser Gly Ser Ser Ser Gly Ser Gly Ser Ser Ser Ser Ser Ser Ser Thr
                485                 490                 495

acc act aag gcc act tcg acg acc ttg aag act acc tcg acc acc agc      1536
Thr Thr Lys Ala Thr Ser Thr Thr Leu Lys Thr Thr Ser Thr Thr Ser
            500                 505                 510

agt gga agc agt tcg aca tcg gcg gcg cag tcg gcc tgc act ctc caa      1584
Ser Gly Ser Ser Ser Thr Ser Ala Ala Gln Ser Ala Cys Thr Leu Gln
        515                 520                 525

tcg gag act cac ccg cct ctg aca tgg cag aaa tgc tcg tct ggt ggc      1632
Ser Glu Thr His Pro Pro Leu Thr Trp Gln Lys Cys Ser Ser Gly Gly
    530                 535                 540

acg tgc act caa cag aca ggc tcc gtg gtc atc gac gcc aac tgg cgc      1680
Thr Cys Thr Gln Gln Thr Gly Ser Val Val Ile Asp Ala Asn Trp Arg
545                 550                 555                 560

tgg act cac gct acg aac agc agc acg aac tgc tac gat ggc aac act      1728
Trp Thr His Ala Thr Asn Ser Ser Thr Asn Cys Tyr Asp Gly Asn Thr
                565                 570                 575

tgg agc tcg acc cta tgt cct gac aac gag acc tgc gcg aag aac tgc      1776
Trp Ser Ser Thr Leu Cys Pro Asp Asn Glu Thr Cys Ala Lys Asn Cys
            580                 585                 590

tgt ctg gac ggt gcc gcc tac gcg tcc acg tac gga gtt acc acg agc      1824
Cys Leu Asp Gly Ala Ala Tyr Ala Ser Thr Tyr Gly Val Thr Thr Ser
        595                 600                 605

ggt aac agc ctc tcc att ggc ttt gtc acc cag tct gcg cag aag aac      1872
Gly Asn Ser Leu Ser Ile Gly Phe Val Thr Gln Ser Ala Gln Lys Asn
    610                 615                 620

gtt ggc gct cgc ctt tac ctt atg gcg agc gac acg acc tac cag gaa      1920
Val Gly Ala Arg Leu Tyr Leu Met Ala Ser Asp Thr Thr Tyr Gln Glu
625                 630                 635                 640

ttc acc ctg ctt ggc aac gag ttc tct ttc gat gtt gat gtt tcg cag      1968
```

```
Phe Thr Leu Leu Gly Asn Glu Phe Ser Phe Asp Val Asp Val Ser Gln
645                 650                 655

ctg ccg tgc ggc ttg aac gga gct ctc tac ttc gtg tcc atg gac gcg      2016
Leu Pro Cys Gly Leu Asn Gly Ala Leu Tyr Phe Val Ser Met Asp Ala
            660                 665                 670

gat ggt ggc gtg agc aag tat ccc acc aac acc gct ggc gcc aag tac      2064
Asp Gly Gly Val Ser Lys Tyr Pro Thr Asn Thr Ala Gly Ala Lys Tyr
        675                 680                 685

ggc acg ggg tac tgt gac agc cag tgt ccc cgc gat ctg aag ttc atc      2112
Gly Thr Gly Tyr Cys Asp Ser Gln Cys Pro Arg Asp Leu Lys Phe Ile
    690                 695                 700

aat ggc cag gcc aac gtt gag ggc tgg gag ccg tca tcc aac aac gcg      2160
Asn Gly Gln Ala Asn Val Glu Gly Trp Glu Pro Ser Ser Asn Asn Ala
705                 710                 715                 720

aac acg ggc att gga gga cac gga agc tgc tgc tct gag atg gat atc      2208
Asn Thr Gly Ile Gly Gly His Gly Ser Cys Cys Ser Glu Met Asp Ile
                725                 730                 735

tgg gag gcc aac tcc atc tcc gag gct ctt acc ccc cac cct tgc acg      2256
Trp Glu Ala Asn Ser Ile Ser Glu Ala Leu Thr Pro His Pro Cys Thr
            740                 745                 750

act gtc ggc cag gag atc tgc gag ggt gat ggg tgc ggc gga act tac      2304
Thr Val Gly Gln Glu Ile Cys Glu Gly Asp Gly Cys Gly Gly Thr Tyr
        755                 760                 765

tcc gat aac aga tat ggc ggc act tgc gat ccc gat ggc tgc gac tgg      2352
Ser Asp Asn Arg Tyr Gly Gly Thr Cys Asp Pro Asp Gly Cys Asp Trp
    770                 775                 780

aac cca tac cgc ctg ggc aac acc agc ttc tac ggc cct ggc tca agc      2400
Asn Pro Tyr Arg Leu Gly Asn Thr Ser Phe Tyr Gly Pro Gly Ser Ser
785                 790                 795                 800

ttt acc ctc gat acc acc aag aaa ttg acc gtt gtc acc cag ttc gag      2448
Phe Thr Leu Asp Thr Thr Lys Lys Leu Thr Val Val Thr Gln Phe Glu
                805                 810                 815

acg tcg ggt gcc atc aac cga tac tat gtc cag aat ggc gtc act ttc      2496
Thr Ser Gly Ala Ile Asn Arg Tyr Tyr Val Gln Asn Gly Val Thr Phe
            820                 825                 830

cag cag ccc aac gcc gag ctt ggt agt tac tct ggc aac gag ctc aac      2544
Gln Gln Pro Asn Ala Glu Leu Gly Ser Tyr Ser Gly Asn Glu Leu Asn
        835                 840                 845

gat gat tac tgc aca gct gag gag gca gaa ttc ggc gga tcc tct ttc      2592
Asp Asp Tyr Cys Thr Ala Glu Glu Ala Glu Phe Gly Gly Ser Ser Phe
    850                 855                 860

tca gac aag ggc ggc ctg act cag ttc aag aag gct acc tct ggc ggc      2640
Ser Asp Lys Gly Gly Leu Thr Gln Phe Lys Lys Ala Thr Ser Gly Gly
865                 870                 875                 880

atg gtt ctg gtc atg agt ctg tgg gat gat tac tac gcc aac atg ctg      2688
Met Val Leu Val Met Ser Leu Trp Asp Asp Tyr Tyr Ala Asn Met Leu
```

```
                885                 890                 895

tgg ctg gac tcc acc tac ccg aca aac gag acc tcc tcc aca ccc ggt      2736
Trp Leu Asp Ser Thr Tyr Pro Thr Asn Glu Thr Ser Ser Thr Pro Gly
            900                 905                 910

gcc gtg cgc gga agc tgc tcc acc agc tcc ggt gtc cct gct cag gtc      2784
Ala Val Arg Gly Ser Cys Ser Thr Ser Ser Gly Val Pro Ala Gln Val
        915                 920                 925

gaa tct cag tct ccc aac gcc aag gtc acc ttc tcc aac atc aag ttc      2832
Glu Ser Gln Ser Pro Asn Ala Lys Val Thr Phe Ser Asn Ile Lys Phe
    930                 935                 940

gga ccc att ggc agc acc ggc aac cct agc ggc ggc aac cct ccc ggc      2880
Gly Pro Ile Gly Ser Thr Gly Asn Pro Ser Gly Gly Asn Pro Pro Gly
945                 950                 955                 960

gga aac ccg cct ggc acc acc acc acc cgc cgc cca gcc act acc act      2928
Gly Asn Pro Pro Gly Thr Thr Thr Thr Arg Arg Pro Ala Thr Thr Thr
                965                 970                 975

gga agc tct ccc gga cct acc cag tct cac tac ggc cag tgc ggc ggt      2976
Gly Ser Ser Pro Gly Pro Thr Gln Ser His Tyr Gly Gln Cys Gly Gly
            980                 985                 990

att ggc tac agc ggc ccc acg gtc  tgc gcc agc ggc aca  act tgc cag    3024
Ile Gly Tyr Ser Gly Pro Thr Val  Cys Ala Ser Gly Thr  Thr Cys Gln
        995                 1000                1005

gtc ctg  aac cct tac tac tct  cag tgc ctg taa                        3057
Val Leu  Asn Pro Tyr Tyr Ser  Gln Cys Leu
    1010                1015
```

<210> 44
<211> 1018
<212> PRT
<213> Seqüência artificial

<220>
<223> Construção Sintética

<400> 44

```
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1               5                   10                  15

Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
            20                  25                  30

Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
        35                  40                  45

Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
    50                  55                  60
```

Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65 70 75 80

Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
85 90 95

Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
100 105 110

Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
115 120 125

Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
130 135 140

Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145 150 155 160

Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
165 170 175

Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
180 185 190

Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
195 200 205

Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
210 215 220

Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225 230 235 240

Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
245 250 255

Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
260 265 270

Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
275 280 285

Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
290 295 300

Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser

305 310 315 320

Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
325 330 335

Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
340 345 350

Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
355 360 365

Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
370 375 380

Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385 390 395 400

Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
405 410 415

Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
420 425 430

Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
435 440 445

Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
450 455 460

Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gly Ser Thr Tyr Ser
465 470 475 480

Ser Gly Ser Ser Ser Gly Ser Gly Ser Ser Ser Ser Ser Ser Ser Thr
485 490 495

Thr Thr Lys Ala Thr Ser Thr Thr Leu Lys Thr Thr Ser Thr Thr Ser
500 505 510

Ser Gly Ser Ser Ser Thr Ser Ala Ala Gln Ser Ala Cys Thr Leu Gln
515 520 525

Ser Glu Thr His Pro Pro Leu Thr Trp Gln Lys Cys Ser Ser Gly Gly
530 535 540

Thr Cys Thr Gln Gln Thr Gly Ser Val Val Ile Asp Ala Asn Trp Arg
545 550 555 560

Trp Thr His Ala Thr Asn Ser Ser Thr Asn Cys Tyr Asp Gly Asn Thr
565 570 575

Trp Ser Ser Thr Leu Cys Pro Asp Asn Glu Thr Cys Ala Lys Asn Cys
580 585 590

Cys Leu Asp Gly Ala Ala Tyr Ala Ser Thr Tyr Gly Val Thr Thr Ser
595 600 605

Gly Asn Ser Leu Ser Ile Gly Phe Val Thr Gln Ser Ala Gln Lys Asn
610 615 620

Val Gly Ala Arg Leu Tyr Leu Met Ala Ser Asp Thr Thr Tyr Gln Glu
625 630 635 640

Phe Thr Leu Leu Gly Asn Glu Phe Ser Phe Asp Val Asp Val Ser Gln
645 650 655

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

Asp Gly Gly Val Ser Lys Tyr Pro Thr Asn Thr Ala Gly Ala Lys Tyr
675 680 685

Gly Thr Gly Tyr Cys Asp Ser Gln Cys Pro Arg Asp Leu Lys Phe Ile
690 695 700

Asn Gly Gln Ala Asn Val Glu Gly Trp Glu Pro Ser Ser Asn Asn Ala
705 710 715 720

Asn Thr Gly Ile Gly Gly His Gly Ser Cys Cys Ser Glu Met Asp Ile
725 730 735

Trp Glu Ala Asn Ser Ile Ser Glu Ala Leu Thr Pro His Pro Cys Thr
740 745 750

Thr Val Gly Gln Glu Ile Cys Glu Gly Asp Gly Cys Gly Gly Thr Tyr
755 760 765

Ser Asp Asn Arg Tyr Gly Gly Thr Cys Asp Pro Asp Gly Cys Asp Trp
770 775 780

Asn Pro Tyr Arg Leu Gly Asn Thr Ser Phe Tyr Gly Pro Gly Ser Ser
785 790 795 800

Phe Thr Leu Asp Thr Thr Lys Lys Leu Thr Val Val Thr Gln Phe Glu
805 810 815

Thr Ser Gly Ala Ile Asn Arg Tyr Tyr Val Gln Asn Gly Val Thr Phe
820 825 830

Gln Gln Pro Asn Ala Glu Leu Gly Ser Tyr Ser Gly Asn Glu Leu Asn
835 840 845

Asp Asp Tyr Cys Thr Ala Glu Glu Ala Glu Phe Gly Gly Ser Ser Phe
850 855 860

Ser Asp Lys Gly Gly Leu Thr Gln Phe Lys Lys Ala Thr Ser Gly Gly
865 870 875 880

Met Val Leu Val Met Ser Leu Trp Asp Asp Tyr Tyr Ala Asn Met Leu
885 890 895

Trp Leu Asp Ser Thr Tyr Pro Thr Asn Glu Thr Ser Ser Thr Pro Gly
900 905 910

Ala Val Arg Gly Ser Cys Ser Thr Ser Ser Gly Val Pro Ala Gln Val
915 920 925

Glu Ser Gln Ser Pro Asn Ala Lys Val Thr Phe Ser Asn Ile Lys Phe
930 935 940

Gly Pro Ile Gly Ser Thr Gly Asn Pro Ser Gly Gly Asn Pro Pro Gly
945 950 955 960

Gly Asn Pro Pro Gly Thr Thr Thr Thr Arg Arg Pro Ala Thr Thr Thr
965 970 975

Gly Ser Ser Pro Gly Pro Thr Gln Ser His Tyr Gly Gln Cys Gly Gly
980 985 990

Ile Gly Tyr Ser Gly Pro Thr Val Cys Ala Ser Gly Thr Thr Cys Gln
995 1000 1005

Val Leu Asn Pro Tyr Tyr Ser Gln Cys Leu
1010 1015

<210> 45
<211> 2919
<212> DNA
<213> Seqüência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2919)

<400> 45

```
cag cag aat tgc gca gca tta ttt ggc caa tgt gga ggc ata ggg tgg        48
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1               5                  10                  15

tcc ggc acc aca tgt tgc gtt gct ggc gcc cag tgc agt ttt gtc aat        96
Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
            20                  25                  30

gac tgg tac tcc cag tgc ctt gcg tca acc ggc gga aac ccc cca aac       144
Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
        35                  40                  45

gga aca act tcc tct agc ttg gtt tca cgg acg tcg tca gca tcc tca       192
Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
    50                  55                  60

tcc gtc ggc tcg tct tca ccc ggc ggc aac tca cca act ggc agt gct       240
Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65                  70                  75                  80

tcc acc tac aca acc aca gat aca gct acc gtg gct cct cat tcg cag       288
Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
                85                  90                  95

tct cct tac ccc agc att gcc gca tcc agt tgc gga tcg tgg acc ctc       336
Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
            100                 105                 110

gtg gat aat gtt tgc tgc cca tca tat tgt gct aat gat gac aca tcc       384
Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
        115                 120                 125

gag tca tgc tca ggc tgc ggt acc tgc act acg ccg ccc tcg gcg gac       432
Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
    130                 135                 140

tgc aaa tcc gga acc atg tat cca gag gtc cat cac gta tcc agc aac       480
Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145                 150                 155                 160

gag agc tgg cac tac agt aga tca acc cac ttt ggc cta acg agc ggc       528
Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
                165                 170                 175

ggg gcc tgt ggc ttt ggc ctg tac ggt ctc tgc aca aag ggc agt gtt       576
Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
            180                 185                 190

aca gcc agc tgg acg gat ccc atg ctt ggc gcg acg tgt gac gct ttt       624
Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
        195                 200                 205
```

209

```
tgt aca gcg tat ccc ctg ctt tgc aaa gac cct acc ggc act acc ctt      672
Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
    210                 215                 220

cgt ggc aac ttc gca gct cca aac ggc gat tac tac acc caa ttc tgg      720
Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225                 230                 235                 240

tcc tcg ttg cca gga gcc ctc gat aac tac ctg tcc tgc ggc gag tgc      768
Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
                245                 250                 255

att gag ctg ata caa aca aag ccc gat ggg acc gat tat gct gtc gga      816
Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
            260                 265                 270

gaa gcc ggc tac acg gat cca att act ctc gag att gtg gac agc tgc      864
Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
        275                 280                 285

ccg tgc agc gcg aac tcc aag tgg tgc tgt ggt ccg ggc gcc gat cat      912
Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
    290                 295                 300

tgc gga gag atc gac ttc aaa tac ggc tgt cct ctt cct gct gac agc      960
Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305                 310                 315                 320

att cat ctc gac ctg tca gac att gcc atg ggc cgt ttg cag ggc aat     1008
Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
                325                 330                 335

gga tca cta acc aat ggc gtc atc ccg act cga tat aga aga gtc caa     1056
Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
            340                 345                 350

tgc ccc aaa gtt ggg aac gcc tac att tgg ctt cga aat ggc gga ggg     1104
Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
        355                 360                 365

cct tac tat ttt gct ctc acg gca gtc aac acc aac gga ccg ggc tca     1152
Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
    370                 375                 380

gtc acc aaa atc gag atc aag ggc gca gac acc gac aac tgg gtt gcc     1200
Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385                 390                 395                 400

ttg gtc cat gac cca aac tat acg agt agc cgc cca caa gaa cgc tat     1248
Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
                405                 410                 415

ggc agt tgg gta atc cca cag gga tca ggg ccc ttt aac ttg cct gtt     1296
Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
            420                 425                 430

gga att cgt ctg act agc cca acg ggg gaa cag att gtg aat gaa cag     1344
Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
        435                 440                 445
```

219

```
gcc atc aag aca ttc act cct ccg gcc aca ggt gac ccc aat ttt tac     1392
Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
    450                 455                 460

tac att gac att ggt gtg cag ttt agc cag aat cag tcg gcc tgc act     1440
Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gln Ser Ala Cys Thr
465                 470                 475                 480

ctc caa tcg gag act cac ccg cct ctg aca tgg cag aaa tgc tcg tct     1488
Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp Gln Lys Cys Ser Ser
                485                 490                 495

ggt ggc acg tgc act caa cag aca ggc tcc gtg gtc atc gac gcc aac     1536
Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val Val Ile Asp Ala Asn
            500                 505                 510

tgg cgc tgg act cac gct acg aac agc agc acg aac tgc tac gat ggc     1584
Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr Asn Cys Tyr Asp Gly
        515                 520                 525

aac act tgg agc tcg acc cta tgt cct gac aac gag acc tgc gcg aag     1632
Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn Glu Thr Cys Ala Lys
    530                 535                 540

aac tgc tgt ctg gac ggt gcc gcc tac gcg tcc acg tac gga gtt acc     1680
Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser Thr Tyr Gly Val Thr
545                 550                 555                 560

acg agc ggt aac agc ctc tcc att ggc ttt gtc acc cag tct gcg cag     1728
Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe Val Thr Gln Ser Ala Gln
                565                 570                 575

aag aac gtt ggc gct cgc ctt tac ctt atg gcg agc gac acg acc tac     1776
Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala Ser Asp Thr Thr Tyr
            580                 585                 590

cag gaa ttc acc ctg ctt ggc aac gag ttc tct ttc gat gtt gat gtt     1824
Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser Phe Asp Val Asp Val
        595                 600                 605

tcg cag ctg ccg tgc ggc ttg aac gga gct ctc tac ttc gtg tcc atg     1872
Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu Tyr Phe Val Ser Met
    610                 615                 620

gac gcg gat ggt ggc gtg agc aag tat ccc acc aac acc gct ggc gcc     1920
Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr Asn Thr Ala Gly Ala
625                 630                 635                 640

aag tac ggc acg ggg tac tgt gac agc cag tgt ccc cgc gat ctg aag     1968
Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys Pro Arg Asp Leu Lys
                645                 650                 655

ttc atc aat ggc cag gcc aac gtt gag ggc tgg gag ccg tca tcc aac     2016
Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp Glu Pro Ser Ser Asn
            660                 665                 670

aac gcg aac acg ggc att gga gga cac gga agc tgc tgc tct gag atg     2064
Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser Cys Cys Ser Glu Met
        675                 680                 685

gat atc tgg gag gcc aac tcc atc tcc gag gct ctt acc ccc cac cct     2112
```

211

```
Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala Leu Thr Pro His Pro
    690                 695                 700

tgc acg act gtc ggc cag gag atc tgc gag ggt gat ggg tgc ggc gga      2160
Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly Asp Gly Cys Gly Gly
705                 710                 715                 720

act tac tcc gat aac aga tat ggc ggc act tgc gat ccc gat ggc tgc      2208
Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr Cys Asp Pro Asp Gly Cys
                725                 730                 735

gac tgg aac cca tac cgc ctg ggc aac acc agc ttc tac ggc cct ggc      2256
Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser Phe Tyr Gly Pro Gly
            740                 745                 750

tca agc ttt acc ctc gat acc acc aag aaa ttg acc gtt gtc acc cag      2304
Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu Thr Val Val Thr Gln
        755                 760                 765

ttc gag acg tcg ggt gcc atc aac cga tac tat gtc cag aat ggc gtc      2352
Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr Val Gln Asn Gly Val
    770                 775                 780

act ttc cag cag ccc aac gcc gag ctt ggt agt tac tct ggc aac gag      2400
Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser Tyr Ser Gly Asn Glu
785                 790                 795                 800

ctc aac gat gat tac tgc aca gct gag gag gca gaa ttc ggc gga tcc      2448
Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu Ala Glu Phe Gly Gly Ser
                805                 810                 815

tct ttc tca gac aag ggc ggc ctg act cag ttc aag aag gct acc tct      2496
Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe Lys Lys Ala Thr Ser
            820                 825                 830

ggc ggc atg gtt ctg gtc atg agt ctg tgg gat gat tac tac gcc aac      2544
Gly Gly Met Val Leu Val Met Ser Leu Trp Asp Asp Tyr Tyr Ala Asn
        835                 840                 845

atg ctg tgg ctg gac tcc acc tac ccg aca aac gag acc tcc tcc aca      2592
Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr Asn Glu Thr Ser Ser Thr
    850                 855                 860

ccc ggt gcc gtg cgc gga agc tgc tcc acc agc tcc ggt gtc cct gct      2640
Pro Gly Ala Val Arg Gly Ser Cys Ser Thr Ser Ser Gly Val Pro Ala
865                 870                 875                 880

cag gtc gaa tct cag tct ccc aac gcc aag gtc acc ttc tcc aac atc      2688
Gln Val Glu Ser Gln Ser Pro Asn Ala Lys Val Thr Phe Ser Asn Ile
                885                 890                 895

aag ttc gga ccc att ggc agc acc ggc aac cct agc ggc ggc aac cct      2736
Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn Pro Ser Gly Gly Asn Pro
            900                 905                 910

ccc ggc gga aac ccg cct ggc acc acc acc acc cgc cgc cca gcc act      2784
Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr Thr Arg Arg Pro Ala Thr
        915                 920                 925

acc act gga agc tct ccc gga cct acc cag tct cac tac ggc cag tgc      2832
Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln Ser His Tyr Gly Gln Cys
```

930 935 940

ggc ggt att ggc tac agc ggc ccc acg gtc tgc gcc agc ggc aca act 2880
Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val Cys Ala Ser Gly Thr Thr
945 950 955 960

tgc cag gtc ctg aac cct tac tac tct cag tgc ctg taa 2919
Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln Cys Leu
965 970

<210> 46
<211> 972
<212> PRT
<213> Sequência artificial

<220>
<223> Construção Sintética

<400> 46

Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1 5 10 15

Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
20 25 30

Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
35 40 45

Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
50 55 60

Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65 70 75 80

Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
85 90 95

Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
100 105 110

Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
115 120 125

Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
130 135 140

Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145 150 155 160

Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
165 170 175

Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
180 185 190

Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
195 200 205

Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
210 215 220

Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225 230 235 240

Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
245 250 255

Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
260 265 270

Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
275 280 285

Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
290 295 300

Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305 310 315 320

Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
325 330 335

Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
340 345 350

Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
355 360 365

Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
370 375 380

Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385 390 395 400

Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr

405 410 415

Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
420 425 430

Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
435 440 445

Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
450 455 460

Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gln Ser Ala Cys Thr
465 470 475 480

Leu Gln Ser Glu Thr His Pro Pro Leu Thr Trp Gln Lys Cys Ser Ser
485 490 495

Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser Val Val Ile Asp Ala Asn
500 505 510

Trp Arg Trp Thr His Ala Thr Asn Ser Ser Thr Asn Cys Tyr Asp Gly
515 520 525

Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp Asn Glu Thr Cys Ala Lys
530 535 540

Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala Ser Thr Tyr Gly Val Thr
545 550 555 560

Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe Val Thr Gln Ser Ala Gln
565 570 575

Lys Asn Val Gly Ala Arg Leu Tyr Leu Met Ala Ser Asp Thr Thr Tyr
580 585 590

Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe Ser Phe Asp Val Asp Val
595 600 605

Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala Leu Tyr Phe Val Ser Met
610 615 620

Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro Thr Asn Thr Ala Gly Ala
625 630 635 640

Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys Pro Arg Asp Leu Lys
645 650 655

Phe Ile Asn Gly Gln Ala Asn Val Glu Gly Trp Glu Pro Ser Ser Asn
660 665 670

Asn Ala Asn Thr Gly Ile Gly Gly His Gly Ser Cys Cys Ser Glu Met
675 680 685

Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu Ala Leu Thr Pro His Pro
690 695 700

Cys Thr Thr Val Gly Gln Glu Ile Cys Glu Gly Asp Gly Cys Gly Gly
705 710 715 720

Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr Cys Asp Pro Asp Gly Cys
725 730 735

Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr Ser Phe Tyr Gly Pro Gly
740 745 750

Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys Leu Thr Val Val Thr Gln
755 760 765

Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr Tyr Val Gln Asn Gly Val
770 775 780

Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly Ser Tyr Ser Gly Asn Glu
785 790 795 800

Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu Ala Glu Phe Gly Gly Ser
805 810 815

Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln Phe Lys Lys Ala Thr Ser
820 825 830

Gly Gly Met Val Leu Val Met Ser Leu Trp Asp Asp Tyr Tyr Ala Asn
835 840 845

Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr Asn Glu Thr Ser Ser Thr
850 855 860

Pro Gly Ala Val Arg Gly Ser Cys Ser Thr Ser Ser Gly Val Pro Ala
865 870 875 880

Gln Val Glu Ser Gln Ser Pro Asn Ala Lys Val Thr Phe Ser Asn Ile
885 890 895

Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn Pro Ser Gly Gly Asn Pro
900 905 910

Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr Thr Arg Arg Pro Ala Thr
915 920 925

Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln Ser His Tyr Gly Gln Cys
930 935 940

Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val Cys Ala Ser Gly Thr Thr
945 950 955 960

Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln Cys Leu
965 970

<210> 47
<211> 3057
<212> DNA
<213> Sequência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(3057)

<400> 47
cag cag aat tgc gca gca tta ttt ggc caa tgt gga ggc ata ggg tgg 48
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1 5 10 15

tcc ggc acc aca tgt tgc gtt gct ggc gcc cag tgc agt ttt gtc aat 96
Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
20 25 30

gac tgg tac tcc cag tgc ctt gcg tca acc ggc gga aac ccc cca aac 144
Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
35 40 45

gga aca act tcc tct agc ttg gtt tca cgg acg tcg tca gca tcc tca 192
Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
50 55 60

tcc gtc ggc tcg tct tca ccc ggc ggc aac tca cca act ggc agt gct 240
Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65 70 75 80

tcc acc tac aca acc aca gat aca gct acc gtg gct cct cat tcg cag 288
Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
85 90 95

tct cct tac ccc agc att gcc gca tcc agt tgc gga tcg tgg acc ctc 336
Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu

```
                100                 105                 110

gtg gat aat gtt tgc tgc cca tca tat tgt gct aat gat gac aca tcc      384
Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
        115                 120                 125

gag tca tgc tca ggc tgc ggt acc tgc act acg ccg ccc tcg gcg gac      432
Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
    130                 135                 140

tgc aaa tcc gga acc atg tat cca gag gtc cat cac gta tcc agc aac      480
Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145                 150                 155                 160

gag agc tgg cac tac agt aga tca acc cac ttt ggc cta acg agc ggc      528
Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
                165                 170                 175

ggg gcc tgt ggc ttt ggc ctg tac ggt ctc tgc aca aag ggc agt gtt      576
Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
            180                 185                 190

aca gcc agc tgg acg gat ccc atg ctt ggc gcg acg tgt gac gct ttt      624
Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
        195                 200                 205

tgt aca gcg tat ccc ctg ctt tgc aaa gac cct acc ggc act acc ctt      672
Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
    210                 215                 220

cgt ggc aac ttc gca gct cca aac ggc gat tac tac acc caa ttc tgg      720
Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225                 230                 235                 240

tcc tcg ttg cca gga gcc ctc gat aac tac ctg tcc tgc ggc gag tgc      768
Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
                245                 250                 255

att gag ctg ata caa aca aag ccc gat ggg acc gat tat gct gtc gga      816
Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
            260                 265                 270

gaa gcc ggc tac acg gat cca att act ctc gag att gtg gac agc tgc      864
Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
        275                 280                 285

ccg tgc agc gcg aac tcc aag tgg tgc tgt ggt ccg ggc gcc gat cat      912
Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
    290                 295                 300

tgc gga gag atc gac ttc aaa tac ggc tgt cct ctt cct gct gac agc      960
Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305                 310                 315                 320

att cat ctc gac ctg tca gac att gcc atg ggc cgt ttg cag ggc aat     1008
Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
                325                 330                 335

gga tca cta acc aat ggc gtc atc ccg act cga tat aga aga gtc caa     1056
Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
            340                 345                 350
```

218

```
tgc ccc aaa gtt ggg aac gcc tac att tgg ctt cga aat ggc gga ggg      1104
Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
        355                 360                 365

cct tac tat ttt gct ctc acg gca gtc aac acc aac gga ccg ggc tca      1152
Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
    370                 375                 380

gtc acc aaa atc gag atc aag ggc gca gac acc gac aac tgg gtt gcc      1200
Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385                 390                 395                 400

ttg gtc cat gac cca aac tat acg agt agc cgc cca caa gaa cgc tat      1248
Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
                405                 410                 415

ggc agt tgg gta atc cca cag gga tca ggg ccc ttt aac ttg cct gtt      1296
Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
            420                 425                 430

gga att cgt ctg act agc cca acg ggg gaa cag att gtg aat gaa cag      1344
Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
        435                 440                 445

gcc atc aag aca ttc act cct ccg gcc aca ggt gac ccc aat ttt tac      1392
Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
    450                 455                 460

tac att gac att ggt gtg cag ttt agc cag aat ggc tcg act tac tcc      1440
Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gly Ser Thr Tyr Ser
465                 470                 475                 480

agt gga tct tct tcg ggg tcg ggg tct agc tcc agc tcg agt tcg act      1488
Ser Gly Ser Ser Ser Gly Ser Gly Ser Ser Ser Ser Ser Ser Ser Thr
                485                 490                 495

acc act aag gcc act tcg acg acc ttg aag act acc tcg acc acc agc      1536
Thr Thr Lys Ala Thr Ser Thr Thr Leu Lys Thr Thr Ser Thr Thr Ser
            500                 505                 510

agt gga agc agt tcg aca tcg gcg gcg cag tcg gcc tgc act ctc caa      1584
Ser Gly Ser Ser Ser Thr Ser Ala Ala Gln Ser Ala Cys Thr Leu Gln
        515                 520                 525

tcg gag act cac ccg cct ctg aca tgg cag aaa tgc tcg tct ggt ggc      1632
Ser Glu Thr His Pro Pro Leu Thr Trp Gln Lys Cys Ser Ser Gly Gly
    530                 535                 540

acg tgc act caa cag aca ggc tcc gtg gtc atc gac gcc aac tgg cgc      1680
Thr Cys Thr Gln Gln Thr Gly Ser Val Val Ile Asp Ala Asn Trp Arg
545                 550                 555                 560

tgg act cac gct acg aac agc agc acg aac tgc tac gat ggc aac act      1728
Trp Thr His Ala Thr Asn Ser Ser Thr Asn Cys Tyr Asp Gly Asn Thr
                565                 570                 575

tgg agc tcg acc cta tgt cct gac aac gag acc tgc gcg aag aac tgc      1776
Trp Ser Ser Thr Leu Cys Pro Asp Asn Glu Thr Cys Ala Lys Asn Cys
            580                 585                 590
```

```
tgt ctg gac ggt gcc gcc tac gcg tcc acg tac gga gtt acc acg agc      1824
Cys Leu Asp Gly Ala Ala Tyr Ala Ser Thr Tyr Gly Val Thr Thr Ser
        595                 600                 605

ggt aac agc ctc tcc att ggc ttt gtc acc cag tct gcg cag aag aac      1872
Gly Asn Ser Leu Ser Ile Gly Phe Val Thr Gln Ser Ala Gln Lys Asn
    610                 615                 620

gtt ggc gct cgc ctt tac ctt atg gcg agc gac acg acc tac cag gaa      1920
Val Gly Ala Arg Leu Tyr Leu Met Ala Ser Asp Thr Thr Tyr Gln Glu
625                 630                 635                 640

ttc acc ctg ctt ggc aac gag ttc tct ttc gat gtt gat gtt tcg cag      1968
Phe Thr Leu Leu Gly Asn Glu Phe Ser Phe Asp Val Asp Val Ser Gln
                645                 650                 655

ctg ccg tgc ggc ttg aac gga gct ctc tac ttc gtg tcc atg gac gcg      2016
Leu Pro Cys Gly Leu Asn Gly Ala Leu Tyr Phe Val Ser Met Asp Ala
            660                 665                 670

gat ggt ggc gtg agc aag tat ccc acc aac acc gct ggc gcc aag tac      2064
Asp Gly Gly Val Ser Lys Tyr Pro Thr Asn Thr Ala Gly Ala Lys Tyr
        675                 680                 685

ggc acg ggg tac tgt gac agc cag tgt ccc cgc gat ctg aag ttc atc      2112
Gly Thr Gly Tyr Cys Asp Ser Gln Cys Pro Arg Asp Leu Lys Phe Ile
    690                 695                 700

aat ggc cag gcc aac gtt gag ggc tgg gag ccg tca tcc aac aac gcg      2160
Asn Gly Gln Ala Asn Val Glu Gly Trp Glu Pro Ser Ser Asn Asn Ala
705                 710                 715                 720

aac acg ggc att gga gga cac gga agc tgc tgc tct gag atg gat atc      2208
Asn Thr Gly Ile Gly Gly His Gly Ser Cys Cys Ser Glu Met Asp Ile
                725                 730                 735

tgg gag gcc aac tcc atc tcc gag gct ctt acc ccc cac cct tgc acg      2256
Trp Glu Ala Asn Ser Ile Ser Glu Ala Leu Thr Pro His Pro Cys Thr
            740                 745                 750

act gtc ggc cag gag atc tgc gag ggt gat ggg tgc ggc gga act tac      2304
Thr Val Gly Gln Glu Ile Cys Glu Gly Asp Gly Cys Gly Gly Thr Tyr
        755                 760                 765

tcc gat aac aga tat ggc ggc act tgc gat ccc gat ggc tgc gac tgg      2352
Ser Asp Asn Arg Tyr Gly Gly Thr Cys Asp Pro Asp Gly Cys Asp Trp
    770                 775                 780

aac cca tac cgc ctg ggc aac acc agc ttc tac ggc cct ggc tca agc      2400
Asn Pro Tyr Arg Leu Gly Asn Thr Ser Phe Tyr Gly Pro Gly Ser Ser
785                 790                 795                 800

ttt acc ctc gat acc acc aag aaa ttg acc gtt gtc acc cag ttc gag      2448
Phe Thr Leu Asp Thr Thr Lys Lys Leu Thr Val Val Thr Gln Phe Glu
                805                 810                 815

acg tcg ggt gcc atc aac cga tac tat gtc cag aat ggc gtc act ttc      2496
Thr Ser Gly Ala Ile Asn Arg Tyr Tyr Val Gln Asn Gly Val Thr Phe
            820                 825                 830

cag cag ccc aac gcc gag ctt ggt agt tac tct ggc aac gag ctc aac      2544
```

```
Gln Gln Pro Asn Ala Glu Leu Gly Ser Tyr Ser Gly Asn Glu Leu Asn
        835                 840                 845

gat gat tac tgc aca gct gag gag gca gaa ttc ggc gga tcc tct ttc      2592
Asp Asp Tyr Cys Thr Ala Glu Glu Ala Glu Phe Gly Gly Ser Ser Phe
    850                 855                 860

tca gac aag ggc ggc ctg act cag ttc aag aag gct acc tct ggc ggc      2640
Ser Asp Lys Gly Gly Leu Thr Gln Phe Lys Lys Ala Thr Ser Gly Gly
865                 870                 875                 880

atg gtt ctg gtc atg agt ctg tgg gat gat tac tac gcc aac atg ctg      2688
Met Val Leu Val Met Ser Leu Trp Asp Asp Tyr Tyr Ala Asn Met Leu
                885                 890                 895

tgg ctg gac tcc acc tac ccg aca aac gag acc tcc tcc aca ccc ggt      2736
Trp Leu Asp Ser Thr Tyr Pro Thr Asn Glu Thr Ser Ser Thr Pro Gly
            900                 905                 910

gcc gtg cgc gga agc tgc tcc acc agc tcc ggt gtc cct gct cag gtc      2784
Ala Val Arg Gly Ser Cys Ser Thr Ser Ser Gly Val Pro Ala Gln Val
        915                 920                 925

gaa tct cag tct ccc aac gcc aag gtc acc ttc tcc aac atc aag ttc      2832
Glu Ser Gln Ser Pro Asn Ala Lys Val Thr Phe Ser Asn Ile Lys Phe
    930                 935                 940

gga ccc att ggc agc acc ggc aac cct agc ggc ggc aac cct ccc ggc      2880
Gly Pro Ile Gly Ser Thr Gly Asn Pro Ser Gly Gly Asn Pro Pro Gly
945                 950                 955                 960

gga aac ccg cct ggc acc acc acc acc cgc cgc cca gcc act acc act      2928
Gly Asn Pro Pro Gly Thr Thr Thr Thr Arg Arg Pro Ala Thr Thr Thr
                965                 970                 975

gga agc tct ccc gga cct acc cag tct cac tac ggc cag tgc ggc ggt      2976
Gly Ser Ser Pro Gly Pro Thr Gln Ser His Tyr Gly Gln Cys Gly Gly
            980                 985                 990

att ggc tac agc ggc ccc acg gtc  tgc gcc agc ggc aca  act tgc cag    3024
Ile Gly Tyr Ser Gly Pro Thr Val  Cys Ala Ser Gly Thr  Thr Cys Gln
        995                 1000                1005

                                                                     3057
gtc ctg  aac cct tac tac tct  cag tgc ctg taa
Val Leu  Asn Pro Tyr Tyr Ser  Gln Cys Leu
    1010                1015
```

<210> 48
<211> 1018
<212> PRT
<213> Seqüência artificial

<220>
<223> Construção Sintética

<400> 48

```
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1               5                   10                  15
```

Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
20 25 30

Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
35 40 45

Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
50 55 60

Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65 70 75 80

Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
85 90 95

Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
100 105 110

Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
115 120 125

Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
130 135 140

Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145 150 155 160

Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
165 170 175

Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
180 185 190

Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
195 200 205

Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
210 215 220

Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225 230 235 240

Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
245 250 255

L22

Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
260 265 270

Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
275 280 285

Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
290 295 300

Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305 310 315 320

Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
325 330 335

Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
340 345 350

Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
355 360 365

Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
370 375 380

Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385 390 395 400

Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
405 410 415

Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
420 425 430

Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
435 440 445

Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
450 455 460

Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gly Ser Thr Tyr Ser
465 470 475 480

Ser Gly Ser Ser Ser Gly Ser Gly Ser Ser Ser Ser Ser Ser Ser Thr
485 490 495

Thr Thr Lys Ala Thr Ser Thr Thr Leu Lys Thr Thr Ser Thr Thr Ser

500 505 510

Ser Gly Ser Ser Ser Thr Ser Ala Ala Gln Ser Ala Cys Thr Leu Gln
515 520 525

Ser Glu Thr His Pro Pro Leu Thr Trp Gln Lys Cys Ser Ser Gly Gly
530 535 540

Thr Cys Thr Gln Gln Thr Gly Ser Val Val Ile Asp Ala Asn Trp Arg
545 550 555 560

Trp Thr His Ala Thr Asn Ser Ser Thr Asn Cys Tyr Asp Gly Asn Thr
565 570 575

Trp Ser Ser Thr Leu Cys Pro Asp Asn Glu Thr Cys Ala Lys Asn Cys
580 585 590

Cys Leu Asp Gly Ala Ala Tyr Ala Ser Thr Tyr Gly Val Thr Thr Ser
595 600 605

Gly Asn Ser Leu Ser Ile Gly Phe Val Thr Gln Ser Ala Gln Lys Asn
610 615 620

Val Gly Ala Arg Leu Tyr Leu Met Ala Ser Asp Thr Thr Tyr Gln Glu
625 630 635 640

Phe Thr Leu Leu Gly Asn Glu Phe Ser Phe Asp Val Asp Val Ser Gln
645 650 655

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

Asp Gly Gly Val Ser Lys Tyr Pro Thr Asn Thr Ala Gly Ala Lys Tyr
675 680 685

Gly Thr Gly Tyr Cys Asp Ser Gln Cys Pro Arg Asp Leu Lys Phe Ile
690 695 700

Asn Gly Gln Ala Asn Val Glu Gly Trp Glu Pro Ser Ser Asn Asn Ala
705 710 715 720

Asn Thr Gly Ile Gly Gly His Gly Ser Cys Cys Ser Glu Met Asp Ile
725 730 735

Trp Glu Ala Asn Ser Ile Ser Glu Ala Leu Thr Pro His Pro Cys Thr
740 745 750

Thr Val Gly Gln Glu Ile Cys Glu Gly Asp Gly Cys Gly Gly Thr Tyr
755 760 765

Ser Asp Asn Arg Tyr Gly Gly Thr Cys Asp Pro Asp Gly Cys Asp Trp
770 775 780

Asn Pro Tyr Arg Leu Gly Asn Thr Ser Phe Tyr Gly Pro Gly Ser Ser
785 790 795 800

Phe Thr Leu Asp Thr Thr Lys Lys Leu Thr Val Val Thr Gln Phe Glu
805 810 815

Thr Ser Gly Ala Ile Asn Arg Tyr Tyr Val Gln Asn Gly Val Thr Phe
820 825 830

Gln Gln Pro Asn Ala Glu Leu Gly Ser Tyr Ser Gly Asn Glu Leu Asn
835 840 845

Asp Asp Tyr Cys Thr Ala Glu Glu Ala Glu Phe Gly Gly Ser Ser Phe
850 855 860

Ser Asp Lys Gly Gly Leu Thr Gln Phe Lys Lys Ala Thr Ser Gly Gly
865 870 875 880

Met Val Leu Val Met Ser Leu Trp Asp Asp Tyr Tyr Ala Asn Met Leu
885 890 895

Trp Leu Asp Ser Thr Tyr Pro Thr Asn Glu Thr Ser Ser Thr Pro Gly
900 905 910

Ala Val Arg Gly Ser Cys Ser Thr Ser Ser Gly Val Pro Ala Gln Val
915 920 925

Glu Ser Gln Ser Pro Asn Ala Lys Val Thr Phe Ser Asn Ile Lys Phe
930 935 940

Gly Pro Ile Gly Ser Thr Gly Asn Pro Ser Gly Gly Asn Pro Pro Gly
945 950 955 960

Gly Asn Pro Pro Gly Thr Thr Thr Thr Arg Arg Pro Ala Thr Thr Thr
965 970 975

Gly Ser Ser Pro Gly Pro Thr Gln Ser His Tyr Gly Gln Cys Gly Gly
980 985 990

Ile Gly Tyr Ser Gly Pro Thr Val Cys Ala Ser Gly Thr Thr Cys Gln
995 1000 1005

Val Leu Asn Pro Tyr Tyr Ser Gln Cys Leu
1010 1015

<210> 49
<211> 2769
<212> DNA
<213> Seqüência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2769)

<400> 49
cag cag aat tgc gca gca tta ttt ggc caa tgt gga ggc ata ggg tgg 48
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1 5 10 15

tcc ggc acc aca tgt tgc gtt gct ggc gcc cag tgc agt ttt gtc aat 96
Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
20 25 30

gac tgg tac tcc cag tgc ctt gcg tca acc ggc gga aac ccc cca aac 144
Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
35 40 45

gga aca act tcc tct agc ttg gtt tca cgg acg tcg tca gca tcc tca 192
Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
50 55 60

tcc gtc ggc tcg tct tca ccc ggc ggc aac tca cca act ggc agt gct 240
Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65 70 75 80

tcc acc tac aca acc aca gat aca gct acc gtg gct cct cat tcg cag 288
Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
85 90 95

tct cct tac ccc agc att gcc gca tcc agt tgc gga tcg tgg acc ctc 336
Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
100 105 110

gtg gat aat gtt tgc tgc cca tca tat tgt gct aat gat gac aca tcc 384
Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
115 120 125

gag tca tgc tca ggc tgc ggt acc tgc act acg ccg ccc tcg gcg gac 432
Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
130 135 140

tgc aaa tcc gga acc atg tat cca gag gtc cat cac gta tcc agc aac 480
Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn

```
145                 150                 155                 160

gag agc tgg cac tac agt aga tca acc cac ttt ggc cta acg agc ggc      528
Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
                165                 170                 175

ggg gcc tgt ggc ttt ggc ctg tac ggt ctc tgc aca aag ggc agt gtt      576
Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
            180                 185                 190

aca gcc agc tgg acg gat ccc atg ctt ggc gcg acg tgt gac gct ttt      624
Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
        195                 200                 205

tgt aca gcg tat ccc ctg ctt tgc aaa gac cct acc ggc act acc ctt      672
Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
    210                 215                 220

cgt ggc aac ttc gca gct cca aac ggc gat tac tac acc caa ttc tgg      720
Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225                 230                 235                 240

tcc tcg ttg cca gga gcc ctc gat aac tac ctg tcc tgc ggc gag tgc      768
Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
                245                 250                 255

att gag ctg ata caa aca aag ccc gat ggg acc gat tat gct gtc gga      816
Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
            260                 265                 270

gaa gcc ggc tac acg gat cca att act ctc gag att gtg gac agc tgc      864
Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
        275                 280                 285

ccg tgc agc gcg aac tcc aag tgg tgc tgt ggt ccg ggc gcc gat cat      912
Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
    290                 295                 300

tgc gga gag atc gac ttc aaa tac ggc tgt cct ctt cct gct gac agc      960
Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305                 310                 315                 320

att cat ctc gac ctg tca gac att gcc atg ggc cgt ttg cag ggc aat     1008
Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
                325                 330                 335

gga tca cta acc aat ggc gtc atc ccg act cga tat aga aga gtc caa     1056
Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
            340                 345                 350

tgc ccc aaa gtt ggg aac gcc tac att tgg ctt cga aat ggc gga ggg     1104
Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
        355                 360                 365

cct tac tat ttt gct ctc acg gca gtc aac acc aac gga ccg ggc tca     1152
Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
    370                 375                 380

gtc acc aaa atc gag atc aag ggc gca gac acc gac aac tgg gtt gcc     1200
Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385                 390                 395                 400
```

```
ttg gtc cat gac cca aac tat acg agt agc cgc cca caa gaa cgc tat    1248
Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
                405                 410                 415

ggc agt tgg gta atc cca cag gga tca ggg ccc ttt aac ttg cct gtt    1296
Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
            420                 425                 430

gga att cgt ctg act agc cca acg ggg gaa cag att gtg aat gaa cag    1344
Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
        435                 440                 445

gcc atc aag aca ttc act cct ccg gcc aca ggt gac ccc aat ttt tac    1392
Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
    450                 455                 460

tac att gac att ggt gtg cag ttt agc cag aat caa gct tgc tca agc    1440
Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gln Ala Cys Ser Ser
465                 470                 475                 480

gtc tgg ggc caa tgt ggt ggc cag aat tgg tcg ggt ccg act tgc tgt    1488
Val Trp Gly Gln Cys Gly Gly Gln Asn Trp Ser Gly Pro Thr Cys Cys
                485                 490                 495

gct tcc gga agc aca tgc gtc tac tcc aac gac tat tac tcc cag tgt    1536
Ala Ser Gly Ser Thr Cys Val Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys
            500                 505                 510

ctt ccc ggc gct gca agc tca agc tcg tcc acg cgc gcc gcg tcg acg    1584
Leu Pro Gly Ala Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr
        515                 520                 525

act tct cga gta tcc ccc aca aca tcc cgg tcg agc tcc gcg acg cct    1632
Thr Ser Arg Val Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro
    530                 535                 540

cca cct ggt tct act act acc aga gta cct cca gtc gga tcg gga acc    1680
Pro Pro Gly Ser Thr Thr Thr Arg Val Pro Pro Val Gly Ser Gly Thr
545                 550                 555                 560

gct acg tat tca ggc aac cct ttt gtt ggg gtc act cct tgg gcc aat    1728
Ala Thr Tyr Ser Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala Asn
                565                 570                 575

gca tat tac gcc tct gaa gtt agc agc ctc gct att cct agc ttg act    1776
Ala Tyr Tyr Ala Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu Thr
            580                 585                 590

gga gcc atg gcc act gct gca gca gct gtc gca aag gtt ccc tct ttt    1824
Gly Ala Met Ala Thr Ala Ala Ala Ala Val Ala Lys Val Pro Ser Phe
        595                 600                 605

atg tgg cta gat act ctt gac aag acc cct ctc atg gag caa acc ttg    1872
Met Trp Leu Asp Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr Leu
    610                 615                 620

gcc gac atc cgc acc gcc aac aag aat ggc ggt aac tat gcg gga cag    1920
Ala Asp Ile Arg Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln
625                 630                 635                 640
```

```
ttt gtg gtg tat gac ttg ccg gat cgc gat tgc gct gcc ctt gcc tcg      1968
Phe Val Val Tyr Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser
                645                 650                 655

aat ggc gaa tac tct att gcc gat ggt ggc gtc gcc aaa tat aag aac      2016
Asn Gly Glu Tyr Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn
            660                 665                 670

tat atc gac acc att cgt caa att gtc gtg gaa tat tcc gat atc cgg      2064
Tyr Ile Asp Thr Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile Arg
        675                 680                 685

acc ctc ctg gtt att gag cct gac tct ctt gcc aac ctg gtg acc aac      2112
Thr Leu Leu Val Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn
    690                 695                 700

ctc ggt act cca aag tgt gcc aat gct cag tca gcc tac ctt gag tgc      2160
Leu Gly Thr Pro Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys
705                 710                 715                 720

atc aac tac gcc gtc aca cag ctg aac ctt cca aat gtt gcg atg tat      2208
Ile Asn Tyr Ala Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr
                725                 730                 735

ttg gac gct ggc cat gca gga tgg ctt ggc tgg ccg gca aac caa gac      2256
Leu Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp
            740                 745                 750

ccg gcc gct cag cta ttt gca aat gtt tac aag aat gca tcg tct ccg      2304
Pro Ala Ala Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro
        755                 760                 765

aga gct ctt cgc gga ttg gca acc aat gtc gcc aac tac aac ggg tgg      2352
Arg Ala Leu Arg Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp
    770                 775                 780

aac att acc agc ccc cca tcg tac acg caa ggc aac gct gtc tac aac      2400
Asn Ile Thr Ser Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn
785                 790                 795                 800

gag aag ctg tac atc cac gct att gga cgt ctt ctt gcc aat cac ggc      2448
Glu Lys Leu Tyr Ile His Ala Ile Gly Arg Leu Leu Ala Asn His Gly
                805                 810                 815

tgg tcc aac gcc ttc ttc atc act gat caa ggt cga tcg gga aag cag      2496
Trp Ser Asn Ala Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln
            820                 825                 830

cct acc gga cag caa cag tgg gga gac tgg tgc aat gtg atc ggc acc      2544
Pro Thr Gly Gln Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr
        835                 840                 845

gga ttt ggt att cgc cca tcc gca aac act ggg gac tcg ttg ctg gat      2592
Gly Phe Gly Ile Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp
    850                 855                 860

tcg ttt gtc tgg gtc aag cca ggc ggc gag tgt gac ggc acc agc gac      2640
Ser Phe Val Trp Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp
865                 870                 875                 880

agc agt gcg cca cga ttt gac tcc cac tgt gcg ctc cca gat gcc ttg      2688
```

229

Ser Ser Ala Pro Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu
885 890 895

caa ccg gcg gct caa gct ggt gct tgg ttc caa gcc tac ttt gtg cag 2736
Gln Pro Ala Ala Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln
900 905 910

ctt ctc aca aac gca aac cca tcg ttc ctg taa 2769
Leu Leu Thr Asn Ala Asn Pro Ser Phe Leu
915 920

<210> 50
<211> 922
<212> PRT
<213> Sequência artificial

<220>
<223> Construção Sintética

<400> 50

Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1 5 10 15

Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
20 25 30

Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
35 40 45

Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
50 55 60

Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65 70 75 80

Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
85 90 95

Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
100 105 110

Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
115 120 125

Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
130 135 140

Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145 150 155 160

Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
165 170 175

Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
180 185 190

Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
195 200 205

Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
210 215 220

Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225 230 235 240

Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
245 250 255

Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
260 265 270

Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
275 280 285

Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
290 295 300

Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305 310 315 320

Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
325 330 335

Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
340 345 350

Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
355 360 365

Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
370 375 380

Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385 390 395 400

Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
405 410 415

Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
420 425 430

Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
435 440 445

Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
450 455 460

Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gln Ala Cys Ser Ser
465 470 475 480

Val Trp Gly Gln Cys Gly Gly Gln Asn Trp Ser Gly Pro Thr Cys Cys
485 490 495

Ala Ser Gly Ser Thr Cys Val Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys
500 505 510

Leu Pro Gly Ala Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr
515 520 525

Thr Ser Arg Val Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro
530 535 540

Pro Pro Gly Ser Thr Thr Thr Arg Val Pro Pro Val Gly Ser Gly Thr
545 550 555 560

Ala Thr Tyr Ser Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala Asn
565 570 575

Ala Tyr Tyr Ala Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu Thr
580 585 590

Gly Ala Met Ala Thr Ala Ala Ala Ala Val Ala Lys Val Pro Ser Phe
595 600 605

Met Trp Leu Asp Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr Leu
610 615 620

Ala Asp Ile Arg Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln
625 630 635 640

Phe Val Val Tyr Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser

645 650 655

Asn Gly Glu Tyr Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn
660 665 670

Tyr Ile Asp Thr Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile Arg
675 680 685

Thr Leu Leu Val Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn
690 695 700

Leu Gly Thr Pro Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys
705 710 715 720

Ile Asn Tyr Ala Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr
725 730 735

Leu Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp
740 745 750

Pro Ala Ala Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro
755 760 765

Arg Ala Leu Arg Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp
770 775 780

Asn Ile Thr Ser Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn
785 790 795 800

Glu Lys Leu Tyr Ile His Ala Ile Gly Arg Leu Leu Ala Asn His Gly
805 810 815

Trp Ser Asn Ala Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln
820 825 830

Pro Thr Gly Gln Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr
835 840 845

Gly Phe Gly Ile Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp
850 855 860

Ser Phe Val Trp Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp
865 870 875 880

Ser Ser Ala Pro Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu
885 890 895

Gln Pro Ala Ala Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln
900 905 910

Leu Leu Thr Asn Ala Asn Pro Ser Phe Leu
915 920

<210> 51
<211> 2907
<212> DNA
<213> Seqüência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2907)

<400> 51
cag cag aat tgc gca gca tta ttt ggc caa tgt gga ggc ata ggg tgg 48
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1 5 10 15

tcc ggc acc aca tgt tgc gtt gct ggc gcc cag tgc agt ttt gtc aat 96
Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
20 25 30

gac tgg tac tcc cag tgc ctt gcg tca acc ggc gga aac ccc cca aac 144
Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
35 40 45

gga aca act tcc tct agc ttg gtt tca cgg acg tcg tca gca tcc tca 192
Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
50 55 60

tcc gtc ggc tcg tct tca ccc ggc ggc aac tca cca act ggc agt gct 240
Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65 70 75 80

tcc acc tac aca acc aca gat aca gct acc gtg gct cct cat tcg cag 288
Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
85 90 95

tct cct tac ccc agc att gcc gca tcc agt tgc gga tcg tgg acc ctc 336
Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
100 105 110

gtg gat aat gtt tgc tgc cca tca tat tgt gct aat gat gac aca tcc 384
Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
115 120 125

gag tca tgc tca ggc tgc ggt acc tgc act acg ccg ccc tcg gcg gac 432
Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
130 135 140

tgc aaa tcc gga acc atg tat cca gag gtc cat cac gta tcc agc aac 480

```
Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145                 150                 155                 160

gag agc tgg cac tac agt aga tca acc cac ttt ggc cta acg agc ggc      528
Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
                165                 170                 175

ggg gcc tgt ggc ttt ggc ctg tac ggt ctc tgc aca aag ggc agt gtt      576
Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
            180                 185                 190

aca gcc agc tgg acg gat ccc atg ctt ggc gcg acg tgt gac gct ttt      624
Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
        195                 200                 205

tgt aca gcg tat ccc ctg ctt tgc aaa gac cct acc ggc act acc ctt      672
Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
    210                 215                 220

cgt ggc aac ttc gca gct cca aac ggc gat tac tac acc caa ttc tgg      720
Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225                 230                 235                 240

tcc tcg ttg cca gga gcc ctc gat aac tac ctg tcc tgc ggc gag tgc      768
Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
                245                 250                 255

att gag ctg ata caa aca aag ccc gat ggg acc gat tat gct gtc gga      816
Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
            260                 265                 270

gaa gcc ggc tac acg gat cca att act ctc gag att gtg gac agc tgc      864
Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
        275                 280                 285

ccg tgc agc gcg aac tcc aag tgg tgc tgt ggt ccg ggc gcc gat cat      912
Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
    290                 295                 300

tgc gga gag atc gac ttc aaa tac ggc tgt cct ctt cct gct gac agc      960
Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305                 310                 315                 320

att cat ctc gac ctg tca gac att gcc atg ggc cgt ttg cag ggc aat     1008
Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
                325                 330                 335

gga tca cta acc aat ggc gtc atc ccg act cga tat aga aga gtc caa     1056
Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
            340                 345                 350

tgc ccc aaa gtt ggg aac gcc tac att tgg ctt cga aat ggc gga ggg     1104
Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
        355                 360                 365

cct tac tat ttt gct ctc acg gca gtc aac acc aac gga ccg ggc tca     1152
Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
    370                 375                 380

gtc acc aaa atc gag atc aag ggc gca gac acc gac aac tgg gtt gcc     1200
Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
```

```
385                 390                 395                 400

ttg gtc cat gac cca aac tat acg agt agc cgc cca caa gaa cgc tat      1248
Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
                405                 410                 415

ggc agt tgg gta atc cca cag gga tca ggg ccc ttt aac ttg cct gtt      1296
Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
            420                 425                 430

gga att cgt ctg act agc cca acg ggg gaa cag att gtg aat gaa cag      1344
Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
        435                 440                 445

gcc atc aag aca ttc act cct ccg gcc aca ggt gac ccc aat ttt tac      1392
Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
    450                 455                 460

tac att gac att ggt gtg cag ttt agc cag aat ggc tcg act tac tcc      1440
Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gly Ser Thr Tyr Ser
465                 470                 475                 480

agt gga tct tct tcg ggg tcg ggg tct agc tcc agc tcg agt tcg act      1488
Ser Gly Ser Ser Ser Gly Ser Gly Ser Ser Ser Ser Ser Ser Thr
                485                 490                 495

acc act aag gcc act tcg acg acc ttg aag act acc tcg acc acc agc      1536
Thr Thr Lys Ala Thr Ser Thr Thr Leu Lys Thr Thr Ser Thr Thr Ser
            500                 505                 510

agt gga agc agt tcg aca tcg gcg gcg caa gct tgc tca agc gtc tgg      1584
Ser Gly Ser Ser Ser Thr Ser Ala Ala Gln Ala Cys Ser Ser Val Trp
        515                 520                 525

ggc caa tgt ggt ggc cag aat tgg tcg ggt ccg act tgc tgt gct tcc      1632
Gly Gln Cys Gly Gly Gln Asn Trp Ser Gly Pro Thr Cys Cys Ala Ser
    530                 535                 540

gga agc aca tgc gtc tac tcc aac gac tat tac tcc cag tgt ctt ccc      1680
Gly Ser Thr Cys Val Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro
545                 550                 555                 560

ggc gct gca agc tca agc tcg tcc acg cgc gcc gcg tcg acg act tct      1728
Gly Ala Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr Thr Ser
                565                 570                 575

cga gta tcc ccc aca aca tcc cgg tcg agc tcc gcg acg cct cca cct      1776
Arg Val Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro Pro Pro
            580                 585                 590

ggt tct act act acc aga gta cct cca gtc gga tcg gga acc gct acg      1824
Gly Ser Thr Thr Thr Arg Val Pro Pro Val Gly Ser Gly Thr Ala Thr
        595                 600                 605

tat tca ggc aac cct ttt gtt ggg gtc act cct tgg gcc aat gca tat      1872
Tyr Ser Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala Asn Ala Tyr
    610                 615                 620

tac gcc tct gaa gtt agc agc ctc gct att cct agc ttg act gga gcc      1920
Tyr Ala Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu Thr Gly Ala
625                 630                 635                 640
```

```
atg gcc act gct gca gca gct gtc gca aag gtt ccc tct ttt atg tgg     1968
Met Ala Thr Ala Ala Ala Ala Val Ala Lys Val Pro Ser Phe Met Trp
                645                 650                 655

cta gat act ctt gac aag acc cct ctc atg gag caa acc ttg gcc gac     2016
Leu Asp Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr Leu Ala Asp
            660                 665                 670

atc cgc acc gcc aac aag aat ggc ggt aac tat gcg gga cag ttt gtg     2064
Ile Arg Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln Phe Val
        675                 680                 685

gtg tat gac ttg ccg gat cgc gat tgc gct gcc ctt gcc tcg aat ggc     2112
Val Tyr Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly
    690                 695                 700

gaa tac tct att gcc gat ggt ggc gtc gcc aaa tat aag aac tat atc     2160
Glu Tyr Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn Tyr Ile
705                 710                 715                 720

gac acc att cgt caa att gtc gtg gaa tat tcc gat atc cgg acc ctc     2208
Asp Thr Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile Arg Thr Leu
                725                 730                 735

ctg gtt att gag cct gac tct ctt gcc aac ctg gtg acc aac ctc ggt     2256
Leu Val Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu Gly
            740                 745                 750

act cca aag tgt gcc aat gct cag tca gcc tac ctt gag tgc atc aac     2304
Thr Pro Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn
        755                 760                 765

tac gcc gtc aca cag ctg aac ctt cca aat gtt gcg atg tat ttg gac     2352
Tyr Ala Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp
    770                 775                 780

gct ggc cat gca gga tgg ctt ggc tgg ccg gca aac caa gac ccg gcc     2400
Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala
785                 790                 795                 800

gct cag cta ttt gca aat gtt tac aag aat gca tcg tct ccg aga gct     2448
Ala Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala
                805                 810                 815

ctt cgc gga ttg gca acc aat gtc gcc aac tac aac ggg tgg aac att     2496
Leu Arg Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile
            820                 825                 830

acc agc ccc cca tcg tac acg caa ggc aac gct gtc tac aac gag aag     2544
Thr Ser Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys
        835                 840                 845

ctg tac atc cac gct att gga cgt ctt ctt gcc aat cac ggc tgg tcc     2592
Leu Tyr Ile His Ala Ile Gly Arg Leu Leu Ala Asn His Gly Trp Ser
    850                 855                 860

aac gcc ttc ttc atc act gat caa ggt cga tcg gga aag cag cct acc     2640
Asn Ala Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr
865                 870                 875                 880
```

```
gga cag caa cag tgg gga gac tgg tgc aat gtg atc ggc acc gga ttt     2688
Gly Gln Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe
                885                 890                 895

ggt att cgc cca tcc gca aac act ggg gac tcg ttg ctg gat tcg ttt     2736
Gly Ile Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe
            900                 905                 910

gtc tgg gtc aag cca ggc ggc gag tgt gac ggc acc agc gac agc agt     2784
Val Trp Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser
        915                 920                 925

gcg cca cga ttt gac tcc cac tgt gcg ctc cca gat gcc ttg caa ccg     2832
Ala Pro Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu Gln Pro
    930                 935                 940

gcg gct caa gct ggt gct tgg ttc caa gcc tac ttt gtg cag ctt ctc     2880
Ala Ala Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu
945                 950                 955                 960

                                                                    2907
aca aac gca aac cca tcg ttc ctg taa
Thr Asn Ala Asn Pro Ser Phe Leu
                965
```

<210> 52
<211> 968
<212> PRT
<213> Seqüência artificial

<220>
<223> Construção Sintética

<400> 52

```
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1               5                  10                  15

Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
            20                  25                  30

Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
        35                  40                  45

Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
    50                  55                  60

Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65                  70                  75                  80

Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
                85                  90                  95

Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
            100                 105                 110
```

Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
115 120 125

Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
130 135 140

Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145 150 155 160

Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
165 170 175

Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
180 185 190

Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
195 200 205

Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
210 215 220

Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225 230 235 240

Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
245 250 255

Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
260 265 270

Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
275 280 285

Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
290 295 300

Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305 310 315 320

Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
325 330 335

Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
340 345 350

Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
355 360 365

Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
370 375 380

Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385 390 395 400

Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
405 410 415

Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
420 425 430

Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
435 440 445

Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
450 455 460

Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gly Ser Thr Tyr Ser
465 470 475 480

Ser Gly Ser Ser Ser Gly Ser Gly Ser Ser Ser Ser Ser Ser Ser Thr
485 490 495

Thr Thr Lys Ala Thr Ser Thr Thr Leu Lys Thr Thr Ser Thr Thr Ser
500 505 510

Ser Gly Ser Ser Ser Thr Ser Ala Ala Gln Ala Cys Ser Ser Val Trp
515 520 525

Gly Gln Cys Gly Gly Gln Asn Trp Ser Gly Pro Thr Cys Cys Ala Ser
530 535 540

Gly Ser Thr Cys Val Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro
545 550 555 560

Gly Ala Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr Thr Ser
565 570 575

Arg Val Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro Pro Pro
580 585 590

Gly Ser Thr Thr Thr Arg Val Pro Pro Val Gly Ser Gly Thr Ala Thr
595 600 605

Tyr Ser Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala Asn Ala Tyr
610 615 620

Tyr Ala Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu Thr Gly Ala
625 630 635 640

Met Ala Thr Ala Ala Ala Ala Val Ala Lys Val Pro Ser Phe Met Trp
645 650 655

Leu Asp Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr Leu Ala Asp
660 665 670

Ile Arg Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln Phe Val
675 680 685

Val Tyr Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly
690 695 700

Glu Tyr Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn Tyr Ile
705 710 715 720

Asp Thr Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile Arg Thr Leu
725 730 735

Leu Val Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu Gly
740 745 750

Thr Pro Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn
755 760 765

Tyr Ala Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp
770 775 780

Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala
785 790 795 800

Ala Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala
805 810 815

Leu Arg Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile
820 825 830

Thr Ser Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys

835 840 845

Leu Tyr Ile His Ala Ile Gly Arg Leu Leu Ala Asn His Gly Trp Ser
850 855 860

Asn Ala Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr
865 870 875 880

Gly Gln Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe
885 890 895

Gly Ile Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe
900 905 910

Val Trp Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser
915 920 925

Ala Pro Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu Gln Pro
930 935 940

Ala Ala Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu
945 950 955 960

Thr Asn Ala Asn Pro Ser Phe Leu
965

<210> 53
<211> 2655
<212> DNA
<213> Seqüência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2655)

<400> 53
cag cag aat tgc gca gca tta ttt ggc caa tgt gga ggc ata ggg tgg 48
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1 5 10 15

tcc ggc acc aca tgt tgc gtt gct ggc gcc cag tgc agt ttt gtc aat 96
Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
20 25 30

gac tgg tac tcc cag tgc ctt gcg tca acc ggc gga aac ccc cca aac 144
Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
35 40 45

```
gga aca act tcc tct agc ttg gtt tca cgg acg tcg tca gca tcc tca      192
Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
    50                  55                  60

tcc gtc ggc tcg tct tca ccc ggc ggc aac tca cca act ggc agt gct      240
Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65                  70                  75                  80

tcc acc tac aca acc aca gat aca gct acc gtg gct cct cat tcg cag      288
Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
                85                  90                  95

tct cct tac ccc agc att gcc gca tcc agt tgc gga tcg tgg acc ctc      336
Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
            100                 105                 110

gtg gat aat gtt tgc tgc cca tca tat tgt gct aat gat gac aca tcc      384
Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
        115                 120                 125

gag tca tgc tca ggc tgc ggt acc tgc act acg ccg ccc tcg gcg gac      432
Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
    130                 135                 140

tgc aaa tcc gga acc atg tat cca gag gtc cat cac gta tcc agc aac      480
Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145                 150                 155                 160

gag agc tgg cac tac agt aga tca acc cac ttt ggc cta acg agc ggc      528
Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
                165                 170                 175

ggg gcc tgt ggc ttt ggc ctg tac ggt ctc tgc aca aag ggc agt gtt      576
Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
            180                 185                 190

aca gcc agc tgg acg gat ccc atg ctt ggc gcg acg tgt gac gct ttt      624
Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
        195                 200                 205

tgt aca gcg tat ccc ctg ctt tgc aaa gac cct acc ggc act acc ctt      672
Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
    210                 215                 220

cgt ggc aac ttc gca gct cca aac ggc gat tac tac acc caa ttc tgg      720
Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225                 230                 235                 240

tcc tcg ttg cca gga gcc ctc gat aac tac ctg tcc tgc ggc gag tgc      768
Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
                245                 250                 255

att gag ctg ata caa aca aag ccc gat ggg acc gat tat gct gtc gga      816
Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
            260                 265                 270

gaa gcc ggc tac acg gat cca att act ctc gag att gtg gac agc tgc      864
Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
        275                 280                 285

ccg tgc agc gcg aac tcc aag tgg tgc tgt ggt ccg ggc gcc gat cat      912
```

```
Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
    290                 295                 300

tgc gga gag atc gac ttc aaa tac ggc tgt cct ctt cct gct gac agc      960
Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305                 310                 315                 320

att cat ctc gac ctg tca gac att gcc atg ggc cgt ttg cag ggc aat     1008
Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
                325                 330                 335

gga tca cta acc aat ggc gtc atc ccg act cga tat aga aga gtc caa     1056
Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
            340                 345                 350

tgc ccc aaa gtt ggg aac gcc tac att tgg ctt cga aat ggc gga ggg     1104
Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
        355                 360                 365

cct tac tat ttt gct ctc acg gca gtc aac acc aac gga ccg ggc tca     1152
Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
    370                 375                 380

gtc acc aaa atc gag atc aag ggc gca gac acc gac aac tgg gtt gcc     1200
Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385                 390                 395                 400

ttg gtc cat gac cca aac tat acg agt agc cgc cca caa gaa cgc tat     1248
Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
                405                 410                 415

ggc agt tgg gta atc cca cag gga tca ggg ccc ttt aac ttg cct gtt     1296
Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
            420                 425                 430

gga att cgt ctg act agc cca acg ggg gaa cag att gtg aat gaa cag     1344
Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
        435                 440                 445

gcc atc aag aca ttc act cct ccg gcc aca ggt gac ccc aat ttt tac     1392
Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
    450                 455                 460

tac att gac att ggt gtg cag ttt agc cag aat ccc ggc gct gca agc     1440
Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Pro Gly Ala Ala Ser
465                 470                 475                 480

tca agc tcg tcc acg cgc gcc gcg tcg acg act tct cga gta tcc ccc     1488
Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr Thr Ser Arg Val Ser Pro
                485                 490                 495

aca aca tcc cgg tcg agc tcc gcg acg cct cca cct ggt tct act act     1536
Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro Pro Pro Gly Ser Thr Thr
            500                 505                 510

acc aga gta cct cca gtc gga tcg gga acc gct acg tat tca ggc aac     1584
Thr Arg Val Pro Pro Val Gly Ser Gly Thr Ala Thr Tyr Ser Gly Asn
        515                 520                 525

cct ttt gtt ggg gtc act cct tgg gcc aat gca tat tac gcc tct gaa     1632
Pro Phe Val Gly Val Thr Pro Trp Ala Asn Ala Tyr Tyr Ala Ser Glu
```

```
    530                 535                 540
gtt agc agc ctc gct att cct agc ttg act gga gcc atg gcc act gct  1680
Val Ser Ser Leu Ala Ile Pro Ser Leu Thr Gly Ala Met Ala Thr Ala
545                 550                 555                 560

gca gca gct gtc gca aag gtt ccc tct ttt atg tgg cta gat act ctt  1728
Ala Ala Ala Val Ala Lys Val Pro Ser Phe Met Trp Leu Asp Thr Leu
                565                 570                 575

gac aag acc cct ctc atg gag caa acc ttg gcc gac atc cgc acc gcc  1776
Asp Lys Thr Pro Leu Met Glu Gln Thr Leu Ala Asp Ile Arg Thr Ala
            580                 585                 590

aac aag aat ggc ggt aac tat gcg gga cag ttt gtg gtg tat gac ttg  1824
Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln Phe Val Val Tyr Asp Leu
        595                 600                 605

ccg gat cgc gat tgc gct gcc ctt gcc tcg aat ggc gaa tac tct att  1872
Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Tyr Ser Ile
    610                 615                 620

gcc gat ggt ggc gtc gcc aaa tat aag aac tat atc gac acc att cgt  1920
Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn Tyr Ile Asp Thr Ile Arg
625                 630                 635                 640

caa att gtc gtg gaa tat tcc gat atc cgg acc ctc ctg gtt att gag  1968
Gln Ile Val Val Glu Tyr Ser Asp Ile Arg Thr Leu Leu Val Ile Glu
                645                 650                 655

cct gac tct ctt gcc aac ctg gtg acc aac ctc ggt act cca aag tgt  2016
Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu Gly Thr Pro Lys Cys
            660                 665                 670

gcc aat gct cag tca gcc tac ctt gag tgc atc aac tac gcc gtc aca  2064
Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn Tyr Ala Val Thr
        675                 680                 685

cag ctg aac ctt cca aat gtt gcg atg tat ttg gac gct ggc cat gca  2112
Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala Gly His Ala
    690                 695                 700

gga tgg ctt ggc tgg ccg gca aac caa gac ccg gcc gct cag cta ttt  2160
Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala Gln Leu Phe
705                 710                 715                 720

gca aat gtt tac aag aat gca tcg tct ccg aga gct ctt cgc gga ttg  2208
Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu Arg Gly Leu
                725                 730                 735

gca acc aat gtc gcc aac tac aac ggg tgg aac att acc agc ccc cca  2256
Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile Thr Ser Pro Pro
            740                 745                 750

tcg tac acg caa ggc aac gct gtc tac aac gag aag ctg tac atc cac  2304
Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu Tyr Ile His
        755                 760                 765

gct att gga cgt ctt ctt gcc aat cac ggc tgg tcc aac gcc ttc ttc  2352
Ala Ile Gly Arg Leu Leu Ala Asn His Gly Trp Ser Asn Ala Phe Phe
    770                 775                 780
```

```
atc act gat caa ggt cga tcg gga aag cag cct acc gga cag caa cag     2400
Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr Gly Gln Gln Gln
785                 790                 795                 800

tgg gga gac tgg tgc aat gtg atc ggc acc gga ttt ggt att cgc cca     2448
Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly Ile Arg Pro
                805                 810                 815

tcc gca aac act ggg gac tcg ttg ctg gat tcg ttt gtc tgg gtc aag     2496
Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe Val Trp Val Lys
            820                 825                 830

cca ggc ggc gag tgt gac ggc acc agc gac agc agt gcg cca cga ttt     2544
Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser Ala Pro Arg Phe
        835                 840                 845

gac tcc cac tgt gcg ctc cca gat gcc ttg caa ccg gcg gct caa gct     2592
Asp Ser His Cys Ala Leu Pro Asp Ala Leu Gln Pro Ala Ala Gln Ala
    850                 855                 860

ggt gct tgg ttc caa gcc tac ttt gtg cag ctt ctc aca aac gca aac     2640
Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu Thr Asn Ala Asn
865                 870                 875                 880

cca tcg ttc ctg taa                                                2655
Pro Ser Phe Leu
```

<210> 54
<211> 884
<212> PRT
<213> Sequência artificial

<220>
<223> Construção Sintética

<400> 54

```
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1               5                   10                  15

Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
            20                  25                  30

Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
        35                  40                  45

Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
    50                  55                  60

Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65                  70                  75                  80

Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
```

85 90 95

Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
100 105 110

Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
115 120 125

Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
130 135 140

Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145 150 155 160

Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
165 170 175

Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
180 185 190

Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
195 200 205

Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
210 215 220

Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225 230 235 240

Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
245 250 255

Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
260 265 270

Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
275 280 285

Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
290 295 300

Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305 310 315 320

Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
325 330 335

Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
340 345 350

Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
355 360 365

Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
370 375 380

Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385 390 395 400

Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
405 410 415

Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
420 425 430

Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
435 440 445

Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
450 455 460

Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Pro Gly Ala Ala Ser
465 470 475 480

Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr Thr Ser Arg Val Ser Pro
485 490 495

Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro Pro Pro Gly Ser Thr Thr
500 505 510

Thr Arg Val Pro Pro Val Gly Ser Gly Thr Ala Thr Tyr Ser Gly Asn
515 520 525

Pro Phe Val Gly Val Thr Pro Trp Ala Asn Ala Tyr Tyr Ala Ser Glu
530 535 540

Val Ser Ser Leu Ala Ile Pro Ser Leu Thr Gly Ala Met Ala Thr Ala
545 550 555 560

Ala Ala Ala Val Ala Lys Val Pro Ser Phe Met Trp Leu Asp Thr Leu
565 570 575

Asp Lys Thr Pro Leu Met Glu Gln Thr Leu Ala Asp Ile Arg Thr Ala
580 585 590

Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln Phe Val Val Tyr Asp Leu
595 600 605

Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Tyr Ser Ile
610 615 620

Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn Tyr Ile Asp Thr Ile Arg
625 630 635 640

Gln Ile Val Val Glu Tyr Ser Asp Ile Arg Thr Leu Leu Val Ile Glu
645 650 655

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

Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn Tyr Ala Val Thr
675 680 685

Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala Gly His Ala
690 695 700

Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala Gln Leu Phe
705 710 715 720

Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu Arg Gly Leu
725 730 735

Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile Thr Ser Pro Pro
740 745 750

Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu Tyr Ile His
755 760 765

Ala Ile Gly Arg Leu Leu Ala Asn His Gly Trp Ser Asn Ala Phe Phe
770 775 780

Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr Gly Gln Gln Gln
785 790 795 800

Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly Ile Arg Pro
805 810 815

Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe Val Trp Val Lys
820 825 830

Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser Ala Pro Arg Phe
835 840 845

Asp Ser His Cys Ala Leu Pro Asp Ala Leu Gln Pro Ala Ala Gln Ala
850 855 860

Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu Thr Asn Ala Asn
865 870 875 880

Pro Ser Phe Leu

<210> 55
<211> 2793
<212> DNA
<213> Sequência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2793)

<400> 55
cag cag aat tgc gca gca tta ttt ggc caa tgt gga ggc ata ggg tgg 48
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1 5 10 15

tcc ggc acc aca tgt tgc gtt gct ggc gcc cag tgc agt ttt gtc aat 96
Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
20 25 30

gac tgg tac tcc cag tgc ctt gcg tca acc ggc gga aac ccc cca aac 144
Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
35 40 45

gga aca act tcc tct agc ttg gtt tca cgg acg tcg tca gca tcc tca 192
Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
50 55 60

tcc gtc ggc tcg tct tca ccc ggc ggc aac tca cca act ggc agt gct 240
Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65 70 75 80

tcc acc tac aca acc aca gat aca gct acc gtg gct cct cat tcg cag 288
Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
85 90 95

tct cct tac ccc agc att gcc gca tcc agt tgc gga tcg tgg acc ctc 336
Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
100 105 110

```
gtg gat aat gtt tgc tgc cca tca tat tgt gct aat gat gac aca tcc      384
Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
        115                 120                 125

gag tca tgc tca ggc tgc ggt acc tgc act acg ccg ccc tcg gcg gac      432
Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
    130                 135                 140

tgc aaa tcc gga acc atg tat cca gag gtc cat cac gta tcc agc aac      480
Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145                 150                 155                 160

gag agc tgg cac tac agt aga tca acc cac ttt ggc cta acg agc ggc      528
Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
                165                 170                 175

ggg gcc tgt ggc ttt ggc ctg tac ggt ctc tgc aca aag ggc agt gtt      576
Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
            180                 185                 190

aca gcc agc tgg acg gat ccc atg ctt ggc gcg acg tgt gac gct ttt      624
Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
        195                 200                 205

tgt aca gcg tat ccc ctg ctt tgc aaa gac cct acc ggc act acc ctt      672
Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
    210                 215                 220

cgt ggc aac ttc gca gct cca aac ggc gat tac tac acc caa ttc tgg      720
Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225                 230                 235                 240

tcc tcg ttg cca gga gcc ctc gat aac tac ctg tcc tgc ggc gag tgc      768
Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
                245                 250                 255

att gag ctg ata caa aca aag ccc gat ggg acc gat tat gct gtc gga      816
Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
            260                 265                 270

gaa gcc ggc tac acg gat cca att act ctc gag att gtg gac agc tgc      864
Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
        275                 280                 285

ccg tgc agc gcg aac tcc aag tgg tgc tgt ggt ccg ggc gcc gat cat      912
Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
    290                 295                 300

tgc gga gag atc gac ttc aaa tac ggc tgt cct ctt cct gct gac agc      960
Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305                 310                 315                 320

att cat ctc gac ctg tca gac att gcc atg ggc cgt ttg cag ggc aat     1008
Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
                325                 330                 335

gga tca cta acc aat ggc gtc atc ccg act cga tat aga aga gtc caa     1056
Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
            340                 345                 350
```

```
tgc ccc aaa gtt ggg aac gcc tac att tgg ctt cga aat ggc gga ggg      1104
Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
        355                 360                 365

cct tac tat ttt gct ctc acg gca gtc aac acc aac gga ccg ggc tca      1152
Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
    370                 375                 380

gtc acc aaa atc gag atc aag ggc gca gac acc gac aac tgg gtt gcc      1200
Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385                 390                 395                 400

ttg gtc cat gac cca aac tat acg agt agc cgc cca caa gaa cgc tat      1248
Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
                405                 410                 415

ggc agt tgg gta atc cca cag gga tca ggg ccc ttt aac ttg cct gtt      1296
Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
            420                 425                 430

gga att cgt ctg act agc cca acg ggg gaa cag att gtg aat gaa cag      1344
Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
        435                 440                 445

gcc atc aag aca ttc act cct ccg gcc aca ggt gac ccc aat ttt tac      1392
Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
    450                 455                 460

tac att gac att ggt gtg cag ttt agc cag aat ggc tcg act tac tcc      1440
Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gly Ser Thr Tyr Ser
465                 470                 475                 480

agt gga tct tct tcg ggg tcg ggg tct agc tcc agc tcg agt tcg act      1488
Ser Gly Ser Ser Ser Gly Ser Gly Ser Ser Ser Ser Ser Ser Ser Thr
                485                 490                 495

acc act aag gcc act tcg acg acc ttg aag act acc tcg acc acc agc      1536
Thr Thr Lys Ala Thr Ser Thr Thr Leu Lys Thr Thr Ser Thr Thr Ser
            500                 505                 510

agt gga agc agt tcg aca tcg gcg gcg ccc ggc gct gca agc tca agc      1584
Ser Gly Ser Ser Ser Thr Ser Ala Ala Pro Gly Ala Ala Ser Ser Ser
        515                 520                 525

tcg tcc acg cgc gcc gcg tcg acg act tct cga gta tcc ccc aca aca      1632
Ser Ser Thr Arg Ala Ala Ser Thr Thr Ser Arg Val Ser Pro Thr Thr
    530                 535                 540

tcc cgg tcg agc tcc gcg acg cct cca cct ggt tct act act acc aga      1680
Ser Arg Ser Ser Ser Ala Thr Pro Pro Pro Gly Ser Thr Thr Thr Arg
545                 550                 555                 560

gta cct cca gtc gga tcg gga acc gct acg tat tca ggc aac cct ttt      1728
Val Pro Pro Val Gly Ser Gly Thr Ala Thr Tyr Ser Gly Asn Pro Phe
                565                 570                 575

gtt ggg gtc act cct tgg gcc aat gca tat tac gcc tct gaa gtt agc      1776
Val Gly Val Thr Pro Trp Ala Asn Ala Tyr Tyr Ala Ser Glu Val Ser
            580                 585                 590

agc ctc gct att cct agc ttg act gga gcc atg gcc act gct gca gca      1824
```

```
Ser Leu Ala Ile Pro Ser Leu Thr Gly Ala Met Ala Thr Ala Ala Ala
        595                 600                 605

gct gtc gca aag gtt ccc tct ttt atg tgg cta gat act ctt gac aag   1872
Ala Val Ala Lys Val Pro Ser Phe Met Trp Leu Asp Thr Leu Asp Lys
    610                 615                 620

acc cct ctc atg gag caa acc ttg gcc gac atc cgc acc gcc aac aag   1920
Thr Pro Leu Met Glu Gln Thr Leu Ala Asp Ile Arg Thr Ala Asn Lys
625                 630                 635                 640

aat ggc ggt aac tat gcg gga cag ttt gtg gtg tat gac ttg ccg gat   1968
Asn Gly Gly Asn Tyr Ala Gly Gln Phe Val Val Tyr Asp Leu Pro Asp
                645                 650                 655

cgc gat tgc gct gcc ctt gcc tcg aat ggc gaa tac tct att gcc gat   2016
Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Tyr Ser Ile Ala Asp
            660                 665                 670

ggt ggc gtc gcc aaa tat aag aac tat atc gac acc att cgt caa att   2064
Gly Gly Val Ala Lys Tyr Lys Asn Tyr Ile Asp Thr Ile Arg Gln Ile
        675                 680                 685

gtc gtg gaa tat tcc gat atc cgg acc ctc ctg gtt att gag cct gac   2112
Val Val Glu Tyr Ser Asp Ile Arg Thr Leu Leu Val Ile Glu Pro Asp
    690                 695                 700

tct ctt gcc aac ctg gtg acc aac ctc ggt act cca aag tgt gcc aat   2160
Ser Leu Ala Asn Leu Val Thr Asn Leu Gly Thr Pro Lys Cys Ala Asn
705                 710                 715                 720

gct cag tca gcc tac ctt gag tgc atc aac tac gcc gtc aca cag ctg   2208
Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn Tyr Ala Val Thr Gln Leu
                725                 730                 735

aac ctt cca aat gtt gcg atg tat ttg gac gct ggc cat gca gga tgg   2256
Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala Gly His Ala Gly Trp
            740                 745                 750

ctt ggc tgg ccg gca aac caa gac ccg gcc gct cag cta ttt gca aat   2304
Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala Gln Leu Phe Ala Asn
        755                 760                 765

gtt tac aag aat gca tcg tct ccg aga gct ctt cgc gga ttg gca acc   2352
Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu Arg Gly Leu Ala Thr
    770                 775                 780

aat gtc gcc aac tac aac ggg tgg aac att acc agc ccc cca tcg tac   2400
Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile Thr Ser Pro Pro Ser Tyr
785                 790                 795                 800

acg caa ggc aac gct gtc tac aac gag aag ctg tac atc cac gct att   2448
Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu Tyr Ile His Ala Ile
                805                 810                 815

gga cgt ctt ctt gcc aat cac ggc tgg tcc aac gcc ttc ttc atc act   2496
Gly Arg Leu Leu Ala Asn His Gly Trp Ser Asn Ala Phe Phe Ile Thr
            820                 825                 830

gat caa ggt cga tcg gga aag cag cct acc gga cag caa cag tgg gga   2544
Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr Gly Gln Gln Gln Trp Gly
```

```
          835                 840                 845

gac tgg tgc aat gtg atc ggc acc gga ttt ggt att cgc cca tcc gca      2592
Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly Ile Arg Pro Ser Ala
     850                 855                 860

aac act ggg gac tcg ttg ctg gat tcg ttt gtc tgg gtc aag cca ggc      2640
Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe Val Trp Val Lys Pro Gly
865                 870                 875                 880

ggc gag tgt gac ggc acc agc gac agc agt gcg cca cga ttt gac tcc      2688
Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser Ala Pro Arg Phe Asp Ser
                885                 890                 895

cac tgt gcg ctc cca gat gcc ttg caa ccg gcg gct caa gct ggt gct      2736
His Cys Ala Leu Pro Asp Ala Leu Gln Pro Ala Ala Gln Ala Gly Ala
            900                 905                 910

tgg ttc caa gcc tac ttt gtg cag ctt ctc aca aac gca aac cca tcg      2784
Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu Thr Asn Ala Asn Pro Ser
        915                 920                 925

ttc ctg taa                                                        2793
Phe Leu
    930
```

<210> 56
<211> 930
<212> PRT
<213> Sequência artificial

<220>
<223> Construção Sintética

<400> 56

```
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1               5                   10                  15

Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
            20                  25                  30

Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
        35                  40                  45

Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
    50                  55                  60

Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65                  70                  75                  80

Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
                85                  90                  95
```

254

Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
100 105 110

Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
115 120 125

Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
130 135 140

Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145 150 155 160

Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
165 170 175

Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
180 185 190

Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
195 200 205

Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
210 215 220

Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225 230 235 240

Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
245 250 255

Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
260 265 270

Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
275 280 285

Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
290 295 300

Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305 310 315 320

Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
325 330 335

Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln

340 345 350

Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
355 360 365

Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
370 375 380

Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385 390 395 400

Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
405 410 415

Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
420 425 430

Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
435 440 445

Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
450 455 460

Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gly Ser Thr Tyr Ser
465 470 475 480

Ser Gly Ser Ser Ser Gly Ser Gly Ser Ser Ser Ser Ser Ser Ser Thr
485 490 495

Thr Thr Lys Ala Thr Ser Thr Thr Leu Lys Thr Thr Ser Thr Thr Ser
500 505 510

Ser Gly Ser Ser Ser Thr Ser Ala Ala Pro Gly Ala Ala Ser Ser Ser
515 520 525

Ser Ser Thr Arg Ala Ala Ser Thr Thr Ser Arg Val Ser Pro Thr Thr
530 535 540

Ser Arg Ser Ser Ser Ala Thr Pro Pro Pro Gly Ser Thr Thr Thr Arg
545 550 555 560

Val Pro Pro Val Gly Ser Gly Thr Ala Thr Tyr Ser Gly Asn Pro Phe
565 570 575

Val Gly Val Thr Pro Trp Ala Asn Ala Tyr Tyr Ala Ser Glu Val Ser
580 585 590

Ser Leu Ala Ile Pro Ser Leu Thr Gly Ala Met Ala Thr Ala Ala Ala
595 600 605

Ala Val Ala Lys Val Pro Ser Phe Met Trp Leu Asp Thr Leu Asp Lys
610 615 620

Thr Pro Leu Met Glu Gln Thr Leu Ala Asp Ile Arg Thr Ala Asn Lys
625 630 635 640

Asn Gly Gly Asn Tyr Ala Gly Gln Phe Val Val Tyr Asp Leu Pro Asp
645 650 655

Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Tyr Ser Ile Ala Asp
660 665 670

Gly Gly Val Ala Lys Tyr Lys Asn Tyr Ile Asp Thr Ile Arg Gln Ile
675 680 685

Val Val Glu Tyr Ser Asp Ile Arg Thr Leu Leu Val Ile Glu Pro Asp
690 695 700

Ser Leu Ala Asn Leu Val Thr Asn Leu Gly Thr Pro Lys Cys Ala Asn
705 710 715 720

Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn Tyr Ala Val Thr Gln Leu
725 730 735

Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala Gly His Ala Gly Trp
740 745 750

Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala Gln Leu Phe Ala Asn
755 760 765

Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu Arg Gly Leu Ala Thr
770 775 780

Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile Thr Ser Pro Pro Ser Tyr
785 790 795 800

Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu Tyr Ile His Ala Ile
805 810 815

Gly Arg Leu Leu Ala Asn His Gly Trp Ser Asn Ala Phe Phe Ile Thr
820 825 830

Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr Gly Gln Gln Gln Trp Gly
835 840 845

Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly Ile Arg Pro Ser Ala
850 855 860

Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe Val Trp Val Lys Pro Gly
865 870 875 880

Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser Ala Pro Arg Phe Asp Ser
885 890 895

His Cys Ala Leu Pro Asp Ala Leu Gln Pro Ala Ala Gln Ala Gly Ala
900 905 910

Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu Thr Asn Ala Asn Pro Ser
915 920 925

Phe Leu
930

<210> 57
<211> 2739
<212> DNA
<213> Sequência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2739)

<400> 57
cag cag aat tgc gca gca tta ttt ggc caa tgt gga ggc ata ggg tgg 48
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1 5 10 15

tcc ggc acc aca tgt tgc gtt gct ggc gcc cag tgc agt ttt gtc aat 96
Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
20 25 30

gac tgg tac tcc cag tgc ctt gcg tca acc ggc gga aac ccc cca aac 144
Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
35 40 45

gga aca act tcc tct agc ttg gtt tca cgg acg tcg tca gca tcc tca 192
Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
50 55 60

tcc gtc ggc tcg tct tca ccc ggc ggc aac tca cca act ggc agt gct 240
Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala

```
65                  70                  75                  80

tcc acc tac aca acc aca gat aca gct acc gtg gct cct cat tcg cag      288
Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
                85                  90                  95

tct cct tac ccc agc att gcc gca tcc agt tgc gga tcg tgg acc ctc      336
Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
            100                 105                 110

gtg gat aat gtt tgc tgc cca tca tat tgt gct aat gat gac aca tcc      384
Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
        115                 120                 125

gag tca tgc tca ggc tgc ggt acc tgc act acg ccg ccc tcg gcg gac      432
Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
    130                 135                 140

tgc aaa tcc gga acc atg tat cca gag gtc cat cac gta tcc agc aac      480
Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145                 150                 155                 160

gag agc tgg cac tac agt aga tca acc cac ttt ggc cta acg agc ggc      528
Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
                165                 170                 175

ggg gcc tgt ggc ttt ggc ctg tac ggt ctc tgc aca aag ggc agt gtt      576
Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
            180                 185                 190

aca gcc agc tgg acg gat ccc atg ctt ggc gcg acg tgt gac gct ttt      624
Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
        195                 200                 205

tgt aca gcg tat ccc ctg ctt tgc aaa gac cct acc ggc act acc ctt      672
Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
    210                 215                 220

cgt ggc aac ttc gca gct cca aac ggc gat tac tac acc caa ttc tgg      720
Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225                 230                 235                 240

tcc tcg ttg cca gga gcc ctc gat aac tac ctg tcc tgc ggc gag tgc      768
Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
                245                 250                 255

att gag ctg ata caa aca aag ccc gat ggg acc gat tat gct gtc gga      816
Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
            260                 265                 270

gaa gcc ggc tac acg gat cca att act ctc gag att gtg gac agc tgc      864
Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
        275                 280                 285

ccg tgc agc gcg aac tcc aag tgg tgc tgt ggt ccg ggc gcc gat cat      912
Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
    290                 295                 300

tgc gga gag atc gac ttc aaa tac ggc tgt cct ctt cct gct gac agc      960
Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305                 310                 315                 320
```

```
att cat ctc gac ctg tca gac att gcc atg ggc cgt ttg cag ggc aat      1008
Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
                325                 330                 335

gga tca cta acc aat ggc gtc atc ccg act cga tat aga aga gtc caa      1056
Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
            340                 345                 350

tgc ccc aaa gtt ggg aac gcc tac att tgg ctt cga aat ggc gga ggg      1104
Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
        355                 360                 365

cct tac tat ttt gct ctc acg gca gtc aac acc aac gga ccg ggc tca      1152
Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
    370                 375                 380

gtc acc aaa atc gag atc aag ggc gca gac acc gac aac tgg gtt gcc      1200
Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385                 390                 395                 400

ttg gtc cat gac cca aac tat acg agt agc cgc cca caa gaa cgc tat      1248
Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
                405                 410                 415

ggc agt tgg gta atc cca cag gga tca ggg ccc ttt aac ttg cct gtt      1296
Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
            420                 425                 430

gga att cgt ctg act agc cca acg ggg gaa cag att gtg aat gaa cag      1344
Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
        435                 440                 445

gcc atc aag aca ttc act cct ccg gcc aca ggt gac ccc aat ttt tac      1392
Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
    450                 455                 460

tac att gac att ggt gtg cag ttt agc cag aat cag caa ccg ggt acc      1440
Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gln Gln Pro Gly Thr
465                 470                 475                 480

agc acc ccc gag gtc cat ccc aag ttg aca acc tac aag tgt aca aag      1488
Ser Thr Pro Glu Val His Pro Lys Leu Thr Thr Tyr Lys Cys Thr Lys
                485                 490                 495

tcc ggg ggg tgc gtg gcc cag gac acc tcg gtg gtc ctt gac tgg aac      1536
Ser Gly Gly Cys Val Ala Gln Asp Thr Ser Val Val Leu Asp Trp Asn
            500                 505                 510

tac cgc tgg atg cac gac gca aac tac aac tcg tgc acc gtc aac ggc      1584
Tyr Arg Trp Met His Asp Ala Asn Tyr Asn Ser Cys Thr Val Asn Gly
        515                 520                 525

ggc gtc aac acc acg ctc tgc cct gac gag gcg acc tgt ggc aag aac      1632
Gly Val Asn Thr Thr Leu Cys Pro Asp Glu Ala Thr Cys Gly Lys Asn
    530                 535                 540

tgc ttc atc gag ggc gtc gac tac gcc gcc tcg ggc gtc acg acc tcg      1680
Cys Phe Ile Glu Gly Val Asp Tyr Ala Ala Ser Gly Val Thr Thr Ser
545                 550                 555                 560
```

```
ggc agc agc ctc acc atg aac cag tac atg ccc agc agc tct ggc ggc      1728
Gly Ser Ser Leu Thr Met Asn Gln Tyr Met Pro Ser Ser Ser Gly Gly
                565                 570                 575

tac agc agc gtc tct cct cgg ctg tat ctc ctg gac tct gac ggt gag      1776
Tyr Ser Ser Val Ser Pro Arg Leu Tyr Leu Leu Asp Ser Asp Gly Glu
            580                 585                 590

tac gtg atg ctg aag ctc aac ggc cag gag ctg agc ttc gac gtc gac      1824
Tyr Val Met Leu Lys Leu Asn Gly Gln Glu Leu Ser Phe Asp Val Asp
        595                 600                 605

ctc tct gct ctg ccg tgt gga gag aac ggc tcg ctc tac ctg tct cag      1872
Leu Ser Ala Leu Pro Cys Gly Glu Asn Gly Ser Leu Tyr Leu Ser Gln
    610                 615                 620

atg gac gag aac ggg ggc gcc aac cag tat aac acg gcc ggt gcc aac      1920
Met Asp Glu Asn Gly Gly Ala Asn Gln Tyr Asn Thr Ala Gly Ala Asn
625                 630                 635                 640

tac ggg agc ggc tac tgc gat gct cag tgc ccc gtc cag aca tgg agg      1968
Tyr Gly Ser Gly Tyr Cys Asp Ala Gln Cys Pro Val Gln Thr Trp Arg
                645                 650                 655

aac ggc acc ctc aac act agc cac cag ggc ttc tgc tgc aac gag atg      2016
Asn Gly Thr Leu Asn Thr Ser His Gln Gly Phe Cys Cys Asn Glu Met
            660                 665                 670

gat atc ctg gag ggc aac tcg agg gcg aat gcc ttg acc cct cac tct      2064
Asp Ile Leu Glu Gly Asn Ser Arg Ala Asn Ala Leu Thr Pro His Ser
        675                 680                 685

tgc acg gcc acg gcc tgc gac tct gcc ggt tgc ggc ttc aac ccc tat      2112
Cys Thr Ala Thr Ala Cys Asp Ser Ala Gly Cys Gly Phe Asn Pro Tyr
    690                 695                 700

ggc agc ggc tac aaa agc tac tac ggc ccc gga gat acc gtt gac acc      2160
Gly Ser Gly Tyr Lys Ser Tyr Tyr Gly Pro Gly Asp Thr Val Asp Thr
705                 710                 715                 720

tcc aag acc ttc acc atc atc acc cag ttc aac acg gac aac ggc tcg      2208
Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe Asn Thr Asp Asn Gly Ser
                725                 730                 735

ccc tcg ggc aac ctt gtg agc atc acc cgc aag tac cag caa aac ggc      2256
Pro Ser Gly Asn Leu Val Ser Ile Thr Arg Lys Tyr Gln Gln Asn Gly
            740                 745                 750

gtc gac atc ccc agc gcc cag ccc ggc ggc gac acc atc tcg tcc tgc      2304
Val Asp Ile Pro Ser Ala Gln Pro Gly Gly Asp Thr Ile Ser Ser Cys
        755                 760                 765

ccg tcc gcc tca gcc tac ggc ggc ctc gcc acc atg ggc aag gcc ctg      2352
Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala Thr Met Gly Lys Ala Leu
    770                 775                 780

agc agc ggc atg gtg ctc gtg ttc agc att tgg aac gac aac agc cag      2400
Ser Ser Gly Met Val Leu Val Phe Ser Ile Trp Asn Asp Asn Ser Gln
785                 790                 795                 800

tac atg aac tgg ctc gac agc ggc aac gcc ggc ccc tgc agc agc acc      2448
```

```
Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala Gly Pro Cys Ser Ser Thr
                805                 810                 815

gag ggc aac cca tcc aac atc ctg gcc aac aac ccc aac acg cac gtc     2496
Glu Gly Asn Pro Ser Asn Ile Leu Ala Asn Asn Pro Asn Thr His Val
            820                 825                 830

gtc ttc tcc aac atc cgc tgg gga gac att ggg tct act acg aac tcg     2544
Val Phe Ser Asn Ile Arg Trp Gly Asp Ile Gly Ser Thr Thr Asn Ser
        835                 840                 845

act gcg ccc ccg ccc ccg cct gcg tcc agc acg acg ttt tcg act aca     2592
Thr Ala Pro Pro Pro Pro Pro Ala Ser Ser Thr Thr Phe Ser Thr Thr
    850                 855                 860

cgg agg agc tcg acg act tcg agc agc ccg agc tgc acg cag act cac     2640
Arg Arg Ser Ser Thr Thr Ser Ser Ser Pro Ser Cys Thr Gln Thr His
865                 870                 875                 880

tgg ggg cag tgc ggt ggc att ggg tac agc ggg tgc aag acg tgc acg     2688
Trp Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Cys Lys Thr Cys Thr
                885                 890                 895

tcg ggc act acg tgc cag tat agc aac gac tac tac tcg caa tgc ctt     2736
Ser Gly Thr Thr Cys Gln Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys Leu
            900                 905                 910

tag                                                                2739
```

<210> 58
<211> 912
<212> PRT
<213> Sequência artificial

<220>
<223> Construção Sintética

<400> 58

```
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1               5                  10                  15

Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
            20                  25                  30

Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
        35                  40                  45

Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
    50                  55                  60

Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65                  70                  75                  80

Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
```

85 90 95

Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
100 105 110

Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
115 120 125

Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
130 135 140

Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145 150 155 160

Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
165 170 175

Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
180 185 190

Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
195 200 205

Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
210 215 220

Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225 230 235 240

Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
245 250 255

Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
260 265 270

Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
275 280 285

Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
290 295 300

Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305 310 315 320

Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
325 330 335

Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
340 345 350

Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
355 360 365

Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
370 375 380

Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385 390 395 400

Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
405 410 415

Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
420 425 430

Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
435 440 445

Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
450 455 460

Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gln Gln Pro Gly Thr
465 470 475 480

Ser Thr Pro Glu Val His Pro Lys Leu Thr Thr Tyr Lys Cys Thr Lys
485 490 495

Ser Gly Gly Cys Val Ala Gln Asp Thr Ser Val Val Leu Asp Trp Asn
500 505 510

Tyr Arg Trp Met His Asp Ala Asn Tyr Asn Ser Cys Thr Val Asn Gly
515 520 525

Gly Val Asn Thr Thr Leu Cys Pro Asp Glu Ala Thr Cys Gly Lys Asn
530 535 540

Cys Phe Ile Glu Gly Val Asp Tyr Ala Ala Ser Gly Val Thr Thr Ser
545 550 555 560

Gly Ser Ser Leu Thr Met Asn Gln Tyr Met Pro Ser Ser Ser Gly Gly
565 570 575

Tyr Ser Ser Val Ser Pro Arg Leu Tyr Leu Leu Asp Ser Asp Gly Glu
580 585 590

Tyr Val Met Leu Lys Leu Asn Gly Gln Glu Leu Ser Phe Asp Val Asp
595 600 605

Leu Ser Ala Leu Pro Cys Gly Glu Asn Gly Ser Leu Tyr Leu Ser Gln
610 615 620

Met Asp Glu Asn Gly Gly Ala Asn Gln Tyr Asn Thr Ala Gly Ala Asn
625 630 635 640

Tyr Gly Ser Gly Tyr Cys Asp Ala Gln Cys Pro Val Gln Thr Trp Arg
645 650 655

Asn Gly Thr Leu Asn Thr Ser His Gln Gly Phe Cys Cys Asn Glu Met
660 665 670

Asp Ile Leu Glu Gly Asn Ser Arg Ala Asn Ala Leu Thr Pro His Ser
675 680 685

Cys Thr Ala Thr Ala Cys Asp Ser Ala Gly Cys Gly Phe Asn Pro Tyr
690 695 700

Gly Ser Gly Tyr Lys Ser Tyr Tyr Gly Pro Gly Asp Thr Val Asp Thr
705 710 715 720

Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe Asn Thr Asp Asn Gly Ser
725 730 735

Pro Ser Gly Asn Leu Val Ser Ile Thr Arg Lys Tyr Gln Gln Asn Gly
740 745 750

Val Asp Ile Pro Ser Ala Gln Pro Gly Gly Asp Thr Ile Ser Ser Cys
755 760 765

Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala Thr Met Gly Lys Ala Leu
770 775 780

Ser Ser Gly Met Val Leu Val Phe Ser Ile Trp Asn Asp Asn Ser Gln
785 790 795 800

Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala Gly Pro Cys Ser Ser Thr
805 810 815

```
Glu Gly Asn Pro Ser Asn Ile Leu Ala Asn Asn Pro Asn Thr His Val
            820                 825                 830

Val Phe Ser Asn Ile Arg Trp Gly Asp Ile Gly Ser Thr Thr Asn Ser
        835                 840                 845

Thr Ala Pro Pro Pro Pro Pro Ala Ser Ser Thr Thr Phe Ser Thr Thr
    850                 855                 860

Arg Arg Ser Ser Thr Thr Ser Ser Ser Pro Ser Cys Thr Gln Thr His
865                 870                 875                 880

Trp Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Cys Lys Thr Cys Thr
                885                 890                 895

Ser Gly Thr Thr Cys Gln Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys Leu
            900                 905                 910
```

<210> 59
<211> 2877
<212> DNA
<213> Sequência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2877)

<400> 59

```
cag cag aat tgc gca gca tta ttt ggc caa tgt gga ggc ata ggg tgg      48
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1               5                   10                  15

tcc ggc acc aca tgt tgc gtt gct ggc gcc cag tgc agt ttt gtc aat      96
Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
            20                  25                  30

gac tgg tac tcc cag tgc ctt gcg tca acc ggc gga aac ccc cca aac     144
Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
        35                  40                  45

gga aca act tcc tct agc ttg gtt tca cgg acg tcg tca gca tcc tca     192
Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
    50                  55                  60

tcc gtc ggc tcg tct tca ccc ggc ggc aac tca cca act ggc agt gct     240
Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65                  70                  75                  80

tcc acc tac aca acc aca gat aca gct acc gtg gct cct cat tcg cag     288
Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
                85                  90                  95
```

```
tct cct tac ccc agc att gcc gca tcc agt tgc gga tcg tgg acc ctc      336
Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
            100                 105                 110

gtg gat aat gtt tgc tgc cca tca tat tgt gct aat gat gac aca tcc      384
Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
        115                 120                 125

gag tca tgc tca ggc tgc ggt acc tgc act acg ccg ccc tcg gcg gac      432
Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
    130                 135                 140

tgc aaa tcc gga acc atg tat cca gag gtc cat cac gta tcc agc aac      480
Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145                 150                 155                 160

gag agc tgg cac tac agt aga tca acc cac ttt ggc cta acg agc ggc      528
Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
                165                 170                 175

ggg gcc tgt ggc ttt ggc ctg tac ggt ctc tgc aca aag ggc agt gtt      576
Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
            180                 185                 190

aca gcc agc tgg acg gat ccc atg ctt ggc gcg acg tgt gac gct ttt      624
Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
        195                 200                 205

tgt aca gcg tat ccc ctg ctt tgc aaa gac cct acc ggc act acc ctt      672
Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
    210                 215                 220

cgt ggc aac ttc gca gct cca aac ggc gat tac tac acc caa ttc tgg      720
Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225                 230                 235                 240

tcc tcg ttg cca gga gcc ctc gat aac tac ctg tcc tgc ggc gag tgc      768
Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
                245                 250                 255

att gag ctg ata caa aca aag ccc gat ggg acc gat tat gct gtc gga      816
Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
            260                 265                 270

gaa gcc ggc tac acg gat cca att act ctc gag att gtg gac agc tgc      864
Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
        275                 280                 285

ccg tgc agc gcg aac tcc aag tgg tgc tgt ggt ccg ggc gcc gat cat      912
Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
    290                 295                 300

tgc gga gag atc gac ttc aaa tac ggc tgt cct ctt cct gct gac agc      960
Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305                 310                 315                 320

att cat ctc gac ctg tca gac att gcc atg ggc cgt ttg cag ggc aat     1008
Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
                325                 330                 335
```

```
gga tca cta acc aat ggc gtc atc ccg act cga tat aga aga gtc caa      1056
Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
            340                 345                 350

tgc ccc aaa gtt ggg aac gcc tac att tgg ctt cga aat ggc gga ggg      1104
Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
        355                 360                 365

cct tac tat ttt gct ctc acg gca gtc aac acc aac gga ccg ggc tca      1152
Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
    370                 375                 380

gtc acc aaa atc gag atc aag ggc gca gac acc gac aac tgg gtt gcc      1200
Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385                 390                 395                 400

ttg gtc cat gac cca aac tat acg agt agc cgc cca caa gaa cgc tat      1248
Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
                405                 410                 415

ggc agt tgg gta atc cca cag gga tca ggg ccc ttt aac ttg cct gtt      1296
Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
            420                 425                 430

gga att cgt ctg act agc cca acg ggg gaa cag att gtg aat gaa cag      1344
Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
        435                 440                 445

gcc atc aag aca ttc act cct ccg gcc aca ggt gac ccc aat ttt tac      1392
Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
    450                 455                 460

tac att gac att ggt gtg cag ttt agc cag aat ggc tcg act tac tcc      1440
Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gly Ser Thr Tyr Ser
465                 470                 475                 480

agt gga tct tct tcg ggg tcg ggg tct agc tcc agc tcg agt tcg act      1488
Ser Gly Ser Ser Ser Gly Ser Gly Ser Ser Ser Ser Ser Ser Ser Thr
                485                 490                 495

acc act aag gcc act tcg acg acc ttg aag act acc tcg acc acc agc      1536
Thr Thr Lys Ala Thr Ser Thr Thr Leu Lys Thr Thr Ser Thr Thr Ser
            500                 505                 510

agt gga agc agt tcg aca tcg gcg gcg cag caa ccg ggt acc agc acc      1584
Ser Gly Ser Ser Ser Thr Ser Ala Ala Gln Gln Pro Gly Thr Ser Thr
        515                 520                 525

ccc gag gtc cat ccc aag ttg aca acc tac aag tgt aca aag tcc ggg      1632
Pro Glu Val His Pro Lys Leu Thr Thr Tyr Lys Cys Thr Lys Ser Gly
    530                 535                 540

ggg tgc gtg gcc cag gac acc tcg gtg gtc ctt gac tgg aac tac cgc      1680
Gly Cys Val Ala Gln Asp Thr Ser Val Val Leu Asp Trp Asn Tyr Arg
545                 550                 555                 560

tgg atg cac gac gca aac tac aac tcg tgc acc gtc aac ggc ggc gtc      1728
Trp Met His Asp Ala Asn Tyr Asn Ser Cys Thr Val Asn Gly Gly Val
                565                 570                 575

aac acc acg ctc tgc cct gac gag gcg acc tgt ggc aag aac tgc ttc      1776
```

```
Asn Thr Thr Leu Cys Pro Asp Glu Ala Thr Cys Gly Lys Asn Cys Phe
            580                 585                 590

atc gag ggc gtc gac tac gcc gcc tcg ggc gtc acg acc tcg ggc agc    1824
Ile Glu Gly Val Asp Tyr Ala Ala Ser Gly Val Thr Thr Ser Gly Ser
        595                 600                 605

agc ctc acc atg aac cag tac atg ccc agc agc tct ggc ggc tac agc    1872
Ser Leu Thr Met Asn Gln Tyr Met Pro Ser Ser Ser Gly Gly Tyr Ser
    610                 615                 620

agc gtc tct cct cgg ctg tat ctc ctg gac tct gac ggt gag tac gtg    1920
Ser Val Ser Pro Arg Leu Tyr Leu Leu Asp Ser Asp Gly Glu Tyr Val
625                 630                 635                 640

atg ctg aag ctc aac ggc cag gag ctg agc ttc gac gtc gac ctc tct    1968
Met Leu Lys Leu Asn Gly Gln Glu Leu Ser Phe Asp Val Asp Leu Ser
                645                 650                 655

gct ctg ccg tgt gga gag aac ggc tcg ctc tac ctg tct cag atg gac    2016
Ala Leu Pro Cys Gly Glu Asn Gly Ser Leu Tyr Leu Ser Gln Met Asp
            660                 665                 670

gag aac ggg ggc gcc aac cag tat aac acg gcc ggt gcc aac tac ggg    2064
Glu Asn Gly Gly Ala Asn Gln Tyr Asn Thr Ala Gly Ala Asn Tyr Gly
        675                 680                 685

agc ggc tac tgc gat gct cag tgc ccc gtc cag aca tgg agg aac ggc    2112
Ser Gly Tyr Cys Asp Ala Gln Cys Pro Val Gln Thr Trp Arg Asn Gly
    690                 695                 700

acc ctc aac act agc cac cag ggc ttc tgc tgc aac gag atg gat atc    2160
Thr Leu Asn Thr Ser His Gln Gly Phe Cys Cys Asn Glu Met Asp Ile
705                 710                 715                 720

ctg gag ggc aac tcg agg gcg aat gcc ttg acc cct cac tct tgc acg    2208
Leu Glu Gly Asn Ser Arg Ala Asn Ala Leu Thr Pro His Ser Cys Thr
                725                 730                 735

gcc acg gcc tgc gac tct gcc ggt tgc ggc ttc aac ccc tat ggc agc    2256
Ala Thr Ala Cys Asp Ser Ala Gly Cys Gly Phe Asn Pro Tyr Gly Ser
            740                 745                 750

ggc tac aaa agc tac tac ggc ccc gga gat acc gtt gac acc tcc aag    2304
Gly Tyr Lys Ser Tyr Tyr Gly Pro Gly Asp Thr Val Asp Thr Ser Lys
        755                 760                 765

acc ttc acc atc atc acc cag ttc aac acg gac aac ggc tcg ccc tcg    2352
Thr Phe Thr Ile Ile Thr Gln Phe Asn Thr Asp Asn Gly Ser Pro Ser
    770                 775                 780

ggc aac ctt gtg agc atc acc cgc aag tac cag caa aac ggc gtc gac    2400
Gly Asn Leu Val Ser Ile Thr Arg Lys Tyr Gln Gln Asn Gly Val Asp
785                 790                 795                 800

atc ccc agc gcc cag ccc ggc ggc gac acc atc tcg tcc tgc ccg tcc    2448
Ile Pro Ser Ala Gln Pro Gly Gly Asp Thr Ile Ser Ser Cys Pro Ser
                805                 810                 815

gcc tca gcc tac ggc ggc ctc gcc acc atg ggc aag gcc ctg agc agc    2496
Ala Ser Ala Tyr Gly Gly Leu Ala Thr Met Gly Lys Ala Leu Ser Ser
```

```
                820                 825                 830

ggc atg gtg ctc gtg ttc agc att tgg aac gac aac agc cag tac atg     2544
Gly Met Val Leu Val Phe Ser Ile Trp Asn Asp Asn Ser Gln Tyr Met
        835                 840                 845

aac tgg ctc gac agc ggc aac gcc ggc ccc tgc agc agc acc gag ggc     2592
Asn Trp Leu Asp Ser Gly Asn Ala Gly Pro Cys Ser Ser Thr Glu Gly
    850                 855                 860

aac cca tcc aac atc ctg gcc aac aac ccc aac acg cac gtc gtc ttc     2640
Asn Pro Ser Asn Ile Leu Ala Asn Asn Pro Asn Thr His Val Val Phe
865                 870                 875                 880

tcc aac atc cgc tgg gga gac att ggg tct act acg aac tcg act gcg     2688
Ser Asn Ile Arg Trp Gly Asp Ile Gly Ser Thr Thr Asn Ser Thr Ala
                885                 890                 895

ccc ccg ccc ccg cct gcg tcc agc acg acg ttt tcg act aca cgg agg     2736
Pro Pro Pro Pro Pro Ala Ser Ser Thr Thr Phe Ser Thr Thr Arg Arg
            900                 905                 910

agc tcg acg act tcg agc agc ccg agc tgc acg cag act cac tgg ggg     2784
Ser Ser Thr Thr Ser Ser Ser Pro Ser Cys Thr Gln Thr His Trp Gly
        915                 920                 925

cag tgc ggt ggc att ggg tac agc ggg tgc aag acg tgc acg tcg ggc     2832
Gln Cys Gly Gly Ile Gly Tyr Ser Gly Cys Lys Thr Cys Thr Ser Gly
    930                 935                 940

act acg tgc cag tat agc aac gac tac tac tcg caa tgc ctt tag         2877
Thr Thr Cys Gln Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys Leu
945                 950                 955
```

<210> 60
<211> 958
<212> PRT
<213> Seqüência artificial

<220>
<223> Construção Sintética

<400> 60

```
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1               5                   10                  15

Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
            20                  25                  30

Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
        35                  40                  45

Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
    50                  55                  60
```

Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65 70 75 80

Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
85 90 95

Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
100 105 110

Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
115 120 125

Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
130 135 140

Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145 150 155 160

Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
165 170 175

Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
180 185 190

Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
195 200 205

Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
210 215 220

Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225 230 235 240

Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
245 250 255

Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
260 265 270

Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
275 280 285

Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
290 295 300

Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser

305 310 315 320

Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
325 330 335

Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
340 345 350

Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
355 360 365

Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
370 375 380

Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385 390 395 400

Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
405 410 415

Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
420 425 430

Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
435 440 445

Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
450 455 460

Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gly Ser Thr Tyr Ser
465 470 475 480

Ser Gly Ser Ser Ser Gly Ser Gly Ser Ser Ser Ser Ser Ser Ser Thr
485 490 495

Thr Thr Lys Ala Thr Ser Thr Thr Leu Lys Thr Thr Ser Thr Thr Ser
500 505 510

Ser Gly Ser Ser Ser Thr Ser Ala Ala Gln Gln Pro Gly Thr Ser Thr
515 520 525

Pro Glu Val His Pro Lys Leu Thr Thr Tyr Lys Cys Thr Lys Ser Gly
530 535 540

Gly Cys Val Ala Gln Asp Thr Ser Val Val Leu Asp Trp Asn Tyr Arg
545 550 555 560

Trp Met His Asp Ala Asn Tyr Asn Ser Cys Thr Val Asn Gly Gly Val
565 570 575

Asn Thr Thr Leu Cys Pro Asp Glu Ala Thr Cys Gly Lys Asn Cys Phe
580 585 590

Ile Glu Gly Val Asp Tyr Ala Ala Ser Gly Val Thr Thr Ser Gly Ser
595 600 605

Ser Leu Thr Met Asn Gln Tyr Met Pro Ser Ser Ser Gly Gly Tyr Ser
610 615 620

Ser Val Ser Pro Arg Leu Tyr Leu Leu Asp Ser Asp Gly Glu Tyr Val
625 630 635 640

Met Leu Lys Leu Asn Gly Gln Glu Leu Ser Phe Asp Val Asp Leu Ser
645 650 655

Ala Leu Pro Cys Gly Glu Asn Gly Ser Leu Tyr Leu Ser Gln Met Asp
660 665 670

Glu Asn Gly Gly Ala Asn Gln Tyr Asn Thr Ala Gly Ala Asn Tyr Gly
675 680 685

Ser Gly Tyr Cys Asp Ala Gln Cys Pro Val Gln Thr Trp Arg Asn Gly
690 695 700

Thr Leu Asn Thr Ser His Gln Gly Phe Cys Cys Asn Glu Met Asp Ile
705 710 715 720

Leu Glu Gly Asn Ser Arg Ala Asn Ala Leu Thr Pro His Ser Cys Thr
725 730 735

Ala Thr Ala Cys Asp Ser Ala Gly Cys Gly Phe Asn Pro Tyr Gly Ser
740 745 750

Gly Tyr Lys Ser Tyr Tyr Gly Pro Gly Asp Thr Val Asp Thr Ser Lys
755 760 765

Thr Phe Thr Ile Ile Thr Gln Phe Asn Thr Asp Asn Gly Ser Pro Ser
770 775 780

Gly Asn Leu Val Ser Ile Thr Arg Lys Tyr Gln Gln Asn Gly Val Asp
785 790 795 800

Ile Pro Ser Ala Gln Pro Gly Gly Asp Thr Ile Ser Ser Cys Pro Ser
805 810 815

Ala Ser Ala Tyr Gly Gly Leu Ala Thr Met Gly Lys Ala Leu Ser Ser
820 825 830

Gly Met Val Leu Val Phe Ser Ile Trp Asn Asp Asn Ser Gln Tyr Met
835 840 845

Asn Trp Leu Asp Ser Gly Asn Ala Gly Pro Cys Ser Ser Thr Glu Gly
850 855 860

Asn Pro Ser Asn Ile Leu Ala Asn Asn Pro Asn Thr His Val Val Phe
865 870 875 880

Ser Asn Ile Arg Trp Gly Asp Ile Gly Ser Thr Thr Asn Ser Thr Ala
885 890 895

Pro Pro Pro Pro Pro Ala Ser Ser Thr Thr Phe Ser Thr Thr Arg Arg
900 905 910

Ser Ser Thr Thr Ser Ser Ser Pro Ser Cys Thr Gln Thr His Trp Gly
915 920 925

Gln Cys Gly Gly Ile Gly Tyr Ser Gly Cys Lys Thr Cys Thr Ser Gly
930 935 940

Thr Thr Cys Gln Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys Leu
945 950 955

<210> 61
<211> 2625
<212> DNA
<213> Seqüência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2625)

<400> 61
cag cag aat tgc gca gca tta ttt ggc caa tgt gga ggc ata ggg tgg 48
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1 5 10 15

tcc ggc acc aca tgt tgc gtt gct ggc gcc cag tgc agt ttt gtc aat 96
Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn

```
                20                  25                  30

gac tgg tac tcc cag tgc ctt gcg tca acc ggc gga aac ccc cca aac      144
Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
        35                  40                  45

gga aca act tcc tct agc ttg gtt tca cgg acg tcg tca gca tcc tca      192
Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
    50                  55                  60

tcc gtc ggc tcg tct tca ccc ggc ggc aac tca cca act ggc agt gct      240
Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65                  70                  75                  80

tcc acc tac aca acc aca gat aca gct acc gtg gct cct cat tcg cag      288
Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
                85                  90                  95

tct cct tac ccc agc att gcc gca tcc agt tgc gga tcg tgg acc ctc      336
Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
            100                 105                 110

gtg gat aat gtt tgc tgc cca tca tat tgt gct aat gat gac aca tcc      384
Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
        115                 120                 125

gag tca tgc tca ggc tgc ggt acc tgc act acg ccg ccc tcg gcg gac      432
Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
    130                 135                 140

tgc aaa tcc gga acc atg tat cca gag gtc cat cac gta tcc agc aac      480
Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145                 150                 155                 160

gag agc tgg cac tac agt aga tca acc cac ttt ggc cta acg agc ggc      528
Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
                165                 170                 175

ggg gcc tgt ggc ttt ggc ctg tac ggt ctc tgc aca aag ggc agt gtt      576
Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
            180                 185                 190

aca gcc agc tgg acg gat ccc atg ctt ggc gcg acg tgt gac gct ttt      624
Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
        195                 200                 205

tgt aca gcg tat ccc ctg ctt tgc aaa gac cct acc ggc act acc ctt      672
Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
    210                 215                 220

cgt ggc aac ttc gca gct cca aac ggc gat tac tac acc caa ttc tgg      720
Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225                 230                 235                 240

tcc tcg ttg cca gga gcc ctc gat aac tac ctg tcc tgc ggc gag tgc      768
Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
                245                 250                 255

att gag ctg ata caa aca aag ccc gat ggg acc gat tat gct gtc gga      816
Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
            260                 265                 270
```

```
gaa gcc ggc tac acg gat cca att act ctc gag att gtg gac agc tgc                 864
Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
        275                 280                 285

ccg tgc agc gcg aac tcc aag tgg tgc tgt ggt ccg ggc gcc gat cat                 912
Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
    290                 295                 300

tgc gga gag atc gac ttc aaa tac ggc tgt cct ctt cct gct gac agc                 960
Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305                 310                 315                 320

att cat ctc gac ctg tca gac att gcc atg ggc cgt ttg cag ggc aat                1008
Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
                325                 330                 335

gga tca cta acc aat ggc gtc atc ccg act cga tat aga aga gtc caa                1056
Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
            340                 345                 350

tgc ccc aaa gtt ggg aac gcc tac att tgg ctt cga aat ggc gga ggg                1104
Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
        355                 360                 365

cct tac tat ttt gct ctc acg gca gtc aac acc aac gga ccg ggc tca                1152
Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
    370                 375                 380

gtc acc aaa atc gag atc aag ggc gca gac acc gac aac tgg gtt gcc                1200
Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385                 390                 395                 400

ttg gtc cat gac cca aac tat acg agt agc cgc cca caa gaa cgc tat                1248
Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
                405                 410                 415

ggc agt tgg gta atc cca cag gga tca ggg ccc ttt aac ttg cct gtt                1296
Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
            420                 425                 430

gga att cgt ctg act agc cca acg ggg gaa cag att gtg aat gaa cag                1344
Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
        435                 440                 445

gcc atc aag aca ttc act cct ccg gcc aca ggt gac ccc aat ttt tac                1392
Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
    450                 455                 460

tac att gac att ggt gtg cag ttt agc cag aat cag caa ccg ggt acc                1440
Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gln Gln Pro Gly Thr
465                 470                 475                 480

agc acc ccc gag gtc cat ccc aag ttg aca acc tac aag tgt aca aag                1488
Ser Thr Pro Glu Val His Pro Lys Leu Thr Thr Tyr Lys Cys Thr Lys
                485                 490                 495

tcc ggg ggg tgc gtg gcc cag gac acc tcg gtg gtc ctt gac tgg aac                1536
Ser Gly Gly Cys Val Ala Gln Asp Thr Ser Val Val Leu Asp Trp Asn
            500                 505                 510
```

```
tac cgc tgg atg cac gac gca aac tac aac tcg tgc acc gtc aac ggc      1584
Tyr Arg Trp Met His Asp Ala Asn Tyr Asn Ser Cys Thr Val Asn Gly
        515                 520                 525

ggc gtc aac acc acg ctc tgc cct gac gag gcg acc tgt ggc aag aac      1632
Gly Val Asn Thr Thr Leu Cys Pro Asp Glu Ala Thr Cys Gly Lys Asn
    530                 535                 540

tgc ttc atc gag ggc gtc gac tac gcc gcc tcg ggc gtc acg acc tcg      1680
Cys Phe Ile Glu Gly Val Asp Tyr Ala Ala Ser Gly Val Thr Thr Ser
545                 550                 555                 560

ggc agc agc ctc acc atg aac cag tac atg ccc agc agc tct ggc ggc      1728
Gly Ser Ser Leu Thr Met Asn Gln Tyr Met Pro Ser Ser Ser Gly Gly
                565                 570                 575

tac agc agc gtc tct cct cgg ctg tat ctc ctg gac tct gac ggt gag      1776
Tyr Ser Ser Val Ser Pro Arg Leu Tyr Leu Leu Asp Ser Asp Gly Glu
            580                 585                 590

tac gtg atg ctg aag ctc aac ggc cag gag ctg agc ttc gac gtc gac      1824
Tyr Val Met Leu Lys Leu Asn Gly Gln Glu Leu Ser Phe Asp Val Asp
        595                 600                 605

ctc tct gct ctg ccg tgt gga gag aac ggc tcg ctc tac ctg tct cag      1872
Leu Ser Ala Leu Pro Cys Gly Glu Asn Gly Ser Leu Tyr Leu Ser Gln
    610                 615                 620

atg gac gag aac ggg ggc gcc aac cag tat aac acg gcc ggt gcc aac      1920
Met Asp Glu Asn Gly Gly Ala Asn Gln Tyr Asn Thr Ala Gly Ala Asn
625                 630                 635                 640

tac ggg agc ggc tac tgc gat gct cag tgc ccc gtc cag aca tgg agg      1968
Tyr Gly Ser Gly Tyr Cys Asp Ala Gln Cys Pro Val Gln Thr Trp Arg
                645                 650                 655

aac ggc acc ctc aac act agc cac cag ggc ttc tgc tgc aac gag atg      2016
Asn Gly Thr Leu Asn Thr Ser His Gln Gly Phe Cys Cys Asn Glu Met
            660                 665                 670

gat atc ctg gag ggc aac tcg agg gcg aat gcc ttg acc cct cac tct      2064
Asp Ile Leu Glu Gly Asn Ser Arg Ala Asn Ala Leu Thr Pro His Ser
        675                 680                 685

tgc acg gcc acg gcc tgc gac tct gcc ggt tgc ggc ttc aac ccc tat      2112
Cys Thr Ala Thr Ala Cys Asp Ser Ala Gly Cys Gly Phe Asn Pro Tyr
    690                 695                 700

ggc agc ggc tac aaa agc tac tac ggc ccc gga gat acc gtt gac acc      2160
Gly Ser Gly Tyr Lys Ser Tyr Tyr Gly Pro Gly Asp Thr Val Asp Thr
705                 710                 715                 720

tcc aag acc ttc acc atc atc acc cag ttc aac acg gac aac ggc tcg      2208
Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe Asn Thr Asp Asn Gly Ser
                725                 730                 735

ccc tcg ggc aac ctt gtg agc atc acc cgc aag tac cag caa aac ggc      2256
Pro Ser Gly Asn Leu Val Ser Ile Thr Arg Lys Tyr Gln Gln Asn Gly
            740                 745                 750

gtc gac atc ccc agc gcc cag ccc ggc ggc gac acc atc tcg tcc tgc      2304
```

Val Asp Ile Pro Ser Ala Gln Pro Gly Gly Asp Thr Ile Ser Ser Cys
755 760 765

ccg tcc gcc tca gcc tac ggc ggc ctc gcc acc atg ggc aag gcc ctg 2352
Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala Thr Met Gly Lys Ala Leu
770 775 780

agc agc ggc atg gtg ctc gtg ttc agc att tgg aac gac aac agc cag 2400
Ser Ser Gly Met Val Leu Val Phe Ser Ile Trp Asn Asp Asn Ser Gln
785 790 795 800

tac atg aac tgg ctc gac agc ggc aac gcc ggc ccc tgc agc agc acc 2448
Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala Gly Pro Cys Ser Ser Thr
805 810 815

gag ggc aac cca tcc aac atc ctg gcc aac aac ccc aac acg cac gtc 2496
Glu Gly Asn Pro Ser Asn Ile Leu Ala Asn Asn Pro Asn Thr His Val
820 825 830

[illegible]c ttc tcc aac atc cgc tgg gga gac att ggg tct act acg aac tcg 2544
[illegible]al Phe Ser Asn Ile Arg Trp Gly Asp Ile Gly Ser Thr Thr Asn Ser
835 840 845

act gcg ccc ccg ccc ccg cct gcg tcc agc acg acg ttt tcg act aca 2592
Thr Ala Pro Pro Pro Pro Pro Ala Ser Ser Thr Thr Phe Ser Thr Thr
850 855 860

cgg agg agc tcg acg act tcg agc agc ccg agc 2625
Arg Arg Ser Ser Thr Thr Ser Ser Ser Pro Ser
865 870 875

<210> 62
<211> 875
<212> PRT
<213> Sequência artificial

<220>
<223> Construção Sintética

<400> 62

Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1 5 10 15

Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
20 25 30

Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
35 40 45

Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
50 55 60

Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65 70 75 80

Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
85 90 95

Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
100 105 110

Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
115 120 125

Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
130 135 140

Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145 150 155 160

Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
165 170 175

Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
180 185 190

Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
195 200 205

Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
210 215 220

Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225 230 235 240

Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
245 250 255

Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
260 265 270

Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
275 280 285

Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
290 295 300

Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305 310 315 320

Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
325 330 335

Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
340 345 350

Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
355 360 365

Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
370 375 380

Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385 390 395 400

Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
405 410 415

Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
420 425 430

Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
435 440 445

Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
450 455 460

Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gln Gln Pro Gly Thr
465 470 475 480

Ser Thr Pro Glu Val His Pro Lys Leu Thr Thr Tyr Lys Cys Thr Lys
485 490 495

Ser Gly Gly Cys Val Ala Gln Asp Thr Ser Val Val Leu Asp Trp Asn
500 505 510

Tyr Arg Trp Met His Asp Ala Asn Tyr Asn Ser Cys Thr Val Asn Gly
515 520 525

Gly Val Asn Thr Thr Leu Cys Pro Asp Glu Ala Thr Cys Gly Lys Asn
530 535 540

Cys Phe Ile Glu Gly Val Asp Tyr Ala Ala Ser Gly Val Thr Thr Ser
545 550 555 560

Gly Ser Ser Leu Thr Met Asn Gln Tyr Met Pro Ser Ser Ser Gly Gly

565 570 575

Tyr Ser Ser Val Ser Pro Arg Leu Tyr Leu Leu Asp Ser Asp Gly Glu
580 585 590

Tyr Val Met Leu Lys Leu Asn Gly Gln Glu Leu Ser Phe Asp Val Asp
595 600 605

Leu Ser Ala Leu Pro Cys Gly Glu Asn Gly Ser Leu Tyr Leu Ser Gln
610 615 620

Met Asp Glu Asn Gly Gly Ala Asn Gln Tyr Asn Thr Ala Gly Ala Asn
625 630 635 640

Tyr Gly Ser Gly Tyr Cys Asp Ala Gln Cys Pro Val Gln Thr Trp Arg
645 650 655

Asn Gly Thr Leu Asn Thr Ser His Gln Gly Phe Cys Cys Asn Glu Met
660 665 670

Asp Ile Leu Glu Gly Asn Ser Arg Ala Asn Ala Leu Thr Pro His Ser
675 680 685

Cys Thr Ala Thr Ala Cys Asp Ser Ala Gly Cys Gly Phe Asn Pro Tyr
690 695 700

Gly Ser Gly Tyr Lys Ser Tyr Tyr Gly Pro Gly Asp Thr Val Asp Thr
705 710 715 720

Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe Asn Thr Asp Asn Gly Ser
725 730 735

Pro Ser Gly Asn Leu Val Ser Ile Thr Arg Lys Tyr Gln Gln Asn Gly
740 745 750

Val Asp Ile Pro Ser Ala Gln Pro Gly Gly Asp Thr Ile Ser Ser Cys
755 760 765

Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala Thr Met Gly Lys Ala Leu
770 775 780

Ser Ser Gly Met Val Leu Val Phe Ser Ile Trp Asn Asp Asn Ser Gln
785 790 795 800

Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala Gly Pro Cys Ser Ser Thr
805 810 815

Glu Gly Asn Pro Ser Asn Ile Leu Ala Asn Asn Pro Asn Thr His Val
820 825 830

Val Phe Ser Asn Ile Arg Trp Gly Asp Ile Gly Ser Thr Thr Asn Ser
835 840 845

Thr Ala Pro Pro Pro Pro Pro Ala Ser Ser Thr Thr Phe Ser Thr Thr
850 855 860

Arg Arg Ser Ser Thr Thr Ser Ser Ser Pro Ser
865 870 875

<210> 63
<211> 2763
<212> DNA
<213> Sequência artificial
<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2763)

<400> 63
cag cag aat tgc gca gca tta ttt ggc caa tgt gga ggc ata ggg tgg 48
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1 5 10 15

tcc ggc acc aca tgt tgc gtt gct ggc gcc cag tgc agt ttt gtc aat 96
Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
20 25 30

gac tgg tac tcc cag tgc ctt gcg tca acc ggc gga aac ccc cca aac 144
Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
35 40 45

gga aca act tcc tct agc ttg gtt tca cgg acg tcg tca gca tcc tca 192
Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
50 55 60

tcc gtc ggc tcg tct tca ccc ggc ggc aac tca cca act ggc agt gct 240
Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65 70 75 80

tcc acc tac aca acc aca gat aca gct acc gtg gct cct cat tcg cag 288
Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
85 90 95

tct cct tac ccc agc att gcc gca tcc agt tgc gga tcg tgg acc ctc 336
Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
100 105 110

gtg gat aat gtt tgc tgc cca tca tat tgt gct aat gat gac aca tcc 384

```
Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
        115                 120                 125

gag tca tgc tca ggc tgc ggt acc tgc act acg ccg ccc tcg gcg gac      432
Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
    130                 135                 140

tgc aaa tcc gga acc atg tat cca gag gtc cat cac gta tcc agc aac      480
Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145                 150                 155                 160

gag agc tgg cac tac agt aga tca acc cac ttt ggc cta acg agc ggc      528
Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
                165                 170                 175

ggg gcc tgt ggc ttt ggc ctg tac ggt ctc tgc aca aag ggc agt gtt      576
Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
            180                 185                 190

aca gcc agc tgg acg gat ccc atg ctt ggc gcg acg tgt gac gct ttt      624
Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
        195                 200                 205

tgt aca gcg tat ccc ctg ctt tgc aaa gac cct acc ggc act acc ctt      672
Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
    210                 215                 220

cgt ggc aac ttc gca gct cca aac ggc gat tac tac acc caa ttc tgg      720
Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225                 230                 235                 240

tcc tcg ttg cca gga gcc ctc gat aac tac ctg tcc tgc ggc gag tgc      768
Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
                245                 250                 255

att gag ctg ata caa aca aag ccc gat ggg acc gat tat gct gtc gga      816
Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
            260                 265                 270

gaa gcc ggc tac acg gat cca att act ctc gag att gtg gac agc tgc      864
Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
        275                 280                 285

ccg tgc agc gcg aac tcc aag tgg tgc tgt ggt ccg ggc gcc gat cat      912
Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
    290                 295                 300

tgc gga gag atc gac ttc aaa tac ggc tgt cct ctt cct gct gac agc      960
Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305                 310                 315                 320

att cat ctc gac ctg tca gac att gcc atg ggc cgt ttg cag ggc aat     1008
Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
                325                 330                 335

gga tca cta acc aat ggc gtc atc ccg act cga tat aga aga gtc caa     1056
Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
            340                 345                 350

tgc ccc aaa gtt ggg aac gcc tac att tgg ctt cga aat ggc gga ggg     1104
Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
```

```
                355                 360                 365
cct tac tat ttt gct ctc acg gca gtc aac acc aac gga ccg ggc tca   1152
Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
    370                 375                 380

gtc acc aaa atc gag atc aag ggc gca gac acc gac aac tgg gtt gcc   1200
Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385                 390                 395                 400

ttg gtc cat gac cca aac tat acg agt agc cgc cca caa gaa cgc tat   1248
Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
                405                 410                 415

ggc agt tgg gta atc cca cag gga tca ggg ccc ttt aac ttg cct gtt   1296
Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
            420                 425                 430

gga att cgt ctg act agc cca acg ggg gaa cag att gtg aat gaa cag   1344
Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
        435                 440                 445

gcc atc aag aca ttc act cct ccg gcc aca ggt gac ccc aat ttt tac   1392
Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
    450                 455                 460

tac att gac att ggt gtg cag ttt agc cag aat ggc tcg act tac tcc   1440
Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gly Ser Thr Tyr Ser
465                 470                 475                 480

agt gga tct tct tcg ggg tcg ggg tct agc tcc agc tcg agt tcg act   1488
Ser Gly Ser Ser Ser Gly Ser Gly Ser Ser Ser Ser Ser Ser Ser Thr
                485                 490                 495

acc act aag gcc act tcg acg acc ttg aag act acc tcg acc acc agc   1536
Thr Thr Lys Ala Thr Ser Thr Thr Leu Lys Thr Thr Ser Thr Thr Ser
            500                 505                 510

agt gga agc agt tcg aca tcg gcg gcg cag caa ccg ggt acc agc acc   1584
Ser Gly Ser Ser Ser Thr Ser Ala Ala Gln Gln Pro Gly Thr Ser Thr
        515                 520                 525

ccc gag gtc cat ccc aag ttg aca acc tac aag tgt aca aag tcc ggg   1632
Pro Glu Val His Pro Lys Leu Thr Thr Tyr Lys Cys Thr Lys Ser Gly
    530                 535                 540

ggg tgc gtg gcc cag gac acc tcg gtg gtc ctt gac tgg aac tac cgc   1680
Gly Cys Val Ala Gln Asp Thr Ser Val Val Leu Asp Trp Asn Tyr Arg
545                 550                 555                 560

tgg atg cac gac gca aac tac aac tcg tgc acc gtc aac ggc ggc gtc   1728
Trp Met His Asp Ala Asn Tyr Asn Ser Cys Thr Val Asn Gly Gly Val
                565                 570                 575

aac acc acg ctc tgc cct gac gag gcg acc tgt ggc aag aac tgc ttc   1776
Asn Thr Thr Leu Cys Pro Asp Glu Ala Thr Cys Gly Lys Asn Cys Phe
            580                 585                 590

atc gag ggc gtc gac tac gcc gcc tcg ggc gtc acg acc tcg ggc agc   1824
Ile Glu Gly Val Asp Tyr Ala Ala Ser Gly Val Thr Thr Ser Gly Ser
        595                 600                 605
```

```
agc ctc acc atg aac cag tac atg ccc agc agc tct ggc ggc tac agc      1872
Ser Leu Thr Met Asn Gln Tyr Met Pro Ser Ser Ser Gly Gly Tyr Ser
    610                 615                 620

agc gtc tct cct cgg ctg tat ctc ctg gac tct gac ggt gag tac gtg      1920
Ser Val Ser Pro Arg Leu Tyr Leu Leu Asp Ser Asp Gly Glu Tyr Val
625                 630                 635                 640

atg ctg aag ctc aac ggc cag gag ctg agc ttc gac gtc gac ctc tct      1968
Met Leu Lys Leu Asn Gly Gln Glu Leu Ser Phe Asp Val Asp Leu Ser
                645                 650                 655

gct ctg ccg tgt gga gag aac ggc tcg ctc tac ctg tct cag atg gac      2016
Ala Leu Pro Cys Gly Glu Asn Gly Ser Leu Tyr Leu Ser Gln Met Asp
            660                 665                 670

gag aac ggg ggc gcc aac cag tat aac acg gcc ggt gcc aac tac ggg      2064
Glu Asn Gly Gly Ala Asn Gln Tyr Asn Thr Ala Gly Ala Asn Tyr Gly
        675                 680                 685

agc ggc tac tgc gat gct cag tgc ccc gtc cag aca tgg agg aac ggc      2112
Ser Gly Tyr Cys Asp Ala Gln Cys Pro Val Gln Thr Trp Arg Asn Gly
    690                 695                 700

acc ctc aac act agc cac cag ggc ttc tgc tgc aac gag atg gat atc      2160
Thr Leu Asn Thr Ser His Gln Gly Phe Cys Cys Asn Glu Met Asp Ile
705                 710                 715                 720

ctg gag ggc aac tcg agg gcg aat gcc ttg acc cct cac tct tgc acg      2208
Leu Glu Gly Asn Ser Arg Ala Asn Ala Leu Thr Pro His Ser Cys Thr
                725                 730                 735

gcc acg gcc tgc gac tct gcc ggt tgc ggc ttc aac ccc tat ggc agc      2256
Ala Thr Ala Cys Asp Ser Ala Gly Cys Gly Phe Asn Pro Tyr Gly Ser
            740                 745                 750

ggc tac aaa agc tac tac ggc ccc gga gat acc gtt gac acc tcc aag      2304
Gly Tyr Lys Ser Tyr Tyr Gly Pro Gly Asp Thr Val Asp Thr Ser Lys
        755                 760                 765

acc ttc acc atc atc acc cag ttc aac acg gac aac ggc tcg ccc tcg      2352
Thr Phe Thr Ile Ile Thr Gln Phe Asn Thr Asp Asn Gly Ser Pro Ser
    770                 775                 780

ggc aac ctt gtg agc atc acc cgc aag tac cag caa aac ggc gtc gac      2400
Gly Asn Leu Val Ser Ile Thr Arg Lys Tyr Gln Gln Asn Gly Val Asp
785                 790                 795                 800

atc ccc agc gcc cag ccc ggc ggc gac acc atc tcg tcc tgc ccg tcc      2448
Ile Pro Ser Ala Gln Pro Gly Gly Asp Thr Ile Ser Ser Cys Pro Ser
                805                 810                 815

gcc tca gcc tac ggc ggc ctc gcc acc atg ggc aag gcc ctg agc agc      2496
Ala Ser Ala Tyr Gly Gly Leu Ala Thr Met Gly Lys Ala Leu Ser Ser
            820                 825                 830

ggc atg gtg ctc gtg ttc agc att tgg aac gac aac agc cag tac atg      2544
Gly Met Val Leu Val Phe Ser Ile Trp Asn Asp Asn Ser Gln Tyr Met
        835                 840                 845
```

```
aac tgg ctc gac agc ggc aac gcc ggc ccc tgc agc agc acc gag ggc      2592
Asn Trp Leu Asp Ser Gly Asn Ala Gly Pro Cys Ser Ser Thr Glu Gly
    850                 855                 860

aac cca tcc aac atc ctg gcc aac aac ccc aac acg cac gtc gtc ttc      2640
Asn Pro Ser Asn Ile Leu Ala Asn Asn Pro Asn Thr His Val Val Phe
865                 870                 875                 880

tcc aac atc cgc tgg gga gac att ggg tct act acg aac tcg act gcg      2688
Ser Asn Ile Arg Trp Gly Asp Ile Gly Ser Thr Thr Asn Ser Thr Ala
                885                 890                 895

ccc ccg ccc ccg cct gcg tcc agc acg acg ttt tcg act aca cgg agg      2736
Pro Pro Pro Pro Pro Ala Ser Ser Thr Thr Phe Ser Thr Thr Arg Arg
            900                 905                 910

agc tcg acg act tcg agc agc ccg agc                                 2763
Ser Ser Thr Thr Ser Ser Ser Pro Ser
        915                 920
```

<210> 64
<211> 921
<212> PRT
<213> Sequência artificial

<220>
<223> Construção Sintética

<400> 64

```
Gln Gln Asn Cys Ala Ala Leu Phe Gly Gln Cys Gly Gly Ile Gly Trp
1               5                   10                  15

Ser Gly Thr Thr Cys Cys Val Ala Gly Ala Gln Cys Ser Phe Val Asn
            20                  25                  30

Asp Trp Tyr Ser Gln Cys Leu Ala Ser Thr Gly Gly Asn Pro Pro Asn
        35                  40                  45

Gly Thr Thr Ser Ser Ser Leu Val Ser Arg Thr Ser Ser Ala Ser Ser
    50                  55                  60

Ser Val Gly Ser Ser Ser Pro Gly Gly Asn Ser Pro Thr Gly Ser Ala
65                  70                  75                  80

Ser Thr Tyr Thr Thr Thr Asp Thr Ala Thr Val Ala Pro His Ser Gln
                85                  90                  95

Ser Pro Tyr Pro Ser Ile Ala Ala Ser Ser Cys Gly Ser Trp Thr Leu
            100                 105                 110

Val Asp Asn Val Cys Cys Pro Ser Tyr Cys Ala Asn Asp Asp Thr Ser
        115                 120                 125
```

Glu Ser Cys Ser Gly Cys Gly Thr Cys Thr Thr Pro Pro Ser Ala Asp
130 135 140

Cys Lys Ser Gly Thr Met Tyr Pro Glu Val His His Val Ser Ser Asn
145 150 155 160

Glu Ser Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr Ser Gly
165 170 175

Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Gly Ser Val
180 185 190

Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ala Thr Cys Asp Ala Phe
195 200 205

Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Thr Gly Thr Thr Leu
210 215 220

Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln Phe Trp
225 230 235 240

Ser Ser Leu Pro Gly Ala Leu Asp Asn Tyr Leu Ser Cys Gly Glu Cys
245 250 255

Ile Glu Leu Ile Gln Thr Lys Pro Asp Gly Thr Asp Tyr Ala Val Gly
260 265 270

Glu Ala Gly Tyr Thr Asp Pro Ile Thr Leu Glu Ile Val Asp Ser Cys
275 280 285

Pro Cys Ser Ala Asn Ser Lys Trp Cys Cys Gly Pro Gly Ala Asp His
290 295 300

Cys Gly Glu Ile Asp Phe Lys Tyr Gly Cys Pro Leu Pro Ala Asp Ser
305 310 315 320

Ile His Leu Asp Leu Ser Asp Ile Ala Met Gly Arg Leu Gln Gly Asn
325 330 335

Gly Ser Leu Thr Asn Gly Val Ile Pro Thr Arg Tyr Arg Arg Val Gln
340 345 350

Cys Pro Lys Val Gly Asn Ala Tyr Ile Trp Leu Arg Asn Gly Gly Gly
355 360 365

Pro Tyr Tyr Phe Ala Leu Thr Ala Val Asn Thr Asn Gly Pro Gly Ser
370 375 380

Val Thr Lys Ile Glu Ile Lys Gly Ala Asp Thr Asp Asn Trp Val Ala
385 390 395 400

Leu Val His Asp Pro Asn Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr
405 410 415

Gly Ser Trp Val Ile Pro Gln Gly Ser Gly Pro Phe Asn Leu Pro Val
420 425 430

Gly Ile Arg Leu Thr Ser Pro Thr Gly Glu Gln Ile Val Asn Glu Gln
435 440 445

Ala Ile Lys Thr Phe Thr Pro Pro Ala Thr Gly Asp Pro Asn Phe Tyr
450 455 460

Tyr Ile Asp Ile Gly Val Gln Phe Ser Gln Asn Gly Ser Thr Tyr Ser
465 470 475 480

Ser Gly Ser Ser Ser Gly Ser Gly Ser Ser Ser Ser Ser Ser Ser Thr
485 490 495

Thr Thr Lys Ala Thr Ser Thr Thr Leu Lys Thr Thr Ser Thr Thr Ser
500 505 510

Ser Gly Ser Ser Ser Thr Ser Ala Ala Gln Gln Pro Gly Thr Ser Thr
515 520 525

Pro Glu Val His Pro Lys Leu Thr Thr Tyr Lys Cys Thr Lys Ser Gly
530 535 540

Gly Cys Val Ala Gln Asp Thr Ser Val Val Leu Asp Trp Asn Tyr Arg
545 550 555 560

Trp Met His Asp Ala Asn Tyr Asn Ser Cys Thr Val Asn Gly Gly Val
565 570 575

Asn Thr Thr Leu Cys Pro Asp Glu Ala Thr Cys Gly Lys Asn Cys Phe
580 585 590

Ile Glu Gly Val Asp Tyr Ala Ala Ser Gly Val Thr Thr Ser Gly Ser
595 600 605

Ser Leu Thr Met Asn Gln Tyr Met Pro Ser Ser Ser Gly Gly Tyr Ser
610 615 620

Ser Val Ser Pro Arg Leu Tyr Leu Leu Asp Ser Asp Gly Glu Tyr Val
625 630 635 640

Met Leu Lys Leu Asn Gly Gln Glu Leu Ser Phe Asp Val Asp Leu Ser
645 650 655

Ala Leu Pro Cys Gly Glu Asn Gly Ser Leu Tyr Leu Ser Gln Met Asp
660 665 670

Glu Asn Gly Gly Ala Asn Gln Tyr Asn Thr Ala Gly Ala Asn Tyr Gly
675 680 685

Ser Gly Tyr Cys Asp Ala Gln Cys Pro Val Gln Thr Trp Arg Asn Gly
690 695 700

Thr Leu Asn Thr Ser His Gln Gly Phe Cys Cys Asn Glu Met Asp Ile
705 710 715 720

Leu Glu Gly Asn Ser Arg Ala Asn Ala Leu Thr Pro His Ser Cys Thr
725 730 735

Ala Thr Ala Cys Asp Ser Ala Gly Cys Gly Phe Asn Pro Tyr Gly Ser
740 745 750

Gly Tyr Lys Ser Tyr Tyr Gly Pro Gly Asp Thr Val Asp Thr Ser Lys
755 760 765

Thr Phe Thr Ile Ile Thr Gln Phe Asn Thr Asp Asn Gly Ser Pro Ser
770 775 780

Gly Asn Leu Val Ser Ile Thr Arg Lys Tyr Gln Gln Asn Gly Val Asp
785 790 795 800

Ile Pro Ser Ala Gln Pro Gly Gly Asp Thr Ile Ser Ser Cys Pro Ser
805 810 815

Ala Ser Ala Tyr Gly Gly Leu Ala Thr Met Gly Lys Ala Leu Ser Ser
820 825 830

Gly Met Val Leu Val Phe Ser Ile Trp Asn Asp Asn Ser Gln Tyr Met
835 840 845

Asn Trp Leu Asp Ser Gly Asn Ala Gly Pro Cys Ser Ser Thr Glu Gly

```
    850                 855                 860

Asn Pro Ser Asn Ile Leu Ala Asn Asn Pro Asn Thr His Val Val Phe
865                 870                 875                 880

Ser Asn Ile Arg Trp Gly Asp Ile Gly Ser Thr Thr Asn Ser Thr Ala
                885                 890                 895

Pro Pro Pro Pro Pro Ala Ser Ser Thr Thr Phe Ser Thr Thr Arg Arg
            900                 905                 910

Ser Ser Thr Thr Ser Ser Ser Pro Ser
        915                 920
```

<210> 65
<211> 2229
<212> DNA
<213> Sequência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2229)

<400> 65

```
cag agc agc tgc gtc tcg gct tgg ggt caa tgt ggc ggt att tct tat      48
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1               5                   10                  15

acc ggg tct acc tgc tgt cag agt ggg aat acc tgc gcc gag att aac      96
Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
            20                  25                  30

tcg tac tac tac cag tgc ata cca gca aca gct gtg agt act tca act     144
Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
        35                  40                  45

acc aca gtg aca tct ccc tct agc tct ggt tcg tct tct gcc aac acg     192
Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
    50                  55                  60

tca ggt tat aca acg acg act gtc ttg ccc agt ccc acg gca aca cag     240
Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65                  70                  75                  80

aac cct tat cct ccg gcc aat gcc agc tca tgt gga tcg tgg gct ctc     288
Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
                85                  90                  95

gtt gat aac gtt tgc tgc cca tac tac tgt ctc tcg gat aat gaa tcc     336
Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
            100                 105                 110
```

```
gag tcc tgc acg agc agc tgt acc ggc ggc tgc ggc agt cct gat tcc      384
Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
        115                 120                 125

tcc atg tgc aag tcc ggg acg atg tgg gga gag caa cac acc gta act      432
Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
    130                 135                 140

tcc aac gag gac tgg cat tac agc cgc tca aca cac ttt ggt ctg acc      480
Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145                 150                 155                 160

agc ggt ggc gcc tgc ggg ttc ggt ctg tac ggc ctc tgc acc aag aac      528
Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
                165                 170                 175

agt gtc acc gcg agc tgg aca gac cca atg ctg ggc tct acc tgc gac      576
Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
            180                 185                 190

tgc ttc tgc acc gcg tat ccg ctc ctc tgc aaa gac ccc gct aac gtc      624
Cys Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
        195                 200                 205

act ctc cgc ggg aac ttt gct gcc ccg aac gga gac tac tac act cag      672
Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
    210                 215                 220

ttc tgg cct tcc ctg gct gca tcc ggc aat ccc gac aac tac ctc tct      720
Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225                 230                 235                 240

tgc ggg gag tgt ttc gag gtc atc cgc acc aag ccc gac ggg aca gac      768
Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
                245                 250                 255

tac gcc gtc ggc gag agc gga tat acc gac ccc ata gtc ctc gag gta      816
Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
            260                 265                 270

gta gac agc tgt ccc tgc aat gcc aat tca aaa tgg tgc tgt aag cgg      864
Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
        275                 280                 285

ccc ccc ccc ccc ccc ttt ttt tcc ccg cct tcc aac gga caa aat ctc      912
Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
    290                 295                 300

aca aga cca ggc ggc agc ggc gca gac cac tgc ggc gaa atc gac ttc      960
Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305                 310                 315                 320

aag tac ggc tgt cct ctg ccg gaa gga tcc cat cac atg gac ctc tcc     1008
Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
                325                 330                 335

gat att gcc atg ggc cga ctc cag gga aac ggc agt ctc gcc gac ggt     1056
Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
            340                 345                 350

gtg att ccc atc cgc tac cgg cgt gtc ccc tgt ccc aag ccg ggg aac     1104
```

```
Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
        355                 360                 365

atc tac atc tgg ctt cat gat ggg gcg gga ccg tat tat ttt gcg ctg     1152
Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
    370                 375                 380

agc gcg gtc aat acc aac ggc ccc ggc tcc gta atc agt atc gaa gtc     1200
Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385                 390                 395                 400

cag gct ggt ggc tcc ggg cca tgg gtt gcc ctc gag cac gat ccg aac     1248
Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
                405                 410                 415

tac acc agt agc cgg ccg cag gag cgg tat ggc tct tgg gtc ctc ccg     1296
Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
            420                 425                 430

cag ggc aag gga ccc att act gtg cct gtt tcg atg agg ctg acg gcg     1344
Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
        435                 440                 445

ccc aat ggg cag cag gtg gtt aag gag ggc gcc att acc agc tat acc     1392
Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
    450                 455                 460

ccg ccg gcg act gcg gtc gag ggc ttt tgg tat att gat ctg gga gtg     1440
Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465                 470                 475                 480

cag ttc acc gcc tcc acg caa ggc atc tcc gaa gac ctc tac aat cgc     1488
Gln Phe Thr Ala Ser Thr Gln Gly Ile Ser Glu Asp Leu Tyr Asn Arg
                485                 490                 495

ttg gta gag atg gcc act atc tcc caa gcc gcc tac gcc gac cta tgc     1536
Leu Val Glu Met Ala Thr Ile Ser Gln Ala Ala Tyr Ala Asp Leu Cys
            500                 505                 510

aat att cca tcg act att atc aaa gga gag aaa att tac aac gct caa     1584
Asn Ile Pro Ser Thr Ile Ile Lys Gly Glu Lys Ile Tyr Asn Ala Gln
        515                 520                 525

act gat atc aac gga tgg atc ctc cgc gac gac acc agc aaa gaa att     1632
Thr Asp Ile Asn Gly Trp Ile Leu Arg Asp Asp Thr Ser Lys Glu Ile
    530                 535                 540

atc acc gtc ttc cgt ggc act ggc agt gac aca aac cta cag ctc gat     1680
Ile Thr Val Phe Arg Gly Thr Gly Ser Asp Thr Asn Leu Gln Leu Asp
545                 550                 555                 560

act aac tac acg ctc acg cca ttc gac act cta cct caa tgc aac gat     1728
Thr Asn Tyr Thr Leu Thr Pro Phe Asp Thr Leu Pro Gln Cys Asn Asp
                565                 570                 575

tgc gag gta cac ggt gga tac tat att gga tgg atc tca gtc caa gac     1776
Cys Glu Val His Gly Gly Tyr Tyr Ile Gly Trp Ile Ser Val Gln Asp
            580                 585                 590

caa gtc gag tcg ctt gtc aaa caa cag gct agc cag tat ccg gac tat     1824
Gln Val Glu Ser Leu Val Lys Gln Gln Ala Ser Gln Tyr Pro Asp Tyr
```

595 600 605

gcg ctt acc gtg aca ggc cat agt ctg gga gcg tcg atg gca gca ctc 1872
Ala Leu Thr Val Thr Gly His Ser Leu Gly Ala Ser Met Ala Ala Leu
610 615 620

act gcc gcc cag ctg tcc gcg aca tac gac aac gtc cgt ctg tac aca 1920
Thr Ala Ala Gln Leu Ser Ala Thr Tyr Asp Asn Val Arg Leu Tyr Thr
625 630 635 640

ttc ggc gaa ccg cgc agc ggc aac cag gcc ttc gcg tcg tac atg aac 1968
Phe Gly Glu Pro Arg Ser Gly Asn Gln Ala Phe Ala Ser Tyr Met Asn
645 650 655

gat gcg ttc cag gtc tcg agc ccg gag acg acc cag tac ttc cgg gtc 2016
Asp Ala Phe Gln Val Ser Ser Pro Glu Thr Thr Gln Tyr Phe Arg Val
660 665 670

act cat tcc aac gac ggc atc cca aac ttg ccc ccg gcg gac gag ggt 2064
Thr His Ser Asn Asp Gly Ile Pro Asn Leu Pro Pro Ala Asp Glu Gly
675 680 685

tac gcc cat ggt ggt gta gag tac tgg agc gtt gat cct tac agc gcc 2112
Tyr Ala His Gly Gly Val Glu Tyr Trp Ser Val Asp Pro Tyr Ser Ala
690 695 700

cag aac acg ttt gtc tgt act ggg gat gaa gta cag tgc tgt gag gca 2160
Gln Asn Thr Phe Val Cys Thr Gly Asp Glu Val Gln Cys Cys Glu Ala
705 710 715 720

cag ggc gga cag ggg gtg aat gat gcg cat act act tat ttt ggg atg 2208
Gln Gly Gly Gln Gly Val Asn Asp Ala His Thr Thr Tyr Phe Gly Met
725 730 735

acg agc gga gct tgt act tgg 2229
Thr Ser Gly Ala Cys Thr Trp
740

<210> 66
<211> 743
<212> PRT
<213> Seqüência artificial

<220>
<223> Construção Sintética

<400> 66

Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1 5 10 15

Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
20 25 30

Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
35 40 45

Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
50 55 60

Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65 70 75 80

Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
85 90 95

Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
100 105 110

Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
115 120 125

Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
130 135 140

Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145 150 155 160

Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
165 170 175

Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
180 185 190

Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
195 200 205

Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
210 215 220

Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225 230 235 240

Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
245 250 255

Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
260 265 270

Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
275 280 285

Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu

290 295 300

Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305 310 315 320

Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
325 330 335

Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
340 345 350

Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
355 360 365

Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
370 375 380

Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385 390 395 400

Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
405 410 415

Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
420 425 430

Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
435 440 445

Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
450 455 460

Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465 470 475 480

Gln Phe Thr Ala Ser Thr Gln Gly Ile Ser Glu Asp Leu Tyr Asn Arg
485 490 495

Leu Val Glu Met Ala Thr Ile Ser Gln Ala Ala Tyr Ala Asp Leu Cys
500 505 510

Asn Ile Pro Ser Thr Ile Ile Lys Gly Glu Lys Ile Tyr Asn Ala Gln
515 520 525

Thr Asp Ile Asn Gly Trp Ile Leu Arg Asp Asp Thr Ser Lys Glu Ile
530 535 540

Ile Thr Val Phe Arg Gly Thr Gly Ser Asp Thr Asn Leu Gln Leu Asp
545 550 555 560

Thr Asn Tyr Thr Leu Thr Pro Phe Asp Thr Leu Pro Gln Cys Asn Asp
565 570 575

Cys Glu Val His Gly Gly Tyr Tyr Ile Gly Trp Ile Ser Val Gln Asp
580 585 590

Gln Val Glu Ser Leu Val Lys Gln Gln Ala Ser Gln Tyr Pro Asp Tyr
595 600 605

Ala Leu Thr Val Thr Gly His Ser Leu Gly Ala Ser Met Ala Ala Leu
610 615 620

Thr Ala Ala Gln Leu Ser Ala Thr Tyr Asp Asn Val Arg Leu Tyr Thr
625 630 635 640

Phe Gly Glu Pro Arg Ser Gly Asn Gln Ala Phe Ala Ser Tyr Met Asn
645 650 655

Asp Ala Phe Gln Val Ser Ser Pro Glu Thr Thr Gln Tyr Phe Arg Val
660 665 670

Thr His Ser Asn Asp Gly Ile Pro Asn Leu Pro Pro Ala Asp Glu Gly
675 680 685

Tyr Ala His Gly Gly Val Glu Tyr Trp Ser Val Asp Pro Tyr Ser Ala
690 695 700

Gln Asn Thr Phe Val Cys Thr Gly Asp Glu Val Gln Cys Cys Glu Ala
705 710 715 720

Gln Gly Gly Gln Gly Val Asn Asp Ala His Thr Thr Tyr Phe Gly Met
725 730 735

Thr Ser Gly Ala Cys Thr Trp
740

<210> 67
<211> 2367
<212> DNA
<213> Seqüência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2367)

<400> 67

```
cag agc agc tgc gtc tcg gct tgg ggt caa tgt ggc ggt att tct tat      48
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1               5                  10                  15

acc ggg tct acc tgc tgt cag agt ggg aat acc tgc gcc gag att aac      96
Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
            20                  25                  30

tcg tac tac tac cag tgc ata cca gca aca gct gtg agt act tca act     144
Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
        35                  40                  45

acc aca gtg aca tct ccc tct agc tct ggt tcg tct tct gcc aac acg     192
Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
    50                  55                  60

tca ggt tat aca acg acg act gtc ttg ccc agt ccc acg gca aca cag     240
Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65                  70                  75                  80

aac cct tat cct ccg gcc aat gcc agc tca tgt gga tcg tgg gct ctc     288
Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
                85                  90                  95

gtt gat aac gtt tgc tgc cca tac tac tgt ctc tcg gat aat gaa tcc     336
Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
            100                 105                 110

gag tcc tgc acg agc agc tgt acc ggc ggc tgc ggc agt cct gat tcc     384
Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
        115                 120                 125

tcc atg tgc aag tcc ggg acg atg tgg gga gag caa cac acc gta act     432
Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
    130                 135                 140

tcc aac gag gac tgg cat tac agc cgc tca aca cac ttt ggt ctg acc     480
Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145                 150                 155                 160

agc ggt ggc gcc tgc ggg ttc ggt ctg tac ggc ctc tgc acc aag aac     528
Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
                165                 170                 175

agt gtc acc gcg agc tgg aca gac cca atg ctg ggc tct acc tgc gac     576
Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
            180                 185                 190

gcc ttc tgc acc gcg tat ccg ctc ctc tgc aaa gac ccc gct aac gtc     624
Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
        195                 200                 205

act ctc cgc ggg aac ttt gct gcc ccg aac gga gac tac tac act cag     672
Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
```

```
    210                 215                 220

ttc tgg cct tcc ctg gct gca tcc ggc aat ccc gac aac tac ctc tct      720
Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225                 230                 235                 240

tgc ggg gag tgt ttc gag gtc atc cgc acc aag ccc gac ggg aca gac      768
Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
                245                 250                 255

tac gcc gtc ggc gag agc gga tat acc gac ccc ata gtc ctc gag gta      816
Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
            260                 265                 270

gta gac agc tgt ccc tgc aat gcc aat tca aaa tgg tgc tgt aag cgg      864
Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
        275                 280                 285

ccc ccc ccc ccc ccc ttt ttt tcc ccg cct tcc aac gga caa aat ctc      912
Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
    290                 295                 300

aca aga cca ggc ggc agc ggc gca gac cac tgc ggc gaa atc gac ttc      960
Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305                 310                 315                 320

aag tac ggc tgt cct ctg ccg gaa gga tcc cat cac atg gac ctc tcc     1008
Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
                325                 330                 335

gat att gcc atg ggc cga ctc cag gga aac ggc agt ctc gcc gac ggt     1056
Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
            340                 345                 350

gtg att ccc atc cgc tac cgg cgt gtc ccc tgt ccc aag ccg ggg aac     1104
Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
        355                 360                 365

atc tac atc tgg ctt cat gat ggg gcg gga ccg tat tat ttt gcg ctg     1152
Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
    370                 375                 380

agc gcg gtc aat acc aac ggc ccc ggc tcc gta atc agt atc gaa gtc     1200
Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385                 390                 395                 400

cag gct ggt ggc tcc ggg cca tgg gtt gcc ctc gag cac gat ccg aac     1248
Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
                405                 410                 415

tac acc agt agc cgg ccg cag gag cgg tat ggc tct tgg gtc ctc ccg     1296
Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
            420                 425                 430

cag ggc aag gga ccc att act gtg cct gtt tcg atg agg ctg acg gcg     1344
Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
        435                 440                 445

ccc aat ggg cag cag gtg gtt aag gag ggc gcc att acc agc tat acc     1392
Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
    450                 455                 460
```

```
ccg ccg gcg act gcg gtc gag ggc ttt tgg tat att gat ctg gga gtg      1440
Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465                 470                 475                 480

cag ttc acc ggc tcg act tac tcc agt gga tct tct tcg ggg tcg ggg      1488
Gln Phe Thr Gly Ser Thr Tyr Ser Ser Gly Ser Ser Ser Gly Ser Gly
                485                 490                 495

tct agc tcc agc tcg agt tcg act acc act aag gcc act tcg acg acc      1536
Ser Ser Ser Ser Ser Ser Ser Thr Thr Thr Lys Ala Thr Ser Thr Thr
            500                 505                 510

ttg aag act acc tcg acc acc agc agt gga agc agt tcg aca tcg gcg      1584
Leu Lys Thr Thr Ser Thr Thr Ser Ser Gly Ser Ser Ser Thr Ser Ala
        515                 520                 525

gcg gcc tcc acg caa ggc atc tcc gaa gac ctc tac aat cgc ttg gta      1632
Ala Ala Ser Thr Gln Gly Ile Ser Glu Asp Leu Tyr Asn Arg Leu Val
    530                 535                 540

gag atg gcc act atc tcc caa gcc gcc tac gcc gac cta tgc aat att      1680
Glu Met Ala Thr Ile Ser Gln Ala Ala Tyr Ala Asp Leu Cys Asn Ile
545                 550                 555                 560

cca tcg act att atc aaa gga gag aaa att tac aac gct caa act gat      1728
Pro Ser Thr Ile Ile Lys Gly Glu Lys Ile Tyr Asn Ala Gln Thr Asp
                565                 570                 575

atc aac gga tgg atc ctc cgc gac gac acc agc aaa gaa att atc acc      1776
Ile Asn Gly Trp Ile Leu Arg Asp Asp Thr Ser Lys Glu Ile Ile Thr
            580                 585                 590

gtc ttc cgt ggc act ggc agt gac aca aac cta cag ctc gat act aac      1824
Val Phe Arg Gly Thr Gly Ser Asp Thr Asn Leu Gln Leu Asp Thr Asn
        595                 600                 605

tac acg ctc acg cca ttc gac act cta cct caa tgc aac gat tgc gag      1872
Tyr Thr Leu Thr Pro Phe Asp Thr Leu Pro Gln Cys Asn Asp Cys Glu
    610                 615                 620

gta cac ggt gga tac tat att gga tgg atc tca gtc caa gac caa gtc      1920
Val His Gly Gly Tyr Tyr Ile Gly Trp Ile Ser Val Gln Asp Gln Val
625                 630                 635                 640

gag tcg ctt gtc aaa caa cag gct agc cag tat ccg gac tat gcg ctt      1968
Glu Ser Leu Val Lys Gln Gln Ala Ser Gln Tyr Pro Asp Tyr Ala Leu
                645                 650                 655

acc gtg aca ggc cat agt ctg gga gcg tcg atg gca gca ctc act gcc      2016
Thr Val Thr Gly His Ser Leu Gly Ala Ser Met Ala Ala Leu Thr Ala
            660                 665                 670

gcc cag ctg tcc gcg aca tac gac aac gtc cgt ctg tac aca ttc ggc      2064
Ala Gln Leu Ser Ala Thr Tyr Asp Asn Val Arg Leu Tyr Thr Phe Gly
        675                 680                 685

gaa ccg cgc agc ggc aac cag gcc ttc gcg tcg tac atg aac gat gcg      2112
Glu Pro Arg Ser Gly Asn Gln Ala Phe Ala Ser Tyr Met Asn Asp Ala
    690                 695                 700
```

```
ttc cag gtc tcg agc ccg gag acg acc cag tac ttc cgg gtc act cat      2160
Phe Gln Val Ser Ser Pro Glu Thr Thr Gln Tyr Phe Arg Val Thr His
705                 710                 715                 720

tcc aac gac ggc atc cca aac ttg ccc ccg gcg gac gag ggt tac gcc      2208
Ser Asn Asp Gly Ile Pro Asn Leu Pro Pro Ala Asp Glu Gly Tyr Ala
                725                 730                 735

cat ggt ggt gta gag tac tgg agc gtt gat cct tac agc gcc cag aac      2256
His Gly Gly Val Glu Tyr Trp Ser Val Asp Pro Tyr Ser Ala Gln Asn
            740                 745                 750

acg ttt gtc tgt act ggg gat gaa gta cag tgc tgt gag gca cag ggc      2304
Thr Phe Val Cys Thr Gly Asp Glu Val Gln Cys Cys Glu Ala Gln Gly
        755                 760                 765

gga cag ggg gtg aat gat gcg cat act act tat ttt ggg atg acg agc      2352
Gly Gln Gly Val Asn Asp Ala His Thr Thr Tyr Phe Gly Met Thr Ser
    770                 775                 780

                                                                    2367
gga gct tgt act tgg
Gly Ala Cys Thr Trp
785
```

<210> 68
<211> 789
<212> PRT
<213> Sequência artificial

<220>
<223> Construção Sintética

<400> 68

```
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1               5                  10                  15

Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
            20                  25                  30

Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
        35                  40                  45

Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
    50                  55                  60

Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65                  70                  75                  80

Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
                85                  90                  95

Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
            100                 105                 110
```

Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
115 120 125

Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
130 135 140

Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145 150 155 160

Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
165 170 175

Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
180 185 190

Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
195 200 205

Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
210 215 220

Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225 230 235 240

Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
245 250 255

Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
260 265 270

Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
275 280 285

Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
290 295 300

Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305 310 315 320

Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
325 330 335

Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
340 345 350

Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
355 360 365

Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
370 375 380

Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385 390 395 400

Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
405 410 415

Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
420 425 430

Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
435 440 445

Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
450 455 460

Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465 470 475 480

Gln Phe Thr Gly Ser Thr Tyr Ser Ser Gly Ser Ser Ser Gly Ser Gly
485 490 495

Ser Ser Ser Ser Ser Ser Ser Thr Thr Thr Lys Ala Thr Ser Thr Thr
500 505 510

Leu Lys Thr Thr Ser Thr Thr Ser Ser Gly Ser Ser Ser Thr Ser Ala
515 520 525

Ala Ala Ser Thr Gln Gly Ile Ser Glu Asp Leu Tyr Asn Arg Leu Val
530 535 540

Glu Met Ala Thr Ile Ser Gln Ala Ala Tyr Ala Asp Leu Cys Asn Ile
545 550 555 560

Pro Ser Thr Ile Ile Lys Gly Glu Lys Ile Tyr Asn Ala Gln Thr Asp
565 570 575

Ile Asn Gly Trp Ile Leu Arg Asp Asp Thr Ser Lys Glu Ile Ile Thr
580 585 590

Val Phe Arg Gly Thr Gly Ser Asp Thr Asn Leu Gln Leu Asp Thr Asn
595 600 605

Tyr Thr Leu Thr Pro Phe Asp Thr Leu Pro Gln Cys Asn Asp Cys Glu
610 615 620

Val His Gly Gly Tyr Tyr Ile Gly Trp Ile Ser Val Gln Asp Gln Val
625 630 635 640

Glu Ser Leu Val Lys Gln Gln Ala Ser Gln Tyr Pro Asp Tyr Ala Leu
645 650 655

Thr Val Thr Gly His Ser Leu Gly Ala Ser Met Ala Ala Leu Thr Ala
660 665 670

Ala Gln Leu Ser Ala Thr Tyr Asp Asn Val Arg Leu Tyr Thr Phe Gly
675 680 685

Glu Pro Arg Ser Gly Asn Gln Ala Phe Ala Ser Tyr Met Asn Asp Ala
690 695 700

Phe Gln Val Ser Ser Pro Glu Thr Thr Gln Tyr Phe Arg Val Thr His
705 710 715 720

Ser Asn Asp Gly Ile Pro Asn Leu Pro Pro Ala Asp Glu Gly Tyr Ala
725 730 735

His Gly Gly Val Glu Tyr Trp Ser Val Asp Pro Tyr Ser Ala Gln Asn
740 745 750

Thr Phe Val Cys Thr Gly Asp Glu Val Gln Cys Cys Glu Ala Gln Gly
755 760 765

Gly Gln Gly Val Asn Asp Ala His Thr Thr Tyr Phe Gly Met Thr Ser
770 775 780

Gly Ala Cys Thr Trp
785

<210> 69
<211> 2961
<212> DNA
<213> Seqüência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2961)

<400> 69

```
cag agc agc tgc gtc tcg gct tgg ggt caa tgt ggc ggt att tct tat        48
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1               5                   10                  15

acc ggg tct acc tgc tgt cag agt ggg aat acc tgc gcc gag att aac        96
Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
            20                  25                  30

tcg tac tac tac cag tgc ata cca gca aca gct gtg agt act tca act       144
Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
        35                  40                  45

acc aca gtg aca tct ccc tct agc tct ggt tcg tct tct gcc aac acg       192
Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
    50                  55                  60

tca ggt tat aca acg acg act gtc ttg ccc agt ccc acg gca aca cag       240
Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65                  70                  75                  80

aac cct tat cct ccg gcc aat gcc agc tca tgt gga tcg tgg gct ctc       288
Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
                85                  90                  95

gtt gat aac gtt tgc tgc cca tac tac tgt ctc tcg gat aat gaa tcc       336
Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
            100                 105                 110

gag tcc tgc acg agc agc tgt acc ggc ggc tgc ggc agt cct gat tcc       384
Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
        115                 120                 125

tcc atg tgc aag tcc ggg acg atg tgg gga gag caa cac acc gta act       432
Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
    130                 135                 140

tcc aac gag gac tgg cat tac agc cgc tca aca cac ttt ggt ctg acc       480
Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145                 150                 155                 160

agc ggt ggc gcc tgc ggg ttc ggt ctg tac ggc ctc tgc acc aag aac       528
Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
                165                 170                 175

agt gtc acc gcg agc tgg aca gac cca atg ctg ggc tct acc tgc gac       576
Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
            180                 185                 190

gcc ttc tgc acc gcg tat ccg ctc ctc tgc aaa gac ccc gct aac gtc       624
Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
        195                 200                 205

act ctc cgc ggg aac ttt gct gcc ccg aac gga gac tac tac act cag       672
Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
    210                 215                 220
```

```
ttc tgg cct tcc ctg gct gca tcc ggc aat ccc gac aac tac ctc tct      720
Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225                 230                 235                 240

tgc ggg gag tgt ttc gag gtc atc cgc acc aag ccc gac ggg aca gac      768
Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
                245                 250                 255

tac gcc gtc ggc gag agc gga tat acc gac ccc ata gtc ctc gag gta      816
Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
            260                 265                 270

gta gac agc tgt ccc tgc aat gcc aat tca aaa tgg tgc tgt aag cgg      864
Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
        275                 280                 285

ccc ccc ccc ccc ccc ttt ttt tcc ccg cct tcc aac gga caa aat ctc      912
Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
    290                 295                 300

aca aga cca ggc ggc agc ggc gca gac cac tgc ggc gaa atc gac ttc      960
Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305                 310                 315                 320

aag tac ggc tgt cct ctg ccg gaa gga tcc cat cac atg gac ctc tcc     1008
Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
                325                 330                 335

gat att gcc atg ggc cga ctc cag gga aac ggc agt ctc gcc gac ggt     1056
Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
            340                 345                 350

gtg att ccc atc cgc tac cgg cgt gtc ccc tgt ccc aag ccg ggg aac     1104
Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
        355                 360                 365

atc tac atc tgg ctt cat gat ggg gcg gga ccg tat tat ttt gcg ctg     1152
Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
    370                 375                 380

agc gcg gtc aat acc aac ggc ccc ggc tcc gta atc agt atc gaa gtc     1200
Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385                 390                 395                 400

cag gct ggt ggc tcc ggg cca tgg gtt gcc ctc gag cac gat ccg aac     1248
Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
                405                 410                 415

tac acc agt agc cgg ccg cag gag cgg tat ggc tct tgg gtc ctc ccg     1296
Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
            420                 425                 430

cag ggc aag gga ccc att act gtg cct gtt tcg atg agg ctg acg gcg     1344
Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
        435                 440                 445

ccc aat ggg cag cag gtg gtt aag gag ggc gcc att acc agc tat acc     1392
Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
    450                 455                 460

ccg ccg gcg act gcg gtc gag ggc ttt tgg tat att gat ctg gga gtg     1440
```

```
Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465                 470                 475                 480

cag ttc acc gcg acc gac ccc ttc cag tcg cgg tgc aat gaa ttc cag      1488
Gln Phe Thr Ala Thr Asp Pro Phe Gln Ser Arg Cys Asn Glu Phe Gln
                485                 490                 495

aac aag atc gac atc gcc aat gtc acc gtc aga tcg gtc gca tac gtt      1536
Asn Lys Ile Asp Ile Ala Asn Val Thr Val Arg Ser Val Ala Tyr Val
            500                 505                 510

gct gct gga cag aac atc tcc caa gcg gag gtc gcc tcc gtg tgt aaa      1584
Ala Ala Gly Gln Asn Ile Ser Gln Ala Glu Val Ala Ser Val Cys Lys
        515                 520                 525

gca tcg gtt caa gcc agt gtc gac ctg tgc cgg gta acc atg aac atc      1632
Ala Ser Val Gln Ala Ser Val Asp Leu Cys Arg Val Thr Met Asn Ile
    530                 535                 540

tcg acg tcg gat cgc agc cat ctg tgg gct gag gcc tgg ctc cca aga      1680
Ser Thr Ser Asp Arg Ser His Leu Trp Ala Glu Ala Trp Leu Pro Arg
545                 550                 555                 560

aat tat acc ggt cgc ttc gtg agc acg ggg aat gga ggt cta gcc ggc      1728
Asn Tyr Thr Gly Arg Phe Val Ser Thr Gly Asn Gly Gly Leu Ala Gly
                565                 570                 575

tgt gtc caa gaa acg gac ctc aac ttt gca gcc aac ttt ggt ttc gct      1776
Cys Val Gln Glu Thr Asp Leu Asn Phe Ala Ala Asn Phe Gly Phe Ala
            580                 585                 590

acc gtg ggc acc aac ggt gga cat gac ggg gac acg gcc aaa tac ttc      1824
Thr Val Gly Thr Asn Gly Gly His Asp Gly Asp Thr Ala Lys Tyr Phe
        595                 600                 605

ctc aac aac tcg gag gtt ctg gcc gat ttt gcc tat cgc tca gtg cac      1872
Leu Asn Asn Ser Glu Val Leu Ala Asp Phe Ala Tyr Arg Ser Val His
    610                 615                 620

gaa ggg acc gtg gtg ggt aag caa cta act caa ttg ttt tat gac gag      1920
Glu Gly Thr Val Val Gly Lys Gln Leu Thr Gln Leu Phe Tyr Asp Glu
625                 630                 635                 640

gga tac aac tac tcc tac tat ttg ggt tgc tcc acc gga ggc cgc caa      1968
Gly Tyr Asn Tyr Ser Tyr Tyr Leu Gly Cys Ser Thr Gly Gly Arg Gln
                645                 650                 655

ggc tac cag caa gtc caa cgg ttt ccc gac gac tat gac gga gtg att      2016
Gly Tyr Gln Gln Val Gln Arg Phe Pro Asp Asp Tyr Asp Gly Val Ile
            660                 665                 670

gcg ggc tcc gca gcg atg aac ttt atc aac ctg atc tcc tgg ggg gcc      2064
Ala Gly Ser Ala Ala Met Asn Phe Ile Asn Leu Ile Ser Trp Gly Ala
        675                 680                 685

ttc ttg tgg aag gcg acg ggg tta gcg gat gat cca gac ttt atc tct      2112
Phe Leu Trp Lys Ala Thr Gly Leu Ala Asp Asp Pro Asp Phe Ile Ser
    690                 695                 700

gca aac ctg tgg tcc gta atc cac cag gag att gtt cgt cag tgc gac      2160
Ala Asn Leu Trp Ser Val Ile His Gln Glu Ile Val Arg Gln Cys Asp
```

306

```
705                 710                 715                 720

ctg gtc gat ggg gct ctg gat gga atc atc gaa gac cct gat ttc tgt  2208
Leu Val Asp Gly Ala Leu Asp Gly Ile Ile Glu Asp Pro Asp Phe Cys
                725                 730                 735

gct cca gtc atc gag cgc ttg atc tgc gac ggg act acc aac ggc acc  2256
Ala Pro Val Ile Glu Arg Leu Ile Cys Asp Gly Thr Thr Asn Gly Thr
            740                 745                 750

tct tgt atc acg gga gcc cag gca gca aag gtc aac cgg gcc ttg agt  2304
Ser Cys Ile Thr Gly Ala Gln Ala Ala Lys Val Asn Arg Ala Leu Ser
        755                 760                 765

gac ttc tat ggc ccc gac ggg aca gtg tac tac ccg cgc ctg aac tat  2352
Asp Phe Tyr Gly Pro Asp Gly Thr Val Tyr Tyr Pro Arg Leu Asn Tyr
    770                 775                 780

ggg ggt gag gcc gac tcg gct tcc ctg tac ttc acg ggg tcg atg tac  2400
Gly Gly Glu Ala Asp Ser Ala Ser Leu Tyr Phe Thr Gly Ser Met Tyr
785                 790                 795                 800

agc cgt acg gag gaa tgg tac aaa tat gtg gtc tat aac gac acc aac  2448
Ser Arg Thr Glu Glu Trp Tyr Lys Tyr Val Val Tyr Asn Asp Thr Asn
                805                 810                 815

tgg aac tcc agc cag tgg acg ctg gag agt gcc aag ctg gcc ctg gag  2496
Trp Asn Ser Ser Gln Trp Thr Leu Glu Ser Ala Lys Leu Ala Leu Glu
            820                 825                 830

cag aat ccg ttc aat atc cag gcg ttt gat ccc aac atc acg gcc ttc  2544
Gln Asn Pro Phe Asn Ile Gln Ala Phe Asp Pro Asn Ile Thr Ala Phe
        835                 840                 845

cgg gac cgg ggt ggc aag ctg ctg tcc tac cac ggc acg cag gat ccc  2592
Arg Asp Arg Gly Gly Lys Leu Leu Ser Tyr His Gly Thr Gln Asp Pro
    850                 855                 860

att atc agc tcc acg gat agc aag ctc tac tac cga cgg gta gcg aat  2640
Ile Ile Ser Ser Thr Asp Ser Lys Leu Tyr Tyr Arg Arg Val Ala Asn
865                 870                 875                 880

gcc ctg aat gcc gcg ccg tcc gag cta gat gag ttc tat cgg ttc ttc  2688
Ala Leu Asn Ala Ala Pro Ser Glu Leu Asp Glu Phe Tyr Arg Phe Phe
                885                 890                 895

cag atc tcc ggc atg ggc cac tgt ggc gat ggc acg gga gca tcg tac  2736
Gln Ile Ser Gly Met Gly His Cys Gly Asp Gly Thr Gly Ala Ser Tyr
            900                 905                 910

atc ggc cag gga tat ggc acg tac acc tcc aag gcg ccc caa gtc aac  2784
Ile Gly Gln Gly Tyr Gly Thr Tyr Thr Ser Lys Ala Pro Gln Val Asn
        915                 920                 925

ctg ctg cgc acg atg gtg gac tgg gtg gaa aac gga aag gcg ccc gag  2832
Leu Leu Arg Thr Met Val Asp Trp Val Glu Asn Gly Lys Ala Pro Glu
    930                 935                 940

tat atg ccg ggc aac aag ctc aac gcg aac ggg tca att gag tac atg  2880
Tyr Met Pro Gly Asn Lys Leu Asn Ala Asn Gly Ser Ile Glu Tyr Met
945                 950                 955                 960
```

cgc aag cac tgc cgg tat ccg aag cat aac att cac acg ggg ccg ggt 2928
Arg Lys His Cys Arg Tyr Pro Lys His Asn Ile His Thr Gly Pro Gly
965 970 975

aac tac acc gat cct aac tcc tgg act tgc gta 2961
Asn Tyr Thr Asp Pro Asn Ser Trp Thr Cys Val
980 985

<210> 70
<211> 987
<212> PRT
<213> Sequência artificial
<220>
<223> Construção Sintética

<400> 70

Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1 5 10 15

Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
20 25 30

Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
35 40 45

Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
50 55 60

Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65 70 75 80

Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
85 90 95

Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
100 105 110

Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
115 120 125

Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
130 135 140

Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145 150 155 160

Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn

308

165 170 175

Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
180 185 190

Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
195 200 205

Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
210 215 220

Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225 230 235 240

Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
245 250 255

Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
260 265 270

Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
275 280 285

Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
290 295 300

Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305 310 315 320

Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
325 330 335

Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
340 345 350

Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
355 360 365

Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
370 375 380

Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385 390 395 400

Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
405 410 415

309

Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
420 425 430

Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
435 440 445

Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
450 455 460

Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465 470 475 480

Gln Phe Thr Ala Thr Asp Pro Phe Gln Ser Arg Cys Asn Glu Phe Gln
485 490 495

Asn Lys Ile Asp Ile Ala Asn Val Thr Val Arg Ser Val Ala Tyr Val
500 505 510

Ala Ala Gly Gln Asn Ile Ser Gln Ala Glu Val Ala Ser Val Cys Lys
515 520 525

Ala Ser Val Gln Ala Ser Val Asp Leu Cys Arg Val Thr Met Asn Ile
530 535 540

Ser Thr Ser Asp Arg Ser His Leu Trp Ala Glu Ala Trp Leu Pro Arg
545 550 555 560

Asn Tyr Thr Gly Arg Phe Val Ser Thr Gly Asn Gly Gly Leu Ala Gly
565 570 575

Cys Val Gln Glu Thr Asp Leu Asn Phe Ala Ala Asn Phe Gly Phe Ala
580 585 590

Thr Val Gly Thr Asn Gly Gly His Asp Gly Asp Thr Ala Lys Tyr Phe
595 600 605

Leu Asn Asn Ser Glu Val Leu Ala Asp Phe Ala Tyr Arg Ser Val His
610 615 620

Glu Gly Thr Val Val Gly Lys Gln Leu Thr Gln Leu Phe Tyr Asp Glu
625 630 635 640

Gly Tyr Asn Tyr Ser Tyr Tyr Leu Gly Cys Ser Thr Gly Gly Arg Gln
645 650 655

310 E

Gly Tyr Gln Gln Val Gln Arg Phe Pro Asp Asp Tyr Asp Gly Val Ile
660 665 670

Ala Gly Ser Ala Ala Met Asn Phe Ile Asn Leu Ile Ser Trp Gly Ala
675 680 685

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

Ala Asn Leu Trp Ser Val Ile His Gln Glu Ile Val Arg Gln Cys Asp
705 710 715 720

Leu Val Asp Gly Ala Leu Asp Gly Ile Ile Glu Asp Pro Asp Phe Cys
725 730 735

Ala Pro Val Ile Glu Arg Leu Ile Cys Asp Gly Thr Thr Asn Gly Thr
740 745 750

Ser Cys Ile Thr Gly Ala Gln Ala Ala Lys Val Asn Arg Ala Leu Ser
755 760 765

Asp Phe Tyr Gly Pro Asp Gly Thr Val Tyr Tyr Pro Arg Leu Asn Tyr
770 775 780

Gly Gly Glu Ala Asp Ser Ala Ser Leu Tyr Phe Thr Gly Ser Met Tyr
785 790 795 800

Ser Arg Thr Glu Glu Trp Tyr Lys Tyr Val Val Tyr Asn Asp Thr Asn
805 810 815

Trp Asn Ser Ser Gln Trp Thr Leu Glu Ser Ala Lys Leu Ala Leu Glu
820 825 830

Gln Asn Pro Phe Asn Ile Gln Ala Phe Asp Pro Asn Ile Thr Ala Phe
835 840 845

Arg Asp Arg Gly Gly Lys Leu Leu Ser Tyr His Gly Thr Gln Asp Pro
850 855 860

Ile Ile Ser Ser Thr Asp Ser Lys Leu Tyr Tyr Arg Arg Val Ala Asn
865 870 875 880

Ala Leu Asn Ala Ala Pro Ser Glu Leu Asp Glu Phe Tyr Arg Phe Phe
885 890 895

311
C

Gln Ile Ser Gly Met Gly His Cys Gly Asp Gly Thr Gly Ala Ser Tyr
900 905 910

Ile Gly Gln Gly Tyr Gly Thr Tyr Thr Ser Lys Ala Pro Gln Val Asn
915 920 925

Leu Leu Arg Thr Met Val Asp Trp Val Glu Asn Gly Lys Ala Pro Glu
930 935 940

Tyr Met Pro Gly Asn Lys Leu Asn Ala Asn Gly Ser Ile Glu Tyr Met
945 950 955 960

Arg Lys His Cys Arg Tyr Pro Lys His Asn Ile His Thr Gly Pro Gly
965 970 975

Asn Tyr Thr Asp Pro Asn Ser Trp Thr Cys Val
980 985

<210> 71
<211> 3099
<212> DNA
<213> Sequência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(3099)

<400> 71
cag agc agc tgc gtc tcg gct tgg ggt caa tgt ggc ggt att tct tat 48
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1 5 10 15

acc ggg tct acc tgc tgt cag agt ggg aat acc tgc gcc gag att aac 96
Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
20 25 30

tcg tac tac tac cag tgc ata cca gca aca gct gtg agt act tca act 144
Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
35 40 45

acc aca gtg aca tct ccc tct agc tct ggt tcg tct tct gcc aac acg 192
Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
50 55 60

tca ggt tat aca acg acg act gtc ttg ccc agt ccc acg gca aca cag 240
Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65 70 75 80

aac cct tat cct ccg gcc aat gcc agc tca tgt gga tcg tgg gct ctc 288
Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
85 90 95

```
gtt gat aac gtt tgc tgc cca tac tac tgt ctc tcg gat aat gaa tcc      336
Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
            100                 105                 110

gag tcc tgc acg agc agc tgt acc ggc ggc tgc ggc agt cct gat tcc      384
Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
        115                 120                 125

tcc atg tgc aag tcc ggg acg atg tgg gga gag caa cac acc gta act      432
Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
    130                 135                 140

tcc aac gag gac tgg cat tac agc cgc tca aca cac ttt ggt ctg acc      480
Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145                 150                 155                 160

agc ggt ggc gcc tgc ggg ttc ggt ctg tac ggc ctc tgc acc aag aac      528
Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
                165                 170                 175

agt gtc acc gcg agc tgg aca gac cca atg ctg ggc tct acc tgc gac      576
Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
            180                 185                 190

gcc ttc tgc acc gcg tat ccg ctc ctc tgc aaa gac ccc gct aac gtc      624
Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
        195                 200                 205

act ctc cgc ggg aac ttt gct gcc ccg aac gga gac tac tac act cag      672
Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
    210                 215                 220

ttc tgg cct tcc ctg gct gca tcc ggc aat ccc gac aac tac ctc tct      720
Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225                 230                 235                 240

tgc ggg gag tgt ttc gag gtc atc cgc acc aag ccc gac ggg aca gac      768
Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
                245                 250                 255

tac gcc gtc ggc gag agc gga tat acc gac ccc ata gtc ctc gag gta      816
Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
            260                 265                 270

gta gac agc tgt ccc tgc aat gcc aat tca aaa tgg tgc tgt aag cgg      864
Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
        275                 280                 285

ccc ccc ccc ccc ccc ttt ttt tcc ccg cct tcc aac gga caa aat ctc      912
Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
    290                 295                 300

aca aga cca ggc ggc agc ggc gca gac cac tgc ggc gaa atc gac ttc      960
Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305                 310                 315                 320

aag tac ggc tgt cct ctg ccg gaa gga tcc cat cac atg gac ctc tcc     1008
Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
                325                 330                 335
```

```
gat att gcc atg ggc cga ctc cag gga aac ggc agt ctc gcc gac ggt      1056
Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
            340                 345                 350

gtg att ccc atc cgc tac cgg cgt gtc ccc tgt ccc aag ccg ggg aac      1104
Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
        355                 360                 365

atc tac atc tgg ctt cat gat ggg gcg gga ccg tat tat ttt gcg ctg      1152
Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
    370                 375                 380

agc gcg gtc aat acc aac ggc ccc ggc tcc gta atc agt atc gaa gtc      1200
Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385                 390                 395                 400

cag gct ggt ggc tcc ggg cca tgg gtt gcc ctc gag cac gat ccg aac      1248
Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
                405                 410                 415

tac acc agt agc cgg ccg cag gag cgg tat ggc tct tgg gtc ctc ccg      1296
Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
            420                 425                 430

cag ggc aag gga ccc att act gtg cct gtt tcg atg agg ctg acg gcg      1344
Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
        435                 440                 445

ccc aat ggg cag cag gtg gtt aag gag ggc gcc att acc agc tat acc      1392
Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
    450                 455                 460

ccg ccg gcg act gcg gtc gag ggc ttt tgg tat att gat ctg gga gtg      1440
Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465                 470                 475                 480

cag ttc acc ggc tcg act tac tcc agt gga tct tct tcg ggg tcg ggg      1488
Gln Phe Thr Gly Ser Thr Tyr Ser Ser Gly Ser Ser Ser Gly Ser Gly
                485                 490                 495

tct agc tcc agc tcg agt tcg act acc act aag gcc act tcg acg acc      1536
Ser Ser Ser Ser Ser Ser Ser Thr Thr Thr Lys Ala Thr Ser Thr Thr
            500                 505                 510

ttg aag act acc tcg acc acc agc agt gga agc agt tcg aca tcg gcg      1584
Leu Lys Thr Thr Ser Thr Thr Ser Ser Gly Ser Ser Ser Thr Ser Ala
        515                 520                 525

gcg gcg acc gac ccc ttc cag tcg cgg tgc aat gaa ttc cag aac aag      1632
Ala Ala Thr Asp Pro Phe Gln Ser Arg Cys Asn Glu Phe Gln Asn Lys
    530                 535                 540

atc gac atc gcc aat gtc acc gtc aga tcg gtc gca tac gtt gct gct      1680
Ile Asp Ile Ala Asn Val Thr Val Arg Ser Val Ala Tyr Val Ala Ala
545                 550                 555                 560

gga cag aac atc tcc caa gcg gag gtc gcc tcc gtg tgt aaa gca tcg      1728
Gly Gln Asn Ile Ser Gln Ala Glu Val Ala Ser Val Cys Lys Ala Ser
                565                 570                 575

gtt caa gcc agt gtc gac ctg tgc cgg gta acc atg aac atc tcg acg      1776
```

```
Val Gln Ala Ser Val Asp Leu Cys Arg Val Thr Met Asn Ile Ser Thr
            580                 585                 590

tcg gat cgc agc cat ctg tgg gct gag gcc tgg ctc cca aga aat tat      1824
Ser Asp Arg Ser His Leu Trp Ala Glu Ala Trp Leu Pro Arg Asn Tyr
        595                 600                 605

acc ggt cgc ttc gtg agc acg ggg aat gga ggt cta gcc ggc tgt gtc      1872
Thr Gly Arg Phe Val Ser Thr Gly Asn Gly Gly Leu Ala Gly Cys Val
    610                 615                 620

caa gaa acg gac ctc aac ttt gca gcc aac ttt ggt ttc gct acc gtg      1920
Gln Glu Thr Asp Leu Asn Phe Ala Ala Asn Phe Gly Phe Ala Thr Val
625                 630                 635                 640

ggc acc aac ggt gga cat gac ggg gac acg gcc aaa tac ttc ctc aac      1968
Gly Thr Asn Gly Gly His Asp Gly Asp Thr Ala Lys Tyr Phe Leu Asn
                645                 650                 655

aac tcg gag gtt ctg gcc gat ttt gcc tat cgc tca gtg cac gaa ggg      2016
Asn Ser Glu Val Leu Ala Asp Phe Ala Tyr Arg Ser Val His Glu Gly
            660                 665                 670

acc gtg gtg ggt aag caa cta act caa ttg ttt tat gac gag gga tac      2064
Thr Val Val Gly Lys Gln Leu Thr Gln Leu Phe Tyr Asp Glu Gly Tyr
        675                 680                 685

aac tac tcc tac tat ttg ggt tgc tcc acc gga ggc cgc caa ggc tac      2112
Asn Tyr Ser Tyr Tyr Leu Gly Cys Ser Thr Gly Gly Arg Gln Gly Tyr
    690                 695                 700

cag caa gtc caa cgg ttt ccc gac gac tat gac gga gtg att gcg ggc      2160
Gln Gln Val Gln Arg Phe Pro Asp Asp Tyr Asp Gly Val Ile Ala Gly
705                 710                 715                 720

tcc gca gcg atg aac ttt atc aac ctg atc tcc tgg ggg gcc ttc ttg      2208
Ser Ala Ala Met Asn Phe Ile Asn Leu Ile Ser Trp Gly Ala Phe Leu
                725                 730                 735

tgg aag gcg acg ggg tta gcg gat gat cca gac ttt atc tct gca aac      2256
Trp Lys Ala Thr Gly Leu Ala Asp Asp Pro Asp Phe Ile Ser Ala Asn
            740                 745                 750

ctg tgg tcc gta atc cac cag gag att gtt cgt cag tgc gac ctg gtc      2304
Leu Trp Ser Val Ile His Gln Glu Ile Val Arg Gln Cys Asp Leu Val
        755                 760                 765

gat ggg gct ctg gat gga atc atc gaa gac cct gat ttc tgt gct cca      2352
Asp Gly Ala Leu Asp Gly Ile Ile Glu Asp Pro Asp Phe Cys Ala Pro
    770                 775                 780

gtc atc gag cgc ttg atc tgc gac ggg act acc aac ggc acc tct tgt      2400
Val Ile Glu Arg Leu Ile Cys Asp Gly Thr Thr Asn Gly Thr Ser Cys
785                 790                 795                 800

atc acg gga gcc cag gca gca aag gtc aac cgg gcc ttg agt gac ttc      2448
Ile Thr Gly Ala Gln Ala Ala Lys Val Asn Arg Ala Leu Ser Asp Phe
                805                 810                 815

tat ggc ccc gac ggg aca gtg tac tac ccg cgc ctg aac tat ggg ggt      2496
Tyr Gly Pro Asp Gly Thr Val Tyr Tyr Pro Arg Leu Asn Tyr Gly Gly
```

```
                820                 825                 830

gag gcc gac tcg gct tcc ctg tac ttc acg ggg tcg atg tac agc cgt      2544
Glu Ala Asp Ser Ala Ser Leu Tyr Phe Thr Gly Ser Met Tyr Ser Arg
        835                 840                 845

acg gag gaa tgg tac aaa tat gtg gtc tat aac gac acc aac tgg aac      2592
Thr Glu Glu Trp Tyr Lys Tyr Val Val Tyr Asn Asp Thr Asn Trp Asn
    850                 855                 860

tcc agc cag tgg acg ctg gag agt gcc aag ctg gcc ctg gag cag aat      2640
Ser Ser Gln Trp Thr Leu Glu Ser Ala Lys Leu Ala Leu Glu Gln Asn
865                 870                 875                 880

ccg ttc aat atc cag gcg ttt gat ccc aac atc acg gcc ttc cgg gac      2688
Pro Phe Asn Ile Gln Ala Phe Asp Pro Asn Ile Thr Ala Phe Arg Asp
                885                 890                 895

cgg ggt ggc aag ctg ctg tcc tac cac ggc acg cag gat ccc att atc      2736
Arg Gly Gly Lys Leu Leu Ser Tyr His Gly Thr Gln Asp Pro Ile Ile
            900                 905                 910

agc tcc acg gat agc aag ctc tac tac cga cgg gta gcg aat gcc ctg      2784
Ser Ser Thr Asp Ser Lys Leu Tyr Tyr Arg Arg Val Ala Asn Ala Leu
        915                 920                 925

aat gcc gcg ccg tcc gag cta gat gag ttc tat cgg ttc ttc cag atc      2832
Asn Ala Ala Pro Ser Glu Leu Asp Glu Phe Tyr Arg Phe Phe Gln Ile
    930                 935                 940

tcc ggc atg ggc cac tgt ggc gat ggc acg gga gca tcg tac atc ggc      2880
Ser Gly Met Gly His Cys Gly Asp Gly Thr Gly Ala Ser Tyr Ile Gly
945                 950                 955                 960

cag gga tat ggc acg tac acc tcc aag gcg ccc caa gtc aac ctg ctg      2928
Gln Gly Tyr Gly Thr Tyr Thr Ser Lys Ala Pro Gln Val Asn Leu Leu
                965                 970                 975

cgc acg atg gtg gac tgg gtg gaa aac gga aag gcg ccc gag tat atg      2976
Arg Thr Met Val Asp Trp Val Glu Asn Gly Lys Ala Pro Glu Tyr Met
            980                 985                 990

ccg ggc aac aag ctc aac gcg aac  ggg tca att gag tac  atg cgc aag   3024
Pro Gly Asn Lys Leu Asn Ala Asn  Gly Ser Ile Glu Tyr  Met Arg Lys
        995                 1000                1005

cac tgc  cgg tat ccg aag cat  aac att cac acg ggg  ccg ggt aac      3069
His Cys  Arg Tyr Pro Lys His  Asn Ile His Thr Gly  Pro Gly Asn
    1010                1015                1020

tac acc  gat cct aac tcc tgg  act tgc gta                          3099
Tyr Thr  Asp Pro Asn Ser Trp  Thr Cys Val
    1025                1030
```

<210> 72
<211> 1033
<212> PRT
<213> Seqüência artificial

<220>

<223> Construção Sintética

<400> 72

Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1 5 10 15

Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
20 25 30

Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
35 40 45

Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
50 55 60

Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65 70 75 80

Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
85 90 95

Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
100 105 110

Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
115 120 125

Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
130 135 140

Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145 150 155 160

Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
165 170 175

Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
180 185 190

Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
195 200 205

Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
210 215 220

Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser

225 230 235 240

Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
245 250 255

Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
260 265 270

Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
275 280 285

Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
290 295 300

Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305 310 315 320

Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
325 330 335

Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
340 345 350

Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
355 360 365

Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
370 375 380

Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385 390 395 400

Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
405 410 415

Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
420 425 430

Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
435 440 445

Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
450 455 460

Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465 470 475 480

Gln Phe Thr Gly Ser Thr Tyr Ser Ser Gly Ser Ser Ser Gly Ser Gly
485 490 495

Ser Ser Ser Ser Ser Ser Ser Thr Thr Thr Lys Ala Thr Ser Thr Thr
500 505 510

Leu Lys Thr Thr Ser Thr Thr Ser Ser Gly Ser Ser Ser Thr Ser Ala
515 520 525

Ala Ala Thr Asp Pro Phe Gln Ser Arg Cys Asn Glu Phe Gln Asn Lys
530 535 540

Ile Asp Ile Ala Asn Val Thr Val Arg Ser Val Ala Tyr Val Ala Ala
545 550 555 560

Gly Gln Asn Ile Ser Gln Ala Glu Val Ala Ser Val Cys Lys Ala Ser
565 570 575

Val Gln Ala Ser Val Asp Leu Cys Arg Val Thr Met Asn Ile Ser Thr
580 585 590

Ser Asp Arg Ser His Leu Trp Ala Glu Ala Trp Leu Pro Arg Asn Tyr
595 600 605

Thr Gly Arg Phe Val Ser Thr Gly Asn Gly Gly Leu Ala Gly Cys Val
610 615 620

Gln Glu Thr Asp Leu Asn Phe Ala Ala Asn Phe Gly Phe Ala Thr Val
625 630 635 640

Gly Thr Asn Gly Gly His Asp Gly Asp Thr Ala Lys Tyr Phe Leu Asn
645 650 655

Asn Ser Glu Val Leu Ala Asp Phe Ala Tyr Arg Ser Val His Glu Gly
660 665 670

Thr Val Val Gly Lys Gln Leu Thr Gln Leu Phe Tyr Asp Glu Gly Tyr
675 680 685

Asn Tyr Ser Tyr Tyr Leu Gly Cys Ser Thr Gly Gly Arg Gln Gly Tyr
690 695 700

Gln Gln Val Gln Arg Phe Pro Asp Asp Tyr Asp Gly Val Ile Ala Gly
705 710 715 720

Ser Ala Ala Met Asn Phe Ile Asn Leu Ile Ser Trp Gly Ala Phe Leu
725 730 735

Trp Lys Ala Thr Gly Leu Ala Asp Asp Pro Asp Phe Ile Ser Ala Asn
740 745 750

Leu Trp Ser Val Ile His Gln Glu Ile Val Arg Gln Cys Asp Leu Val
755 760 765

Asp Gly Ala Leu Asp Gly Ile Ile Glu Asp Pro Asp Phe Cys Ala Pro
770 775 780

Val Ile Glu Arg Leu Ile Cys Asp Gly Thr Thr Asn Gly Thr Ser Cys
785 790 795 800

Ile Thr Gly Ala Gln Ala Ala Lys Val Asn Arg Ala Leu Ser Asp Phe
805 810 815

Tyr Gly Pro Asp Gly Thr Val Tyr Tyr Pro Arg Leu Asn Tyr Gly Gly
820 825 830

Glu Ala Asp Ser Ala Ser Leu Tyr Phe Thr Gly Ser Met Tyr Ser Arg
835 840 845

Thr Glu Glu Trp Tyr Lys Tyr Val Val Tyr Asn Asp Thr Asn Trp Asn
850 855 860

Ser Ser Gln Trp Thr Leu Glu Ser Ala Lys Leu Ala Leu Glu Gln Asn
865 870 875 880

Pro Phe Asn Ile Gln Ala Phe Asp Pro Asn Ile Thr Ala Phe Arg Asp
885 890 895

Arg Gly Gly Lys Leu Leu Ser Tyr His Gly Thr Gln Asp Pro Ile Ile
900 905 910

Ser Ser Thr Asp Ser Lys Leu Tyr Tyr Arg Arg Val Ala Asn Ala Leu
915 920 925

Asn Ala Ala Pro Ser Glu Leu Asp Glu Phe Tyr Arg Phe Phe Gln Ile
930 935 940

Ser Gly Met Gly His Cys Gly Asp Gly Thr Gly Ala Ser Tyr Ile Gly
945 950 955 960

320
C

Gln Gly Tyr Gly Thr Tyr Thr Ser Lys Ala Pro Gln Val Asn Leu Leu
965 970 975

Arg Thr Met Val Asp Trp Val Glu Asn Gly Lys Ala Pro Glu Tyr Met
980 985 990

Pro Gly Asn Lys Leu Asn Ala Asn Gly Ser Ile Glu Tyr Met Arg Lys
995 1000 1005

His Cys Arg Tyr Pro Lys His Asn Ile His Thr Gly Pro Gly Asn
1010 1015 1020

Tyr Thr Asp Pro Asn Ser Trp Thr Cys Val
1025 1030

<210> 73
<211> 2013
<212> DNA
<213> Sequência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2013)

<400> 73
cag agc agc tgc gtc tcg gct tgg ggt caa tgt ggc ggt att tct tat 48
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1 5 10 15

acc ggg tct acc tgc tgt cag agt ggg aat acc tgc gcc gag att aac 96
Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
20 25 30

tcg tac tac tac cag tgc ata cca gca aca gct gtg agt act tca act 144
Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
35 40 45

acc aca gtg aca tct ccc tct agc tct ggt tcg tct tct gcc aac acg 192
Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
50 55 60

tca ggt tat aca acg acg act gtc ttg ccc agt ccc acg gca aca cag 240
Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65 70 75 80

aac cct tat cct ccg gcc aat gcc agc tca tgt gga tcg tgg gct ctc 288
Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
85 90 95

gtt gat aac gtt tgc tgc cca tac tac tgt ctc tcg gat aat gaa tcc 336
Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
100 105 110

321 C

```
gag tcc tgc acg agc agc tgt acc ggc ggc tgc ggc agt cct gat tcc      384
Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
        115                 120                 125

tcc atg tgc aag tcc ggg acg atg tgg gga gag caa cac acc gta act      432
Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
    130                 135                 140

tcc aac gag gac tgg cat tac agc cgc tca aca cac ttt ggt ctg acc      480
Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145                 150                 155                 160

agc ggt ggc gcc tgc ggg ttc ggt ctg tac ggc ctc tgc acc aag aac      528
Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
                165                 170                 175

agt gtc acc gcg agc tgg aca gac cca atg ctg ggc tct acc tgc gac      576
Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
            180                 185                 190

gcc ttc tgc acc gcg tat ccg ctc ctc tgc aaa gac ccc gct aac gtc      624
Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
        195                 200                 205

act ctc cgc ggg aac ttt gct gcc ccg aac gga gac tac tac act cag      672
Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
    210                 215                 220

ttc tgg cct tcc ctg gct gca tcc ggc aat ccc gac aac tac ctc tct      720
Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225                 230                 235                 240

tgc ggg gag tgt ttc gag gtc atc cgc acc aag ccc gac ggg aca gac      768
Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
                245                 250                 255

tac gcc gtc ggc gag agc gga tat acc gac ccc ata gtc ctc gag gta      816
Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
            260                 265                 270

gta gac agc tgt ccc tgc aat gcc aat tca aaa tgg tgc tgt aag cgg      864
Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
        275                 280                 285

ccc ccc ccc ccc ccc ttt ttt tcc ccg cct tcc aac gga caa aat ctc      912
Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
    290                 295                 300

aca aga cca ggc ggc agc ggc gca gac cac tgc ggc gaa atc gac ttc      960
Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305                 310                 315                 320

aag tac ggc tgt cct ctg ccg gaa gga tcc cat cac atg gac ctc tcc     1008
Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
                325                 330                 335

gat att gcc atg ggc cga ctc cag gga aac ggc agt ctc gcc gac ggt     1056
Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
            340                 345                 350
```

```
gtg att ccc atc cgc tac cgg cgt gtc ccc tgt ccc aag ccg ggg aac      1104
Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
        355                 360                 365

atc tac atc tgg ctt cat gat ggg gcg gga ccg tat tat ttt gcg ctg      1152
Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
    370                 375                 380

agc gcg gtc aat acc aac ggc ccc ggc tcc gta atc agt atc gaa gtc      1200
Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385                 390                 395                 400

cag gct ggt ggc tcc ggg cca tgg gtt gcc ctc gag cac gat ccg aac      1248
Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
                405                 410                 415

tac acc agt agc cgg ccg cag gag cgg tat ggc tct tgg gtc ctc ccg      1296
Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
            420                 425                 430

cag ggc aag gga ccc att act gtg cct gtt tcg atg agg ctg acg gcg      1344
Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
        435                 440                 445

ccc aat ggg cag cag gtg gtt aag gag ggc gcc att acc agc tat acc      1392
Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
    450                 455                 460

ccg ccg gcg act gcg gtc gag ggc ttt tgg tat att gat ctg gga gtg      1440
Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465                 470                 475                 480

cag ttc acc tcg acc ccg agc tcg acc ggc gag aac aac ggc ttc tac      1488
Gln Phe Thr Ser Thr Pro Ser Ser Thr Gly Glu Asn Asn Gly Phe Tyr
                485                 490                 495

tac tcc ttc tgg acc gac ggc ggt gga gac gtg acc tac acc aac gga      1536
Tyr Ser Phe Trp Thr Asp Gly Gly Gly Asp Val Thr Tyr Thr Asn Gly
            500                 505                 510

gat gct ggt gcc tac act gtt gag tgg tcc aac gtg ggc aac ttt gtc      1584
Asp Ala Gly Ala Tyr Thr Val Glu Trp Ser Asn Val Gly Asn Phe Val
        515                 520                 525

ggt gga aag ggc tgg aac ccc gga agt gcg cag gac atc acc tac agc      1632
Gly Gly Lys Gly Trp Asn Pro Gly Ser Ala Gln Asp Ile Thr Tyr Ser
    530                 535                 540

ggc acc ttc acc cct agc ggc aac ggc tac ctc tcc gtc tat ggc tgg      1680
Gly Thr Phe Thr Pro Ser Gly Asn Gly Tyr Leu Ser Val Tyr Gly Trp
545                 550                 555                 560

acc act gac cct ctg atc gag tac tac atc gtc gag tct tac ggc gac      1728
Thr Thr Asp Pro Leu Ile Glu Tyr Tyr Ile Val Glu Ser Tyr Gly Asp
                565                 570                 575

tac aac ccc ggc agt gga ggc acg tac aag ggc acc gtc acc tcg gac      1776
Tyr Asn Pro Gly Ser Gly Gly Thr Tyr Lys Gly Thr Val Thr Ser Asp
            580                 585                 590

gga tcc gtt tac gat atc tac acg gct acc cgt acc aat gct gct tcc      1824
```

```
Gly Ser Val Tyr Asp Ile Tyr Thr Ala Thr Arg Thr Asn Ala Ala Ser
        595                 600                 605

att cag gga acc gct acc ttc act cag tac tgg tcc gtt cgc cag aac      1872
Ile Gln Gly Thr Ala Thr Phe Thr Gln Tyr Trp Ser Val Arg Gln Asn
    610                 615                 620

aag aga gtt ggc gga acc gtt acc acc tcc aac cac ttc aat gct tgg      1920
Lys Arg Val Gly Gly Thr Val Thr Thr Ser Asn His Phe Asn Ala Trp
625                 630                 635                 640

gct aag ctg gga atg aac ctg ggt act cac aac tac cag atc gtg gct      1968
Ala Lys Leu Gly Met Asn Leu Gly Thr His Asn Tyr Gln Ile Val Ala
                645                 650                 655

acc gag ggt tac cag agc agt gga tct tcg tcc atc act gtt cag          2013
Thr Glu Gly Tyr Gln Ser Ser Gly Ser Ser Ser Ile Thr Val Gln
            660                 665                 670
```

<210> 74
<211> 671
<212> PRT
<213> Seqüência artificial

<220>
<223> Construção Sintética

<400> 74

```
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1               5                   10                  15

Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
            20                  25                  30

Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
        35                  40                  45

Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
    50                  55                  60

Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65                  70                  75                  80

Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
                85                  90                  95

Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
            100                 105                 110

Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
        115                 120                 125
```

Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
130 135 140

Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145 150 155 160

Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
165 170 175

Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
180 185 190

Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
195 200 205

Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
210 215 220

Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225 230 235 240

Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
245 250 255

Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
260 265 270

Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
275 280 285

Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
290 295 300

Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305 310 315 320

Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
325 330 335

Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
340 345 350

Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
355 360 365

Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
370 375 380

Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385 390 395 400

Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
405 410 415

Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
420 425 430

Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
435 440 445

Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
450 455 460

Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465 470 475 480

Gln Phe Thr Ser Thr Pro Ser Ser Thr Gly Glu Asn Asn Gly Phe Tyr
485 490 495

Tyr Ser Phe Trp Thr Asp Gly Gly Gly Asp Val Thr Tyr Thr Asn Gly
500 505 510

Asp Ala Gly Ala Tyr Thr Val Glu Trp Ser Asn Val Gly Asn Phe Val
515 520 525

Gly Gly Lys Gly Trp Asn Pro Gly Ser Ala Gln Asp Ile Thr Tyr Ser
530 535 540

Gly Thr Phe Thr Pro Ser Gly Asn Gly Tyr Leu Ser Val Tyr Gly Trp
545 550 555 560

Thr Thr Asp Pro Leu Ile Glu Tyr Tyr Ile Val Glu Ser Tyr Gly Asp
565 570 575

Tyr Asn Pro Gly Ser Gly Gly Thr Tyr Lys Gly Thr Val Thr Ser Asp
580 585 590

Gly Ser Val Tyr Asp Ile Tyr Thr Ala Thr Arg Thr Asn Ala Ala Ser
595 600 605

Ile Gln Gly Thr Ala Thr Phe Thr Gln Tyr Trp Ser Val Arg Gln Asn

610 615 620

Lys Arg Val Gly Gly Thr Val Thr Thr Ser Asn His Phe Asn Ala Trp
625 630 635 640

Ala Lys Leu Gly Met Asn Leu Gly Thr His Asn Tyr Gln Ile Val Ala
645 650 655

Thr Glu Gly Tyr Gln Ser Ser Gly Ser Ser Ser Ile Thr Val Gln
660 665 670

<210> 75
<211> 2151
<212> DNA
<213> Sequência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2151)

<400> 75

```
cag agc agc tgc gtc tcg gct tgg ggt caa tgt ggc ggt att tct tat      48
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1               5                  10                  15

acc ggg tct acc tgc tgt cag agt ggg aat acc tgc gcc gag att aac      96
Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
            20                  25                  30

tcg tac tac tac cag tgc ata cca gca aca gct gtg agt act tca act     144
Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
        35                  40                  45

acc aca gtg aca tct ccc tct agc tct ggt tcg tct tct gcc aac acg     192
Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ala Asn Thr
    50                  55                  60

tca ggt tat aca acg acg act gtc ttg ccc agt ccc acg gca aca cag     240
Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65                  70                  75                  80

aac cct tat cct ccg gcc aat gcc agc tca tgt gga tcg tgg gct ctc     288
Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
                85                  90                  95

gtt gat aac gtt tgc tgc cca tac tac tgt ctc tcg gat aat gaa tcc     336
Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
            100                 105                 110

gag tcc tgc acg agc agc tgt acc ggc ggc tgc ggc agt cct gat tcc     384
Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
        115                 120                 125
```

```
tcc atg tgc aag tcc ggg acg atg tgg gga gag caa cac acc gta act      432
Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
    130                 135                 140

tcc aac gag gac tgg cat tac agc cgc tca aca cac ttt ggt ctg acc      480
Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145                 150                 155                 160

agc ggt ggc gcc tgc ggg ttc ggt ctg tac ggc ctc tgc acc aag aac      528
Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
                165                 170                 175

agt gtc acc gcg agc tgg aca gac cca atg ctg ggc tct acc tgc gac      576
Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
            180                 185                 190

gcc ttc tgc acc gcg tat ccg ctc ctc tgc aaa gac ccc gct aac gtc      624
Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
        195                 200                 205

act ctc cgc ggg aac ttt gct gcc ccg aac gga gac tac tac act cag      672
Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
    210                 215                 220

ttc tgg cct tcc ctg gct gca tcc ggc aat ccc gac aac tac ctc tct      720
Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225                 230                 235                 240

tgc ggg gag tgt ttc gag gtc atc cgc acc aag ccc gac ggg aca gac      768
Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
                245                 250                 255

tac gcc gtc ggc gag agc gga tat acc gac ccc ata gtc ctc gag gta      816
Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
            260                 265                 270

gta gac agc tgt ccc tgc aat gcc aat tca aaa tgg tgc tgt aag cgg      864
Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
        275                 280                 285

ccc ccc ccc ccc ccc ttt ttt tcc ccg cct tcc aac gga caa aat ctc      912
Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
    290                 295                 300

aca aga cca ggc ggc agc ggc gca gac cac tgc ggc gaa atc gac ttc      960
Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305                 310                 315                 320

aag tac ggc tgt cct ctg ccg gaa gga tcc cat cac atg gac ctc tcc     1008
Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
                325                 330                 335

gat att gcc atg ggc cga ctc cag gga aac ggc agt ctc gcc gac ggt     1056
Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
            340                 345                 350

gtg att ccc atc cgc tac cgg cgt gtc ccc tgt ccc aag ccg ggg aac     1104
Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
        355                 360                 365

atc tac atc tgg ctt cat gat ggg gcg gga ccg tat tat ttt gcg ctg     1152
```

```
Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
    370                 375                 380

agc gcg gtc aat acc aac ggc ccc ggc tcc gta atc agt atc gaa gtc     1200
Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385                 390                 395                 400

cag gct ggt ggc tcc ggg cca tgg gtt gcc ctc gag cac gat ccg aac     1248
Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
                405                 410                 415

tac acc agt agc cgg ccg cag gag cgg tat ggc tct tgg gtc ctc ccg     1296
Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
            420                 425                 430

cag ggc aag gga ccc att act gtg cct gtt tcg atg agg ctg acg gcg     1344
Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
        435                 440                 445

ccc aat ggg cag cag gtg gtt aag gag ggc gcc att acc agc tat acc     1392
Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
    450                 455                 460

ccg ccg gcg act gcg gtc gag ggc ttt tgg tat att gat ctg gga gtg     1440
Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465                 470                 475                 480

cag ttc acc ggc tcg act tac tcc agt gga tct tct tcg ggg tcg ggg     1488
Gln Phe Thr Gly Ser Thr Tyr Ser Ser Gly Ser Ser Ser Gly Ser Gly
                485                 490                 495

tct agc tcc agc tcg agt tcg act acc act aag gcc act tcg acg acc     1536
Ser Ser Ser Ser Ser Ser Ser Thr Thr Thr Lys Ala Thr Ser Thr Thr
            500                 505                 510

ttg aag act acc tcg acc acc agc agt gga agc agt tcg aca tcg gcg     1584
Leu Lys Thr Thr Ser Thr Thr Ser Ser Gly Ser Ser Ser Thr Ser Ala
        515                 520                 525

gcg tcg acc ccg agc tcg acc ggc gag aac aac ggc ttc tac tac tcc     1632
Ala Ser Thr Pro Ser Ser Thr Gly Glu Asn Asn Gly Phe Tyr Tyr Ser
    530                 535                 540

ttc tgg acc gac ggc ggt gga gac gtg acc tac acc aac gga gat gct     1680
Phe Trp Thr Asp Gly Gly Gly Asp Val Thr Tyr Thr Asn Gly Asp Ala
545                 550                 555                 560

ggt gcc tac act gtt gag tgg tcc aac gtg ggc aac ttt gtc ggt gga     1728
Gly Ala Tyr Thr Val Glu Trp Ser Asn Val Gly Asn Phe Val Gly Gly
                565                 570                 575

aag ggc tgg aac ccc gga agt gcg cag gac atc acc tac agc ggc acc     1776
Lys Gly Trp Asn Pro Gly Ser Ala Gln Asp Ile Thr Tyr Ser Gly Thr
            580                 585                 590

ttc acc cct agc ggc aac ggc tac ctc tcc gtc tat ggc tgg acc act     1824
Phe Thr Pro Ser Gly Asn Gly Tyr Leu Ser Val Tyr Gly Trp Thr Thr
        595                 600                 605

gac cct ctg atc gag tac tac atc gtc gag tct tac ggc gac tac aac     1872
Asp Pro Leu Ile Glu Tyr Tyr Ile Val Glu Ser Tyr Gly Asp Tyr Asn
```

610 615 620

ccc ggc agt gga ggc acg tac aag ggc acc gtc acc tcg gac gga tcc 1920
Pro Gly Ser Gly Gly Thr Tyr Lys Gly Thr Val Thr Ser Asp Gly Ser
625 630 635 640

gtt tac gat atc tac acg gct acc cgt acc aat gct gct tcc att cag 1968
Val Tyr Asp Ile Tyr Thr Ala Thr Arg Thr Asn Ala Ala Ser Ile Gln
645 650 655

gga acc gct acc ttc act cag tac tgg tcc gtt cgc cag aac aag aga 2016
Gly Thr Ala Thr Phe Thr Gln Tyr Trp Ser Val Arg Gln Asn Lys Arg
660 665 670

gtt ggc gga acc gtt acc acc tcc aac cac ttc aat gct tgg gct aag 2064
Val Gly Gly Thr Val Thr Thr Ser Asn His Phe Asn Ala Trp Ala Lys
675 680 685

ctg gga atg aac ctg ggt act cac aac tac cag atc gtg gct acc gag 2112
Leu Gly Met Asn Leu Gly Thr His Asn Tyr Gln Ile Val Ala Thr Glu
690 695 700

ggt tac cag agc agt gga tct tcg tcc atc act gtt cag 2151
Gly Tyr Gln Ser Ser Gly Ser Ser Ser Ile Thr Val Gln
705 710 715

<210> 76
<211> 717
<212> PRT
<213> Sequência artificial

<220>
<223> Construção Sintética

<400> 76

Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1 5 10 15

Ser Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
20 25 30

Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
35 40 45

Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
50 55 60

Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65 70 75 80

Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
85 90 95

330
C

Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
100 105 110

Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
115 120 125

Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
130 135 140

Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145 150 155 160

Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
165 170 175

Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
180 185 190

Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
195 200 205

Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
210 215 220

Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225 230 235 240

Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
245 250 255

Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
260 265 270

Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
275 280 285

Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
290 295 300

Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305 310 315 320

Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
325 330 335

Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly

331
e

340 345 350

Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
355 360 365

Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
370 375 380

Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385 390 395 400

Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
405 410 415

yr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
420 425 430

Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
435 440 445

Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
450 455 460

Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465 470 475 480

Gln Phe Thr Gly Ser Thr Tyr Ser Ser Gly Ser Ser Ser Gly Ser Gly
485 490 495

er Ser Ser Ser Ser Ser Ser Thr Thr Thr Lys Ala Thr Ser Thr Thr
500 505 510

Leu Lys Thr Thr Ser Thr Thr Ser Ser Gly Ser Ser Ser Thr Ser Ala
515 520 525

Ala Ser Thr Pro Ser Ser Thr Gly Glu Asn Asn Gly Phe Tyr Tyr Ser
530 535 540

Phe Trp Thr Asp Gly Gly Gly Asp Val Thr Tyr Thr Asn Gly Asp Ala
545 550 555 560

Gly Ala Tyr Thr Val Glu Trp Ser Asn Val Gly Asn Phe Val Gly Gly
565 570 575

Lys Gly Trp Asn Pro Gly Ser Ala Gln Asp Ile Thr Tyr Ser Gly Thr
580 585 590

Phe Thr Pro Ser Gly Asn Gly Tyr Leu Ser Val Tyr Gly Trp Thr Thr
595 600 605

Asp Pro Leu Ile Glu Tyr Tyr Ile Val Glu Ser Tyr Gly Asp Tyr Asn
610 615 620

Pro Gly Ser Gly Gly Thr Tyr Lys Gly Thr Val Thr Ser Asp Gly Ser
625 630 635 640

Val Tyr Asp Ile Tyr Thr Ala Thr Arg Thr Asn Ala Ala Ser Ile Gln
645 650 655

Gly Thr Ala Thr Phe Thr Gln Tyr Trp Ser Val Arg Gln Asn Lys Arg
660 665 670

Val Gly Gly Thr Val Thr Thr Ser Asn His Phe Asn Ala Trp Ala Lys
675 680 685

Leu Gly Met Asn Leu Gly Thr His Asn Tyr Gln Ile Val Ala Thr Glu
690 695 700

Gly Tyr Gln Ser Ser Gly Ser Ser Ser Ile Thr Val Gln
705 710 715

<210> 77
<211> 2943
<212> DNA
<213> Seqüência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2943)

<400> 77
cag agc agc tgc gtc tcg gct tgg ggt caa tgt ggc ggt att tct tat 48
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1 5 10 15

acc ggg tct acc tgc tgt cag agt ggg aat acc tgc gcc gag att aac 96
Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
20 25 30

tcg tac tac tac cag tgc ata cca gca aca gct gtg agt act tca act 144
Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
35 40 45

acc aca gtg aca tct ccc tct agc tct ggt tcg tct tct gcc aac acg 192

```
Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
    50                  55                  60

tca ggt tat aca acg acg act gtc ttg ccc agt ccc acg gca aca cag      240
Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65                  70                  75                  80

aac cct tat cct ccg gcc aat gcc agc tca tgt gga tcg tgg gct ctc      288
Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
                85                  90                  95

gtt gat aac gtt tgc tgc cca tac tac tgt ctc tcg gat aat gaa tcc      336
Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
            100                 105                 110

gag tcc tgc acg agc agc tgt acc ggc ggc tgc ggc agt cct gat tcc      384
Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
        115                 120                 125

tcc atg tgc aag tcc ggg acg atg tgg gga gag caa cac acc gta act      432
Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
    130                 135                 140

tcc aac gag gac tgg cat tac agc cgc tca aca cac ttt ggt ctg acc      480
Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145                 150                 155                 160

agc ggt ggc gcc tgc ggg ttc ggt ctg tac ggc ctc tgc acc aag aac      528
Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
                165                 170                 175

agt gtc acc gcg agc tgg aca gac cca atg ctg ggc tct acc tgc gac      576
Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
            180                 185                 190

gcc ttc tgc acc gcg tat ccg ctc ctc tgc aaa gac ccc gct aac gtc      624
Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
        195                 200                 205

act ctc cgc ggg aac ttt gct gcc ccg aac gga gac tac tac act cag      672
Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
    210                 215                 220

ttc tgg cct tcc ctg gct gca tcc ggc aat ccc gac aac tac ctc tct      720
Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225                 230                 235                 240

tgc ggg gag tgt ttc gag gtc atc cgc acc aag ccc gac ggg aca gac      768
Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
                245                 250                 255

tac gcc gtc ggc gag agc gga tat acc gac ccc ata gtc ctc gag gta      816
Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
            260                 265                 270

gta gac agc tgt ccc tgc aat gcc aat tca aaa tgg tgc tgt aag cgg      864
Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
        275                 280                 285

ccc ccc ccc ccc ccc ttt ttt tcc ccg cct tcc aac gga caa aat ctc      912
Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
```

```
    290                 295                 300

aca aga cca ggc ggc agc ggc gca gac cac tgc ggc gaa atc gac ttc      960
Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305                 310                 315                 320

aag tac ggc tgt cct ctg ccg gaa gga tcc cat cac atg gac ctc tcc     1008
Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
                325                 330                 335

gat att gcc atg ggc cga ctc cag gga aac ggc agt ctc gcc gac ggt     1056
Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
            340                 345                 350

gtg att ccc atc cgc tac cgg cgt gtc ccc tgt ccc aag ccg ggg aac     1104
Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
        355                 360                 365

atc tac atc tgg ctt cat gat ggg gcg gga ccg tat tat ttt gcg ctg     1152
Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
    370                 375                 380

agc gcg gtc aat acc aac ggc ccc ggc tcc gta atc agt atc gaa gtc     1200
Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385                 390                 395                 400

cag gct ggt ggc tcc ggg cca tgg gtt gcc ctc gag cac gat ccg aac     1248
Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
                405                 410                 415

tac acc agt agc cgg ccg cag gag cgg tat ggc tct tgg gtc ctc ccg     1296
Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
            420                 425                 430

cag ggc aag gga ccc att act gtg cct gtt tcg atg agg ctg acg gcg     1344
Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
        435                 440                 445

ccc aat ggg cag cag gtg gtt aag gag ggc gcc att acc agc tat acc     1392
Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
    450                 455                 460

ccg ccg gcg act gcg gtc gag ggc ttt tgg tat att gat ctg gga gtg     1440
Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465                 470                 475                 480

cag ttc acc cag tcg gcc tgc act ctc caa tcg gag act cac ccg cct     1488
Gln Phe Thr Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro
                485                 490                 495

ctg aca tgg cag aaa tgc tcg tct ggt ggc acg tgc act caa cag aca     1536
Leu Thr Trp Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr
            500                 505                 510

ggc tcc gtg gtc atc gac gcc aac tgg cgc tgg act cac gct acg aac     1584
Gly Ser Val Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn
        515                 520                 525

agc agc acg aac tgc tac gat ggc aac act tgg agc tcg acc cta tgt     1632
Ser Ser Thr Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys
    530                 535                 540
```

```
cct gac aac gag acc tgc gcg aag aac tgc tgt ctg gac ggt gcc gcc      1680
Pro Asp Asn Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala
545                 550                 555                 560

tac gcg tcc acg tac gga gtt acc acg agc ggt aac agc ctc tcc att      1728
Tyr Ala Ser Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile
                565                 570                 575

ggc ttt gtc acc cag tct gcg cag aag aac gtt ggc gct cgc ctt tac      1776
Gly Phe Val Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr
            580                 585                 590

ctt atg gcg agc gac acg acc tac cag gaa ttc acc ctg ctt ggc aac      1824
Leu Met Ala Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn
        595                 600                 605

gag ttc tct ttc gat gtt gat gtt tcg cag ctg ccg tgc ggc ttg aac      1872
Glu Phe Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn
    610                 615                 620

gga gct ctc tac ttc gtg tcc atg gac gcg gat ggt ggc gtg agc aag      1920
Gly Ala Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys
625                 630                 635                 640

tat ccc acc aac acc gct ggc gcc aag tac ggc acg ggg tac tgt gac      1968
Tyr Pro Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp
                645                 650                 655

agc cag tgt ccc cgc gat ctg aag ttc atc aat ggc cag gcc aac gtt      2016
Ser Gln Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val
            660                 665                 670

gag ggc tgg gag ccg tca tcc aac aac gcg aac acg ggc att gga gga      2064
Glu Gly Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly
        675                 680                 685

cac gga agc tgc tgc tct gag atg gat atc tgg gag gcc aac tcc atc      2112
His Gly Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile
    690                 695                 700

tcc gag gct ctt acc ccc cac cct tgc acg act gtc ggc cag gag atc      2160
Ser Glu Ala Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile
705                 710                 715                 720

tgc gag ggt gat ggg tgc ggc gga act tac tcc gat aac aga tat ggc      2208
Cys Glu Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly
                725                 730                 735

ggc act tgc gat ccc gat ggc tgc gac tgg aac cca tac cgc ctg ggc      2256
Gly Thr Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly
            740                 745                 750

aac acc agc ttc tac ggc cct ggc tca agc ttt acc ctc gat acc acc      2304
Asn Thr Ser Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr
        755                 760                 765

aag aaa ttg acc gtt gtc acc cag ttc gag acg tcg ggt gcc atc aac      2352
Lys Lys Leu Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn
    770                 775                 780
```

```
cga tac tat gtc cag aat ggc gtc act ttc cag cag ccc aac gcc gag      2400
Arg Tyr Tyr Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu
785                 790                 795                 800

ctt ggt agt tac tct ggc aac gag ctc aac gat gat tac tgc aca gct      2448
Leu Gly Ser Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala
                805                 810                 815

gag gag gca gaa ttc ggc gga tcc tct ttc tca gac aag ggc ggc ctg      2496
Glu Glu Ala Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu
            820                 825                 830

act cag ttc aag aag gct acc tct ggc ggc atg gtt ctg gtc atg agt      2544
Thr Gln Phe Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser
        835                 840                 845

ctg tgg gat gat tac tac gcc aac atg ctg tgg ctg gac tcc acc tac      2592
Leu Trp Asp Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr
    850                 855                 860

ccg aca aac gag acc tcc tcc aca ccc ggt gcc gtg cgc gga agc tgc      2640
Pro Thr Asn Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys
865                 870                 875                 880

tcc acc agc tcc ggt gtc cct gct cag gtc gaa tct cag tct ccc aac      2688
Ser Thr Ser Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn
                885                 890                 895

gcc aag gtc acc ttc tcc aac atc aag ttc gga ccc att ggc agc acc      2736
Ala Lys Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr
            900                 905                 910

ggc aac cct agc ggc ggc aac cct ccc ggc gga aac ccg cct ggc acc      2784
Gly Asn Pro Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr
        915                 920                 925

acc acc acc cgc cgc cca gcc act acc act gga agc tct ccc gga cct      2832
Thr Thr Thr Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro
    930                 935                 940

acc cag tct cac tac ggc cag tgc ggc ggt att ggc tac agc ggc ccc      2880
Thr Gln Ser His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro
945                 950                 955                 960

acg gtc tgc gcc agc ggc aca act tgc cag gtc ctg aac cct tac tac      2928
Thr Val Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr
                965                 970                 975

tct cag tgc ctg taa                                                 2943
Ser Gln Cys Leu
            980
```

<210> 78
<211> 980
<212> PRT
<213> Seqüência artificial

<220>
<223> Construção Sintética

<400> 78

Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1 5 10 15

Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
20 25 30

Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
35 40 45

Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
50 55 60

Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65 70 75 80

Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
85 90 95

Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
100 105 110

Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
115 120 125

Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
130 135 140

Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145 150 155 160

Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
165 170 175

Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
180 185 190

Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
195 200 205

Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
210 215 220

Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225 230 235 240

Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
245 250 255

Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
260 265 270

Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
275 280 285

Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
290 295 300

Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305 310 315 320

Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
325 330 335

Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
340 345 350

Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
355 360 365

Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
370 375 380

Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385 390 395 400

Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
405 410 415

Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
420 425 430

Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
435 440 445

Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
450 455 460

Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465 470 475 480

Gln Phe Thr Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro
485 490 495

Leu Thr Trp Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr
500 505 510

Gly Ser Val Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn
515 520 525

Ser Ser Thr Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys
530 535 540

Pro Asp Asn Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala
545 550 555 560

Tyr Ala Ser Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile
565 570 575

Gly Phe Val Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr
580 585 590

Leu Met Ala Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn
595 600 605

Glu Phe Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn
610 615 620

Gly Ala Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys
625 630 635 640

Tyr Pro Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp
645 650 655

Ser Gln Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val
660 665 670

Glu Gly Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly
675 680 685

His Gly Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile
690 695 700

Ser Glu Ala Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile
705 710 715 720

Cys Glu Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly

725 730 735

Gly Thr Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly
740 745 750

Asn Thr Ser Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr
755 760 765

Lys Lys Leu Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn
770 775 780

Arg Tyr Tyr Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu
785 790 795 800

Leu Gly Ser Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala
805 810 815

Glu Glu Ala Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu
820 825 830

Thr Gln Phe Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser
835 840 845

Leu Trp Asp Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr
850 855 860

Pro Thr Asn Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys
865 870 875 880

Ser Thr Ser Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn
885 890 895

Ala Lys Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr
900 905 910

Gly Asn Pro Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr
915 920 925

Thr Thr Thr Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro
930 935 940

Thr Gln Ser His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro
945 950 955 960

Thr Val Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr
965 970 975

Ser Gln Cys Leu
980

<210> 79
<211> 3081
<212> DNA
<213> Seqüência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(3081)

<400> 79

```
cag agc agc tgc gtc tcg gct tgg ggt caa tgt ggc ggt att tct tat      48
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1               5                  10                  15

acc ggg tct acc tgc tgt cag agt ggg aat acc tgc gcc gag att aac      96
Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
            20                  25                  30

tcg tac tac tac cag tgc ata cca gca aca gct gtg agt act tca act     144
Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
        35                  40                  45

acc aca gtg aca tct ccc tct agc tct ggt tcg tct tct gcc aac acg     192
Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
    50                  55                  60

tca ggt tat aca acg acg act gtc ttg ccc agt ccc acg gca aca cag     240
Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65                  70                  75                  80

aac cct tat cct ccg gcc aat gcc agc tca tgt gga tcg tgg gct ctc     288
Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
                85                  90                  95

gtt gat aac gtt tgc tgc cca tac tac tgt ctc tcg gat aat gaa tcc     336
Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
            100                 105                 110

gag tcc tgc acg agc agc tgt acc ggc ggc tgc ggc agt cct gat tcc     384
Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
        115                 120                 125

tcc atg tgc aag tcc ggg acg atg tgg gga gag caa cac acc gta act     432
Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
    130                 135                 140

tcc aac gag gac tgg cat tac agc cgc tca aca cac ttt ggt ctg acc     480
Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145                 150                 155                 160

agc ggt ggc gcc tgc ggg ttc ggt ctg tac ggc ctc tgc acc aag aac     528
```

```
Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
                165                 170                 175

agt gtc acc gcg agc tgg aca gac cca atg ctg ggc tct acc tgc gac   576
Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
            180                 185                 190

gcc ttc tgc acc gcg tat ccg ctc ctc tgc aaa gac ccc gct aac gtc   624
Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
        195                 200                 205

act ctc cgc ggg aac ttt gct gcc ccg aac gga gac tac tac act cag   672
Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
    210                 215                 220

ttc tgg cct tcc ctg gct gca tcc ggc aat ccc gac aac tac ctc tct   720
Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225                 230                 235                 240

tgc ggg gag tgt ttc gag gtc atc cgc acc aag ccc gac ggg aca gac   768
Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
                245                 250                 255

tac gcc gtc ggc gag agc gga tat acc gac ccc ata gtc ctc gag gta   816
Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
            260                 265                 270

gta gac agc tgt ccc tgc aat gcc aat tca aaa tgg tgc tgt aag cgg   864
Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
        275                 280                 285

ccc ccc ccc ccc ccc ttt ttt tcc ccg cct tcc aac gga caa aat ctc   912
Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
    290                 295                 300

aca aga cca ggc ggc agc ggc gca gac cac tgc ggc gaa atc gac ttc   960
Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305                 310                 315                 320

aag tac ggc tgt cct ctg ccg gaa gga tcc cat cac atg gac ctc tcc  1008
Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
                325                 330                 335

gat att gcc atg ggc cga ctc cag gga aac ggc agt ctc gcc gac ggt  1056
Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
            340                 345                 350

gtg att ccc atc cgc tac cgg cgt gtc ccc tgt ccc aag ccg ggg aac  1104
Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
        355                 360                 365

atc tac atc tgg ctt cat gat ggg gcg gga ccg tat tat ttt gcg ctg  1152
Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
    370                 375                 380

agc gcg gtc aat acc aac ggc ccc ggc tcc gta atc agt atc gaa gtc  1200
Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385                 390                 395                 400

cag gct ggt ggc tcc ggg cca tgg gtt gcc ctc gag cac gat ccg aac  1248
Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
```

343

```
                405                 410                 415

tac acc agt agc cgg ccg cag gag cgg tat ggc tct tgg gtc ctc ccg      1296
Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
            420                 425                 430

cag ggc aag gga ccc att act gtg cct gtt tcg atg agg ctg acg gcg      1344
Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
        435                 440                 445

ccc aat ggg cag cag gtg gtt aag gag ggc gcc att acc agc tat acc      1392
Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
    450                 455                 460

ccg ccg gcg act gcg gtc gag ggc ttt tgg tat att gat ctg gga gtg      1440
Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465                 470                 475                 480

cag ttc acc ggc tcg act tac tcc agt gga tct tct tcg ggg tcg ggg      1488
Gln Phe Thr Gly Ser Thr Tyr Ser Ser Gly Ser Ser Ser Gly Ser Gly
                485                 490                 495

tct agc tcc agc tcg agt tcg act acc act aag gcc act tcg acg acc      1536
Ser Ser Ser Ser Ser Ser Ser Thr Thr Thr Lys Ala Thr Ser Thr Thr
            500                 505                 510

ttg aag act acc tcg acc acc agc agt gga agc agt tcg aca tcg gcg      1584
Leu Lys Thr Thr Ser Thr Thr Ser Ser Gly Ser Ser Ser Thr Ser Ala
        515                 520                 525

gcg cag tcg gcc tgc act ctc caa tcg gag act cac ccg cct ctg aca      1632
Ala Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr
    530                 535                 540

tgg cag aaa tgc tcg tct ggt ggc acg tgc act caa cag aca ggc tcc      1680
Trp Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser
545                 550                 555                 560

gtg gtc atc gac gcc aac tgg cgc tgg act cac gct acg aac agc agc      1728
Val Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser
                565                 570                 575

acg aac tgc tac gat ggc aac act tgg agc tcg acc cta tgt cct gac      1776
Thr Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp
            580                 585                 590

aac gag acc tgc gcg aag aac tgc tgt ctg gac ggt gcc gcc tac gcg      1824
Asn Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala
        595                 600                 605

tcc acg tac gga gtt acc acg agc ggt aac agc ctc tcc att ggc ttt      1872
Ser Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe
    610                 615                 620

gtc acc cag tct gcg cag aag aac gtt ggc gct cgc ctt tac ctt atg      1920
Val Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met
625                 630                 635                 640

gcg agc gac acg acc tac cag gaa ttc acc ctg ctt ggc aac gag ttc      1968
Ala Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe
                645                 650                 655
```

```
tct ttc gat gtt gat gtt tcg cag ctg ccg tgc ggc ttg aac gga gct      2016
Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala
            660                 665                 670

ctc tac ttc gtg tcc atg gac gcg gat ggt ggc gtg agc aag tat ccc      2064
Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro
        675                 680                 685

acc aac acc gct ggc gcc aag tac ggc acg ggg tac tgt gac agc cag      2112
Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln
    690                 695                 700

tgt ccc cgc gat ctg aag ttc atc aat ggc cag gcc aac gtt gag ggc      2160
Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly
705                 710                 715                 720

tgg gag ccg tca tcc aac aac gcg aac acg ggc att gga gga cac gga      2208
Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly
                725                 730                 735

tgc tgc tgc tct gag atg gat atc tgg gag gcc aac tcc atc tcc gag      2256
Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu
            740                 745                 750

gct ctt acc ccc cac cct tgc acg act gtc ggc cag gag atc tgc gag      2304
Ala Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu
        755                 760                 765

ggt gat ggg tgc ggc gga act tac tcc gat aac aga tat ggc ggc act      2352
Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr
    770                 775                 780

tgc gat ccc gat ggc tgc gac tgg aac cca tac cgc ctg ggc aac acc      2400
Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr
785                 790                 795                 800

agc ttc tac ggc cct ggc tca agc ttt acc ctc gat acc acc aag aaa      2448
Ser Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys
                805                 810                 815

ctg acc gtt gtc acc cag ttc gag acg tcg ggt gcc atc aac cga tac      2496
Leu Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr
            820                 825                 830

tat gtc cag aat ggc gtc act ttc cag cag ccc aac gcc gag ctt ggt      2544
Tyr Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly
        835                 840                 845

agt tac tct ggc aac gag ctc aac gat gat tac tgc aca gct gag gag      2592
Ser Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu
    850                 855                 860

gca gaa ttc ggc gga tcc tct ttc tca gac aag ggc ggc ctg act cag      2640
Ala Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln
865                 870                 875                 880

ttc aag aag gct acc tct ggc ggc atg gtt ctg gtc atg agt ctg tgg      2688
Phe Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp
                885                 890                 895
```

```
gat gat tac tac gcc aac atg ctg tgg ctg gac tcc acc tac ccg aca      2736
Asp Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr
            900                 905                 910

aac gag acc tcc tcc aca ccc ggt gcc gtg cgc gga agc tgc tcc acc      2784
Asn Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr
        915                 920                 925

agc tcc ggt gtc cct gct cag gtc gaa tct cag tct ccc aac gcc aag      2832
Ser Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys
    930                 935                 940

gtc acc ttc tcc aac atc aag ttc gga ccc att ggc agc acc ggc aac      2880
Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn
945                 950                 955                 960

cct agc ggc ggc aac cct ccc ggc gga aac ccg cct ggc acc acc acc      2928
Pro Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr
                965                 970                 975

acc cgc cgc cca gcc act acc act gga agc tct ccc gga cct acc cag      2976
Thr Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln
            980                 985                 990

tct cac tac ggc cag tgc ggc ggt  att ggc tac agc ggc  ccc acg gtc    3024
Ser His Tyr Gly Gln Cys Gly Gly  Ile Gly Tyr Ser Gly  Pro Thr Val
        995                 1000                1005

tgc gcc  agc ggc aca act tgc  cag gtc ctg aac cct  tac tac tct       3069
Cys Ala  Ser Gly Thr Thr Cys  Gln Val Leu Asn Pro  Tyr Tyr Ser
    1010                1015                1020

                                                                     3081
cag tgc  ctg taa
Gln Cys  Leu
    1025
```

<210> 80
<211> 1026
<212> PRT
<213> Seqüência artificial

<220>
<223> Construção Sintética

<400> 80

```
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1               5                   10                  15

Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
            20                  25                  30

Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
        35                  40                  45

Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
    50                  55                  60
```

Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65 70 75 80

Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
85 90 95

Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
100 105 110

Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
115 120 125

Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
130 135 140

Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145 150 155 160

Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
165 170 175

Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
180 185 190

Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
195 200 205

Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
210 215 220

Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225 230 235 240

Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
245 250 255

Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
260 265 270

Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
275 280 285

Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
290 295 300

Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305 310 315 320

Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
325 330 335

Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
340 345 350

Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
355 360 365

Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
370 375 380

Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385 390 395 400

Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
405 410 415

Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
420 425 430

Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
435 440 445

Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
450 455 460

Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465 470 475 480

Gln Phe Thr Gly Ser Thr Tyr Ser Ser Gly Ser Ser Ser Gly Ser Gly
485 490 495

Ser Ser Ser Ser Ser Ser Ser Thr Thr Thr Lys Ala Thr Ser Thr Thr
500 505 510

Leu Lys Thr Thr Ser Thr Thr Ser Ser Gly Ser Ser Ser Thr Ser Ala
515 520 525

Ala Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr
530 535 540

Trp Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser
545 550 555 560

Val Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser
565 570 575

Thr Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp
580 585 590

Asn Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala
595 600 605

Ser Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe
610 615 620

Val Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met
625 630 635 640

Ala Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe
645 650 655

Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala
660 665 670

Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro
675 680 685

Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln
690 695 700

Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly
705 710 715 720

Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly
725 730 735

Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu
740 745 750

Ala Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu
755 760 765

Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr
770 775 780

Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr

349

785 790 795 800

Ser Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys
805 810 815

Leu Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr
820 825 830

Tyr Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly
835 840 845

Ser Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu
850 855 860

Ala Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln
865 870 875 880

Phe Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp
885 890 895

Asp Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr
900 905 910

Asn Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr
915 920 925

Ser Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys
930 935 940

Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn
945 950 955 960

Pro Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr
965 970 975

Thr Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln
980 985 990

Ser His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val
995 1000 1005

Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser
1010 1015 1020

Gln Cys Leu
1025

<210> 81
<211> 2943
<212> DNA
<213> Seqüência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2943)

<400> 81

```
cag agc agc tgc gtc tcg gct tgg ggt caa tgt ggc ggt att tct tat       48
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1               5                   10                  15

acc ggg tct acc tgc tgt cag agt ggg aat acc tgc gcc gag att aac       96
Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
            20                  25                  30

tcg tac tac tac cag tgc ata cca gca aca gct gtg agt act tca act      144
Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
        35                  40                  45

acc aca gtg aca tct ccc tct agc tct ggt tcg tct tct gcc aac acg      192
Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
    50                  55                  60

tca ggt tat aca acg acg act gtc ttg ccc agt ccc acg gca aca cag      240
Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65                  70                  75                  80

aac cct tat cct ccg gcc aat gcc agc tca tgt gga tcg tgg gct ctc      288
Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
                85                  90                  95

gtt gat aac gtt tgc tgc cca tac tac tgt ctc tcg gat aat gaa tcc      336
Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
            100                 105                 110

gag tcc tgc acg agc agc tgt acc ggc ggc tgc ggc agt cct gat tcc      384
Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
        115                 120                 125

tcc atg tgc aag tcc ggg acg atg tgg gga gag caa cac acc gta act      432
Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
    130                 135                 140

tcc aac gag gac tgg cat tac agc cgc tca aca cac ttt ggt ctg acc      480
Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145                 150                 155                 160

agc ggt ggc gcc tgc ggg ttc ggt ctg tac ggc ctc tgc acc aag aac      528
Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
                165                 170                 175

agt gtc acc gcg agc tgg aca gac cca atg ctg ggc tct acc tgc gac      576
```

```
Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
            180                 185                 190

gcc ttc tgc acc gcg tat ccg ctc ctc tgc aaa gac ccc gct aac gtc      624
Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
        195                 200                 205

act ctc cgc ggg aac ttt gct gcc ccg aac gga gac tac tac act cag      672
Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
    210                 215                 220

ttc tgg cct tcc ctg gct gca tcc ggc aat ccc gac aac tac ctc tct      720
Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225                 230                 235                 240

tgc ggg gag tgt ttc gag gtc atc cgc acc aag ccc gac ggg aca gac      768
Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
                245                 250                 255

tac gcc gtc ggc gag agc gga tat acc gac ccc ata gtc ctc gag gta      816
Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
            260                 265                 270

gta gac agc tgt ccc tgc aat gcc aat tca aaa tgg tgc tgt aag cgg      864
Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
        275                 280                 285

ccc ccc ccc ccc ccc ttt ttt tcc ccg cct tcc aac gga caa aat ctc      912
Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
    290                 295                 300

aca aga cca ggc ggc agc ggc gca gac cac tgc ggc gaa atc gac ttc      960
Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305                 310                 315                 320

aag tac ggc tgt cct ctg ccg gaa gga tcc cat cac atg gac ctc tcc     1008
Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
                325                 330                 335

gat att gcc atg ggc cga ctc cag gga aac ggc agt ctc gcc gac ggt     1056
Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
            340                 345                 350

gtg att ccc atc cgc tac cgg cgt gtc ccc tgt ccc aag ccg ggg aac     1104
Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
        355                 360                 365

atc tac atc tgg ctt cat gat ggg gcg gga ccg tat tat ttt gcg ctg     1152
Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
    370                 375                 380

agc gcg gtc aat acc aac ggc ccc ggc tcc gta atc agt atc gaa gtc     1200
Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385                 390                 395                 400

cag gct ggt ggc tcc ggg cca tgg gtt gcc ctc gag cac gat ccg aac     1248
Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
                405                 410                 415

tac acc agt agc cgg ccg cag gag cgg tat ggc tct tgg gtc ctc ccg     1296
Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
```

```
                420                 425                 430
cag ggc aag gga ccc att act gtg cct gtt tcg atg agg ctg acg gcg      1344
Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
        435                 440                 445

ccc aat ggg cag cag gtg gtt aag gag ggc gcc att acc agc tat acc      1392
Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
    450                 455                 460

ccg ccg gcg act gcg gtc gag ggc ttt tgg tat att gat ctg gga gtg      1440
Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465                 470                 475                 480

cag ttc acc cag tcg gcc tgc act ctc caa tcg gag act cac ccg cct      1488
Gln Phe Thr Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro
                485                 490                 495

ctg aca tgg cag aaa tgc tcg tct ggt ggc acg tgc act caa cag aca      1536
Leu Thr Trp Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr
            500                 505                 510

ggc tcc gtg gtc atc gac gcc aac tgg cgc tgg act cac gct acg aac      1584
Gly Ser Val Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn
        515                 520                 525

agc agc acg aac tgc tac gat ggc aac act tgg agc tcg acc cta tgt      1632
Ser Ser Thr Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys
    530                 535                 540

cct gac aac gag acc tgc gcg aag aac tgc tgt ctg gac ggt gcc gcc      1680
Pro Asp Asn Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala
545                 550                 555                 560

tac gcg tcc acg tac gga gtt acc acg agc ggt aac agc ctc tcc att      1728
Tyr Ala Ser Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile
                565                 570                 575

ggc ttt gtc acc cag tct gcg cag aag aac gtt ggc gct cgc ctt tac      1776
Gly Phe Val Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr
            580                 585                 590

ctt atg gcg agc gac acg acc tac cag gaa ttc acc ctg ctt ggc aac      1824
Leu Met Ala Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn
        595                 600                 605

gag ttc tct ttc gat gtt gat gtt tcg cag ctg ccg tgc ggc ttg aac      1872
Glu Phe Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn
    610                 615                 620

gga gct ctc tac ttc gtg tcc atg gac gcg gat ggt ggc gtg agc aag      1920
Gly Ala Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys
625                 630                 635                 640

tat ccc acc aac acc gct ggc gcc aag tac ggc acg ggg tac tgt gac      1968
Tyr Pro Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp
                645                 650                 655

agc cag tgt ccc cgc gat ctg aag ttc atc aat ggc cag gcc aac gtt      2016
Ser Gln Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val
            660                 665                 670
```

```
gag ggc tgg gag ccg tca tcc aac aac gcg aac acg ggc att gga gga      2064
Glu Gly Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly
        675                 680                 685

cac gga agc tgc tgc tct gag atg gat atc tgg gag gcc aac tcc atc      2112
His Gly Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile
    690                 695                 700

tcc gag gct ctt acc ccc cac cct tgc acg act gtc ggc cag gag atc      2160
Ser Glu Ala Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile
705                 710                 715                 720

tgc gag ggt gat ggg tgc ggc gga act tac tcc gat aac aga tat ggc      2208
Cys Glu Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly
                725                 730                 735

ggc act tgc gat ccc gat ggc tgc gac tgg aac cca tac cgc ctg ggc      2256
Gly Thr Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly
            740                 745                 750

aac acc agc ttc tac ggc cct ggc tca agc ttt acc ctc gat acc acc      2304
Asn Thr Ser Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr
        755                 760                 765

aag aaa ttg acc gtt gtc acc cag ttc gag acg tcg ggt gcc atc aac      2352
Lys Lys Leu Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn
    770                 775                 780

cga tac tat gtc cag aat ggc gtc act ttc cag cag ccc aac gcc gag      2400
Arg Tyr Tyr Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu
785                 790                 795                 800

ctt ggt agt tac tct ggc aac gag ctc aac gat gat tac tgc aca gct      2448
Leu Gly Ser Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala
                805                 810                 815

gag gag gca gaa ttc ggc gga tcc tct ttc tca gac aag ggc ggc ctg      2496
Glu Glu Ala Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu
            820                 825                 830

act cag ttc aag aag gct acc tct ggc ggc atg gtt ctg gtc atg agt      2544
Thr Gln Phe Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser
        835                 840                 845

ctg tgg gat gat tac tac gcc aac atg ctg tgg ctg gac tcc acc tac      2592
Leu Trp Asp Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr
    850                 855                 860

ccg aca aac gag acc tcc tcc aca ccc ggt gcc gtg cgc gga agc tgc      2640
Pro Thr Asn Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys
865                 870                 875                 880

tcc acc agc tcc ggt gtc cct gct cag gtc gaa tct cag tct ccc aac      2688
Ser Thr Ser Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn
                885                 890                 895

gcc aag gtc acc ttc tcc aac atc aag ttc gga ccc att ggc agc acc      2736
Ala Lys Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr
            900                 905                 910
```

```
ggc aac cct agc ggc ggc aac cct ccc ggc gga aac ccg cct ggc acc      2784
Gly Asn Pro Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr
        915                 920                 925

acc acc acc cgc cgc cca gcc act acc act gga agc tct ccc gga cct      2832
Thr Thr Thr Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro
    930                 935                 940

acc cag tct cac tac ggc cag tgc ggc ggt att ggc tac agc ggc ccc      2880
Thr Gln Ser His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro
945                 950                 955                 960

acg gtc tgc gcc agc ggc aca act tgc cag gtc ctg aac cct tac tac      2928
Thr Val Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr
                965                 970                 975

tct cag tgc ctg taa                                                 2943
Ser Gln Cys Leu
            980
```

<210> 82
<211> 980
<212> PRT
<213> Sequência artificial

<220>
<223> Construção Sintética

<400> 82

```
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1               5                   10                  15

Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
            20                  25                  30

Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
        35                  40                  45

Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
    50                  55                  60

Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65                  70                  75                  80

Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
                85                  90                  95

Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
            100                 105                 110

Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
        115                 120                 125
```

Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
130 135 140

Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145 150 155 160

Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
165 170 175

Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
180 185 190

Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
195 200 205

Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
210 215 220

Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225 230 235 240

Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
245 250 255

Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
260 265 270

Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
275 280 285

Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
290 295 300

Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305 310 315 320

Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
325 330 335

Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
340 345 350

Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
355 360 365

Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
370 375 380

Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385 390 395 400

Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
405 410 415

Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
420 425 430

Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
435 440 445

Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
450 455 460

Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465 470 475 480

Gln Phe Thr Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro
485 490 495

Leu Thr Trp Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr
500 505 510

Gly Ser Val Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn
515 520 525

Ser Ser Thr Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys
530 535 540

Pro Asp Asn Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala
545 550 555 560

Tyr Ala Ser Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile
565 570 575

Gly Phe Val Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr
580 585 590

Leu Met Ala Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn
595 600 605

Glu Phe Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn
610 615 620

Gly Ala Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys
625 630 635 640

Tyr Pro Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp
645 650 655

Ser Gln Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val
660 665 670

Glu Gly Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly
675 680 685

His Gly Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile
690 695 700

Ser Glu Ala Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile
705 710 715 720

Cys Glu Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly
725 730 735

Gly Thr Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly
740 745 750

Asn Thr Ser Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr
755 760 765

Lys Lys Leu Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn
770 775 780

Arg Tyr Tyr Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu
785 790 795 800

Leu Gly Ser Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala
805 810 815

Glu Glu Ala Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu
820 825 830

Thr Gln Phe Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser
835 840 845

Leu Trp Asp Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr

850 855 860

Pro Thr Asn Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys
865 870 875 880

Ser Thr Ser Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn
885 890 895

Ala Lys Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr
900 905 910

Gly Asn Pro Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr
915 920 925

Thr Thr Thr Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro
930 935 940

Thr Gln Ser His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro
945 950 955 960

Thr Val Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr
965 970 975

Ser Gln Cys Leu
980

<210> 83
<211> 3081
<212> DNA
<213> Sequência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(3081)

<400> 83
cag agc agc tgc gtc tcg gct tgg ggt caa tgt ggc ggt att tct tat 48
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1 5 10 15

acc ggg tct acc tgc tgt cag agt ggg aat acc tgc gcc gag att aac 96
Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
20 25 30

tcg tac tac tac cag tgc ata cca gca aca gct gtg agt act tca act 144
Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
35 40 45

```
acc aca gtg aca tct ccc tct agc tct ggt tcg tct tct gcc aac acg      192
Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
    50                  55                  60

tca ggt tat aca acg acg act gtc ttg ccc agt ccc acg gca aca cag      240
Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65                  70                  75                  80

aac cct tat cct ccg gcc aat gcc agc tca tgt gga tcg tgg gct ctc      288
Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
                85                  90                  95

gtt gat aac gtt tgc tgc cca tac tac tgt ctc tcg gat aat gaa tcc      336
Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
            100                 105                 110

gag tcc tgc acg agc agc tgt acc ggc ggc tgc ggc agt cct gat tcc      384
Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
        115                 120                 125

tcc atg tgc aag tcc ggg acg atg tgg gga gag caa cac acc gta act      432
Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
    130                 135                 140

tcc aac gag gac tgg cat tac agc cgc tca aca cac ttt ggt ctg acc      480
Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145                 150                 155                 160

agc ggt ggc gcc tgc ggg ttc ggt ctg tac ggc ctc tgc acc aag aac      528
Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
                165                 170                 175

agt gtc acc gcg agc tgg aca gac cca atg ctg ggc tct acc tgc gac      576
Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
            180                 185                 190

gcc ttc tgc acc gcg tat ccg ctc ctc tgc aaa gac ccc gct aac gtc      624
Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
        195                 200                 205

act ctc cgc ggg aac ttt gct gcc ccg aac gga gac tac tac act cag      672
Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
    210                 215                 220

ttc tgg cct tcc ctg gct gca tcc ggc aat ccc gac aac tac ctc tct      720
Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225                 230                 235                 240

tgc ggg gag tgt ttc gag gtc atc cgc acc aag ccc gac ggg aca gac      768
Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
                245                 250                 255

tac gcc gtc ggc gag agc gga tat acc gac ccc ata gtc ctc gag gta      816
Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
            260                 265                 270

gta gac agc tgt ccc tgc aat gcc aat tca aaa tgg tgc tgt aag cgg      864
Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
        275                 280                 285

ccc ccc ccc ccc ccc ttt ttt tcc ccg cct tcc aac gga caa aat ctc      912
```

```
Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
    290                 295                 300

aca aga cca ggc ggc agc ggc gca gac cac tgc ggc gaa atc gac ttc      960
Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305                 310                 315                 320

aag tac ggc tgt cct ctg ccg gaa gga tcc cat cac atg gac ctc tcc     1008
Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
                325                 330                 335

gat att gcc atg ggc cga ctc cag gga aac ggc agt ctc gcc gac ggt     1056
Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
            340                 345                 350

gtg att ccc atc cgc tac cgg cgt gtc ccc tgt ccc aag ccg ggg aac     1104
Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
        355                 360                 365

atc tac atc tgg ctt cat gat ggg gcg gga ccg tat tat ttt gcg ctg     1152
Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
    370                 375                 380

agc gcg gtc aat acc aac ggc ccc ggc tcc gta atc agt atc gaa gtc     1200
Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385                 390                 395                 400

cag gct ggt ggc tcc ggg cca tgg gtt gcc ctc gag cac gat ccg aac     1248
Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
                405                 410                 415

tac acc agt agc cgg ccg cag gag cgg tat ggc tct tgg gtc ctc ccg     1296
Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
            420                 425                 430

cag ggc aag gga ccc att act gtg cct gtt tcg atg agg ctg acg gcg     1344
Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
        435                 440                 445

ccc aat ggg cag cag gtg gtt aag gag ggc gcc att acc agc tat acc     1392
Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
    450                 455                 460

ccg ccg gcg act gcg gtc gag ggc ttt tgg tat att gat ctg gga gtg     1440
Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465                 470                 475                 480

cag ttc acc ggc tcg act tac tcc agt gga tct tct tcg ggg tcg ggg     1488
Gln Phe Thr Gly Ser Thr Tyr Ser Ser Gly Ser Ser Ser Gly Ser Gly
                485                 490                 495

tct agc tcc agc tcg agt tcg act acc act aag gcc act tcg acg acc     1536
Ser Ser Ser Ser Ser Ser Ser Thr Thr Thr Lys Ala Thr Ser Thr Thr
            500                 505                 510

ttg aag act acc tcg acc acc agc agt gga agc agt tcg aca tcg gcg     1584
Leu Lys Thr Thr Ser Thr Thr Ser Ser Gly Ser Ser Ser Thr Ser Ala
        515                 520                 525

gcg cag tcg gcc tgc act ctc caa tcg gag act cac ccg cct ctg aca     1632
Ala Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr
```

```
    530                 535                 540

tgg cag aaa tgc tcg tct ggt ggc acg tgc act caa cag aca ggc tcc  1680
Trp Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser
545                 550                 555                 560

gtg gtc atc gac gcc aac tgg cgc tgg act cac gct acg aac agc agc  1728
Val Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser
                565                 570                 575

acg aac tgc tac gat ggc aac act tgg agc tcg acc cta tgt cct gac  1776
Thr Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp
            580                 585                 590

aac gag acc tgc gcg aag aac tgc tgt ctg gac ggt gcc gcc tac gcg  1824
Asn Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala
        595                 600                 605

tcc acg tac gga gtt acc acg agc ggt aac agc ctc tcc att ggc ttt  1872
Ser Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe
    610                 615                 620

gtc acc cag tct gcg cag aag aac gtt ggc gct cgc ctt tac ctt atg  1920
Val Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met
625                 630                 635                 640

gcg agc gac acg acc tac cag gaa ttc acc ctg ctt ggc aac gag ttc  1968
Ala Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe
                645                 650                 655

tct ttc gat gtt gat gtt tcg cag ctg ccg tgc ggc ttg aac gga gct  2016
Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala
            660                 665                 670

ctc tac ttc gtg tcc atg gac gcg gat ggt ggc gtg agc aag tat ccc  2064
Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro
        675                 680                 685

acc aac acc gct ggc gcc aag tac ggc acg ggg tac tgt gac agc cag  2112
Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln
    690                 695                 700

tgt ccc cgc gat ctg aag ttc atc aat ggc cag gcc aac gtt gag ggc  2160
Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly
705                 710                 715                 720

tgg gag ccg tca tcc aac aac gcg aac acg ggc att gga gga cac gga  2208
Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly
                725                 730                 735

agc tgc tgc tct gag atg gat atc tgg gag gcc aac tcc atc tcc gag  2256
Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu
            740                 745                 750

gct ctt acc ccc cac cct tgc acg act gtc ggc cag gag atc tgc gag  2304
Ala Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu
        755                 760                 765

ggt gat ggg tgc ggc gga act tac tcc gat aac aga tat ggc ggc act  2352
Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr
    770                 775                 780
```

```
tgc gat ccc gat ggc tgc gac tgg aac cca tac cgc ctg ggc aac acc     2400
Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr
785                 790                 795                 800

agc ttc tac ggc cct ggc tca agc ttt acc ctc gat acc acc aag aaa     2448
Ser Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys
                805                 810                 815

ttg acc gtt gtc acc cag ttc gag acg tcg ggt gcc atc aac cga tac     2496
Leu Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr
            820                 825                 830

tat gtc cag aat ggc gtc act ttc cag cag ccc aac gcc gag ctt ggt     2544
Tyr Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly
        835                 840                 845

agt tac tct ggc aac gag ctc aac gat gat tac tgc aca gct gag gag     2592
Ser Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu
    850                 855                 860

gca gaa ttc ggc gga tcc tct ttc tca gac aag ggc ggc ctg act cag     2640
Ala Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln
865                 870                 875                 880

ttc aag aag gct acc tct ggc ggc atg gtt ctg gtc atg agt ctg tgg     2688
Phe Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp
                885                 890                 895

gat gat tac tac gcc aac atg ctg tgg ctg gac tcc acc tac ccg aca     2736
Asp Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr
            900                 905                 910

aac gag acc tcc tcc aca ccc ggt gcc gtg cgc gga agc tgc tcc acc     2784
Asn Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr
        915                 920                 925

agc tcc ggt gtc cct gct cag gtc gaa tct cag tct ccc aac gcc aag     2832
Ser Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys
    930                 935                 940

gtc acc ttc tcc aac atc aag ttc gga ccc att ggc agc acc ggc aac     2880
Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn
945                 950                 955                 960

cct agc ggc ggc aac cct ccc ggc gga aac ccg cct ggc acc acc acc     2928
Pro Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr
                965                 970                 975

acc cgc cgc cca gcc act acc act gga agc tct ccc gga cct acc cag     2976
Thr Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln
            980                 985                 990

tct cac tac ggc cag tgc ggc ggt  att ggc tac agc ggc  ccc acg gtc   3024
Ser His Tyr Gly Gln Cys Gly Gly  Ile Gly Tyr Ser Gly  Pro Thr Val
        995                 1000                1005

tgc gcc  agc ggc aca act tgc  cag gtc ctg aac cct  tac tac tct      3069
Cys Ala  Ser Gly Thr Thr Cys  Gln Val Leu Asn Pro  Tyr Tyr Ser
    1010                1015                1020
```

3081

cag tgc ctg taa
Gln Cys Leu
1025

<210> 84
<211> 1026
<212> PRT
<213> Seqüência artificial

<220>
<223> Construção Sintética

<400> 84

Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1 5 10 15

Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
20 25 30

Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
35 40 45

Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
50 55 60

Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65 70 75 80

Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
85 90 95

Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
100 105 110

Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
115 120 125

Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
130 135 140

Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145 150 155 160

Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
165 170 175

Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
180 185 190

Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
195 200 205

Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
210 215 220

Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225 230 235 240

Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
245 250 255

Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
260 265 270

Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
275 280 285

Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
290 295 300

Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305 310 315 320

Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
325 330 335

Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
340 345 350

Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
355 360 365

Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
370 375 380

Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385 390 395 400

Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
405 410 415

Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
420 425 430

Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
435 440 445

Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
450 455 460

Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465 470 475 480

Gln Phe Thr Gly Ser Thr Tyr Ser Ser Gly Ser Ser Ser Gly Ser Gly
485 490 495

Ser Ser Ser Ser Ser Ser Ser Thr Thr Thr Lys Ala Thr Ser Thr Thr
500 505 510

[redacted] Lys Thr Thr Ser Thr Thr Ser Ser Gly Ser Ser Ser Thr Ser Ala
515 520 525

Ala Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr
530 535 540

Trp Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser
545 550 555 560

Val Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser
565 570 575

Thr Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp
580 585 590

[redacted] Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala
595 600 605

Ser Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe
610 615 620

Val Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met
625 630 635 640

Ala Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe
645 650 655

Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala
660 665 670

Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro
675 680 685

Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln
690 695 700

Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly
705 710 715 720

Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly
725 730 735

Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu
740 745 750

a Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu
755 760 765

Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr
770 775 780

Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr
785 790 795 800

Ser Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys
805 810 815

Leu Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr
820 825 830

yr Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly
835 840 845

Ser Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu
850 855 860

Ala Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln
865 870 875 880

Phe Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp
885 890 895

Asp Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr
900 905 910

Asn Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr

915 920 925

Ser Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys
930 935 940

Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn
945 950 955 960

Pro Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr
965 970 975

Thr Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln
980 985 990

Ser His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val
995 1000 1005

Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser
1010 1015 1020

Gln Cys Leu
1025

<210> 85
<211> 2793
<212> DNA
<213> Sequência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2793)

<400> 85
cag agc agc tgc gtc tcg gct tgg ggt caa tgt ggc ggt att tct tat 48
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1 5 10 15

acc ggg tct acc tgc tgt cag agt ggg aat acc tgc gcc gag att aac 96
Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
20 25 30

tcg tac tac tac cag tgc ata cca gca aca gct gtg agt act tca act 144
Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
35 40 45

acc aca gtg aca tct ccc tct agc tct ggt tcg tct tct gcc aac acg 192
Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
50 55 60

```
tca ggt tat aca acg acg act gtc ttg ccc agt ccc acg gca aca cag      240
Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65                  70                  75                  80

aac cct tat cct ccg gcc aat gcc agc tca tgt gga tcg tgg gct ctc      288
Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
                85                  90                  95

gtt gat aac gtt tgc tgc cca tac tac tgt ctc tcg gat aat gaa tcc      336
Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
            100                 105                 110

gag tcc tgc acg agc agc tgt acc ggc ggc tgc ggc agt cct gat tcc      384
Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
        115                 120                 125

tcc atg tgc aag tcc ggg acg atg tgg gga gag caa cac acc gta act      432
Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
    130                 135                 140

tcc aac gag gac tgg cat tac agc cgc tca aca cac ttt ggt ctg acc      480
Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145                 150                 155                 160

agc ggt ggc gcc tgc ggg ttc ggt ctg tac ggc ctc tgc acc aag aac      528
Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
                165                 170                 175

agt gtc acc gcg agc tgg aca gac cca atg ctg ggc tct acc tgc gac      576
Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
            180                 185                 190

gcc ttc tgc acc gcg tat ccg ctc ctc tgc aaa gac ccc gct aac gtc      624
Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
        195                 200                 205

act ctc cgc ggg aac ttt gct gcc ccg aac gga gac tac tac act cag      672
Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
    210                 215                 220

ttc tgg cct tcc ctg gct gca tcc ggc aat ccc gac aac tac ctc tct      720
Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225                 230                 235                 240

tgc ggg gag tgt ttc gag gtc atc cgc acc aag ccc gac ggg aca gac      768
Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
                245                 250                 255

tac gcc gtc ggc gag agc gga tat acc gac ccc ata gtc ctc gag gta      816
Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
            260                 265                 270

gta gac agc tgt ccc tgc aat gcc aat tca aaa tgg tgc tgt aag cgg      864
Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
        275                 280                 285

ccc ccc ccc ccc ccc ttt ttt tcc ccg cct tcc aac gga caa aat ctc      912
Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
    290                 295                 300

aca aga cca ggc ggc agc ggc gca gac cac tgc ggc gaa atc gac ttc      960
```

```
Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305                 310                 315                 320

aag tac ggc tgt cct ctg ccg gaa gga tcc cat cac atg gac ctc tcc     1008
Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
                325                 330                 335

gat att gcc atg ggc cga ctc cag gga aac ggc agt ctc gcc gac ggt     1056
Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
            340                 345                 350

gtg att ccc atc cgc tac cgg cgt gtc ccc tgt ccc aag ccg ggg aac     1104
Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
        355                 360                 365

atc tac atc tgg ctt cat gat ggg gcg gga ccg tat tat ttt gcg ctg     1152
Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
    370                 375                 380

agc gcg gtc aat acc aac ggc ccc ggc tcc gta atc agt atc gaa gtc     1200
Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385                 390                 395                 400

cag gct ggt ggc tcc ggg cca tgg gtt gcc ctc gag cac gat ccg aac     1248
Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
                405                 410                 415

tac acc agt agc cgg ccg cag gag cgg tat ggc tct tgg gtc ctc ccg     1296
Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
            420                 425                 430

cag ggc aag gga ccc att act gtg cct gtt tcg atg agg ctg acg gcg     1344
Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
        435                 440                 445

ccc aat ggg cag cag gtg gtt aag gag ggc gcc att acc agc tat acc     1392
Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
    450                 455                 460

ccg ccg gcg act gcg gtc gag ggc ttt tgg tat att gat ctg gga gtg     1440
Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465                 470                 475                 480

cag ttc acc caa gct tgc tca agc gtc tgg ggc caa tgt ggt ggc cag     1488
Gln Phe Thr Gln Ala Cys Ser Ser Val Trp Gly Gln Cys Gly Gly Gln
                485                 490                 495

aat tgg tcg ggt ccg act tgc tgt gct tcc gga agc aca tgc gtc tac     1536
Asn Trp Ser Gly Pro Thr Cys Cys Ala Ser Gly Ser Thr Cys Val Tyr
            500                 505                 510

tcc aac gac tat tac tcc cag tgt ctt ccc ggc gct gca agc tca agc     1584
Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Gly Ala Ala Ser Ser Ser
        515                 520                 525

tcg tcc acg cgc gcc gcg tcg acg act tct cga gta tcc ccc aca aca     1632
Ser Ser Thr Arg Ala Ala Ser Thr Thr Ser Arg Val Ser Pro Thr Thr
    530                 535                 540

tcc cgg tcg agc tcc gcg acg cct cca cct ggt tct act act acc aga     1680
Ser Arg Ser Ser Ser Ala Thr Pro Pro Pro Gly Ser Thr Thr Thr Arg
```

```
545                 550                 555                 560

gta cct cca gtc gga tcg gga acc gct acg tat tca ggc aac cct ttt   1728
Val Pro Pro Val Gly Ser Gly Thr Ala Thr Tyr Ser Gly Asn Pro Phe
                565                 570                 575

gtt ggg gtc act cct tgg gcc aat gca tat tac gcc tct gaa gtt agc   1776
Val Gly Val Thr Pro Trp Ala Asn Ala Tyr Tyr Ala Ser Glu Val Ser
            580                 585                 590

agc ctc gct att cct agc ttg act gga gcc atg gcc act gct gca gca   1824
Ser Leu Ala Ile Pro Ser Leu Thr Gly Ala Met Ala Thr Ala Ala Ala
        595                 600                 605

gct gtc gca aag gtt ccc tct ttt atg tgg cta gat act ctt gac aag   1872
Ala Val Ala Lys Val Pro Ser Phe Met Trp Leu Asp Thr Leu Asp Lys
    610                 615                 620

acc cct ctc atg gag caa acc ttg gcc gac atc cgc acc gcc aac aag   1920
Thr Pro Leu Met Glu Gln Thr Leu Ala Asp Ile Arg Thr Ala Asn Lys
625                 630                 635                 640

aat ggc ggt aac tat gcg gga cag ttt gtg gtg tat gac ttg ccg gat   1968
Asn Gly Gly Asn Tyr Ala Gly Gln Phe Val Val Tyr Asp Leu Pro Asp
                645                 650                 655

cgc gat tgc gct gcc ctt gcc tcg aat ggc gaa tac tct att gcc gat   2016
Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Tyr Ser Ile Ala Asp
            660                 665                 670

ggt ggc gtc gcc aaa tat aag aac tat atc gac acc att cgt caa att   2064
Gly Gly Val Ala Lys Tyr Lys Asn Tyr Ile Asp Thr Ile Arg Gln Ile
        675                 680                 685

gtc gtg gaa tat tcc gat atc cgg acc ctc ctg gtt att gag cct gac   2112
Val Val Glu Tyr Ser Asp Ile Arg Thr Leu Leu Val Ile Glu Pro Asp
    690                 695                 700

tct ctt gcc aac ctg gtg acc aac ctc ggt act cca aag tgt gcc aat   2160
Ser Leu Ala Asn Leu Val Thr Asn Leu Gly Thr Pro Lys Cys Ala Asn
705                 710                 715                 720

gct cag tca gcc tac ctt gag tgc atc aac tac gcc gtc aca cag ctg   2208
Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn Tyr Ala Val Thr Gln Leu
                725                 730                 735

aac ctt cca aat gtt gcg atg tat ttg gac gct ggc cat gca gga tgg   2256
Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala Gly His Ala Gly Trp
            740                 745                 750

ctt ggc tgg ccg gca aac caa gac ccg gcc gct cag cta ttt gca aat   2304
Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala Gln Leu Phe Ala Asn
        755                 760                 765

gtt tac aag aat gca tcg tct ccg aga gct ctt cgc gga ttg gca acc   2352
Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu Arg Gly Leu Ala Thr
    770                 775                 780

aat gtc gcc aac tac aac ggg tgg aac att acc agc ccc cca tcg tac   2400
Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile Thr Ser Pro Pro Ser Tyr
785                 790                 795                 800
```

```
acg caa ggc aac gct gtc tac aac gag aag ctg tac atc cac gct att     2448
Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu Tyr Ile His Ala Ile
                805                 810                 815

gga cgt ctt ctt gcc aat cac ggc tgg tcc aac gcc ttc ttc atc act     2496
Gly Arg Leu Leu Ala Asn His Gly Trp Ser Asn Ala Phe Phe Ile Thr
            820                 825                 830

gat caa ggt cga tcg gga aag cag cct acc gga cag caa cag tgg gga     2544
Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr Gly Gln Gln Gln Trp Gly
        835                 840                 845

gac tgg tgc aat gtg atc ggc acc gga ttt ggt att cgc cca tcc gca     2592
Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly Ile Arg Pro Ser Ala
    850                 855                 860

aac act ggg gac tcg ttg ctg gat tcg ttt gtc tgg gtc aag cca ggc     2640
Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe Val Trp Val Lys Pro Gly
865                 870                 875                 880

ggc gag tgt gac ggc acc agc gac agc agt gcg cca cga ttt gac tcc     2688
Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser Ala Pro Arg Phe Asp Ser
                885                 890                 895

cac tgt gcg ctc cca gat gcc ttg caa ccg gcg gct caa gct ggt gct     2736
His Cys Ala Leu Pro Asp Ala Leu Gln Pro Ala Ala Gln Ala Gly Ala
            900                 905                 910

tgg ttc caa gcc tac ttt gtg cag ctt ctc aca aac gca aac cca tcg     2784
Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu Thr Asn Ala Asn Pro Ser
        915                 920                 925

ttc ctg taa                                                       2793
Phe Leu
    930
```

<210> 86
<211> 930
<212> PRT
<213> Seqüência artificial

<220>
<223> Construção Sintética

<400> 86

```
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1               5                  10                  15

Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
            20                  25                  30

Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
        35                  40                  45

Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
```

50 55 60

Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65 70 75 80

Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
85 90 95

Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
100 105 110

Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
115 120 125

Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
130 135 140

Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145 150 155 160

Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
165 170 175

Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
180 185 190

Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
195 200 205

Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
210 215 220

Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225 230 235 240

Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
245 250 255

Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
260 265 270

Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
275 280 285

Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
290 295 300

Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305 310 315 320

Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
325 330 335

Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
340 345 350

Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
355 360 365

Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
370 375 380

Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385 390 395 400

Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
405 410 415

Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
420 425 430

Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
435 440 445

Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
450 455 460

Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465 470 475 480

Gln Phe Thr Gln Ala Cys Ser Ser Val Trp Gly Gln Cys Gly Gly Gln
485 490 495

Asn Trp Ser Gly Pro Thr Cys Cys Ala Ser Gly Ser Thr Cys Val Tyr
500 505 510

Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Gly Ala Ala Ser Ser Ser
515 520 525

Ser Ser Thr Arg Ala Ala Ser Thr Thr Ser Arg Val Ser Pro Thr Thr
530 535 540

Ser Arg Ser Ser Ser Ala Thr Pro Pro Pro Gly Ser Thr Thr Thr Arg
545 550 555 560

Val Pro Pro Val Gly Ser Gly Thr Ala Thr Tyr Ser Gly Asn Pro Phe
565 570 575

Val Gly Val Thr Pro Trp Ala Asn Ala Tyr Tyr Ala Ser Glu Val Ser
580 585 590

Ser Leu Ala Ile Pro Ser Leu Thr Gly Ala Met Ala Thr Ala Ala Ala
595 600 605

Ala Val Ala Lys Val Pro Ser Phe Met Trp Leu Asp Thr Leu Asp Lys
610 615 620

Thr Pro Leu Met Glu Gln Thr Leu Ala Asp Ile Arg Thr Ala Asn Lys
625 630 635 640

Asn Gly Gly Asn Tyr Ala Gly Gln Phe Val Val Tyr Asp Leu Pro Asp
645 650 655

Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Tyr Ser Ile Ala Asp
660 665 670

Gly Gly Val Ala Lys Tyr Lys Asn Tyr Ile Asp Thr Ile Arg Gln Ile
675 680 685

Val Val Glu Tyr Ser Asp Ile Arg Thr Leu Leu Val Ile Glu Pro Asp
690 695 700

Ser Leu Ala Asn Leu Val Thr Asn Leu Gly Thr Pro Lys Cys Ala Asn
705 710 715 720

Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn Tyr Ala Val Thr Gln Leu
725 730 735

Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala Gly His Ala Gly Trp
740 745 750

Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala Gln Leu Phe Ala Asn
755 760 765

Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu Arg Gly Leu Ala Thr
770 775 780

Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile Thr Ser Pro Pro Ser Tyr
785 790 795 800

Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu Tyr Ile His Ala Ile
805 810 815

Gly Arg Leu Leu Ala Asn His Gly Trp Ser Asn Ala Phe Phe Ile Thr
820 825 830

Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr Gly Gln Gln Gln Trp Gly
835 840 845

Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly Ile Arg Pro Ser Ala
850 855 860

Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe Val Trp Val Lys Pro Gly
865 870 875 880

Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser Ala Pro Arg Phe Asp Ser
885 890 895

His Cys Ala Leu Pro Asp Ala Leu Gln Pro Ala Ala Gln Ala Gly Ala
900 905 910

Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu Thr Asn Ala Asn Pro Ser
915 920 925

Phe Leu
930

<210> 87
<211> 2931
<212> DNA
<213> Seqüência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2931)

<400> 87
cag agc agc tgc gtc tcg gct tgg ggt caa tgt ggc ggt att tct tat 48
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1 5 10 15

acc ggg tct acc tgc tgt cag agt ggg aat acc tgc gcc gag att aac 96
Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
20 25 30

```
tcg tac tac tac cag tgc ata cca gca aca gct gtg agt act tca act      144
Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
        35                  40                  45

acc aca gtg aca tct ccc tct agc tct ggt tcg tct tct gcc aac acg      192
Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
    50                  55                  60

tca ggt tat aca acg acg act gtc ttg ccc agt ccc acg gca aca cag      240
Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65                  70                  75                  80

aac cct tat cct ccg gcc aat gcc agc tca tgt gga tcg tgg gct ctc      288
Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
                85                  90                  95

gtt gat aac gtt tgc tgc cca tac tac tgt ctc tcg gat aat gaa tcc      336
Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
            100                 105                 110

gag tcc tgc acg agc agc tgt acc ggc ggc tgc ggc agt cct gat tcc      384
Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
        115                 120                 125

tcc atg tgc aag tcc ggg acg atg tgg gga gag caa cac acc gta act      432
Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
    130                 135                 140

tcc aac gag gac tgg cat tac agc cgc tca aca cac ttt ggt ctg acc      480
Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145                 150                 155                 160

agc ggt ggc gcc tgc ggg ttc ggt ctg tac ggc ctc tgc acc aag aac      528
Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
                165                 170                 175

agt gtc acc gcg agc tgg aca gac cca atg ctg ggc tct acc tgc gac      576
Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
            180                 185                 190

gcc ttc tgc acc gcg tat ccg ctc ctc tgc aaa gac ccc gct aac gtc      624
Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
        195                 200                 205

act ctc cgc ggg aac ttt gct gcc ccg aac gga gac tac tac act cag      672
Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
    210                 215                 220

ttc tgg cct tcc ctg gct gca tcc ggc aat ccc gac aac tac ctc tct      720
Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225                 230                 235                 240

tgc ggg gag tgt ttc gag gtc atc cgc acc aag ccc gac ggg aca gac      768
Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
                245                 250                 255

tac gcc gtc ggc gag agc gga tat acc gac ccc ata gtc ctc gag gta      816
Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
            260                 265                 270
```

```
gta gac agc tgt ccc tgc aat gcc aat tca aaa tgg tgc tgt aag cgg      864
Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
        275                 280                 285

ccc ccc ccc ccc ccc ttt ttt tcc ccg cct tcc aac gga caa aat ctc      912
Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
    290                 295                 300

aca aga cca ggc ggc agc ggc gca gac cac tgc ggc gaa atc gac ttc      960
Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305                 310                 315                 320

aag tac ggc tgt cct ctg ccg gaa gga tcc cat cac atg gac ctc tcc     1008
Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
                325                 330                 335

gat att gcc atg ggc cga ctc cag gga aac ggc agt ctc gcc gac ggt     1056
Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
            340                 345                 350

[illegible]tg att ccc atc cgc tac cgg cgt gtc ccc tgt ccc aag ccg ggg aac     1104
[illegible]l Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
        355                 360                 365

atc tac atc tgg ctt cat gat ggg gcg gga ccg tat tat ttt gcg ctg     1152
Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
    370                 375                 380

agc gcg gtc aat acc aac ggc ccc ggc tcc gta atc agt atc gaa gtc     1200
Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385                 390                 395                 400

cag gct ggt ggc tcc ggg cca tgg gtt gcc ctc gag cac gat ccg aac     1248
Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
                405                 410                 415

tac acc agt agc cgg ccg cag gag cgg tat ggc tct tgg gtc ctc ccg     1296
Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
            420                 425                 430

[illegible]g ggc aag gga ccc att act gtg cct gtt tcg atg agg ctg acg gcg     1344
[illegible]n Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
        435                 440                 445

ccc aat ggg cag cag gtg gtt aag gag ggc gcc att acc agc tat acc     1392
Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
    450                 455                 460

ccg ccg gcg act gcg gtc gag ggc ttt tgg tat att gat ctg gga gtg     1440
Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465                 470                 475                 480

cag ttc acc ggc tcg act tac tcc agt gga tct tct tcg ggg tcg ggg     1488
Gln Phe Thr Gly Ser Thr Tyr Ser Ser Gly Ser Ser Ser Gly Ser Gly
                485                 490                 495

tct agc tcc agc tcg agt tcg act acc act aag gcc act tcg acg acc     1536
Ser Ser Ser Ser Ser Ser Ser Thr Thr Thr Lys Ala Thr Ser Thr Thr
            500                 505                 510

ttg aag act acc tcg acc acc agc agt gga agc agt tcg aca tcg gcg     1584
```

```
Leu Lys Thr Thr Ser Thr Thr Ser Ser Gly Ser Ser Ser Thr Ser Ala
        515                 520                 525

gcg caa gct tgc tca agc gtc tgg ggc caa tgt ggt ggc cag aat tgg     1632
Ala Gln Ala Cys Ser Ser Val Trp Gly Gln Cys Gly Gly Gln Asn Trp
    530                 535                 540

tcg ggt ccg act tgc tgt gct tcc gga agc aca tgc gtc tac tcc aac     1680
Ser Gly Pro Thr Cys Cys Ala Ser Gly Ser Thr Cys Val Tyr Ser Asn
545                 550                 555                 560

gac tat tac tcc cag tgt ctt ccc ggc gct gca agc tca agc tcg tcc     1728
Asp Tyr Tyr Ser Gln Cys Leu Pro Gly Ala Ala Ser Ser Ser Ser Ser
                565                 570                 575

acg cgc gcc gcg tcg acg act tct cga gta tcc ccc aca aca tcc cgg     1776
Thr Arg Ala Ala Ser Thr Thr Ser Arg Val Ser Pro Thr Thr Ser Arg
            580                 585                 590

tcg agc tcc gcg acg cct cca cct ggt tct act act acc aga gta cct     1824
Ser Ser Ser Ala Thr Pro Pro Pro Gly Ser Thr Thr Thr Arg Val Pro
        595                 600                 605

cca gtc gga tcg gga acc gct acg tat tca ggc aac cct ttt gtt ggg     1872
Pro Val Gly Ser Gly Thr Ala Thr Tyr Ser Gly Asn Pro Phe Val Gly
    610                 615                 620

gtc act cct tgg gcc aat gca tat tac gcc tct gaa gtt agc agc ctc     1920
Val Thr Pro Trp Ala Asn Ala Tyr Tyr Ala Ser Glu Val Ser Ser Leu
625                 630                 635                 640

gct att cct agc ttg act gga gcc atg gcc act gct gca gca gct gtc     1968
Ala Ile Pro Ser Leu Thr Gly Ala Met Ala Thr Ala Ala Ala Ala Val
                645                 650                 655

gca aag gtt ccc tct ttt atg tgg cta gat act ctt gac aag acc cct     2016
Ala Lys Val Pro Ser Phe Met Trp Leu Asp Thr Leu Asp Lys Thr Pro
            660                 665                 670

ctc atg gag caa acc ttg gcc gac atc cgc acc gcc aac aag aat ggc     2064
Leu Met Glu Gln Thr Leu Ala Asp Ile Arg Thr Ala Asn Lys Asn Gly
        675                 680                 685

ggt aac tat gcg gga cag ttt gtg gtg tat gac ttg ccg gat cgc gat     2112
Gly Asn Tyr Ala Gly Gln Phe Val Val Tyr Asp Leu Pro Asp Arg Asp
    690                 695                 700

tgc gct gcc ctt gcc tcg aat ggc gaa tac tct att gcc gat ggt ggc     2160
Cys Ala Ala Leu Ala Ser Asn Gly Glu Tyr Ser Ile Ala Asp Gly Gly
705                 710                 715                 720

gtc gcc aaa tat aag aac tat atc gac acc att cgt caa att gtc gtg     2208
Val Ala Lys Tyr Lys Asn Tyr Ile Asp Thr Ile Arg Gln Ile Val Val
                725                 730                 735

gaa tat tcc gat atc cgg acc ctc ctg gtt att gag cct gac tct ctt     2256
Glu Tyr Ser Asp Ile Arg Thr Leu Leu Val Ile Glu Pro Asp Ser Leu
            740                 745                 750

gcc aac ctg gtg acc aac ctc ggt act cca aag tgt gcc aat gct cag     2304
Ala Asn Leu Val Thr Asn Leu Gly Thr Pro Lys Cys Ala Asn Ala Gln
```

```
        755                 760                 765

tca gcc tac ctt gag tgc atc aac tac gcc gtc aca cag ctg aac ctt      2352
Ser Ala Tyr Leu Glu Cys Ile Asn Tyr Ala Val Thr Gln Leu Asn Leu
    770                 775                 780

cca aat gtt gcg atg tat ttg gac gct ggc cat gca gga tgg ctt ggc      2400
Pro Asn Val Ala Met Tyr Leu Asp Ala Gly His Ala Gly Trp Leu Gly
785                 790                 795                 800

tgg ccg gca aac caa gac ccg gcc gct cag cta ttt gca aat gtt tac      2448
Trp Pro Ala Asn Gln Asp Pro Ala Ala Gln Leu Phe Ala Asn Val Tyr
                805                 810                 815

aag aat gca tcg tct ccg aga gct ctt cgc gga ttg gca acc aat gtc      2496
Lys Asn Ala Ser Ser Pro Arg Ala Leu Arg Gly Leu Ala Thr Asn Val
            820                 825                 830

gcc aac tac aac ggg tgg aac att acc agc ccc cca tcg tac acg caa      2544
Ala Asn Tyr Asn Gly Trp Asn Ile Thr Ser Pro Pro Ser Tyr Thr Gln
        835                 840                 845

ggc aac gct gtc tac aac gag aag ctg tac atc cac gct att gga cgt      2592
Gly Asn Ala Val Tyr Asn Glu Lys Leu Tyr Ile His Ala Ile Gly Arg
    850                 855                 860

ctt ctt gcc aat cac ggc tgg tcc aac gcc ttc ttc atc act gat caa      2640
Leu Leu Ala Asn His Gly Trp Ser Asn Ala Phe Phe Ile Thr Asp Gln
865                 870                 875                 880

ggt cga tcg gga aag cag cct acc gga cag caa cag tgg gga gac tgg      2688
Gly Arg Ser Gly Lys Gln Pro Thr Gly Gln Gln Gln Trp Gly Asp Trp
                885                 890                 895

tgc aat gtg atc ggc acc gga ttt ggt att cgc cca tcc gca aac act      2736
Cys Asn Val Ile Gly Thr Gly Phe Gly Ile Arg Pro Ser Ala Asn Thr
            900                 905                 910

ggg gac tcg ttg ctg gat tcg ttt gtc tgg gtc aag cca ggc ggc gag      2784
Gly Asp Ser Leu Leu Asp Ser Phe Val Trp Val Lys Pro Gly Gly Glu
        915                 920                 925

tgt gac ggc acc agc gac agc agt gcg cca cga ttt gac tcc cac tgt      2832
Cys Asp Gly Thr Ser Asp Ser Ser Ala Pro Arg Phe Asp Ser His Cys
    930                 935                 940

gcg ctc cca gat gcc ttg caa ccg gcg gct caa gct ggt gct tgg ttc      2880
Ala Leu Pro Asp Ala Leu Gln Pro Ala Ala Gln Ala Gly Ala Trp Phe
945                 950                 955                 960

caa gcc tac ttt gtg cag ctt ctc aca aac gca aac cca tcg ttc ctg      2928
Gln Ala Tyr Phe Val Gln Leu Leu Thr Asn Ala Asn Pro Ser Phe Leu
                965                 970                 975

taa                                                                 2931
```

<210> 88
<211> 976
<212> PRT
<213> Seqüência artificial

<220>
<223> Construção Sintética

<400> 88

Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1 5 10 15

Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
20 25 30

Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
35 40 45

Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
50 55 60

Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65 70 75 80

Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
85 90 95

Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
100 105 110

Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
115 120 125

Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
130 135 140

Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145 150 155 160

Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
165 170 175

Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
180 185 190

Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
195 200 205

Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
210 215 220

Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225 230 235 240

Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
245 250 255

Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
260 265 270

Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
275 280 285

Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
290 295 300

Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305 310 315 320

Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
325 330 335

Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
340 345 350

Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
355 360 365

Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
370 375 380

Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385 390 395 400

Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
405 410 415

Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
420 425 430

Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
435 440 445

Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
450 455 460

Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465 470 475 480

Gln Phe Thr Gly Ser Thr Tyr Ser Ser Gly Ser Ser Ser Gly Ser Gly
485 490 495

Ser Ser Ser Ser Ser Ser Ser Thr Thr Thr Lys Ala Thr Ser Thr Thr
500 505 510

Leu Lys Thr Thr Ser Thr Thr Ser Ser Gly Ser Ser Ser Thr Ser Ala
515 520 525

Ala Gln Ala Cys Ser Ser Val Trp Gly Gln Cys Gly Gly Gln Asn Trp
530 535 540

Ser Gly Pro Thr Cys Cys Ala Ser Gly Ser Thr Cys Val Tyr Ser Asn
545 550 555 560

Asp Tyr Tyr Ser Gln Cys Leu Pro Gly Ala Ala Ser Ser Ser Ser Ser
565 570 575

Thr Arg Ala Ala Ser Thr Thr Ser Arg Val Ser Pro Thr Thr Ser Arg
580 585 590

Ser Ser Ser Ala Thr Pro Pro Pro Gly Ser Thr Thr Thr Arg Val Pro
595 600 605

Pro Val Gly Ser Gly Thr Ala Thr Tyr Ser Gly Asn Pro Phe Val Gly
610 615 620

Val Thr Pro Trp Ala Asn Ala Tyr Tyr Ala Ser Glu Val Ser Ser Leu
625 630 635 640

Ala Ile Pro Ser Leu Thr Gly Ala Met Ala Thr Ala Ala Ala Ala Val
645 650 655

Ala Lys Val Pro Ser Phe Met Trp Leu Asp Thr Leu Asp Lys Thr Pro
660 665 670

Leu Met Glu Gln Thr Leu Ala Asp Ile Arg Thr Ala Asn Lys Asn Gly
675 680 685

Gly Asn Tyr Ala Gly Gln Phe Val Val Tyr Asp Leu Pro Asp Arg Asp
690 695 700

Cys Ala Ala Leu Ala Ser Asn Gly Glu Tyr Ser Ile Ala Asp Gly Gly

705 710 715 720

Val Ala Lys Tyr Lys Asn Tyr Ile Asp Thr Ile Arg Gln Ile Val Val
725 730 735

Glu Tyr Ser Asp Ile Arg Thr Leu Leu Val Ile Glu Pro Asp Ser Leu
740 745 750

Ala Asn Leu Val Thr Asn Leu Gly Thr Pro Lys Cys Ala Asn Ala Gln
755 760 765

Ser Ala Tyr Leu Glu Cys Ile Asn Tyr Ala Val Thr Gln Leu Asn Leu
770 775 780

Pro Asn Val Ala Met Tyr Leu Asp Ala Gly His Ala Gly Trp Leu Gly
785 790 795 800

Trp Pro Ala Asn Gln Asp Pro Ala Ala Gln Leu Phe Ala Asn Val Tyr
805 810 815

Lys Asn Ala Ser Ser Pro Arg Ala Leu Arg Gly Leu Ala Thr Asn Val
820 825 830

Ala Asn Tyr Asn Gly Trp Asn Ile Thr Ser Pro Pro Ser Tyr Thr Gln
835 840 845

Gly Asn Ala Val Tyr Asn Glu Lys Leu Tyr Ile His Ala Ile Gly Arg
850 855 860

Leu Leu Ala Asn His Gly Trp Ser Asn Ala Phe Phe Ile Thr Asp Gln
865 870 875 880

Gly Arg Ser Gly Lys Gln Pro Thr Gly Gln Gln Gln Trp Gly Asp Trp
885 890 895

Cys Asn Val Ile Gly Thr Gly Phe Gly Ile Arg Pro Ser Ala Asn Thr
900 905 910

Gly Asp Ser Leu Leu Asp Ser Phe Val Trp Val Lys Pro Gly Gly Glu
915 920 925

Cys Asp Gly Thr Ser Asp Ser Ser Ala Pro Arg Phe Asp Ser His Cys
930 935 940

Ala Leu Pro Asp Ala Leu Gln Pro Ala Ala Gln Ala Gly Ala Trp Phe
945 950 955 960

Gln Ala Tyr Phe Val Gln Leu Leu Thr Asn Ala Asn Pro Ser Phe Leu
965 970 975

<210> 89
<211> 2679
<212> DNA
<213> Sequência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2679)

<400> 89

```
cag agc agc tgc gtc tcg gct tgg ggt caa tgt ggc ggt att tct tat      48
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1               5                  10                  15

acc ggg tct acc tgc tgt cag agt ggg aat acc tgc gcc gag att aac      96
Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
            20                  25                  30

tcg tac tac tac cag tgc ata cca gca aca gct gtg agt act tca act     144
Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
        35                  40                  45

acc aca gtg aca tct ccc tct agc tct ggt tcg tct tct gcc aac acg     192
Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
    50                  55                  60

tca ggt tat aca acg acg act gtc ttg ccc agt ccc acg gca aca cag     240
Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65                  70                  75                  80

aac cct tat cct ccg gcc aat gcc agc tca tgt gga tcg tgg gct ctc     288
Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
                85                  90                  95

gtt gat aac gtt tgc tgc cca tac tac tgt ctc tcg gat aat gaa tcc     336
Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
            100                 105                 110

gag tcc tgc acg agc agc tgt acc ggc ggc tgc ggc agt cct gat tcc     384
Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
        115                 120                 125

tcc atg tgc aag tcc ggg acg atg tgg gga gag caa cac acc gta act     432
Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
    130                 135                 140

tcc aac gag gac tgg cat tac agc cgc tca aca cac ttt ggt ctg acc     480
Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145                 150                 155                 160

agc ggt ggc gcc tgc ggg ttc ggt ctg tac ggc ctc tgc acc aag aac     528
```

```
Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
                165                 170                 175

agt gtc acc gcg agc tgg aca gac cca atg ctg ggc tct acc tgc gac   576
Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
            180                 185                 190

gcc ttc tgc acc gcg tat ccg ctc ctc tgc aaa gac ccc gct aac gtc   624
Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
        195                 200                 205

act ctc cgc ggg aac ttt gct gcc ccg aac gga gac tac tac act cag   672
Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
    210                 215                 220

ttc tgg cct tcc ctg gct gca tcc ggc aat ccc gac aac tac ctc tct   720
Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225                 230                 235                 240

tgc ggg gag tgt ttc gag gtc atc cgc acc aag ccc gac ggg aca gac   768
Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
                245                 250                 255

tac gcc gtc ggc gag agc gga tat acc gac ccc ata gtc ctc gag gta   816
Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
            260                 265                 270

gta gac agc tgt ccc tgc aat gcc aat tca aaa tgg tgc tgt aag cgg   864
Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
        275                 280                 285

ccc ccc ccc ccc ccc ttt ttt tcc ccg cct tcc aac gga caa aat ctc   912
Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
    290                 295                 300

aca aga cca ggc ggc agc ggc gca gac cac tgc ggc gaa atc gac ttc   960
Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305                 310                 315                 320

aag tac ggc tgt cct ctg ccg gaa gga tcc cat cac atg gac ctc tcc  1008
Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
                325                 330                 335

gat att gcc atg ggc cga ctc cag gga aac ggc agt ctc gcc gac ggt  1056
Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
            340                 345                 350

gtg att ccc atc cgc tac cgg cgt gtc ccc tgt ccc aag ccg ggg aac  1104
Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
        355                 360                 365

atc tac atc tgg ctt cat gat ggg gcg gga ccg tat tat ttt gcg ctg  1152
Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
    370                 375                 380

agc gcg gtc aat acc aac ggc ccc ggc tcc gta atc agt atc gaa gtc  1200
Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385                 390                 395                 400

cag gct ggt ggc tcc ggg cca tgg gtt gcc ctc gag cac gat ccg aac  1248
Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
```

```
                405                 410                 415

tac acc agt agc cgg ccg cag gag cgg tat ggc tct tgg gtc ctc ccg      1296
Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
            420                 425                 430

cag ggc aag gga ccc att act gtg cct gtt tcg atg agg ctg acg gcg      1344
Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
        435                 440                 445

ccc aat ggg cag cag gtg gtt aag gag ggc gcc att acc agc tat acc      1392
Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
    450                 455                 460

ccg ccg gcg act gcg gtc gag ggc ttt tgg tat att gat ctg gga gtg      1440
Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465                 470                 475                 480

cag ttc acc ccc ggc gct gca agc tca agc tcg tcc acg cgc gcc gcg      1488
Gln Phe Thr Pro Gly Ala Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala
                485                 490                 495

tcg acg act tct cga gta tcc ccc aca aca tcc cgg tcg agc tcc gcg      1536
Ser Thr Thr Ser Arg Val Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala
            500                 505                 510

acg cct cca cct ggt tct act act acc aga gta cct cca gtc gga tcg      1584
Thr Pro Pro Pro Gly Ser Thr Thr Thr Arg Val Pro Pro Val Gly Ser
        515                 520                 525

gga acc gct acg tat tca ggc aac cct ttt gtt ggg gtc act cct tgg      1632
Gly Thr Ala Thr Tyr Ser Gly Asn Pro Phe Val Gly Val Thr Pro Trp
    530                 535                 540

gcc aat gca tat tac gcc tct gaa gtt agc agc ctc gct att cct agc      1680
Ala Asn Ala Tyr Tyr Ala Ser Glu Val Ser Ser Leu Ala Ile Pro Ser
545                 550                 555                 560

ttg act gga gcc atg gcc act gct gca gca gct gtc gca aag gtt ccc      1728
Leu Thr Gly Ala Met Ala Thr Ala Ala Ala Ala Val Ala Lys Val Pro
                565                 570                 575

tct ttt atg tgg cta gat act ctt gac aag acc cct ctc atg gag caa      1776
Ser Phe Met Trp Leu Asp Thr Leu Asp Lys Thr Pro Leu Met Glu Gln
            580                 585                 590

acc ttg gcc gac atc cgc acc gcc aac aag aat ggc ggt aac tat gcg      1824
Thr Leu Ala Asp Ile Arg Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala
        595                 600                 605

gga cag ttt gtg gtg tat gac ttg ccg gat cgc gat tgc gct gcc ctt      1872
Gly Gln Phe Val Val Tyr Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu
    610                 615                 620

gcc tcg aat ggc gaa tac tct att gcc gat ggt ggc gtc gcc aaa tat      1920
Ala Ser Asn Gly Glu Tyr Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr
625                 630                 635                 640

aag aac tat atc gac acc att cgt caa att gtc gtg gaa tat tcc gat      1968
Lys Asn Tyr Ile Asp Thr Ile Arg Gln Ile Val Val Glu Tyr Ser Asp
                645                 650                 655
```

```
atc cgg acc ctc ctg gtt att gag cct gac tct ctt gcc aac ctg gtg      2016
Ile Arg Thr Leu Leu Val Ile Glu Pro Asp Ser Leu Ala Asn Leu Val
            660                 665                 670

acc aac ctc ggt act cca aag tgt gcc aat gct cag tca gcc tac ctt      2064
Thr Asn Leu Gly Thr Pro Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu
        675                 680                 685

gag tgc atc aac tac gcc gtc aca cag ctg aac ctt cca aat gtt gcg      2112
Glu Cys Ile Asn Tyr Ala Val Thr Gln Leu Asn Leu Pro Asn Val Ala
    690                 695                 700

atg tat ttg gac gct ggc cat gca gga tgg ctt ggc tgg ccg gca aac      2160
Met Tyr Leu Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn
705                 710                 715                 720

caa gac ccg gcc gct cag cta ttt gca aat gtt tac aag aat gca tcg      2208
Gln Asp Pro Ala Ala Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser
                725                 730                 735

tct ccg aga gct ctt cgc gga ttg gca acc aat gtc gcc aac tac aac      2256
Ser Pro Arg Ala Leu Arg Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn
            740                 745                 750

ggg tgg aac att acc agc ccc cca tcg tac acg caa ggc aac gct gtc      2304
Gly Trp Asn Ile Thr Ser Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val
        755                 760                 765

tac aac gag aag ctg tac atc cac gct att gga cgt ctt ctt gcc aat      2352
Tyr Asn Glu Lys Leu Tyr Ile His Ala Ile Gly Arg Leu Leu Ala Asn
    770                 775                 780

cac ggc tgg tcc aac gcc ttc ttc atc act gat caa ggt cga tcg gga      2400
His Gly Trp Ser Asn Ala Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly
785                 790                 795                 800

aag cag cct acc gga cag caa cag tgg gga gac tgg tgc aat gtg atc      2448
Lys Gln Pro Thr Gly Gln Gln Gln Trp Gly Asp Trp Cys Asn Val Ile
                805                 810                 815

ggc acc gga ttt ggt att cgc cca tcc gca aac act ggg gac tcg ttg      2496
Gly Thr Gly Phe Gly Ile Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu
            820                 825                 830

ctg gat tcg ttt gtc tgg gtc aag cca ggc ggc gag tgt gac ggc acc      2544
Leu Asp Ser Phe Val Trp Val Lys Pro Gly Gly Glu Cys Asp Gly Thr
        835                 840                 845

agc gac agc agt gcg cca cga ttt gac tcc cac tgt gcg ctc cca gat      2592
Ser Asp Ser Ser Ala Pro Arg Phe Asp Ser His Cys Ala Leu Pro Asp
    850                 855                 860

gcc ttg caa ccg gcg gct caa gct ggt gct tgg ttc caa gcc tac ttt      2640
Ala Leu Gln Pro Ala Ala Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe
865                 870                 875                 880

gtg cag ctt ctc aca aac gca aac cca tcg ttc ctg taa                  2679
Val Gln Leu Leu Thr Asn Ala Asn Pro Ser Phe Leu
                885                 890
```

<210> 90
<211> 892
<212> PRT
<213> Seqüência artificial

<220>
<223> Construção Sintética

<400> 90

Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1 5 10 15

Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
20 25 30

Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
35 40 45

Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
50 55 60

Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65 70 75 80

Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
85 90 95

Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
100 105 110

Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
115 120 125

Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
130 135 140

Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145 150 155 160

Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
165 170 175

Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
180 185 190

Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
195 200 205

Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
210 215 220

Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225 230 235 240

Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
245 250 255

Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
260 265 270

Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
275 280 285

Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
290 295 300

Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305 310 315 320

Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
325 330 335

Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
340 345 350

Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
355 360 365

Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
370 375 380

Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385 390 395 400

Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
405 410 415

Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
420 425 430

Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
435 440 445

Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
450 455 460

Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465 470 475 480

Gln Phe Thr Pro Gly Ala Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala
485 490 495

Ser Thr Thr Ser Arg Val Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala
500 505 510

Thr Pro Pro Pro Gly Ser Thr Thr Thr Arg Val Pro Pro Val Gly Ser
515 520 525

Gly Thr Ala Thr Tyr Ser Gly Asn Pro Phe Val Gly Val Thr Pro Trp
530 535 540

Ala Asn Ala Tyr Tyr Ala Ser Glu Val Ser Ser Leu Ala Ile Pro Ser
545 550 555 560

Leu Thr Gly Ala Met Ala Thr Ala Ala Ala Ala Val Ala Lys Val Pro
565 570 575

Ser Phe Met Trp Leu Asp Thr Leu Asp Lys Thr Pro Leu Met Glu Gln
580 585 590

Thr Leu Ala Asp Ile Arg Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala
595 600 605

Gly Gln Phe Val Val Tyr Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu
610 615 620

Ala Ser Asn Gly Glu Tyr Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr
625 630 635 640

Lys Asn Tyr Ile Asp Thr Ile Arg Gln Ile Val Val Glu Tyr Ser Asp
645 650 655

Ile Arg Thr Leu Leu Val Ile Glu Pro Asp Ser Leu Ala Asn Leu Val
660 665 670

Thr Asn Leu Gly Thr Pro Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu
675 680 685

Glu Cys Ile Asn Tyr Ala Val Thr Gln Leu Asn Leu Pro Asn Val Ala
690 695 700

Met Tyr Leu Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn
705 710 715 720

Gln Asp Pro Ala Ala Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser
725 730 735

Ser Pro Arg Ala Leu Arg Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn
740 745 750

Gly Trp Asn Ile Thr Ser Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val
755 760 765

Tyr Asn Glu Lys Leu Tyr Ile His Ala Ile Gly Arg Leu Leu Ala Asn
770 775 780

His Gly Trp Ser Asn Ala Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly
785 790 795 800

Lys Gln Pro Thr Gly Gln Gln Gln Trp Gly Asp Trp Cys Asn Val Ile
805 810 815

Gly Thr Gly Phe Gly Ile Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu
820 825 830

Leu Asp Ser Phe Val Trp Val Lys Pro Gly Gly Glu Cys Asp Gly Thr
835 840 845

Ser Asp Ser Ser Ala Pro Arg Phe Asp Ser His Cys Ala Leu Pro Asp
850 855 860

Ala Leu Gln Pro Ala Ala Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe
865 870 875 880

Val Gln Leu Leu Thr Asn Ala Asn Pro Ser Phe Leu
885 890

<210> 91
<211> 2817
<212> DNA
<213> Seqüência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2817)

<400> 91

```
cag agc agc tgc gtc tcg gct tgg ggt caa tgt ggc ggt att tct tat        48
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1               5                   10                  15

acc ggg tct acc tgc tgt cag agt ggg aat acc tgc gcc gag att aac        96
Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
            20                  25                  30

tcg tac tac tac cag tgc ata cca gca aca gct gtg agt act tca act       144
Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
        35                  40                  45

acc aca gtg aca tct ccc tct agc tct ggt tcg tct tct gcc aac acg       192
Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
    50                  55                  60

tca ggt tat aca acg acg act gtc ttg ccc agt ccc acg gca aca cag       240
Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65                  70                  75                  80

aac cct tat cct ccg gcc aat gcc agc tca tgt gga tcg tgg gct ctc       288
Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
                85                  90                  95

gtt gat aac gtt tgc tgc cca tac tac tgt ctc tcg gat aat gaa tcc       336
Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
            100                 105                 110

gag tcc tgc acg agc agc tgt acc ggc ggc tgc ggc agt cct gat tcc       384
Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
        115                 120                 125

tcc atg tgc aag tcc ggg acg atg tgg gga gag caa cac acc gta act       432
Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
    130                 135                 140

tcc aac gag gac tgg cat tac agc cgc tca aca cac ttt ggt ctg acc       480
Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145                 150                 155                 160

agc ggt ggc gcc tgc ggg ttc ggt ctg tac ggc ctc tgc acc aag aac       528
Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
                165                 170                 175

agt gtc acc gcg agc tgg aca gac cca atg ctg ggc tct acc tgc gac       576
Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
            180                 185                 190

gcc ttc tgc acc gcg tat ccg ctc ctc tgc aaa gac ccc gct aac gtc       624
Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
        195                 200                 205

act ctc cgc ggg aac ttt gct gcc ccg aac gga gac tac tac act cag       672
Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
    210                 215                 220
```

```
ttc tgg cct tcc ctg gct gca tcc ggc aat ccc gac aac tac ctc tct      720
Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225                 230                 235                 240

tgc ggg gag tgt ttc gag gtc atc cgc acc aag ccc gac ggg aca gac      768
Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
                245                 250                 255

tac gcc gtc ggc gag agc gga tat acc gac ccc ata gtc ctc gag gta      816
Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
            260                 265                 270

gta gac agc tgt ccc tgc aat gcc aat tca aaa tgg tgc tgt aag cgg      864
Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
        275                 280                 285

ccc ccc ccc ccc ccc ttt ttt tcc ccg cct tcc aac gga caa aat ctc      912
Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
    290                 295                 300

aca aga cca ggc ggc agc ggc gca gac cac tgc ggc gaa atc gac ttc      960
Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305                 310                 315                 320

aag tac ggc tgt cct ctg ccg gaa gga tcc cat cac atg gac ctc tcc     1008
Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
                325                 330                 335

gat att gcc atg ggc cga ctc cag gga aac ggc agt ctc gcc gac ggt     1056
Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
            340                 345                 350

gtg att ccc atc cgc tac cgg cgt gtc ccc tgt ccc aag ccg ggg aac     1104
Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
        355                 360                 365

atc tac atc tgg ctt cat gat ggg gcg gga ccg tat tat ttt gcg ctg     1152
Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
    370                 375                 380

agc gcg gtc aat acc aac ggc ccc ggc tcc gta atc agt atc gaa gtc     1200
Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385                 390                 395                 400

cag gct ggt ggc tcc ggg cca tgg gtt gcc ctc gag cac gat ccg aac     1248
Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
                405                 410                 415

tac acc agt agc cgg ccg cag gag cgg tat ggc tct tgg gtc ctc ccg     1296
Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
            420                 425                 430

cag ggc aag gga ccc att act gtg cct gtt tcg atg agg ctg acg gcg     1344
Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
        435                 440                 445

ccc aat ggg cag cag gtg gtt aag gag ggc gcc att acc agc tat acc     1392
Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
    450                 455                 460

ccg ccg gcg act gcg gtc gag ggc ttt tgg tat att gat ctg gga gtg     1440
```

```
Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465                 470                 475                 480

cag ttc acc ggc tcg act tac tcc agt gga tct tct tcg ggg tcg ggg      1488
Gln Phe Thr Gly Ser Thr Tyr Ser Ser Gly Ser Ser Ser Gly Ser Gly
                485                 490                 495

tct agc tcc agc tcg agt tcg act acc act aag gcc act tcg acg acc      1536
Ser Ser Ser Ser Ser Ser Ser Thr Thr Thr Lys Ala Thr Ser Thr Thr
            500                 505                 510

ttg aag act acc tcg acc acc agc agt gga agc agt tcg aca tcg gcg      1584
Leu Lys Thr Thr Ser Thr Thr Ser Ser Gly Ser Ser Ser Thr Ser Ala
        515                 520                 525

gcg ccc ggc gct gca agc tca agc tcg tcc acg cgc gcc gcg tcg acg      1632
Ala Pro Gly Ala Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr
    530                 535                 540

act tct cga gta tcc ccc aca aca tcc cgg tcg agc tcc gcg acg cct      1680
Thr Ser Arg Val Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro
545                 550                 555                 560

cca cct ggt tct act act acc aga gta cct cca gtc gga tcg gga acc      1728
Pro Pro Gly Ser Thr Thr Thr Arg Val Pro Pro Val Gly Ser Gly Thr
                565                 570                 575

gct acg tat tca ggc aac cct ttt gtt ggg gtc act cct tgg gcc aat      1776
Ala Thr Tyr Ser Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala Asn
            580                 585                 590

gca tat tac gcc tct gaa gtt agc agc ctc gct att cct agc ttg act      1824
Ala Tyr Tyr Ala Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu Thr
        595                 600                 605

gga gcc atg gcc act gct gca gca gct gtc gca aag gtt ccc tct ttt      1872
Gly Ala Met Ala Thr Ala Ala Ala Ala Val Ala Lys Val Pro Ser Phe
    610                 615                 620

atg tgg cta gat act ctt gac aag acc cct ctc atg gag caa acc ttg      1920
Met Trp Leu Asp Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr Leu
625                 630                 635                 640

gcc gac atc cgc acc gcc aac aag aat ggc ggt aac tat gcg gga cag      1968
Ala Asp Ile Arg Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln
                645                 650                 655

ttt gtg gtg tat gac ttg ccg gat cgc gat tgc gct gcc ctt gcc tcg      2016
Phe Val Val Tyr Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser
            660                 665                 670

aat ggc gaa tac tct att gcc gat ggt ggc gtc gcc aaa tat aag aac      2064
Asn Gly Glu Tyr Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn
        675                 680                 685

tat atc gac acc att cgt caa att gtc gtg gaa tat tcc gat atc cgg      2112
Tyr Ile Asp Thr Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile Arg
    690                 695                 700

acc ctc ctg gtt att gag cct gac tct ctt gcc aac ctg gtg acc aac      2160
Thr Leu Leu Val Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn
```

```
705                 710                 715                 720

ctc ggt act cca aag tgt gcc aat gct cag tca gcc tac ctt gag tgc     2208
Leu Gly Thr Pro Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys
                725                 730                 735

atc aac tac gcc gtc aca cag ctg aac ctt cca aat gtt gcg atg tat     2256
Ile Asn Tyr Ala Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr
            740                 745                 750

ttg gac gct ggc cat gca gga tgg ctt ggc tgg ccg gca aac caa gac     2304
Leu Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp
        755                 760                 765

ccg gcc gct cag cta ttt gca aat gtt tac aag aat gca tcg tct ccg     2352
Pro Ala Ala Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro
    770                 775                 780

aga gct ctt cgc gga ttg gca acc aat gtc gcc aac tac aac ggg tgg     2400
Arg Ala Leu Arg Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp
785                 790                 795                 800

aac att acc agc ccc cca tcg tac acg caa ggc aac gct gtc tac aac     2448
Asn Ile Thr Ser Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn
                805                 810                 815

gag aag ctg tac atc cac gct att gga cgt ctt ctt gcc aat cac ggc     2496
Glu Lys Leu Tyr Ile His Ala Ile Gly Arg Leu Leu Ala Asn His Gly
            820                 825                 830

tgg tcc aac gcc ttc ttc atc act gat caa ggt cga tcg gga aag cag     2544
Trp Ser Asn Ala Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln
        835                 840                 845

cct acc gga cag caa cag tgg gga gac tgg tgc aat gtg atc ggc acc     2592
Pro Thr Gly Gln Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr
    850                 855                 860

gga ttt ggt att cgc cca tcc gca aac act ggg gac tcg ttg ctg gat     2640
Gly Phe Gly Ile Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp
865                 870                 875                 880

tcg ttt gtc tgg gtc aag cca ggc ggc gag tgt gac ggc acc agc gac     2688
Ser Phe Val Trp Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp
                885                 890                 895

agc agt gcg cca cga ttt gac tcc cac tgt gcg ctc cca gat gcc ttg     2736
Ser Ser Ala Pro Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu
            900                 905                 910

caa ccg gcg gct caa gct ggt gct tgg ttc caa gcc tac ttt gtg cag     2784
Gln Pro Ala Ala Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln
        915                 920                 925

ctt ctc aca aac gca aac cca tcg ttc ctg taa                        2817
Leu Leu Thr Asn Ala Asn Pro Ser Phe Leu
    930                 935
```

<210> 92
<211> 938

<212> PRT
<213> Seqüência artificial

<220>
<223> Construção Sintética

<400> 92

Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1 5 10 15

Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
20 25 30

Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
35 40 45

Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
50 55 60

Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65 70 75 80

Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
85 90 95

Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
100 105 110

Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
115 120 125

er Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
130 135 140

Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145 150 155 160

Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
165 170 175

Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
180 185 190

Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
195 200 205

Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln

210 215 220

Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225 230 235 240

Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
245 250 255

Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
260 265 270

Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
275 280 285

Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
290 295 300

Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305 310 315 320

Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
325 330 335

Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
340 345 350

Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
355 360 365

Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
370 375 380

Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385 390 395 400

Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
405 410 415

Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
420 425 430

Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
435 440 445

Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
450 455 460

Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465 470 475 480

Gln Phe Thr Gly Ser Thr Tyr Ser Ser Gly Ser Ser Ser Gly Ser Gly
485 490 495

Ser Ser Ser Ser Ser Ser Ser Thr Thr Thr Lys Ala Thr Ser Thr Thr
500 505 510

Leu Lys Thr Thr Ser Thr Thr Ser Ser Gly Ser Ser Ser Thr Ser Ala
515 520 525

Ala Pro Gly Ala Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr
530 535 540

Thr Ser Arg Val Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro
545 550 555 560

Pro Pro Gly Ser Thr Thr Thr Arg Val Pro Pro Val Gly Ser Gly Thr
565 570 575

Ala Thr Tyr Ser Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala Asn
580 585 590

Ala Tyr Tyr Ala Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu Thr
595 600 605

Gly Ala Met Ala Thr Ala Ala Ala Ala Val Ala Lys Val Pro Ser Phe
610 615 620

Met Trp Leu Asp Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr Leu
625 630 635 640

Ala Asp Ile Arg Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln
645 650 655

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

Asn Gly Glu Tyr Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn
675 680 685

Tyr Ile Asp Thr Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile Arg
690 695 700

Thr Leu Leu Val Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn
705 710 715 720

Leu Gly Thr Pro Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys
725 730 735

Ile Asn Tyr Ala Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr
740 745 750

Leu Asp Ala Gly His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp
755 760 765

Pro Ala Ala Gln Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro
770 775 780

Arg Ala Leu Arg Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp
785 790 795 800

Asn Ile Thr Ser Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn
805 810 815

Glu Lys Leu Tyr Ile His Ala Ile Gly Arg Leu Leu Ala Asn His Gly
820 825 830

Trp Ser Asn Ala Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln
835 840 845

Pro Thr Gly Gln Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr
850 855 860

Gly Phe Gly Ile Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp
865 870 875 880

Ser Phe Val Trp Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp
885 890 895

Ser Ser Ala Pro Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu
900 905 910

Gln Pro Ala Ala Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln
915 920 925

Leu Leu Thr Asn Ala Asn Pro Ser Phe Leu
930 935

<210> 93
<211> 2763
<212> DNA
<213> Seqüência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2763)

<400> 93

```
cag agc agc tgc gtc tcg gct tgg ggt caa tgt ggc ggt att tct tat       48
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1               5                   10                  15

acc ggg tct acc tgc tgt cag agt ggg aat acc tgc gcc gag att aac       96
Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
            20                  25                  30

tcg tac tac tac cag tgc ata cca gca aca gct gtg agt act tca act      144
Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
        35                  40                  45

acc aca gtg aca tct ccc tct agc tct ggt tcg tct tct gcc aac acg      192
Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
    50                  55                  60

tca ggt tat aca acg acg act gtc ttg ccc agt ccc acg gca aca cag      240
Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65                  70                  75                  80

aac cct tat cct ccg gcc aat gcc agc tca tgt gga tcg tgg gct ctc      288
Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
                85                  90                  95

gtt gat aac gtt tgc tgc cca tac tac tgt ctc tcg gat aat gaa tcc      336
Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
            100                 105                 110

gag tcc tgc acg agc agc tgt acc ggc ggc tgc ggc agt cct gat tcc      384
Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
        115                 120                 125

tcc atg tgc aag tcc ggg acg atg tgg gga gag caa cac acc gta act      432
Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
    130                 135                 140

tcc aac gag gac tgg cat tac agc cgc tca aca cac ttt ggt ctg acc      480
Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145                 150                 155                 160

agc ggt ggc gcc tgc ggg ttc ggt ctg tac ggc ctc tgc acc aag aac      528
Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
                165                 170                 175

agt gtc acc gcg agc tgg aca gac cca atg ctg ggc tct acc tgc gac      576
Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
            180                 185                 190
```

```
gcc ttc tgc acc gcg tat ccg ctc ctc tgc aaa gac ccc gct aac gtc      624
Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
        195                 200                 205

act ctc cgc ggg aac ttt gct gcc ccg aac gga gac tac tac act cag      672
Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
    210                 215                 220

ttc tgg cct tcc ctg gct gca tcc ggc aat ccc gac aac tac ctc tct      720
Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225                 230                 235                 240

tgc ggg gag tgt ttc gag gtc atc cgc acc aag ccc gac ggg aca gac      768
Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
                245                 250                 255

tac gcc gtc ggc gag agc gga tat acc gac ccc ata gtc ctc gag gta      816
Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
            260                 265                 270

gta gac agc tgt ccc tgc aat gcc aat tca aaa tgg tgc tgt aag cgg      864
Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
        275                 280                 285

ccc ccc ccc ccc ccc ttt ttt tcc ccg cct tcc aac gga caa aat ctc      912
Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
    290                 295                 300

aca aga cca ggc ggc agc ggc gca gac cac tgc ggc gaa atc gac ttc      960
Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305                 310                 315                 320

aag tac ggc tgt cct ctg ccg gaa gga tcc cat cac atg gac ctc tcc     1008
Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
                325                 330                 335

gat att gcc atg ggc cga ctc cag gga aac ggc agt ctc gcc gac ggt     1056
Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
            340                 345                 350

gtg att ccc atc cgc tac cgg cgt gtc ccc tgt ccc aag ccg ggg aac     1104
Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
        355                 360                 365

atc tac atc tgg ctt cat gat ggg gcg gga ccg tat tat ttt gcg ctg     1152
Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
    370                 375                 380

agc gcg gtc aat acc aac ggc ccc ggc tcc gta atc agt atc gaa gtc     1200
Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385                 390                 395                 400

cag gct ggt ggc tcc ggg cca tgg gtt gcc ctc gag cac gat ccg aac     1248
Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
                405                 410                 415

tac acc agt agc cgg ccg cag gag cgg tat ggc tct tgg gtc ctc ccg     1296
Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
            420                 425                 430
```

```
cag ggc aag gga ccc att act gtg cct gtt tcg atg agg ctg acg gcg    1344
Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
        435                 440                 445

ccc aat ggg cag cag gtg gtt aag gag ggc gcc att acc agc tat acc    1392
Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
    450                 455                 460

ccg ccg gcg act gcg gtc gag ggc ttt tgg tat att gat ctg gga gtg    1440
Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465                 470                 475                 480

cag ttc acc cag caa ccg ggt acc agc acc ccc gag gtc cat ccc aag    1488
Gln Phe Thr Gln Gln Pro Gly Thr Ser Thr Pro Glu Val His Pro Lys
                485                 490                 495

ttg aca acc tac aag tgt aca aag tcc ggg ggg tgc gtg gcc cag gac    1536
Leu Thr Thr Tyr Lys Cys Thr Lys Ser Gly Gly Cys Val Ala Gln Asp
            500                 505                 510

acc tcg gtg gtc ctt gac tgg aac tac cgc tgg atg cac gac gca aac    1584
Thr Ser Val Val Leu Asp Trp Asn Tyr Arg Trp Met His Asp Ala Asn
        515                 520                 525

tac aac tcg tgc acc gtc aac ggc ggc gtc aac acc acg ctc tgc cct    1632
Tyr Asn Ser Cys Thr Val Asn Gly Gly Val Asn Thr Thr Leu Cys Pro
    530                 535                 540

gac gag gcg acc tgt ggc aag aac tgc ttc atc gag ggc gtc gac tac    1680
Asp Glu Ala Thr Cys Gly Lys Asn Cys Phe Ile Glu Gly Val Asp Tyr
545                 550                 555                 560

gcc gcc tcg ggc gtc acg acc tcg ggc agc agc ctc acc atg aac cag    1728
Ala Ala Ser Gly Val Thr Thr Ser Gly Ser Ser Leu Thr Met Asn Gln
                565                 570                 575

tac atg ccc agc agc tct ggc ggc tac agc agc gtc tct cct cgg ctg    1776
Tyr Met Pro Ser Ser Ser Gly Gly Tyr Ser Ser Val Ser Pro Arg Leu
            580                 585                 590

tat ctc ctg gac tct gac ggt gag tac gtg atg ctg aag ctc aac ggc    1824
Tyr Leu Leu Asp Ser Asp Gly Glu Tyr Val Met Leu Lys Leu Asn Gly
        595                 600                 605

cag gag ctg agc ttc gac gtc gac ctc tct gct ctg ccg tgt gga gag    1872
Gln Glu Leu Ser Phe Asp Val Asp Leu Ser Ala Leu Pro Cys Gly Glu
    610                 615                 620

aac ggc tcg ctc tac ctg tct cag atg gac gag aac ggg ggc gcc aac    1920
Asn Gly Ser Leu Tyr Leu Ser Gln Met Asp Glu Asn Gly Gly Ala Asn
625                 630                 635                 640

cag tat aac acg gcc ggt gcc aac tac ggg agc ggc tac tgc gat gct    1968
Gln Tyr Asn Thr Ala Gly Ala Asn Tyr Gly Ser Gly Tyr Cys Asp Ala
                645                 650                 655

cag tgc ccc gtc cag aca tgg agg aac ggc acc ctc aac act agc cac    2016
Gln Cys Pro Val Gln Thr Trp Arg Asn Gly Thr Leu Asn Thr Ser His
            660                 665                 670

cag ggc ttc tgc tgc aac gag atg gat atc ctg gag ggc aac tcg agg    2064
```

```
Gln Gly Phe Cys Cys Asn Glu Met Asp Ile Leu Glu Gly Asn Ser Arg
        675                 680                 685

gcg aat gcc ttg acc cct cac tct tgc acg gcc acg gcc tgc gac tct     2112
Ala Asn Ala Leu Thr Pro His Ser Cys Thr Ala Thr Ala Cys Asp Ser
    690                 695                 700

gcc ggt tgc ggc ttc aac ccc tat ggc agc ggc tac aaa agc tac tac     2160
Ala Gly Cys Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys Ser Tyr Tyr
705                 710                 715                 720

ggc ccc gga gat acc gtt gac acc tcc aag acc ttc acc atc atc acc     2208
Gly Pro Gly Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr
                725                 730                 735

cag ttc aac acg gac aac ggc tcg ccc tcg ggc aac ctt gtg agc atc     2256
Gln Phe Asn Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile
            740                 745                 750

acc cgc aag tac cag caa aac ggc gtc gac atc ccc agc gcc cag ccc     2304
Thr Arg Lys Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro
        755                 760                 765

ggc ggc gac acc atc tcg tcc tgc ccg tcc gcc tca gcc tac ggc ggc     2352
Gly Gly Asp Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly
    770                 775                 780

ctc gcc acc atg ggc aag gcc ctg agc agc ggc atg gtg ctc gtg ttc     2400
Leu Ala Thr Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe
785                 790                 795                 800

agc att tgg aac gac aac agc cag tac atg aac tgg ctc gac agc ggc     2448
Ser Ile Trp Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly
                805                 810                 815

aac gcc ggc ccc tgc agc agc acc gag ggc aac cca tcc aac atc ctg     2496
Asn Ala Gly Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Ile Leu
            820                 825                 830

gcc aac aac ccc aac acg cac gtc gtc ttc tcc aac atc cgc tgg gga     2544
Ala Asn Asn Pro Asn Thr His Val Val Phe Ser Asn Ile Arg Trp Gly
        835                 840                 845

gac att ggg tct act acg aac tcg act gcg ccc ccg ccc ccg cct gcg     2592
Asp Ile Gly Ser Thr Thr Asn Ser Thr Ala Pro Pro Pro Pro Pro Ala
    850                 855                 860

tcc agc acg acg ttt tcg act aca cgg agg agc tcg acg act tcg agc     2640
Ser Ser Thr Thr Phe Ser Thr Thr Arg Arg Ser Ser Thr Thr Ser Ser
865                 870                 875                 880

agc ccg agc tgc acg cag act cac tgg ggg cag tgc ggt ggc att ggg     2688
Ser Pro Ser Cys Thr Gln Thr His Trp Gly Gln Cys Gly Gly Ile Gly
                885                 890                 895

tac agc ggg tgc aag acg tgc acg tcg ggc act acg tgc cag tat agc     2736
Tyr Ser Gly Cys Lys Thr Cys Thr Ser Gly Thr Thr Cys Gln Tyr Ser
            900                 905                 910

aac gac tac tac tcg caa tgc ctt tag                                2763
Asn Asp Tyr Tyr Ser Gln Cys Leu
```

915 920

<210> 94
<211> 920
<212> PRT
<213> Seqüência artificial

<220>
<223> Construção Sintética

<400> 94

Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1 5 10 15

Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
20 25 30

Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
35 40 45

Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
50 55 60

Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65 70 75 80

Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
85 90 95

Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
100 105 110

Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
115 120 125

Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
130 135 140

Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145 150 155 160

Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
165 170 175

Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
180 185 190

Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
195 200 205

Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
210 215 220

Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225 230 235 240

Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
245 250 255

Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
260 265 270

Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
275 280 285

Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
290 295 300

Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305 310 315 320

Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
325 330 335

Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
340 345 350

Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
355 360 365

Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
370 375 380

Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385 390 395 400

Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
405 410 415

Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
420 425 430

Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala

435 440 445

Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
450 455 460

Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465 470 475 480

Gln Phe Thr Gln Gln Pro Gly Thr Ser Thr Pro Glu Val His Pro Lys
485 490 495

Leu Thr Thr Tyr Lys Cys Thr Lys Ser Gly Gly Cys Val Ala Gln Asp
500 505 510

Thr Ser Val Val Leu Asp Trp Asn Tyr Arg Trp Met His Asp Ala Asn
515 520 525

Tyr Asn Ser Cys Thr Val Asn Gly Gly Val Asn Thr Thr Leu Cys Pro
530 535 540

Asp Glu Ala Thr Cys Gly Lys Asn Cys Phe Ile Glu Gly Val Asp Tyr
545 550 555 560

Ala Ala Ser Gly Val Thr Thr Ser Gly Ser Ser Leu Thr Met Asn Gln
565 570 575

Tyr Met Pro Ser Ser Ser Gly Gly Tyr Ser Ser Val Ser Pro Arg Leu
580 585 590

Tyr Leu Leu Asp Ser Asp Gly Glu Tyr Val Met Leu Lys Leu Asn Gly
595 600 605

Gln Glu Leu Ser Phe Asp Val Asp Leu Ser Ala Leu Pro Cys Gly Glu
610 615 620

Asn Gly Ser Leu Tyr Leu Ser Gln Met Asp Glu Asn Gly Gly Ala Asn
625 630 635 640

Gln Tyr Asn Thr Ala Gly Ala Asn Tyr Gly Ser Gly Tyr Cys Asp Ala
645 650 655

Gln Cys Pro Val Gln Thr Trp Arg Asn Gly Thr Leu Asn Thr Ser His
660 665 670

Gln Gly Phe Cys Cys Asn Glu Met Asp Ile Leu Glu Gly Asn Ser Arg
675 680 685

Ala Asn Ala Leu Thr Pro His Ser Cys Thr Ala Thr Ala Cys Asp Ser
690 695 700

Ala Gly Cys Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys Ser Tyr Tyr
705 710 715 720

Gly Pro Gly Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr
725 730 735

Gln Phe Asn Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile
740 745 750

Thr Arg Lys Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro
755 760 765

Gly Gly Asp Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly
770 775 780

Leu Ala Thr Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe
785 790 795 800

Ser Ile Trp Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly
805 810 815

Asn Ala Gly Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Ile Leu
820 825 830

Ala Asn Asn Pro Asn Thr His Val Val Phe Ser Asn Ile Arg Trp Gly
835 840 845

Asp Ile Gly Ser Thr Thr Asn Ser Thr Ala Pro Pro Pro Pro Pro Ala
850 855 860

Ser Ser Thr Thr Phe Ser Thr Thr Arg Arg Ser Ser Thr Thr Ser Ser
865 870 875 880

Ser Pro Ser Cys Thr Gln Thr His Trp Gly Gln Cys Gly Gly Ile Gly
885 890 895

Tyr Ser Gly Cys Lys Thr Cys Thr Ser Gly Thr Thr Cys Gln Tyr Ser
900 905 910

Asn Asp Tyr Tyr Ser Gln Cys Leu
915 920

<210> 95
<211> 2901
<212> DNA
<213> Seqüência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2901)

<400> 95

```
cag agc agc tgc gtc tcg gct tgg ggt caa tgt ggc ggt att tct tat      48
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1               5                  10                  15

acc ggg tct acc tgc tgt cag agt ggg aat acc tgc gcc gag att aac      96
Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
            20                  25                  30

tcg tac tac tac cag tgc ata cca gca aca gct gtg agt act tca act     144
Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
        35                  40                  45

acc aca gtg aca tct ccc tct agc tct ggt tcg tct tct gcc aac acg     192
Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
    50                  55                  60

tca ggt tat aca acg acg act gtc ttg ccc agt ccc acg gca aca cag     240
Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65                  70                  75                  80

aac cct tat cct ccg gcc aat gcc agc tca tgt gga tcg tgg gct ctc     288
Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
                85                  90                  95

gtt gat aac gtt tgc tgc cca tac tac tgt ctc tcg gat aat gaa tcc     336
Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
            100                 105                 110

gag tcc tgc acg agc agc tgt acc ggc ggc tgc ggc agt cct gat tcc     384
Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
        115                 120                 125

tcc atg tgc aag tcc ggg acg atg tgg gga gag caa cac acc gta act     432
Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
    130                 135                 140

tcc aac gag gac tgg cat tac agc cgc tca aca cac ttt ggt ctg acc     480
Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145                 150                 155                 160

agc ggt ggc gcc tgc ggg ttc ggt ctg tac ggc ctc tgc acc aag aac     528
Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
                165                 170                 175

agt gtc acc gcg agc tgg aca gac cca atg ctg ggc tct acc tgc gac     576
Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
```

```
                180                 185                 190

gcc ttc tgc acc gcg tat ccg ctc ctc tgc aaa gac ccc gct aac gtc      624
Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
        195                 200                 205

act ctc cgc ggg aac ttt gct gcc ccg aac gga gac tac tac act cag      672
Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
    210                 215                 220

ttc tgg cct tcc ctg gct gca tcc ggc aat ccc gac aac tac ctc tct      720
Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225                 230                 235                 240

tgc ggg gag tgt ttc gag gtc atc cgc acc aag ccc gac ggg aca gac      768
Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
                245                 250                 255

tac gcc gtc ggc gag agc gga tat acc gac ccc ata gtc ctc gag gta      816
Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
            260                 265                 270

gta gac agc tgt ccc tgc aat gcc aat tca aaa tgg tgc tgt aag cgg      864
Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
        275                 280                 285

ccc ccc ccc ccc ccc ttt ttt tcc ccg cct tcc aac gga caa aat ctc      912
Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
    290                 295                 300

aca aga cca ggc ggc agc ggc gca gac cac tgc ggc gaa atc gac ttc      960
Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305                 310                 315                 320

aag tac ggc tgt cct ctg ccg gaa gga tcc cat cac atg gac ctc tcc     1008
Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
                325                 330                 335

gat att gcc atg ggc cga ctc cag gga aac ggc agt ctc gcc gac ggt     1056
Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
            340                 345                 350

gtg att ccc atc cgc tac cgg cgt gtc ccc tgt ccc aag ccg ggg aac     1104
Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
        355                 360                 365

atc tac atc tgg ctt cat gat ggg gcg gga ccg tat tat ttt gcg ctg     1152
Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
    370                 375                 380

agc gcg gtc aat acc aac ggc ccc ggc tcc gta atc agt atc gaa gtc     1200
Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385                 390                 395                 400

cag gct ggt ggc tcc ggg cca tgg gtt gcc ctc gag cac gat ccg aac     1248
Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
                405                 410                 415

tac acc agt agc cgg ccg cag gag cgg tat ggc tct tgg gtc ctc ccg     1296
Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
            420                 425                 430
```

```
cag ggc aag gga ccc att act gtg cct gtt tcg atg agg ctg acg gcg      1344
Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
        435                 440                 445

ccc aat ggg cag cag gtg gtt aag gag ggc gcc att acc agc tat acc      1392
Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
    450                 455                 460

ccg ccg gcg act gcg gtc gag ggc ttt tgg tat att gat ctg gga gtg      1440
Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465                 470                 475                 480

cag ttc acc ggc tcg act tac tcc agt gga tct tct tcg ggg tcg ggg      1488
Gln Phe Thr Gly Ser Thr Tyr Ser Ser Gly Ser Ser Ser Gly Ser Gly
                485                 490                 495

tct agc tcc agc tcg agt tcg act acc act aag gcc act tcg acg acc      1536
Ser Ser Ser Ser Ser Ser Ser Thr Thr Thr Lys Ala Thr Ser Thr Thr
            500                 505                 510

ctg aag act acc tcg acc acc agc agt gga agc agt tcg aca tcg gcg      1584
Leu Lys Thr Thr Ser Thr Thr Ser Ser Gly Ser Ser Ser Thr Ser Ala
        515                 520                 525

gcg cag caa ccg ggt acc agc acc ccc gag gtc cat ccc aag ttg aca      1632
Ala Gln Gln Pro Gly Thr Ser Thr Pro Glu Val His Pro Lys Leu Thr
    530                 535                 540

acc tac aag tgt aca aag tcc ggg ggg tgc gtg gcc cag gac acc tcg      1680
Thr Tyr Lys Cys Thr Lys Ser Gly Gly Cys Val Ala Gln Asp Thr Ser
545                 550                 555                 560

gtg gtc ctt gac tgg aac tac cgc tgg atg cac gac gca aac tac aac      1728
Val Val Leu Asp Trp Asn Tyr Arg Trp Met His Asp Ala Asn Tyr Asn
                565                 570                 575

tcg tgc acc gtc aac ggc ggc gtc aac acc acg ctc tgc cct gac gag      1776
Ser Cys Thr Val Asn Gly Gly Val Asn Thr Thr Leu Cys Pro Asp Glu
            580                 585                 590

gcg acc tgt ggc aag aac tgc ttc atc gag ggc gtc gac tac gcc gcc      1824
Ala Thr Cys Gly Lys Asn Cys Phe Ile Glu Gly Val Asp Tyr Ala Ala
        595                 600                 605

tcg ggc gtc acg acc tcg ggc agc agc ctc acc atg aac cag tac atg      1872
Ser Gly Val Thr Thr Ser Gly Ser Ser Leu Thr Met Asn Gln Tyr Met
    610                 615                 620

ccc agc agc tct ggc ggc tac agc agc gtc tct cct cgg ctg tat ctc      1920
Pro Ser Ser Ser Gly Gly Tyr Ser Ser Val Ser Pro Arg Leu Tyr Leu
625                 630                 635                 640

ctg gac tct gac ggt gag tac gtg atg ctg aag ctc aac ggc cag gag      1968
Leu Asp Ser Asp Gly Glu Tyr Val Met Leu Lys Leu Asn Gly Gln Glu
                645                 650                 655

ctg agc ttc gac gtc gac ctc tct gct ctg ccg tgt gga gag aac ggc      2016
Leu Ser Phe Asp Val Asp Leu Ser Ala Leu Pro Cys Gly Glu Asn Gly
            660                 665                 670
```

```
tcg ctc tac ctg tct cag atg gac gag aac ggg ggc gcc aac cag tat  2064
Ser Leu Tyr Leu Ser Gln Met Asp Glu Asn Gly Gly Ala Asn Gln Tyr
        675                 680                 685

aac acg gcc ggt gcc aac tac ggg agc ggc tac tgc gat gct cag tgc  2112
Asn Thr Ala Gly Ala Asn Tyr Gly Ser Gly Tyr Cys Asp Ala Gln Cys
    690                 695                 700

ccc gtc cag aca tgg agg aac ggc acc ctc aac act agc cac cag ggc  2160
Pro Val Gln Thr Trp Arg Asn Gly Thr Leu Asn Thr Ser His Gln Gly
705                 710                 715                 720

ttc tgc tgc aac gag atg gat atc ctg gag ggc aac tcg agg gcg aat  2208
Phe Cys Cys Asn Glu Met Asp Ile Leu Glu Gly Asn Ser Arg Ala Asn
                725                 730                 735

gcc ttg acc cct cac tct tgc acg gcc acg gcc tgc gac tct gcc ggt  2256
Ala Leu Thr Pro His Ser Cys Thr Ala Thr Ala Cys Asp Ser Ala Gly
            740                 745                 750

tgc ggc ttc aac ccc tat ggc agc ggc tac aaa agc tac tac ggc ccc  2304
Cys Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys Ser Tyr Tyr Gly Pro
        755                 760                 765

gga gat acc gtt gac acc tcc aag acc ttc acc atc atc acc cag ttc  2352
Gly Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe
    770                 775                 780

aac acg gac aac ggc tcg ccc tcg ggc aac ctt gtg agc atc acc cgc  2400
Asn Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile Thr Arg
785                 790                 795                 800

aag tac cag caa aac ggc gtc gac atc ccc agc gcc cag ccc ggc ggc  2448
Lys Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro Gly Gly
                805                 810                 815

gac acc atc tcg tcc tgc ccg tcc gcc tca gcc tac ggc ggc ctc gcc  2496
Asp Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala
            820                 825                 830

acc atg ggc aag gcc ctg agc agc ggc atg gtg ctc gtg ttc agc att  2544
Thr Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe Ser Ile
        835                 840                 845

tgg aac gac aac agc cag tac atg aac tgg ctc gac agc ggc aac gcc  2592
Trp Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala
    850                 855                 860

ggc ccc tgc agc agc acc gag ggc aac cca tcc aac atc ctg gcc aac  2640
Gly Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Ile Leu Ala Asn
865                 870                 875                 880

aac ccc aac acg cac gtc gtc ttc tcc aac atc cgc tgg gga gac att  2688
Asn Pro Asn Thr His Val Val Phe Ser Asn Ile Arg Trp Gly Asp Ile
                885                 890                 895

ggg tct act acg aac tcg act gcg ccc ccg ccc ccg cct gcg tcc agc  2736
Gly Ser Thr Thr Asn Ser Thr Ala Pro Pro Pro Pro Pro Ala Ser Ser
            900                 905                 910

acg acg ttt tcg act aca cgg agg agc tcg acg act tcg agc agc ccg  2784
```

```
Thr Thr Phe Ser Thr Thr Arg Arg Ser Ser Thr Thr Ser Ser Ser Pro
        915                 920                 925

agc tgc acg cag act cac tgg ggg cag tgc ggt ggc att ggg tac agc     2832
Ser Cys Thr Gln Thr His Trp Gly Gln Cys Gly Gly Ile Gly Tyr Ser
    930                 935                 940

ggg tgc aag acg tgc acg tcg ggc act acg tgc cag tat agc aac gac     2880
Gly Cys Lys Thr Cys Thr Ser Gly Thr Thr Cys Gln Tyr Ser Asn Asp
945                 950                 955                 960

                                                                    2901
tac tac tcg caa tgc ctt tag
Tyr Tyr Ser Gln Cys Leu
                965
```

<210> 96
<211> 966
<212> PRT
<213> Sequência artificial

<220>
<223> Construção Sintética

<400> 96

```
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1               5                   10                  15

Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
            20                  25                  30

Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
        35                  40                  45

Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
    50                  55                  60

Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65                  70                  75                  80

Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
                85                  90                  95

Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
            100                 105                 110

Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
        115                 120                 125

Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
    130                 135                 140
```

Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145 150 155 160

Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
165 170 175

Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
180 185 190

Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
195 200 205

Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
210 215 220

Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225 230 235 240

Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
245 250 255

Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
260 265 270

Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
275 280 285

Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
290 295 300

Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305 310 315 320

Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
325 330 335

Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
340 345 350

Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
355 360 365

Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
370 375 380

Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385 390 395 400

Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
405 410 415

Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
420 425 430

Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
435 440 445

Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
450 455 460

Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465 470 475 480

Gln Phe Thr Gly Ser Thr Tyr Ser Ser Gly Ser Ser Ser Gly Ser Gly
485 490 495

Ser Ser Ser Ser Ser Ser Ser Thr Thr Thr Lys Ala Thr Ser Thr Thr
500 505 510

Leu Lys Thr Thr Ser Thr Thr Ser Ser Gly Ser Ser Ser Thr Ser Ala
515 520 525

Ala Gln Gln Pro Gly Thr Ser Thr Pro Glu Val His Pro Lys Leu Thr
530 535 540

Thr Tyr Lys Cys Thr Lys Ser Gly Gly Cys Val Ala Gln Asp Thr Ser
545 550 555 560

Val Val Leu Asp Trp Asn Tyr Arg Trp Met His Asp Ala Asn Tyr Asn
565 570 575

Ser Cys Thr Val Asn Gly Gly Val Asn Thr Thr Leu Cys Pro Asp Glu
580 585 590

Ala Thr Cys Gly Lys Asn Cys Phe Ile Glu Gly Val Asp Tyr Ala Ala
595 600 605

Ser Gly Val Thr Thr Ser Gly Ser Ser Leu Thr Met Asn Gln Tyr Met
610 615 620

Pro Ser Ser Ser Gly Gly Tyr Ser Ser Val Ser Pro Arg Leu Tyr Leu

625 630 635 640

Leu Asp Ser Asp Gly Glu Tyr Val Met Leu Lys Leu Asn Gly Gln Glu
645 650 655

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

Ser Leu Tyr Leu Ser Gln Met Asp Glu Asn Gly Gly Ala Asn Gln Tyr
675 680 685

Asn Thr Ala Gly Ala Asn Tyr Gly Ser Gly Tyr Cys Asp Ala Gln Cys
690 695 700

Pro Val Gln Thr Trp Arg Asn Gly Thr Leu Asn Thr Ser His Gln Gly
705 710 715 720

Phe Cys Cys Asn Glu Met Asp Ile Leu Glu Gly Asn Ser Arg Ala Asn
725 730 735

Ala Leu Thr Pro His Ser Cys Thr Ala Thr Ala Cys Asp Ser Ala Gly
740 745 750

Cys Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys Ser Tyr Tyr Gly Pro
755 760 765

Gly Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe
770 775 780

Asn Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile Thr Arg
785 790 795 800

Lys Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro Gly Gly
805 810 815

Asp Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala
820 825 830

Thr Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe Ser Ile
835 840 845

Trp Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala
850 855 860

Gly Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Ile Leu Ala Asn
865 870 875 880

Asn Pro Asn Thr His Val Val Phe Ser Asn Ile Arg Trp Gly Asp Ile
885 890 895

Gly Ser Thr Thr Asn Ser Thr Ala Pro Pro Pro Pro Pro Ala Ser Ser
900 905 910

Thr Thr Phe Ser Thr Thr Arg Arg Ser Ser Thr Thr Ser Ser Ser Pro
915 920 925

Ser Cys Thr Gln Thr His Trp Gly Gln Cys Gly Gly Ile Gly Tyr Ser
930 935 940

Gly Cys Lys Thr Cys Thr Ser Gly Thr Thr Cys Gln Tyr Ser Asn Asp
945 950 955 960

Tyr Tyr Ser Gln Cys Leu
965

<210> 97
<211> 2649
<212> DNA
<213> Sequência artificial Sequence

<220>
<223> Proteína de fusão n

<220>
<221> CDS
<222> (1)..(2649)

<400> 97
cag agc agc tgc gtc tcg gct tgg ggt caa tgt ggc ggt att tct tat 48
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1 5 10 15

acc ggg tct acc tgc tgt cag agt ggg aat acc tgc gcc gag att aac 96
Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
20 25 30

tcg tac tac tac cag tgc ata cca gca aca gct gtg agt act tca act 144
Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
35 40 45

acc aca gtg aca tct ccc tct agc tct ggt tcg tct tct gcc aac acg 192
Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
50 55 60

tca ggt tat aca acg acg act gtc ttg ccc agt ccc acg gca aca cag 240
Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65 70 75 80

aac cct tat cct ccg gcc aat gcc agc tca tgt gga tcg tgg gct ctc 288

```
Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
                85                  90                  95

gtt gat aac gtt tgc tgc cca tac tac tgt ctc tcg gat aat gaa tcc      336
Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
            100                 105                 110

gag tcc tgc acg agc agc tgt acc ggc ggc tgc ggc agt cct gat tcc      384
Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
        115                 120                 125

tcc atg tgc aag tcc ggg acg atg tgg gga gag caa cac acc gta act      432
Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
    130                 135                 140

tcc aac gag gac tgg cat tac agc cgc tca aca cac ttt ggt ctg acc      480
Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145                 150                 155                 160

agc ggt ggc gcc tgc ggg ttc ggt ctg tac ggc ctc tgc acc aag aac      528
Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
                165                 170                 175

agt gtc acc gcg agc tgg aca gac cca atg ctg ggc tct acc tgc gac      576
Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
            180                 185                 190

gcc ttc tgc acc gcg tat ccg ctc ctc tgc aaa gac ccc gct aac gtc      624
Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
        195                 200                 205

act ctc cgc ggg aac ttt gct gcc ccg aac gga gac tac tac act cag      672
Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
    210                 215                 220

ttc tgg cct tcc ctg gct gca tcc ggc aat ccc gac aac tac ctc tct      720
Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225                 230                 235                 240

tgc ggg gag tgt ttc gag gtc atc cgc acc aag ccc gac ggg aca gac      768
Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
                245                 250                 255

tac gcc gtc ggc gag agc gga tat acc gac ccc ata gtc ctc gag gta      816
Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
            260                 265                 270

gta gac agc tgt ccc tgc aat gcc aat tca aaa tgg tgc tgt aag cgg      864
Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
        275                 280                 285

ccc ccc ccc ccc ccc ttt ttt tcc ccg cct tcc aac gga caa aat ctc      912
Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
    290                 295                 300

aca aga cca ggc ggc agc ggc gca gac cac tgc ggc gaa atc gac ttc      960
Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305                 310                 315                 320

aag tac ggc tgt cct ctg ccg gaa gga tcc cat cac atg gac ctc tcc     1008
Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
```

```
                    325                 330                 335

gat att gcc atg ggc cga ctc cag gga aac ggc agt ctc gcc gac ggt   1056
Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
            340                 345                 350

gtg att ccc atc cgc tac cgg cgt gtc ccc tgt ccc aag ccg ggg aac   1104
Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
        355                 360                 365

atc tac atc tgg ctt cat gat ggg gcg gga ccg tat tat ttt gcg ctg   1152
Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
    370                 375                 380

agc gcg gtc aat acc aac ggc ccc ggc tcc gta atc agt atc gaa gtc   1200
Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385                 390                 395                 400

cag gct ggt ggc tcc ggg cca tgg gtt gcc ctc gag cac gat ccg aac   1248
Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
                405                 410                 415

tac acc agt agc cgg ccg cag gag cgg tat ggc tct tgg gtc ctc ccg   1296
Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
            420                 425                 430

cag ggc aag gga ccc att act gtg cct gtt tcg atg agg ctg acg gcg   1344
Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
        435                 440                 445

ccc aat ggg cag cag gtg gtt aag gag ggc gcc att acc agc tat acc   1392
Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
    450                 455                 460

ccg ccg gcg act gcg gtc gag ggc ttt tgg tat att gat ctg gga gtg   1440
Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465                 470                 475                 480

cag ttc acc cag caa ccg ggt acc agc acc ccc gag gtc cat ccc aag   1488
Gln Phe Thr Gln Gln Pro Gly Thr Ser Thr Pro Glu Val His Pro Lys
                485                 490                 495

ttg aca acc tac aag tgt aca aag tcc ggg ggg tgc gtg gcc cag gac   1536
Leu Thr Thr Tyr Lys Cys Thr Lys Ser Gly Gly Cys Val Ala Gln Asp
            500                 505                 510

acc tcg gtg gtc ctt gac tgg aac tac cgc tgg atg cac gac gca aac   1584
Thr Ser Val Val Leu Asp Trp Asn Tyr Arg Trp Met His Asp Ala Asn
        515                 520                 525

tac aac tcg tgc acc gtc aac ggc ggc gtc aac acc acg ctc tgc cct   1632
Tyr Asn Ser Cys Thr Val Asn Gly Gly Val Asn Thr Thr Leu Cys Pro
    530                 535                 540

gac gag gcg acc tgt ggc aag aac tgc ttc atc gag ggc gtc gac tac   1680
Asp Glu Ala Thr Cys Gly Lys Asn Cys Phe Ile Glu Gly Val Asp Tyr
545                 550                 555                 560

gcc gcc tcg ggc gtc acg acc tcg ggc agc agc ctc acc atg aac cag   1728
Ala Ala Ser Gly Val Thr Thr Ser Gly Ser Ser Leu Thr Met Asn Gln
                565                 570                 575
```

```
tac atg ccc agc agc tct ggc ggc tac agc agc gtc tct cct cgg ctg      1776
Tyr Met Pro Ser Ser Ser Gly Gly Tyr Ser Ser Val Ser Pro Arg Leu
            580                 585                 590

tat ctc ctg gac tct gac ggt gag tac gtg atg ctg aag ctc aac ggc      1824
Tyr Leu Leu Asp Ser Asp Gly Glu Tyr Val Met Leu Lys Leu Asn Gly
        595                 600                 605

cag gag ctg agc ttc gac gtc gac ctc tct gct ctg ccg tgt gga gag      1872
Gln Glu Leu Ser Phe Asp Val Asp Leu Ser Ala Leu Pro Cys Gly Glu
    610                 615                 620

aac ggc tcg ctc tac ctg tct cag atg gac gag aac ggg ggc gcc aac      1920
Asn Gly Ser Leu Tyr Leu Ser Gln Met Asp Glu Asn Gly Gly Ala Asn
625                 630                 635                 640

cag tat aac acg gcc ggt gcc aac tac ggg agc ggc tac tgc gat gct      1968
Gln Tyr Asn Thr Ala Gly Ala Asn Tyr Gly Ser Gly Tyr Cys Asp Ala
                645                 650                 655

cag tgc ccc gtc cag aca tgg agg aac ggc acc ctc aac act agc cac      2016
Gln Cys Pro Val Gln Thr Trp Arg Asn Gly Thr Leu Asn Thr Ser His
            660                 665                 670

cag ggc ttc tgc tgc aac gag atg gat atc ctg gag ggc aac tcg agg      2064
Gln Gly Phe Cys Cys Asn Glu Met Asp Ile Leu Glu Gly Asn Ser Arg
        675                 680                 685

gcg aat gcc ttg acc cct cac tct tgc acg gcc acg gcc tgc gac tct      2112
Ala Asn Ala Leu Thr Pro His Ser Cys Thr Ala Thr Ala Cys Asp Ser
    690                 695                 700

gcc ggt tgc ggc ttc aac ccc tat ggc agc ggc tac aaa agc tac tac      2160
Ala Gly Cys Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys Ser Tyr Tyr
705                 710                 715                 720

ggc ccc gga gat acc gtt gac acc tcc aag acc ttc acc atc atc acc      2208
Gly Pro Gly Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr
                725                 730                 735

cag ttc aac acg gac aac ggc tcg ccc tcg ggc aac ctt gtg agc atc      2256
Gln Phe Asn Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile
            740                 745                 750

acc cgc aag tac cag caa aac ggc gtc gac atc ccc agc gcc cag ccc      2304
Thr Arg Lys Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro
        755                 760                 765

ggc ggc gac acc atc tcg tcc tgc ccg tcc gcc tca gcc tac ggc ggc      2352
Gly Gly Asp Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly
    770                 775                 780

ctc gcc acc atg ggc aag gcc ctg agc agc ggc atg gtg ctc gtg ttc      2400
Leu Ala Thr Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe
785                 790                 795                 800

agc att tgg aac gac aac agc cag tac atg aac tgg ctc gac agc ggc      2448
Ser Ile Trp Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly
                805                 810                 815
```

```
aac gcc ggc ccc tgc agc agc acc gag ggc aac cca tcc aac atc ctg      2496
Asn Ala Gly Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Ile Leu
            820                 825                 830

gcc aac aac ccc aac acg cac gtc gtc ttc tcc aac atc cgc tgg gga      2544
Ala Asn Asn Pro Asn Thr His Val Val Phe Ser Asn Ile Arg Trp Gly
        835                 840                 845

gac att ggg tct act acg aac tcg act gcg ccc ccg ccc ccg cct gcg      2592
Asp Ile Gly Ser Thr Thr Asn Ser Thr Ala Pro Pro Pro Pro Pro Ala
    850                 855                 860

tcc agc acg acg ttt tcg act aca cgg agg agc tcg acg act tcg agc      2640
Ser Ser Thr Thr Phe Ser Thr Thr Arg Arg Ser Ser Thr Thr Ser Ser
865                 870                 875                 880

agc ccg agc                                                         2649
Ser Pro Ser
```

<210> 98
<211> 883
<212> PRT
<213> Sequência artificial

<220>
<223> Construção Sintética

<400> 98

```
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1               5                   10                  15

Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
            20                  25                  30

Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
        35                  40                  45

Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
    50                  55                  60

Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65                  70                  75                  80

Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
                85                  90                  95

Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
            100                 105                 110

Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
        115                 120                 125
```

Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
130 135 140

Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145 150 155 160

Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
165 170 175

Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
180 185 190

Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
195 200 205

Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
210 215 220

Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225 230 235 240

Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
245 250 255

Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
260 265 270

Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
275 280 285

Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
290 295 300

Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305 310 315 320

Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
325 330 335

Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
340 345 350

Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
355 360 365

Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
370 375 380

Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385 390 395 400

Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
405 410 415

Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
420 425 430

Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
435 440 445

Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
450 455 460

Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465 470 475 480

Gln Phe Thr Gln Gln Pro Gly Thr Ser Thr Pro Glu Val His Pro Lys
485 490 495

Leu Thr Thr Tyr Lys Cys Thr Lys Ser Gly Gly Cys Val Ala Gln Asp
500 505 510

Thr Ser Val Val Leu Asp Trp Asn Tyr Arg Trp Met His Asp Ala Asn
515 520 525

Tyr Asn Ser Cys Thr Val Asn Gly Gly Val Asn Thr Thr Leu Cys Pro
530 535 540

Asp Glu Ala Thr Cys Gly Lys Asn Cys Phe Ile Glu Gly Val Asp Tyr
545 550 555 560

Ala Ala Ser Gly Val Thr Thr Ser Gly Ser Ser Leu Thr Met Asn Gln
565 570 575

Tyr Met Pro Ser Ser Ser Gly Gly Tyr Ser Ser Val Ser Pro Arg Leu
580 585 590

Tyr Leu Leu Asp Ser Asp Gly Glu Tyr Val Met Leu Lys Leu Asn Gly
595 600 605

Gln Glu Leu Ser Phe Asp Val Asp Leu Ser Ala Leu Pro Cys Gly Glu
610 615 620

Asn Gly Ser Leu Tyr Leu Ser Gln Met Asp Glu Asn Gly Gly Ala Asn
625 630 635 640

Gln Tyr Asn Thr Ala Gly Ala Asn Tyr Gly Ser Gly Tyr Cys Asp Ala
645 650 655

Gln Cys Pro Val Gln Thr Trp Arg Asn Gly Thr Leu Asn Thr Ser His
660 665 670

Gln Gly Phe Cys Cys Asn Glu Met Asp Ile Leu Glu Gly Asn Ser Arg
675 680 685

[redacted] Asn Ala Leu Thr Pro His Ser Cys Thr Ala Thr Ala Cys Asp Ser
690 695 700

Ala Gly Cys Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys Ser Tyr Tyr
705 710 715 720

Gly Pro Gly Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr
725 730 735

Gln Phe Asn Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile
740 745 750

Thr Arg Lys Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro
755 760 765

[redacted] Gly Asp Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly
770 775 780

Leu Ala Thr Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe
785 790 795 800

Ser Ile Trp Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly
805 810 815

Asn Ala Gly Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Ile Leu
820 825 830

Ala Asn Asn Pro Asn Thr His Val Val Phe Ser Asn Ile Arg Trp Gly
835 840 845

Asp Ile Gly Ser Thr Thr Asn Ser Thr Ala Pro Pro Pro Pro Pro Ala

850 855 860

Ser Ser Thr Thr Phe Ser Thr Thr Arg Arg Ser Ser Thr Thr Ser Ser
865 870 875 880

Ser Pro Ser

<210> 99
<211> 2787
<212> DNA
<213> Seqüência artificial

<220>
<223> Proteína de fusão

<220>
<221> CDS
<222> (1)..(2787)

<400> 99
cag agc agc tgc gtc tcg gct tgg ggt caa tgt ggc ggt att tct tat 48
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1 5 10 15

acc ggg tct acc tgc tgt cag agt ggg aat acc tgc gcc gag att aac 96
Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
20 25 30

tcg tac tac tac cag tgc ata cca gca aca gct gtg agt act tca act 144
Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
35 40 45

acc aca gtg aca tct ccc tct agc tct ggt tcg tct tct gcc aac acg 192
Thr Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
50 55 60

tca ggt tat aca acg acg act gtc ttg ccc agt ccc acg gca aca cag 240
Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65 70 75 80

aac cct tat cct ccg gcc aat gcc agc tca tgt gga tcg tgg gct ctc 288
Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
85 90 95

gtt gat aac gtt tgc tgc cca tac tac tgt ctc tcg gat aat gaa tcc 336
Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
100 105 110

gag tcc tgc acg agc agc tgt acc ggc ggc tgc ggc agt cct gat tcc 384
Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
115 120 125

tcc atg tgc aag tcc ggg acg atg tgg gga gag caa cac acc gta act 432
Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
130 135 140

```
tcc aac gag gac tgg cat tac agc cgc tca aca cac ttt ggt ctg acc      480
Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145                 150                 155                 160

agc ggt ggc gcc tgc ggg ttc ggt ctg tac ggc ctc tgc acc aag aac      528
Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
                165                 170                 175

agt gtc acc gcg agc tgg aca gac cca atg ctg ggc tct acc tgc gac      576
Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
            180                 185                 190

gcc ttc tgc acc gcg tat ccg ctc ctc tgc aaa gac ccc gct aac gtc      624
Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
        195                 200                 205

act ctc cgc ggg aac ttt gct gcc ccg aac gga gac tac tac act cag      672
Thr Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
    210                 215                 220

[redacted]c tgg cct tcc ctg gct gca tcc ggc aat ccc gac aac tac ctc tct      720
Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225                 230                 235                 240

tgc ggg gag tgt ttc gag gtc atc cgc acc aag ccc gac ggg aca gac      768
Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
                245                 250                 255

tac gcc gtc ggc gag agc gga tat acc gac ccc ata gtc ctc gag gta      816
Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
            260                 265                 270

gta gac agc tgt ccc tgc aat gcc aat tca aaa tgg tgc tgt aag cgg      864
Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
        275                 280                 285

ccc ccc ccc ccc ccc ttt ttt tcc ccg cct tcc aac gga caa aat ctc      912
Pro Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
    290                 295                 300

[redacted]ca aga cca ggc ggc agc ggc gca gac cac tgc ggc gaa atc gac ttc      960
Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305                 310                 315                 320

aag tac ggc tgt cct ctg ccg gaa gga tcc cat cac atg gac ctc tcc     1008
Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
                325                 330                 335

gat att gcc atg ggc cga ctc cag gga aac ggc agt ctc gcc gac ggt     1056
Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
            340                 345                 350

gtg att ccc atc cgc tac cgg cgt gtc ccc tgt ccc aag ccg ggg aac     1104
Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
        355                 360                 365

atc tac atc tgg ctt cat gat ggg gcg gga ccg tat tat ttt gcg ctg     1152
Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
    370                 375                 380

agc gcg gtc aat acc aac ggc ccc ggc tcc gta atc agt atc gaa gtc     1200
```

```
Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385                 390                 395                 400

cag gct ggt ggc tcc ggg cca tgg gtt gcc ctc gag cac gat ccg aac      1248
Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
                405                 410                 415

tac acc agt agc cgg ccg cag gag cgg tat ggc tct tgg gtc ctc ccg      1296
Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
            420                 425                 430

cag ggc aag gga ccc att act gtg cct gtt tcg atg agg ctg acg gcg      1344
Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
        435                 440                 445

ccc aat ggg cag cag gtg gtt aag gag ggc gcc att acc agc tat acc      1392
Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
    450                 455                 460

[redacted]ccg gcg act gcg gtc gag ggc ttt tgg tat att gat ctg gga gtg      1440
[redacted]o Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465                 470                 475                 480

cag ttc acc ggc tcg act tac tcc agt gga tct tct tcg ggg tcg ggg      1488
Gln Phe Thr Gly Ser Thr Tyr Ser Ser Gly Ser Ser Ser Gly Ser Gly
                485                 490                 495

tct agc tcc agc tcg agt tcg act acc act aag gcc act tcg acg acc      1536
Ser Ser Ser Ser Ser Ser Ser Thr Thr Thr Lys Ala Thr Ser Thr Thr
            500                 505                 510

ttg aag act acc tcg acc acc agc agt gga agc agt tcg aca tcg gcg      1584
Leu Lys Thr Thr Ser Thr Thr Ser Ser Gly Ser Ser Ser Thr Ser Ala
        515                 520                 525

gcg cag caa ccg ggt acc agc acc ccc gag gtc cat ccc aag ttg aca      1632
Ala Gln Gln Pro Gly Thr Ser Thr Pro Glu Val His Pro Lys Leu Thr
    530                 535                 540

[redacted]c tac aag tgt aca aag tcc ggg ggg tgc gtg gcc cag gac acc tcg      1680
[redacted]r Tyr Lys Cys Thr Lys Ser Gly Gly Cys Val Ala Gln Asp Thr Ser
545                 550                 555                 560

gtg gtc ctt gac tgg aac tac cgc tgg atg cac gac gca aac tac aac      1728
Val Val Leu Asp Trp Asn Tyr Arg Trp Met His Asp Ala Asn Tyr Asn
                565                 570                 575

tcg tgc acc gtc aac ggc ggc gtc aac acc acg ctc tgc cct gac gag      1776
Ser Cys Thr Val Asn Gly Gly Val Asn Thr Thr Leu Cys Pro Asp Glu
            580                 585                 590

gcg acc tgt ggc aag aac tgc ttc atc gag ggc gtc gac tac gcc gcc      1824
Ala Thr Cys Gly Lys Asn Cys Phe Ile Glu Gly Val Asp Tyr Ala Ala
        595                 600                 605

tcg ggc gtc acg acc tcg ggc agc agc ctc acc atg aac cag tac atg      1872
Ser Gly Val Thr Thr Ser Gly Ser Ser Leu Thr Met Asn Gln Tyr Met
    610                 615                 620

ccc agc agc tct ggc ggc tac agc agc gtc tct cct cgg ctg tat ctc      1920
Pro Ser Ser Ser Gly Gly Tyr Ser Ser Val Ser Pro Arg Leu Tyr Leu
```

625 630 635 640

ctg gac tct gac ggt gag tac gtg atg ctg aag ctc aac ggc cag gag 1968
Leu Asp Ser Asp Gly Glu Tyr Val Met Leu Lys Leu Asn Gly Gln Glu
645 650 655

ctg agc ttc gac gtc gac ctc tct gct ctg ccg tgt gga gag aac ggc 2016
Leu Ser Phe Asp Val Asp Leu Ser Ala Leu Pro Cys Gly Glu Asn Gly
660 665 670

tcg ctc tac ctg tct cag atg gac gag aac ggg ggc gcc aac cag tat 2064
Ser Leu Tyr Leu Ser Gln Met Asp Glu Asn Gly Gly Ala Asn Gln Tyr
675 680 685

aac acg gcc ggt gcc aac tac ggg agc ggc tac tgc gat gct cag tgc 2112
Asn Thr Ala Gly Ala Asn Tyr Gly Ser Gly Tyr Cys Asp Ala Gln Cys
690 695 700

ccc gtc cag aca tgg agg aac ggc acc ctc aac act agc cac cag ggc 2160
[redacted] Val Gln Thr Trp Arg Asn Gly Thr Leu Asn Thr Ser His Gln Gly
[redacted] 710 715 720

ttc tgc tgc aac gag atg gat atc ctg gag ggc aac tcg agg gcg aat 2208
Phe Cys Cys Asn Glu Met Asp Ile Leu Glu Gly Asn Ser Arg Ala Asn
725 730 735

gcc ttg acc cct cac tct tgc acg gcc acg gcc tgc gac tct gcc ggt 2256
Ala Leu Thr Pro His Ser Cys Thr Ala Thr Ala Cys Asp Ser Ala Gly
740 745 750

tgc ggc ttc aac ccc tat ggc agc ggc tac aaa agc tac tac ggc ccc 2304
Cys Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys Ser Tyr Tyr Gly Pro
755 760 765

gga gat acc gtt gac acc tcc aag acc ttc acc atc atc acc cag ttc 2352
Gly Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe
770 775 780

[redacted] acg gac aac ggc tcg ccc tcg ggc aac ctt gtg agc atc acc cgc 2400
[redacted] Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile Thr Arg
[redacted] 790 795 800

aag tac cag caa aac ggc gtc gac atc ccc agc gcc cag ccc ggc ggc 2448
Lys Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro Gly Gly
805 810 815

gac acc atc tcg tcc tgc ccg tcc gcc tca gcc tac ggc ggc ctc gcc 2496
Asp Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala
820 825 830

acc atg ggc aag gcc ctg agc agc ggc atg gtg ctc gtg ttc agc att 2544
Thr Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe Ser Ile
835 840 845

tgg aac gac aac agc cag tac atg aac tgg ctc gac agc ggc aac gcc 2592
Trp Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala
850 855 860

ggc ccc tgc agc agc acc gag ggc aac cca tcc aac atc ctg gcc aac 2640
Gly Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Ile Leu Ala Asn
865 870 875 880

```
aac ccc aac acg cac gtc gtc ttc tcc aac atc cgc tgg gga gac att      2688
Asn Pro Asn Thr His Val Val Phe Ser Asn Ile Arg Trp Gly Asp Ile
                885                 890                 895

ggg tct act acg aac tcg act gcg ccc ccg ccc ccg cct gcg tcc agc      2736
Gly Ser Thr Thr Asn Ser Thr Ala Pro Pro Pro Pro Pro Ala Ser Ser
            900                 905                 910

acg acg ttt tcg act aca cgg agg agc tcg acg act tcg agc agc ccg      2784
Thr Thr Phe Ser Thr Thr Arg Arg Ser Ser Thr Thr Ser Ser Ser Pro
        915                 920                 925

agc                                                                 2787
Ser
```

<210> 100
<211> 929
<212> PRT
<213> Sequência artificial
<220>
<223> Construção Sintética

<400> 100

```
Gln Ser Ser Cys Val Ser Ala Trp Gly Gln Cys Gly Gly Ile Ser Tyr
1               5                  10                  15

Thr Gly Ser Thr Cys Cys Gln Ser Gly Asn Thr Cys Ala Glu Ile Asn
            20                  25                  30

Ser Tyr Tyr Tyr Gln Cys Ile Pro Ala Thr Ala Val Ser Thr Ser Thr
        35                  40                  45

[redacted] Thr Val Thr Ser Pro Ser Ser Ser Gly Ser Ser Ser Ala Asn Thr
    50                  55                  60

Ser Gly Tyr Thr Thr Thr Thr Val Leu Pro Ser Pro Thr Ala Thr Gln
65                  70                  75                  80

Asn Pro Tyr Pro Pro Ala Asn Ala Ser Ser Cys Gly Ser Trp Ala Leu
                85                  90                  95

Val Asp Asn Val Cys Cys Pro Tyr Tyr Cys Leu Ser Asp Asn Glu Ser
            100                 105                 110

Glu Ser Cys Thr Ser Ser Cys Thr Gly Gly Cys Gly Ser Pro Asp Ser
        115                 120                 125

Ser Met Cys Lys Ser Gly Thr Met Trp Gly Glu Gln His Thr Val Thr
```

130 135 140

Ser Asn Glu Asp Trp His Tyr Ser Arg Ser Thr His Phe Gly Leu Thr
145 150 155 160

Ser Gly Gly Ala Cys Gly Phe Gly Leu Tyr Gly Leu Cys Thr Lys Asn
165 170 175

Ser Val Thr Ala Ser Trp Thr Asp Pro Met Leu Gly Ser Thr Cys Asp
180 185 190

Ala Phe Cys Thr Ala Tyr Pro Leu Leu Cys Lys Asp Pro Ala Asn Val
195 200 205

[redacted] Leu Arg Gly Asn Phe Ala Ala Pro Asn Gly Asp Tyr Tyr Thr Gln
210 215 220

Phe Trp Pro Ser Leu Ala Ala Ser Gly Asn Pro Asp Asn Tyr Leu Ser
225 230 235 240

Cys Gly Glu Cys Phe Glu Val Ile Arg Thr Lys Pro Asp Gly Thr Asp
245 250 255

Tyr Ala Val Gly Glu Ser Gly Tyr Thr Asp Pro Ile Val Leu Glu Val
260 265 270

Val Asp Ser Cys Pro Cys Asn Ala Asn Ser Lys Trp Cys Cys Lys Arg
275 280 285

[redacted]o Pro Pro Pro Pro Phe Phe Ser Pro Pro Ser Asn Gly Gln Asn Leu
290 295 300

Thr Arg Pro Gly Gly Ser Gly Ala Asp His Cys Gly Glu Ile Asp Phe
305 310 315 320

Lys Tyr Gly Cys Pro Leu Pro Glu Gly Ser His His Met Asp Leu Ser
325 330 335

Asp Ile Ala Met Gly Arg Leu Gln Gly Asn Gly Ser Leu Ala Asp Gly
340 345 350

Val Ile Pro Ile Arg Tyr Arg Arg Val Pro Cys Pro Lys Pro Gly Asn
355 360 365

Ile Tyr Ile Trp Leu His Asp Gly Ala Gly Pro Tyr Tyr Phe Ala Leu
370 375 380

Ser Ala Val Asn Thr Asn Gly Pro Gly Ser Val Ile Ser Ile Glu Val
385 390 395 400

Gln Ala Gly Gly Ser Gly Pro Trp Val Ala Leu Glu His Asp Pro Asn
405 410 415

Tyr Thr Ser Ser Arg Pro Gln Glu Arg Tyr Gly Ser Trp Val Leu Pro
420 425 430

Gln Gly Lys Gly Pro Ile Thr Val Pro Val Ser Met Arg Leu Thr Ala
435 440 445

Pro Asn Gly Gln Gln Val Val Lys Glu Gly Ala Ile Thr Ser Tyr Thr
450 455 460

Pro Pro Ala Thr Ala Val Glu Gly Phe Trp Tyr Ile Asp Leu Gly Val
465 470 475 480

Gln Phe Thr Gly Ser Thr Tyr Ser Ser Gly Ser Ser Ser Gly Ser Gly
485 490 495

Ser Ser Ser Ser Ser Ser Ser Thr Thr Thr Lys Ala Thr Ser Thr Thr
500 505 510

Leu Lys Thr Thr Ser Thr Thr Ser Ser Gly Ser Ser Ser Thr Ser Ala
515 520 525

Ala Gln Gln Pro Gly Thr Ser Thr Pro Glu Val His Pro Lys Leu Thr
530 535 540

Thr Tyr Lys Cys Thr Lys Ser Gly Gly Cys Val Ala Gln Asp Thr Ser
545 550 555 560

Val Val Leu Asp Trp Asn Tyr Arg Trp Met His Asp Ala Asn Tyr Asn
565 570 575

Ser Cys Thr Val Asn Gly Gly Val Asn Thr Thr Leu Cys Pro Asp Glu
580 585 590

Ala Thr Cys Gly Lys Asn Cys Phe Ile Glu Gly Val Asp Tyr Ala Ala
595 600 605

Ser Gly Val Thr Thr Ser Gly Ser Ser Leu Thr Met Asn Gln Tyr Met
610 615 620

Pro Ser Ser Ser Gly Gly Tyr Ser Ser Val Ser Pro Arg Leu Tyr Leu
625 630 635 640

Leu Asp Ser Asp Gly Glu Tyr Val Met Leu Lys Leu Asn Gly Gln Glu
645 650 655

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

Ser Leu Tyr Leu Ser Gln Met Asp Glu Asn Gly Gly Ala Asn Gln Tyr
675 680 685

Asn Thr Ala Gly Ala Asn Tyr Gly Ser Gly Tyr Cys Asp Ala Gln Cys
690 695 700

Pro Val Gln Thr Trp Arg Asn Gly Thr Leu Asn Thr Ser His Gln Gly
705 710 715 720

Phe Cys Cys Asn Glu Met Asp Ile Leu Glu Gly Asn Ser Arg Ala Asn
725 730 735

Ala Leu Thr Pro His Ser Cys Thr Ala Thr Ala Cys Asp Ser Ala Gly
740 745 750

Cys Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys Ser Tyr Tyr Gly Pro
755 760 765

Gly Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe
770 775 780

Asn Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile Thr Arg
785 790 795 800

Lys Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro Gly Gly
805 810 815

Asp Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala
820 825 830

Thr Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe Ser Ile
835 840 845

Trp Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala
850 855 860

Gly Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Ile Leu Ala Asn
865 870 875 880

Asn Pro Asn Thr His Val Val Phe Ser Asn Ile Arg Trp Gly Asp Ile
885 890 895

Gly Ser Thr Thr Asn Ser Thr Ala Pro Pro Pro Pro Pro Ala Ser Ser
900 905 910

Thr Thr Phe Ser Thr Thr Arg Arg Ser Ser Thr Thr Ser Ser Ser Pro
915 920 925

Ser

<210> 101
<211> 54
<212> DNA
<213> Trichoderma reesei

<220>
<221> CDS
<222> (1)..(54)

<400> 101
atg gct ggt aag ctt atc ctc gtg gct cta gca agc ctt gta tca ctc 48
Met Ala Gly Lys Leu Ile Leu Val Ala Leu Ala Ser Leu Val Ser Leu
1 5 10 15

tct att 54
Ser Ile

<210> 102
<211> 18
<212> PRT
<213> Trichoderma reesei

<400> 102

Met Ala Gly Lys Leu Ile Leu Val Ala Leu Ala Ser Leu Val Ser Leu
1 5 10 15

Ser Ile

<210> 103
<211> 51
<212> DNA
<213> Trichoderma reesei

REIVINDICAÇÕES

1. – Proteínas de fusão, caracterizadas por compreender:

- pelo menos uma swolenina, isto é, uma proteína contendo um domínio de molécula de ligação a carboidratos (CBM) que direciona para a celulose das plantas, e um domínio de expansina que decompõe as ligações de hidrogênio entre as microfibrilas da celulose,

- e pelo menos uma enzima degradadora da parede celular de plantas, a referida enzima sendo de tal forma que ela contém um domínio CBM ou não, contanto que contenha uma CBM, o último pode ser deletado, se necessário,

a referida swolenina e a enzima degradadora da parede celular de plantas sendo proteínas recombinantes correspondendo a proteínas nativas em fungos, ou formas mutadas destes.

2. – Proteínas de fusão, de acordo com a reivindicação 1, caracterizadas pelo fato de que a swolenina corresponde a proteínas nativas, ou a formas mutadas destas, de fungos escolhidos entre ascomicetes, tais como:

- Linhagens de *Trichoderma*, e mais particularmente *Trichoderma reesei*, ou

- linhagens de *Aspergillus*, e mais particularmente *Aspergillus fumigatus*.

3. – Proteínas de fusão, de acordo com a reivindicação 1 ou 2, caracterizadas pelo fato de que a swolenina

corresponde a enzimas nativas, ou suas formas mutadas, de linhagens de *Trichoderma*, tal como *Trichoderma reesei.*

4. – Proteínas de fusão, de acordo com qualquer uma das reivindicações 1 a 3, caracterizadas pelo fato de que a swolenina é a proteína de *Trichoderma reesei*, representada pela SEQ ID NO : 2 com seu peptídeo de sinal, ou pela SEQ ID NO : 4 em seu estado maduro.

5. – Proteínas de fusão, de acordo com a reivindicação 1 ou 2, caracterizadas pelo fato de que a swolenina corresponde a enzimas nativas, ou suas formas mutadas, de linhagens de *Aspergillus*, tal como *Aspergillus fumigatus.*

6. – Proteínas de fusão, de acordo com a reivindicação 5, caracterizadas pelo fato de que a swolenina é a proteína de *Aspergillus fumigatus*, representada pela SEQ ID NO : 6 com seu peptídeo de sinal, ou pela SEQ ID NO : 8 em seu estado maduro.

7. – Proteínas de fusão, de acordo com qualquer uma das reivindicações 1 a 6, caracterizadas pelo fato de que em que as enzimas degradadoras da parede celular de plantas são escolhidas entre enzimas capazes de hidrolizar a celulose, a hemicelulose e degradar a lignina.

8. – Proteínas de fusão, de acordo com qualquer uma das reivindicações 1 a 7, caracterizadas pelo fato de que as enzimas degradadoras da parede celular de plantas são hidrolases escolhidas entre:

- celulases, tais como endoglucanases, exoglucanases, tais como celobiohidrolases, ou β-glucosidases,

- hemicelulases, tais como xilanases,

- ligninases capazes de degradar ligninas, tais como lacases, manganês peroxidases, lignina peroxidases, peroxidases versáteis ou enzimas suplementares, tais como celobiose deidrogenases, e aril álcool oxidases,

- cinamoil éster hidrolases capazes de liberar ácidos cinâmicos, tais como ácidos ferúlicos e de hidrolizar ligações cruzadas de ácido diferúlico entre cadeias de hemicelulose, tais como feruloil esterases, cinamoil esterases e ácido clorogênico hidrolases.

9. – Proteínas de fusão, de acordo com qualquer uma das reivindicações 1 a 8, caracterizadas pelo fato de que as enzimas degradadoras da parede celular de plantas são escolhidas entre feruloil esterases, celobiohidrolases com ou sem seus domínios CBM, endoglucanases com ou sem seus domínios CBM, xilanases e lacases.

10. – Proteínas de fusão, de acordo com qualquer uma das reivindicações 1 a 9, caracterizadas pelo fato de que as enzimas degradadoras da parede celular de plantas correspondem a enzimas nativas, ou a suas formas mutadas, de fungos selecionados entre:

* ascomicetes, tais como:

- linhagens de *Aspergillus*, e mais particularmente, *Aspergillus niger*,

- linhagens de Trichoderma, e mais particularmente, *Trichoderma reesei*,

- Linhagens de *Magnaporthe*, e mais particularmente, *Magnaporthe grisea*,

* basidiomicetes, como linhagens de *Pycnoporus*, *Halocyphina* ou *Phanerochaete*, e mais particularmente, *Pycnoporus cinnabarinus, Pycnoporus sanguineus* ou *Halocyphina villosa*, ou *Phanerochaete chrysosporium*.

11. – Proteínas de fusão, de acordo com qualquer uma das reivindicações 1 a 10, caracterizadas pelo fato de que as enzimas degradadoras da parede celular de plantas correspondem a enzimas nativas, ou a suas formas mutadas, de linhagens de *Aspergillus*, tal como *Aspergillus niger*.

12. – Proteínas de fusão, de acordo com qualquer uma das reivindicações 1 a 11, caracterizadas pelo fato de que pelo menos uma das enzimas degradadoras da parede celular de plantas é uma feruloil esterase, tal como a escolhida entre:

- a feruloil esterase A de *A. niger*, representada pela SEQ ID NO : 10, ou

- a feruloil esterase B de *A. niger* representada pela SEQ ID NO : 12.

13. – Proteínas de fusão, de acordo com qualquer uma das reivindicações 1 a 11, caracterizadas pelo fato de que pelo menos uma das enzimas degradadoras da parede

celular de plantas é uma xilanase, tal como a xilanase B de *A. niger*, representada pela SEQ ID NO : 14.

14. – Proteínas de fusão, de acordo com qualquer uma das reivindicações 1 a 10, caracterizadas pelo fato de que as enzimas degradadoras da parede celular de plantas correspondem a enzimas nativas, ou a suas formas mutadas, de linhagens de *Trichoderma*, tal como *Trichoderma reesei*.

15. – Proteínas de fusão, de acordo com a reivindicação 14, caracterizadas pelo fato de que pelo menos uma das enzimas degradadoras da parede celular de plantas é uma celobiohidrolase, tal como a escolhida entre:

- a celobiohidrolase I de *T. reesei*, e representada pela SEQ ID NO : 16,

- a celobiohidrolase I de *T. reesei*, em que o domínio CBM foi deletado, e representada pela SEQ ID NO : 18,

- a celobiohidrolase II de *T. reesei*, e representada pela SEQ ID NO : 20,

- a celobiohidrolase II de *T. reesei*, em que o domínio CBM foi deletado, e representada pela SEQ ID NO : 22.

16. – Proteínas de fusão, de acordo com a reivindicação 14, caracterizadas pelo fato de que pelo menos uma das enzimas degradadoras da parede celular de plantas é uma endoglucanase, tal como a escolhida entre:

- a endoglucanase I de *T. reesei*, e representada pela SEQ ID NO : 24,

- a endoglucanase I de *T. reesei*, em que o domínio CBM foi deletado, e representada pela SEQ ID NO : 26.

17. – Proteínas de fusão, de acordo com qualquer uma das reivindicações 1 a 16, caracterizadas por compreender peptídeos de ligação entre pelo menos duas das proteínas compreendidas nas referidas proteínas de fusão, os referidos peptídeos de ligação sendo polipeptídeos de 10 a 100 aminoácidos, de preferência de cerca de 50 aminoácidos.

18. – Proteínas de fusão, de acordo com qualquer uma das reivindicações 1 a 17, caracterizadas pelo fato de que um peptídeo de ligação é incluído entre cada proteína compreendida nas referidas proteínas de fusão.

19. – Proteínas de fusão, de acordo com qualquer uma das reivindicações 1 a 18, caracterizadas pelo fato de que o peptídeo de ligação é um polipeptídeo hiperglicosilado, tal como a seqüência representada pela SEQ ID NO : 28, presente na celobiohidrolase B de *A. niger*.

20. Proteínas de fusão, de acordo com qualquer uma das reivindicações 1 a 19, caracterizadas por serem escolhidas entre as proteínas de fusão da swolenina de *Trichoderma reesei* representada pela SEQ ID NO : 4, com:

- a feruloil esterase A de *A. niger*, representada pelo SEQ ID NO : 10, a referida proteína de fusão sendo representada pela SEQ ID NO : 30,

- a feruloil esterase A de *A. niger*, representada pela SEQ ID NO : 10, a referida proteína de fusão

compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 4 e a SEQ ID NO : 10, e sendo representada pela SEQ ID NO : 32,

- a feruloil esterase B de *A. niger*, representada pela SEQ ID NO : 12, a referida proteína de fusão sendo representada pela SEQ ID NO : 34,

- a feruloil esterase B de *A. niger*, representada pela SEQ ID NO : 12, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 4 e a SEQ ID NO : 12, e sendo representada pela SEQ ID NO : 36,

- a xilanase B de *A. niger*, representada pela SEQ ID NO : 14, a referida proteína de fusão sendo representada pela SEQ ID NO : 38,

- a xilanase B de *A. niger*, representada pela SEQ ID NO : 14, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 4 e a SEQ ID NO : 14, e sendo representada pela SEQ ID NO : 40,

- a celobiohidrolase I de *T. reesei* representada pela SEQ ID NO : 16, a referida proteína de fusão sendo representada pela SEQ ID NO : 42,

- a celobiohidrolase I de *T. reesei*, representada pela SEQ ID NO : 16, a referida proteína de fusão

compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 4 e a SEQ ID NO : 16, e sendo representada pela SEQ ID NO : 44,

- a celobiohidrolase I de *T. reesei* sem sua CBM endógena representada pela SEQ ID NO : 18, a referida proteína de fusão sendo representada pela SEQ ID NO : 46,

- a celobiohidrolase I de *T. reesei*, sem sua CBM endógena representada pela SEQ ID NO : 18, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 4 e a SEQ ID NO : 18, e sendo representada pela SEQ ID NO : 48,

- a celobiohidrolase II de *T. reesei* pela SEQ ID NO : 20, a referida proteína de fusão sendo representada pela SEQ ID NO : 50,

- a celobiohidrolase II de *T. reesei*, representada pela SEQ ID NO : 20, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 4 e a SEQ ID NO : 20, e sendo representada pela SEQ ID NO : 52,

- a celobiohidrolase II de *T. reesei* sem sua CBM endógena representada pela SEQ ID NO : 22, a referida proteína de fusão sendo representada pela SEQ ID NO : 54,

- a celobiohidrolase II de *T. reesei*, sem sua CBM endógena representada pela SEQ ID NO : 22, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 4 e a SEQ ID NO : 22, e sendo representada pela SEQ ID NO : 56,

- a endoglucanase I de *T. reesei* representada pela SEQ ID NO : 24, a referida proteína de fusão sendo representada pela SEQ ID NO : 58,

- a endoglucanase I de *T. reesei*, representada pela SEQ ID NO : 24, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 4 e a SEQ ID NO : 24, e sendo representada pela SEQ ID NO : 60,

- a endoglucanase I de *T. reesei* sem sua CBM endógena representada pela SEQ ID NO : 26, a referida proteína de fusão sendo representada pela SEQ ID NO : 62,

- a endoglucanase I de *T. reesei*, sem sua CBM endógena representada pela SEQ ID NO : 26, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 4 e a SEQ ID NO : 26, e sendo representada pela SEQ ID NO : 64.

21. – Proteínas de fusão, de acordo com qualquer uma das reivindicações 1 a 19, caracterizadas por serem

escolhidas entre as proteínas de fusão da swolenina de *Aspergillus fumigatus* representada pela SEQ ID NO : 8, com:

- a feruloil esterase A de *A. niger*, representada pelo SEQ ID NO : 10, a referida proteína de fusão sendo representada pela SEQ ID NO : 66,

- a feruloil esterase A de *A. niger*, representada pela SEQ ID NO : 10, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 8 e a SEQ ID NO : 10, e sendo representada pela SEQ ID NO : 68,

- a feruloil esterase B de *A. niger*, representada pela SEQ ID NO : 12, a referida proteína de fusão sendo representada pela SEQ ID NO : 70,

- a feruloil esterase B de *A. niger*, representada pela SEQ ID NO : 12, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 8 e a SEQ ID NO : 12, e sendo representada pela SEQ ID NO : 72,

- a xilanase B de *A. niger*, representada pela SEQ ID NO : 14, a referida proteína de fusão sendo representada pela SEQ ID NO : 74,

- a xilanase B de *A. niger*, representada pela SEQ ID NO : 14, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo

de ligação hiperglicosilado entre a SEQ ID NO : 8 e a SEQ ID NO : 14, e sendo representada pela SEQ ID NO : 76,

- a celobiohidrolase I de *T. reesei* representada pela SEQ ID NO : 16, a referida proteína de fusão sendo representada pela SEQ ID NO : 78,

- a celobiohidrolase I de *T. reesei*, representada pela SEQ ID NO : 16, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 8 e a SEQ ID NO : 16, e sendo representada pela SEQ ID NO : 80,

- a celobiohidrolase I de *T. reesei* sem sua CBM endógena representada pela SEQ ID NO : 18, a referida proteína de fusão sendo representada pela SEQ ID NO : 82,

- a celobiohidrolase I de *T. reesei*, sem sua CBM endógena representada pela SEQ ID NO : 18, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 8 e a SEQ ID NO : 18, e sendo representada pela SEQ ID NO : 84,

- a celobiohidrolase II de *T. reesei* pela SEQ ID NO : 20, a referida proteína de fusão sendo representada pela SEQ ID NO : 86,

- a celobiohidrolase II de *T. reesei*, representada pela SEQ ID NO : 20, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28

como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 8 e a SEQ ID NO : 20, e sendo representada pela SEQ ID NO : 88,

- a celobiohidrolase II de *T. reesei* sem sua CBM endógena representada pela SEQ ID NO : 22, a referida proteína de fusão sendo representada pela SEQ ID NO : 90,

- a celobiohidrolase II de *T. reesei*, sem sua CBM endógena representada pela SEQ ID NO : 22, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 8 e a SEQ ID NO : 22, e sendo representada pela SEQ ID NO : 92,

- a endoglucanase I de *T. reesei* representada pela SEQ ID NO : 24, a referida proteína de fusão sendo representada pela SEQ ID NO : 94,

- a endoglucanase I de *T. reesei*, representada pela SEQ ID NO : 24, a referida proteína de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 8 e a SEQ ID NO : 24, e sendo representada pela SEQ ID NO : 96,

- a endoglucanase I de *T. reesei* sem sua CBM endógena representada pela SEQ ID NO : 26, a referida proteína de fusão sendo representada pela SEQ ID NO : 98,

- a endoglucanase I de *T. reesei*, sem sua CBM endógena representada pela SEQ ID NO : 26, a referida proteína

de fusão compreendendo a seqüência representada pela SEQ ID NO : 28 como um peptídeo de ligação hiperglicosilado entre a SEQ ID NO : 4 e a SEQ ID NO : 26, e sendo representada pela SEQ ID NO : 100.

22. – Ácidos nucléicos, caracterizados por codificarem uma proteína de fusão, conforme definida em qualquer uma das reivindicações 1 a 21.

23. – Vetores, caracterizados por serem transformados com um ácido nucléico conforme definido na reivindicação 22.

24. – Células hospedeiras, caracterizadas por serem transformadas com um ácido nucléico conforme definido na reivindicação 22, usando um vetor conforme definido na reivindicação 23.

25. – Células hospedeiras transformadas, de acordo com a reivindicação 24, caracterizadas por serem escolhidas entre células de fungos, tais como os fungos definidos na reivindicação 10, e mais especificamente *A. niger*, *A. fumigatus*, *Trichoderma reesei* ou *Pycnoporus cinnabarinus*.

26. – Processo para a preparação de proteínas de fusão, de acordo com a reivindicação 1 a 21, caracterizado por compreender a cultura *in vitro* de células hospedeiras de acordo com a reivindicação 24 ou 25, a recuperação, e, se necessária, a purificação das proteínas de fusão produzidas pelas referidas células hospedeiras na cultura.

27. – Uso de proteínas de fusão, de acordo com qualquer uma das reivindicações 1 a 21, caracterizado por ser para realizar processos de degradação da parede celular de plantas no âmbito da preparação, a partir de plantas ou subprodutos vegetais, de compostos de interesse localizados na parede celular de plantas, ou no âmbito do branqueamento da polpa e do papel, para a produção de biocombustíveis ou nas indústrias alimentícias.

28. – Uso, de acordo com a reivindicação 27, caracterizado por ser para realizar processos de degradação de parede celular de plantas no âmbito da preparação dos seguintes compostos de interesse:

- bioetanol,

- antioxidantes, como ácido ferúlico ou ácido caféico, que são ácidos cinâmicos, e hidroxitirosol, ou ácido gálico,

- aromas, como vanilina ou *p*-hidroxibenzaldeído, obtidos da biotransformação do ácido ferúlico ou do ácido *p*-coumárico, respectivamente.

29. – Processo de degradação de parede celular de plantas no âmbito da preparação, a partir de plantas ou subprodutos vegetais, de compostos de interesse localizados na parede celular de plantas, caracterizado por compreender as seguintes etapas:

- o tratamento enzimático de plantas ou subprodutos vegetais ou resíduos industriais, com proteínas de fusão de acordo com qualquer uma das reivindicações 1 a 21, ou

com células transformadas de acordo com a reivindicação 24 ou 25,

- opcionalmente, o tratamento físico de plantas ou subprodutos vegetais por explosão a vapor em combinação com a ação de proteínas de fusão,

- opcionalmente, a biotransformação com microorganismos ou enzimas apropriados dos compostos contidos nas paredes celulares e liberados durante o tratamento enzimático anterior,

- a recuperação, e se necessária, a purificação do composto de interesse liberado pelas paredes celulares durante o tratamento enzimático anterior ou obtido durante a etapa de biotransformação anterior.

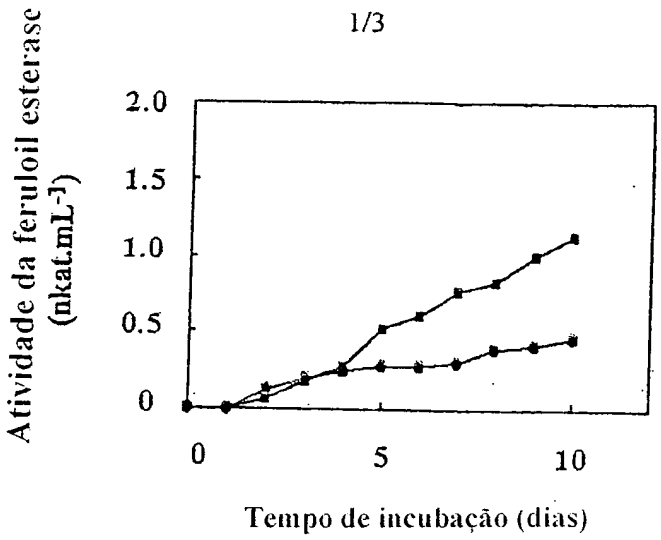

Figura 1

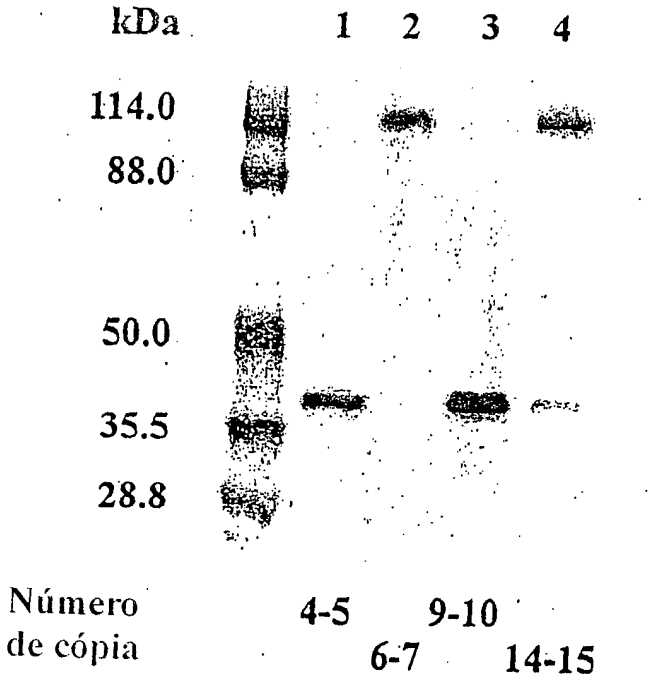

Figura 2

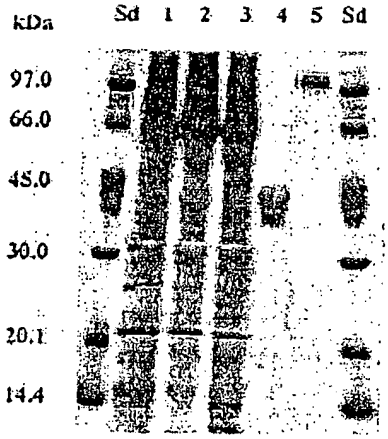

Figura 3

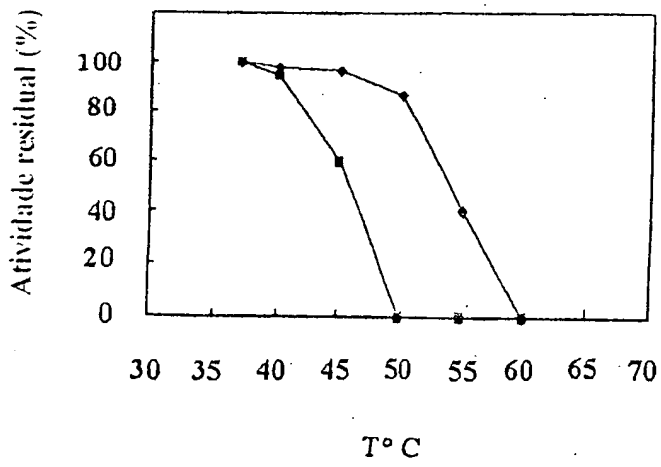

Figura 4

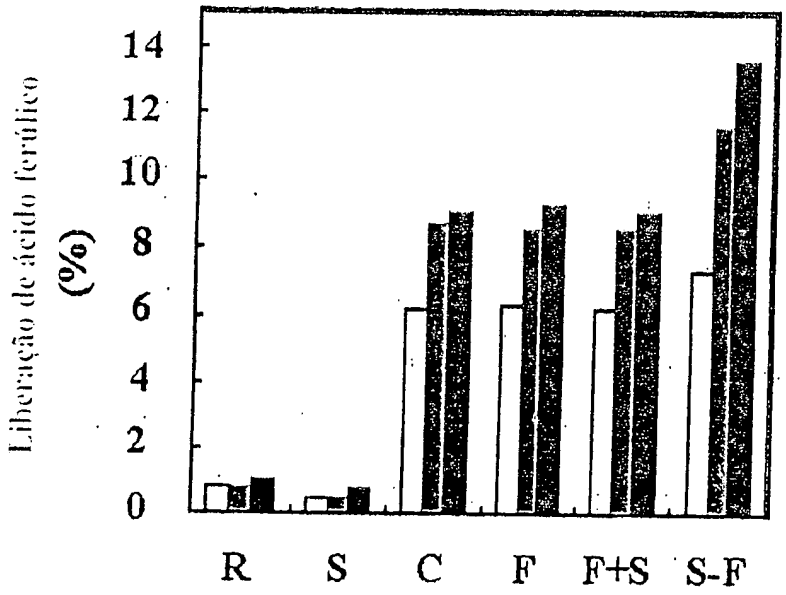

Figura 5

PI0704346-0

RESUMO

Patente de Invenção para "**PROTEÍNAS DE FUSÃO ENTRE ENZIMAS DEGRADADORAS DA PAREDE DE CELULAR DE PLANTAS E UMA SWOLENINA, E SEUS USOS**".

A invenção refere-se a proteínas de fusão compreendendo pelo menos uma swolenina e pelo menos uma enzima degradadora da parede celular de plantas, a referida swolenina e a enzima degradadora da parede celular de plantas sendo proteínas recombinantes correspondendo a proteínas nativas em fungos, ou suas formas mutadas. A invenção também se refere ao uso de proteínas de fusão conforme definidas acima, para realizar processos de degradação da parede celular de plantas no âmbito da preparação, a partir de plantas ou subprodutos vegetais, de compostos de interesse localizados na parede celular de plantas, ou no âmbito do branqueamento da polpa e do papel, para a produção de biocombustíveis ou nas indústrias alimentícias.