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(54) **METHOD TO SCREEN COMPOUNDS FOR ANTIFUNGAL ACTIVITY AND PHARMACEUTICAL COMPOSITIONS AND METHODS TO TREAT FUNGAL DISEASES BY INHIBITING SPORE GERMINATION**

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(51) **Int. Cl.**

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A01N 37/44	(2006.01)
A01N 41/12	(2006.01)
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A61K 31/137	(2006.01)
A61K 31/145	(2006.01)
A61K 31/155	(2006.01)
A61K 31/24	(2006.01)
A61P 31/10	(2006.01)
C12Q 1/66	(2006.01)

(52) **U.S. Cl.**

CPC ***C12Q 1/18*** (2013.01); ***A01N 33/10*** (2013.01); ***A01N 37/44*** (2013.01); ***A01N 41/12*** (2013.01); ***A01N 47/40*** (2013.01); ***A61K 31/137*** (2013.01); ***A61K 31/145*** (2013.01); ***A61K 31/155*** (2013.01); ***A61K 31/24*** (2013.01); ***A61P 31/10*** (2018.01); *C12Q 1/66* (2013.01); *G01N 2333/375* (2013.01)

(58) **Field of Classification Search**

CPC C12Q 1/18
See application file for complete search history.

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(57) **ABSTRACT**

A method of testing compounds for activity to inhibit germination of spores. The method includes the steps of providing bacterial, fungal, or plant spores transformed to contain and express a detectable marker, wherein the marker when expressed, is operationally linked to a spore-specific or yeast-specific protein, in a medium and under environmental conditions in which the spores will germinate, and measuring a first signal output generated by the marker prior to the spores initiating germination; contacting the spores of step (a) with a compound whose activity to inhibit germination of spores is to be measured; incubating the spores of step (b) under environmental conditions and for a time wherein spores not treated with the compound will germinate; and determining extent of germination of the spores by measuring a second signal output generated by the marker, wherein a difference between the first signal output and the second signal output is proportional to the extent of germination of the spores. Also described are compositions of matter for inhibiting spore germination in vitro and in vivo.

16 Claims, 13 Drawing Sheets

Specification includes a Sequence Listing.

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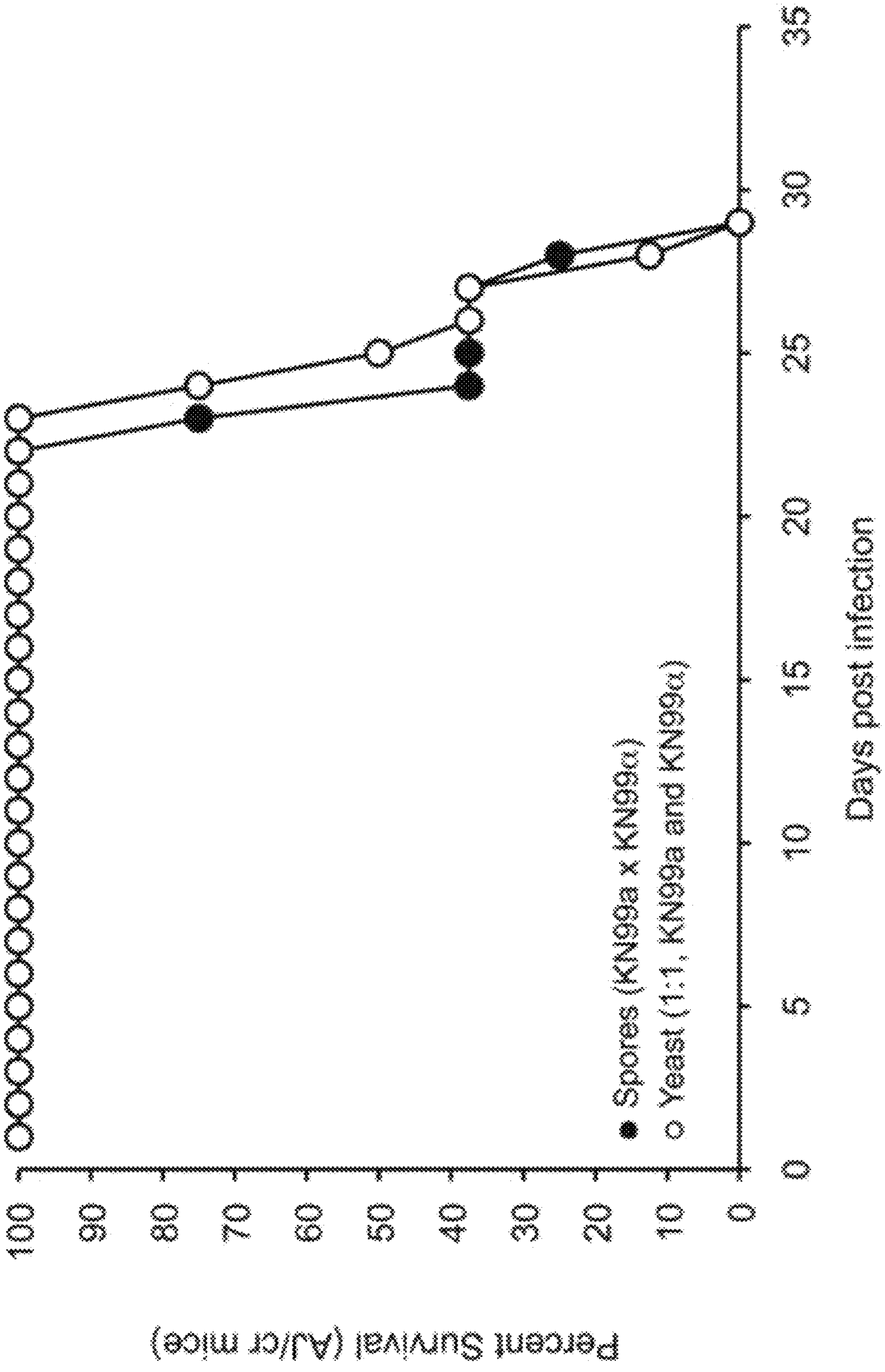

Percent Survival (AJ/cr mice)
100
90
80
70
60
50
40
30
20
10
0
0
5
10
15
20
25
30
35
Days post infection
● Spores (KN99a x KN99α)
○ Yeast (1:1, KN99a and KN99α)

FIG. 1

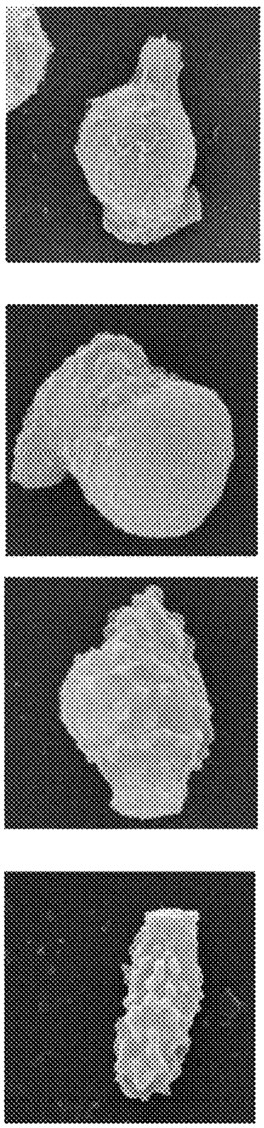


FIG. 2A

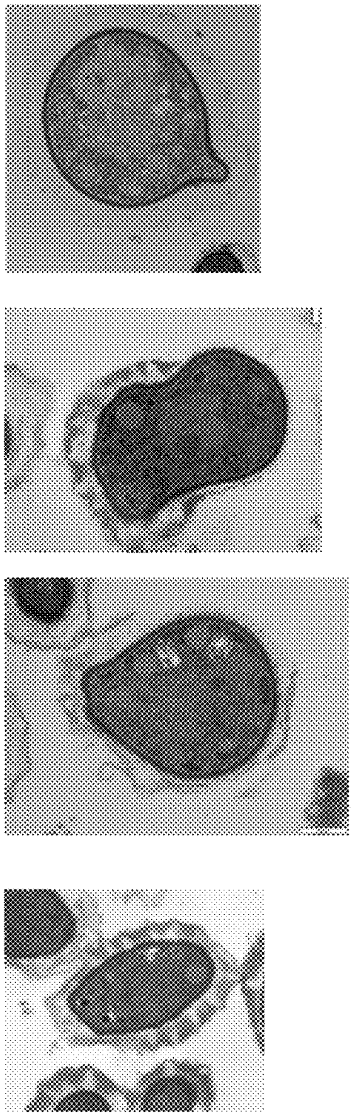


FIG. 2B

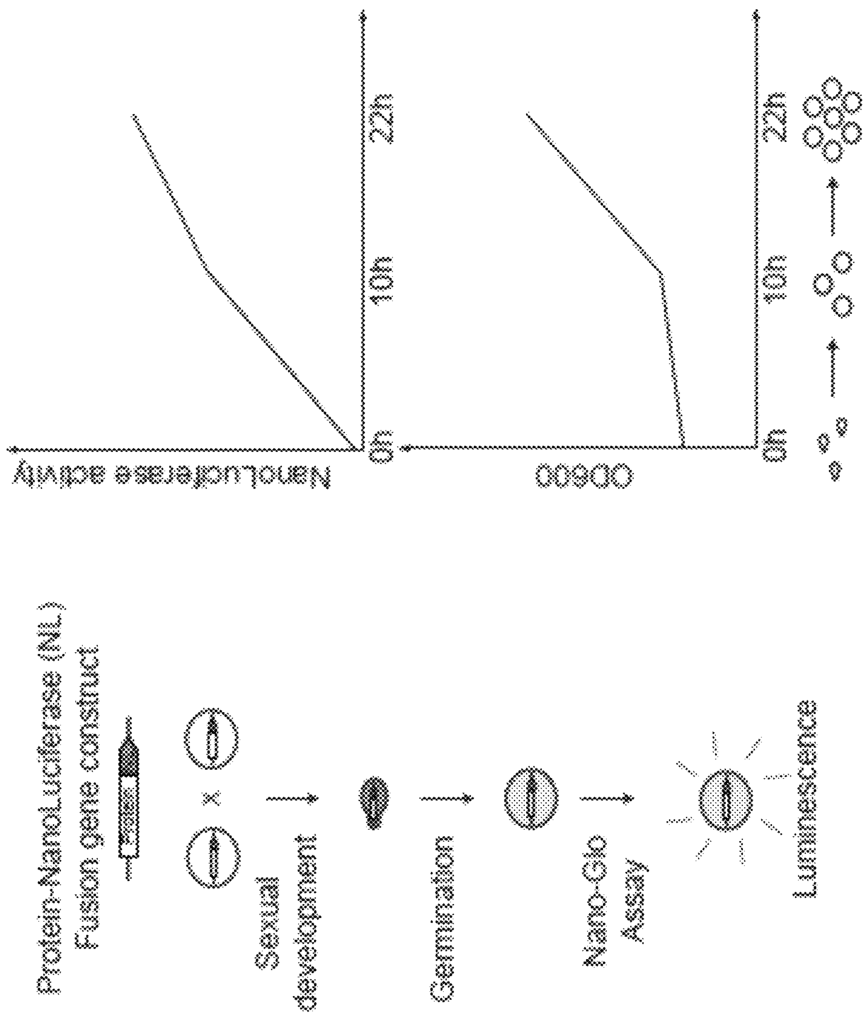

Protein-NanoLuciferase (NL)
Fusion gene construct
x
Sexual development
Germination
Nano-Glo Assay
Luminescence
NanoLuciferase activity
0h
10h
22h
OD600
0h
10h
22h

FIG. 3A

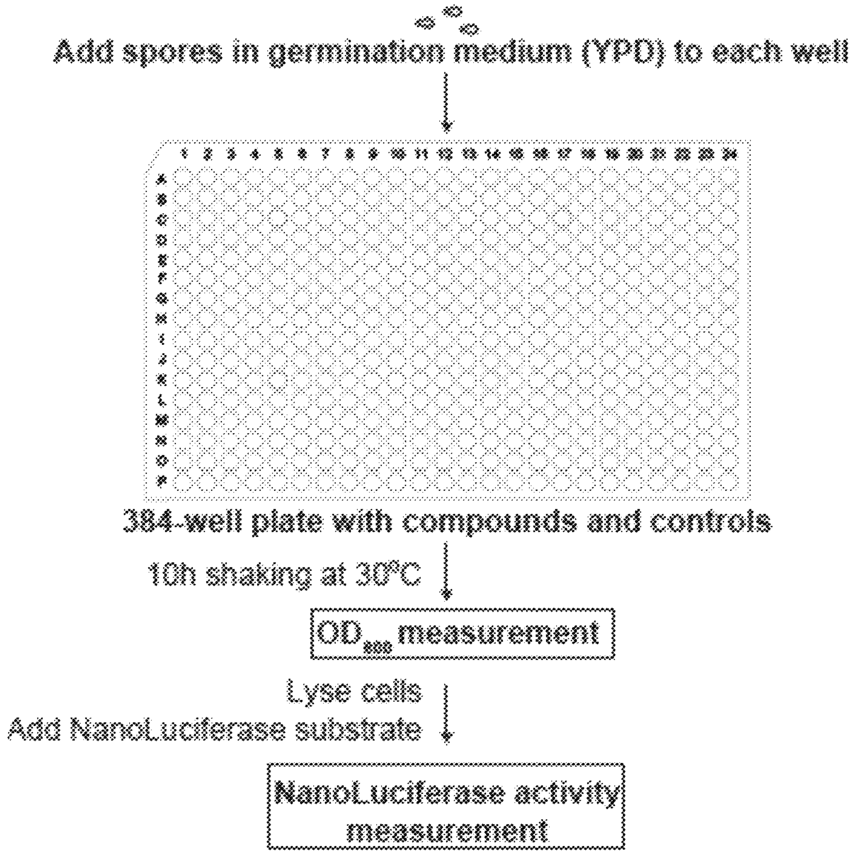

Add spores in germination medium (YPD) to each well
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24
A B C D E F G H I J K L M N O P
384-well plate with compounds and controls
10h shaking at 30°C
OD600 measurement
Lyse cells
Add NanoLuciferase substrate
NanoLuciferase activity measurement

FIG. 3B

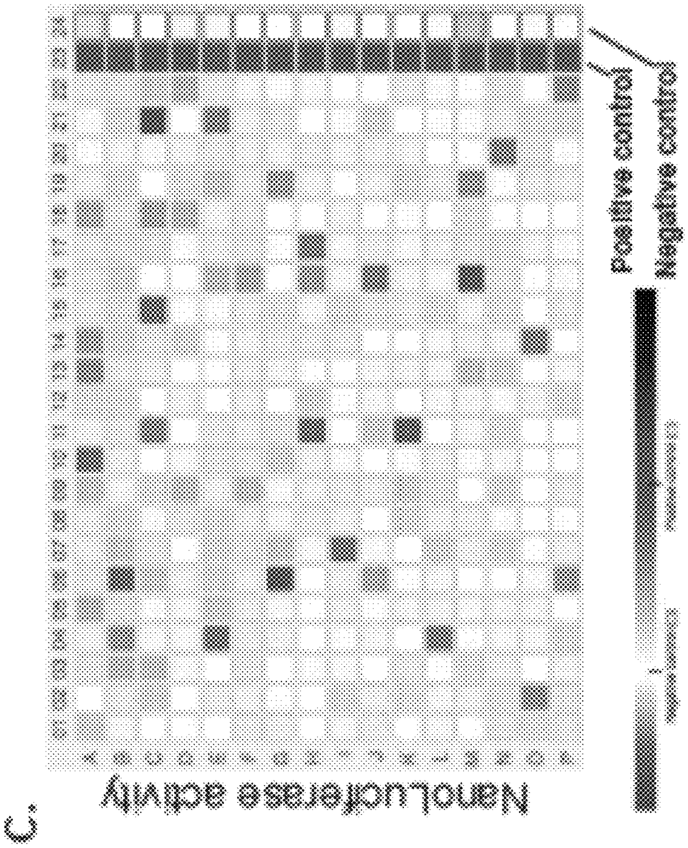

C.
NanoLuciferase activity
Positive control
Negative control

FIG. 3C

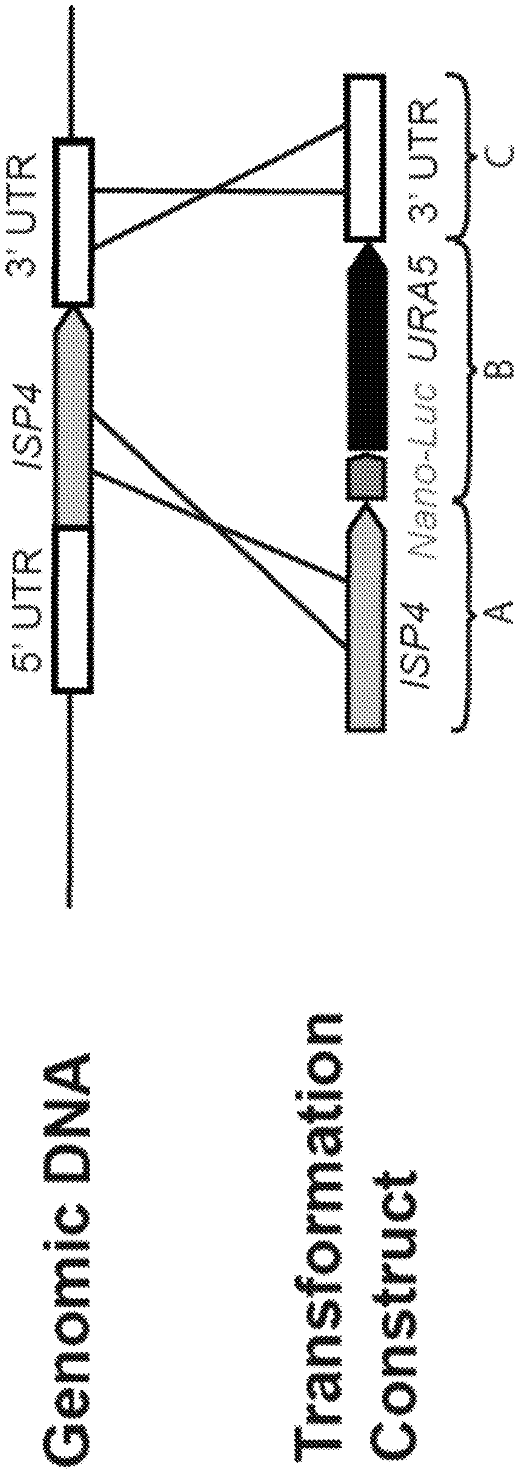

Genomic DNA
5' UTR
ISP4
3' UTR
Transformation Construct
ISP4
Nano-Luc
URA5
3' UTR
A
B
C

FIG. 3D

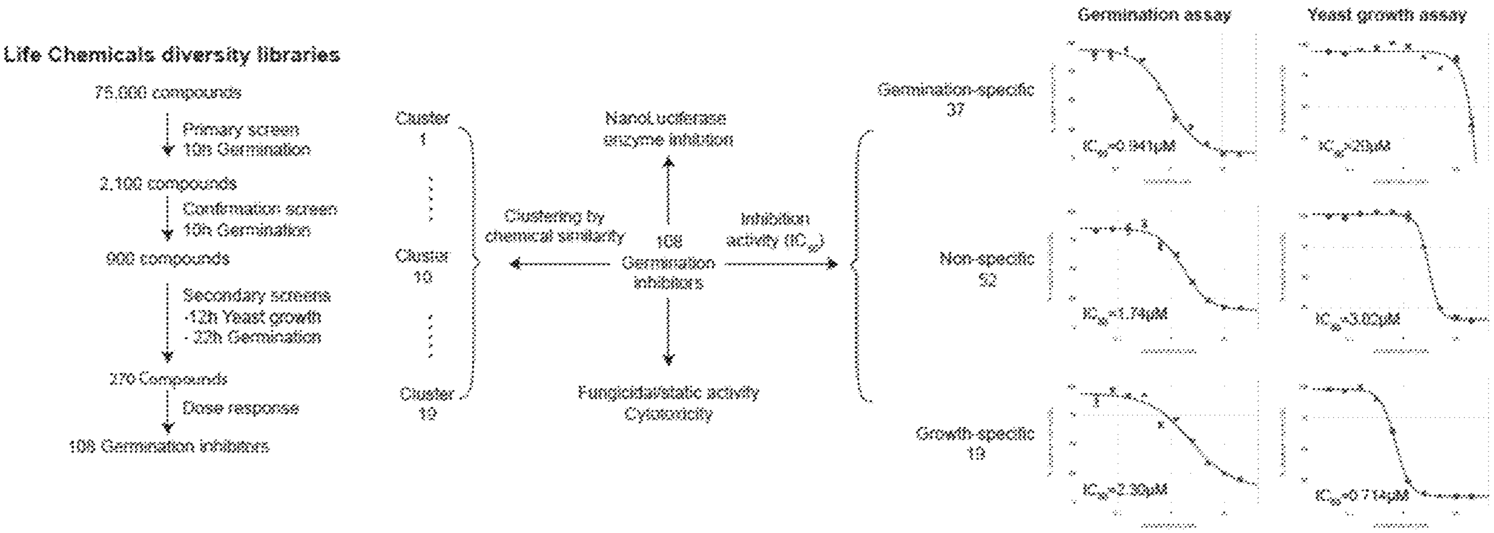

Life Chemicals diversity libraries
75,000 compounds
Primary screen
10h Germination
2,100 compounds
Confirmation screen
10h Germination
900 compounds
Secondary screens
-12h Yeast growth
- 22h Germination
270 Compounds
Dose response
108 Germination inhibitors
Cluster 1
Cluster 10
Cluster 19
Clustering by chemical similarity
NanoLuciferase enzyme inhibition
108 Germination inhibitors
Fungicidal/static activity Cytotoxicity
Inhibition activity (IC_{50})
Germination-specific 37
Non-specific 52
Growth-specific 19
Germination assay
Yeast growth assay
IC_{50}=0.941μM
IC_{50}>20μM
IC_{50}=1.74μM
IC_{50}=3.02μM
IC_{50}=2.30μM
IC_{50}=0.714μM

FIG. 4

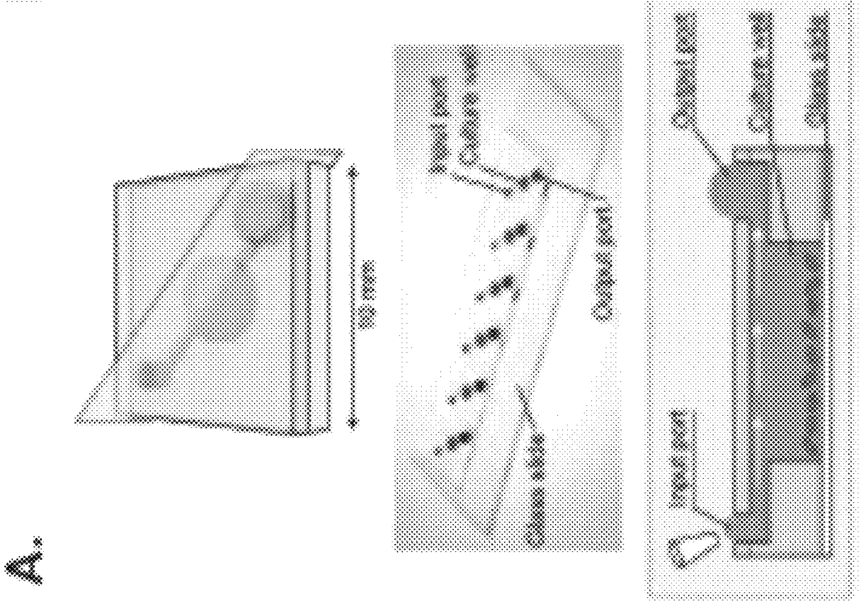


FIG. 5A

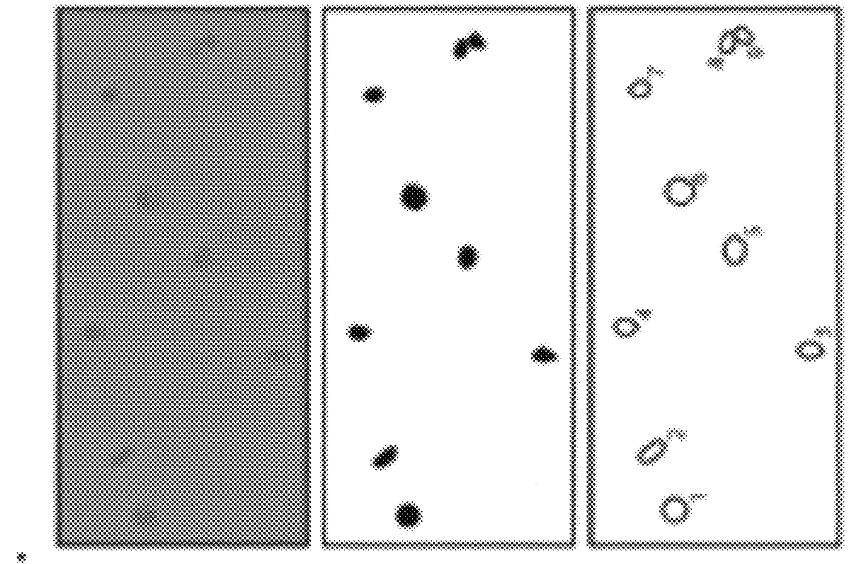


FIG. 5B

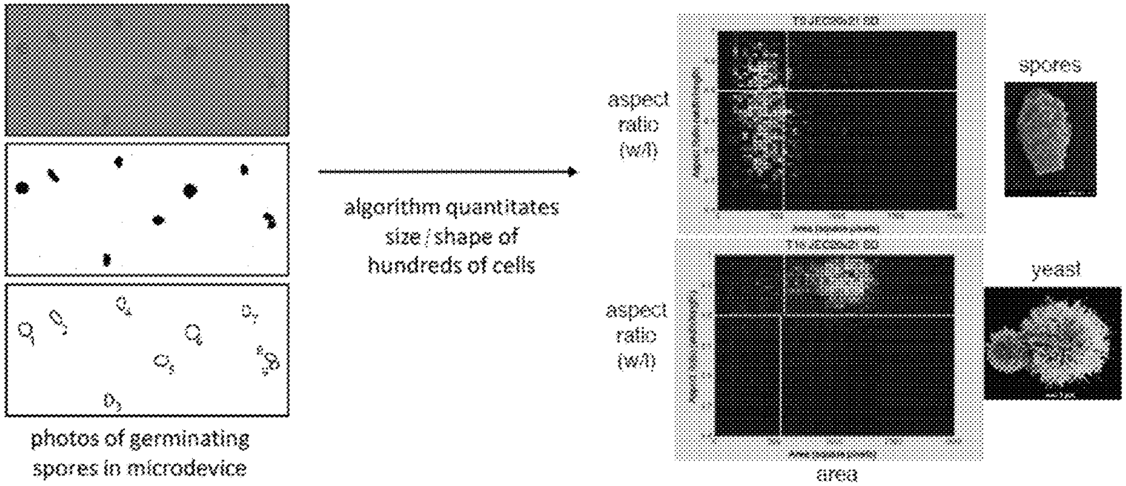

photos of germinating
spores in microdevice
algorithm quantitates
size / shape of
hundreds of cells
aspect
ratio
(w/l)
aspect
ratio
(w/l)
area
spores
yeast

FIG. 6

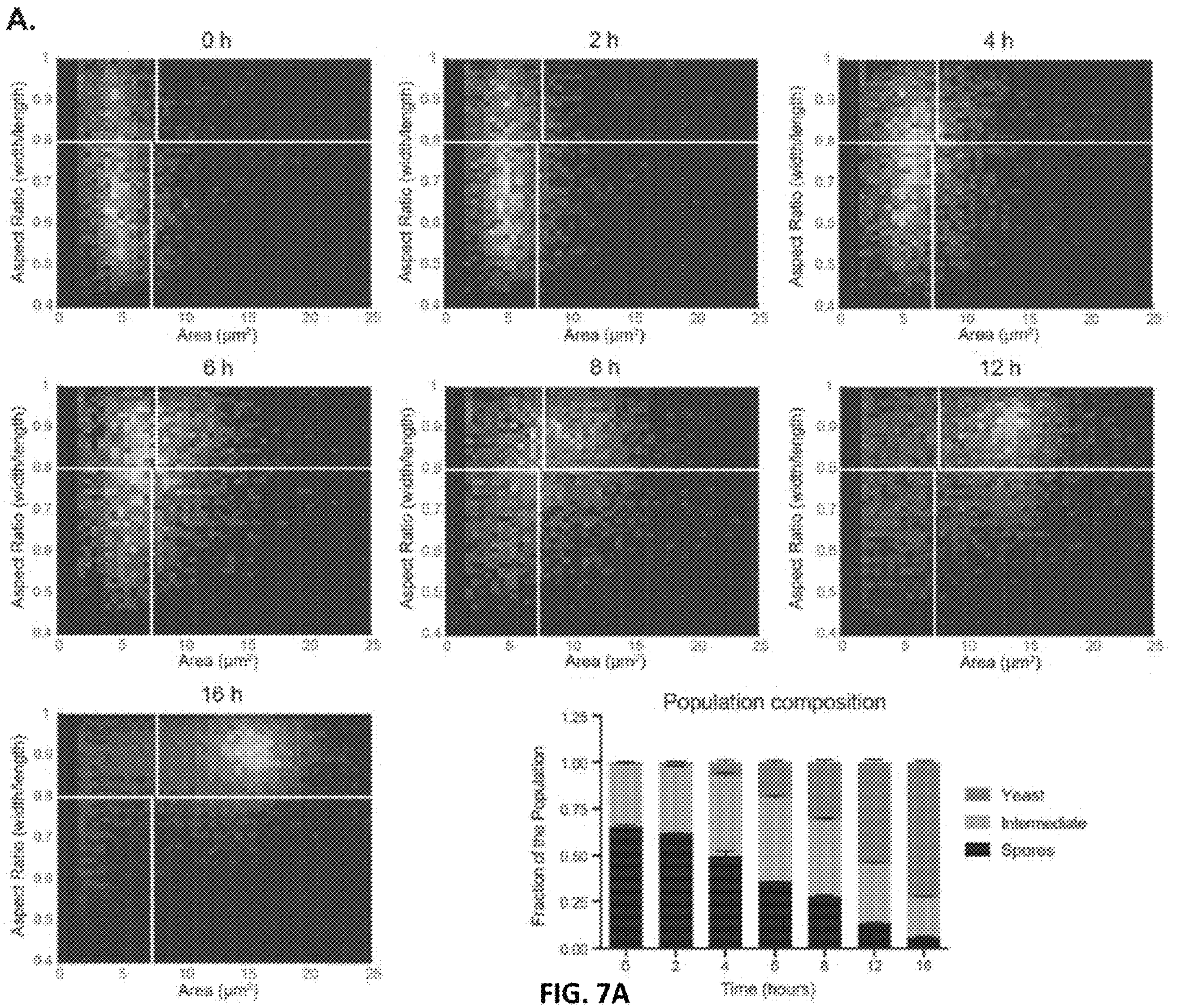

A.
0 h
2 h
4 h
6 h
8 h
12 h
16 h
Aspect Ratio (width/length)
1
0.9
0.8
0.7
0.6
0.5
0.4
Area (μm²)
0
5
10
15
20
25
Population composition
Fraction of the Population
1.25
1.00
0.75
0.50
0.25
0.00
Time (hours)
0
2
4
6
8
12
16
Yeast
Intermediate
Spores

FIG. 7A

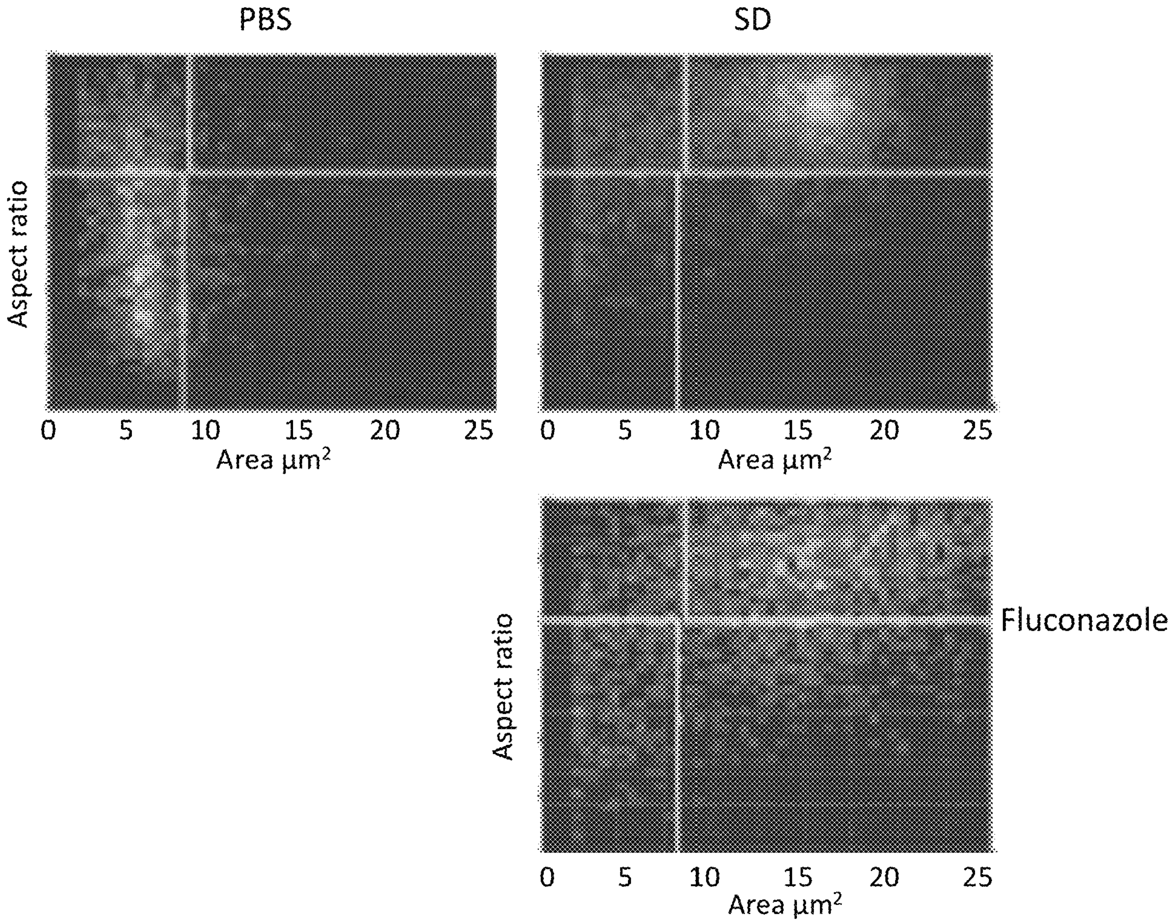

PBS
SD
Fluconazole
Aspect ratio
Aspect ratio
0
5
10
15
20
25
Area µm2
0
5
10
15
20
25
Area µm2
0
5
10
15
20
25
Area µm2

FIG. 7B

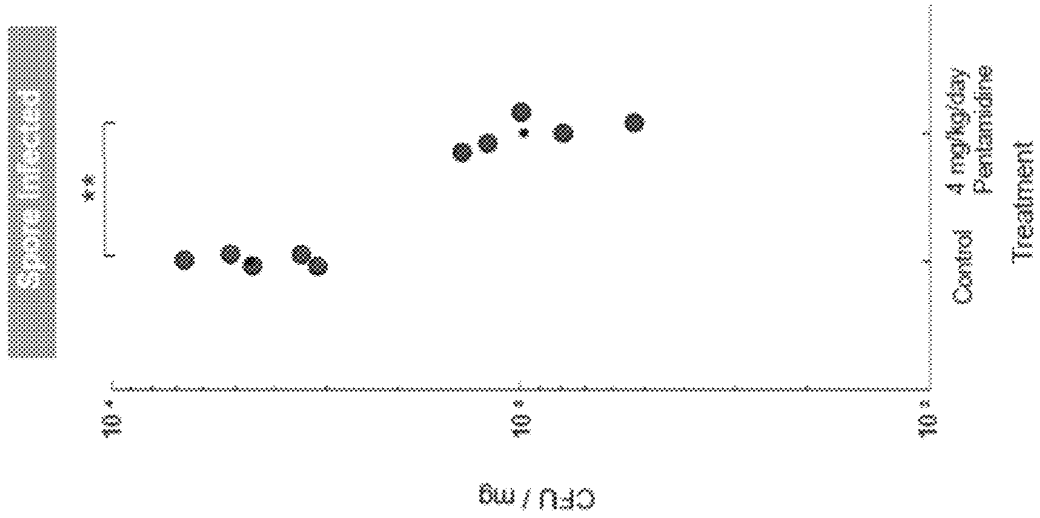

Spore Infected
**
CFU / mg
10^4
10^3
10^2
Control
4 mg/kg/day Pentamidine
Treatment

FIG. 8B

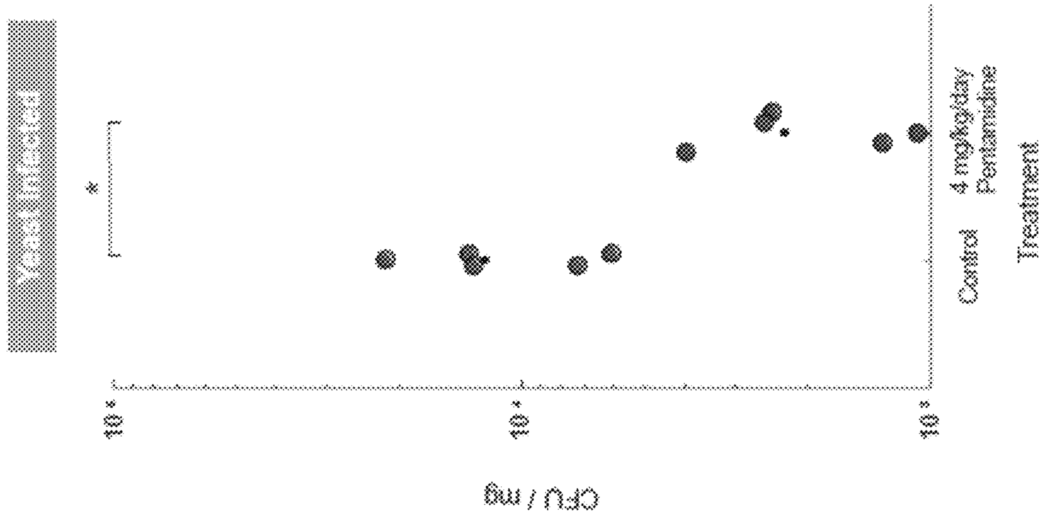

Yeast Infected
*
CFU / mg
10^4
10^3
10^2
Control
4 mg/kg/day Pentamidine
Treatment

FIG. 8A

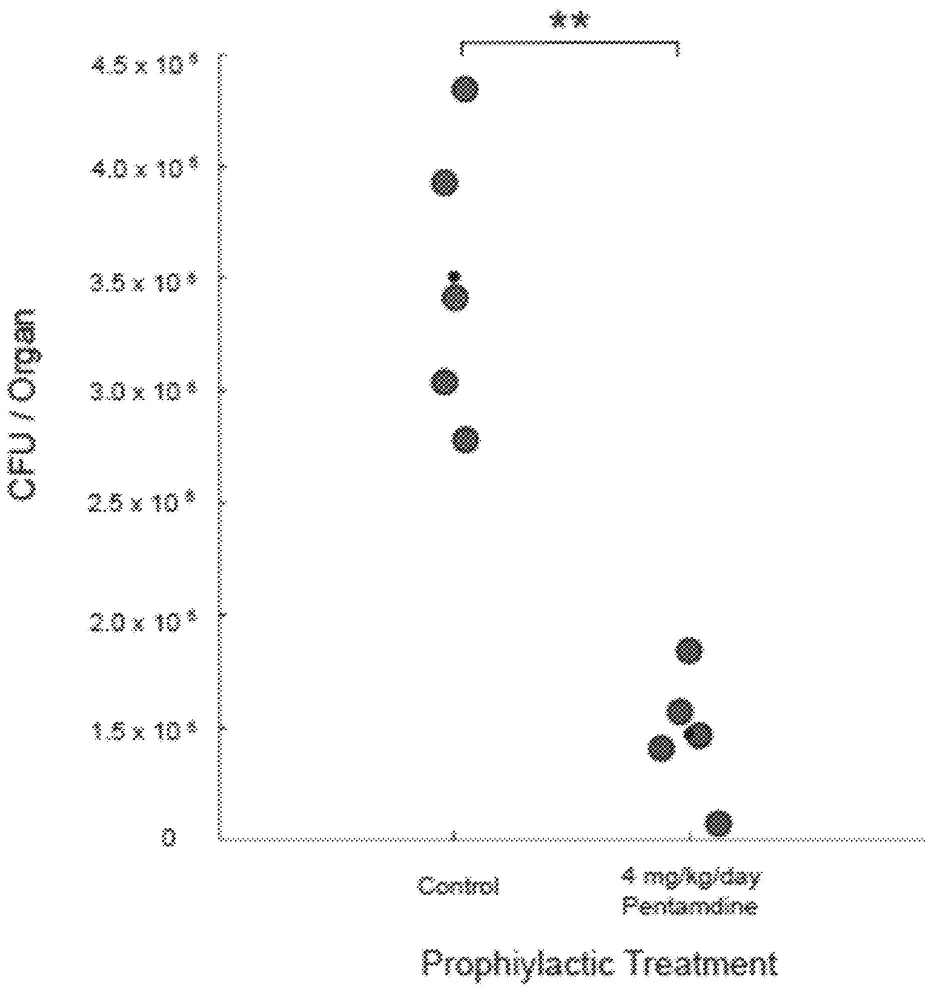

**
4.5 x 10^8
4.0 x 10^8
3.5 x 10^8
3.0 x 10^8
2.5 x 10^8
2.0 x 10^8
1.5 x 10^8
0
CFU / Organ
Control
4 mg/kg/day
Pentamdine
Prophiylactic Treatment

FIG. 9

METHOD TO SCREEN COMPOUNDS FOR ANTIFUNGAL ACTIVITY AND PHARMACEUTICAL COMPOSITIONS AND METHODS TO TREAT FUNGAL DISEASES BY INHIBITING SPORE GERMINATION

CROSS-REFERENCE TO RELATED APPLICATIONS

Priority is hereby claimed to provisional application Ser. No. 62/649,802, filed Mar. 29, 2018, which is incorporated herein by reference.

FEDERAL FUNDING STATEMENT

This invention was made with government support under AI089370 awarded by the National Institutes of Health. The government has certain rights in the invention.

BACKGROUND

Spores are an essential cell type required for long-term survival across diverse organisms and are a hallmark of fungal reproduction, persistence, and dispersal. Among human fungal pathogens, spores are presumed infectious particles, but relatively little is known about this robust cell type. Sporulation enables a relative quiescence—a type of hibernation—that contributes to the survival of fungi. However, sporulation also requires a transition back into a vegetative form so that the fungi can replicate—i.e., germination. Germination, despite its central importance in fungal reproduction and pathology in plants and animals, is not well understood.

Spores are a particularly successful cell type used by many microorganisms, including bacteria, fungi, and protozoa to survive unsuitable growth conditions and/or to disperse to new environments. Among eukaryotes, some of the most environmentally resistant spores are those of fungi, and much of our current understanding of spores comes from studies in model fungi such as *Saccharomyces cerevisiae* and *Aspergillus nidulans*. There are two general categories of fungal spores—sexual and asexual, and both forms occur across diverse fungal species via myriad developmental strategies. For example, in the budding yeast *S. cerevisiae* sexual spores are formed when yeast diploids are subject to nitrogen starvation and a non-fermentable carbon source, resulting in four haploid ascospores; *S. cerevisiae* does not produce asexual spores. In contrast, the filamentous fungus *Aspergillus nidulans* produces both asexual and sexual spores via the development of multicellular fruiting structures with thousands of spores per structure. In all instances, however, spores are adapted for general survivability.

As a consequence, fungal spores share three basic characteristics: First, mature spores are relatively metabolically quiescent, allowing them to remain dormant for long periods of time under sub-optimal growth conditions (e.g. in the absence of nutrients). Second, spores are resistant to environmental stresses, such as high temperatures, desiccation, and UV radiation, thus facilitating long-term survival and/or dispersal across great distances. Third, upon encountering growth-promoting environments, spores rapidly escape quiescence and germinate to resume vegetative growth. As a result, fungi are ubiquitous across all ecosystems on earth.

Spore-producing fungi commonly generate spores with thick, protective coats and robust stress resistance. Spores respond to different environmental signals to initiate germination, depending on their adapted niches. For example, spores of *S. cerevisiae* germinate readily in response to the presence of a fermentable carbon source. In contrast, spores of *Talaromyces macrosporus* require nutrients and a rigorous external trigger of very high temperature or pressure. These triggers generally result in responses such as water uptake, cell wall remodeling, and activation of nutrient metabolism and protein synthesis, leading to active fungal growth.

The transition from dormant particle to actively growing cell is particularly important because fungal survival cannot occur in the absence of the ability to germinate when (and only when) appropriate for vegetative growth. Environmental fungi are well adapted to their niches, and interestingly, these adaptations have led to a handful of fungi with the ability to cause life-threatening diseases in humans. *Histoplasma capsulatum, Blastomyces dermatitidis, Aspergillus fumigatus, Coccidioides immitis, Sporothrix schenkii, Penicillium marneffei*, and *Cryptococcus neoformans* are the most common environmental fungi that can cause disease in humans. The general route of infection is by inhaling cells from environmental sources. Spores (sexual or asexual, depending on the fungus) are the most likely infectious particles for all of these pathogens; however, very little is known about their basic spore biology, making the development of disease prevention and treatment strategies challenging.

Among human fungal pathogens, the most common cause of fatal fungal disease (and a well-developed model for study) is *Cryptococcus neoformans*, a primarily opportunistic pathogenic yeast that causes meningoencephalitis. People with AIDS are particularly susceptible, and there are an over 200,000 cases and nearly as many deaths annually worldwide from cryptococcosis. Rajasingjam R, Smith R M, Park B J, Jarvis J M, Govender N, Chiller T M, Denning D W, Loyse A, Boulware D R (2017) "Global burden of disease of HIV-associated cryptococcal meningitis: and updated analysis" *Lancet Infectious Disease* 17: 873-881 (pmid:2848341). *C. neoformans* is ubiquitous in the environment, and inhalation of aerosolized spores and/or yeast is the most common route of infection of humans. Under laboratory conditions, spores are produced through sexual development between haploid yeast of opposite mating types (a and α) or by α fruiting. In response to specific environmental conditions, cells form filaments and fruiting bodies (basidia) from which haploid, recombinant spores bud in chains.

Spores of *C. neoformans* exhibit the fundamental properties of most fungal spores, such as stability in the absence of nutrients and resistance to a variety of environmental stresses, including high temperature, desiccation, and oxidative stress. These spores have also been shown to germinate efficiently and synchronously in response to nutrients, and they germinate and cause disease in a mouse inhalation model of infection. See Velagapudi R, Hsueh Y-P, Geunes-Boyer S, Wright J R, Heitman J (2009) "Spores as infectious propagules of *Cryptococcus neoformans,*" *Infect Immun.* 77:4345-4355 (pmid:19620339) and Giles S S, Dagenais T R T, Botts M R, Keller N P, Hull C M (2009) "Elucidating the pathogenesis of spores from the human fungal pathogen *Cryptococcus neoformans,*" *Infect Immun* 77:3491-3500 (pmid:19451235). These findings indicate that *C. neoformans* spores harbor intrinsic properties that facilitate survival in the environment, maintain spore viability and stability, and initiate germination in response to external signals, including those of a mammalian host.

Current antifungal therapeutics are relatively limited because of high toxicity or insufficient efficacy. These issues arise because, unlike bacteria, fungi are eukaryotes. Thus, fungi are far more similar (metabolically and biochemically) to plants and animals than are bacteria. In short, compounds that interfere with fungal biology or are toxic to fungi, tend also to interfere with or be toxic to humans and animals.

A comparatively small number of antifungal compounds are approved for human, veterinary, and agricultural use in the United States. Focusing on antifungal drugs approved for use in humans, the gold standard by which all other antifungal pharmaceuticals are measured in terms of systemic antifungal activity is the polyene amphotericin B, first marketed in 1955. It is widely used to treat life-threatening fungal infections such as invasive mucormycosis, cryptococcal meningitis, aspergillosis, and candidiasis. While highly effective against fungi, amphotericin B itself has a slew of well-known and potentially life-threatening side effects. When administered intravenously, amphotericin B typically induces a debilitating set of symptoms, including high fever, shaking chills, hypotension, anorexia, nausea, vomiting, headache, dyspnea and tachypnea, drowsiness, and generalized weakness. Kidney damage is a commonly reported side effect. As a result, amphotericin B is administered with very close monitoring of the patient by healthcare professionals.

Other antifungal compounds approved for use in humans include imidazoles (e.g., miconazole), triazoles (e.g., fluconazole), and thiazole antifungals (e.g., abafungin). Most of these types of antifungal compounds, however, are used topically, rather than systemically. They are much less toxic that amphotericin B, but not as efficacious.

Echinocandins are a much newer class of systemic antifungal compounds approved for use in humans. The echinocandins are macrocyclic lipopeptides. Their structure is characterized by (typically) a 6-mer macrocyclic peptoid moiety bonded to a long (e.g., >C10) hydrocarbon tail. Echinocandins inhibit the synthesis of glucan in the cell wall of fungi via noncompetitive inhibition of the enzyme 1,3-β glucan synthase. In this sense, they exert a pharmacological activity against fungi that is analogous to the pharmacological activity of beta-lactam antibiotics against bacteria. Echinocandins are also far less toxic than amphotericin B, but again, not as effective.

Thus, there remains a long-felt and unmet need for a method to test new and existing compounds for their ability to inhibit fungal growth.

SUMMARY

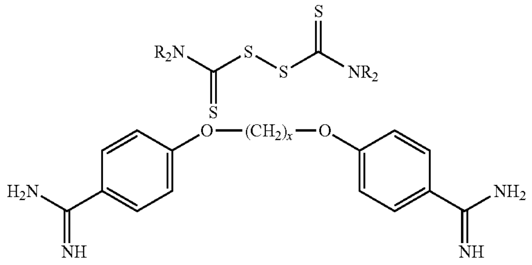
While vegetative fungi are similar metabolically and biochemically to other eukaryotic cells, fungi also sporulate and germinate. Thus, chemical inhibitors of fungal germination are potentially highly useful compounds in antifungal compositions (i.e., human and veterinary pharmaceuticals, topical and systemic pharmaceuticals, and agricultural and industrial fungicides). Thus, disclosed herein is a fluorescence-based quantitative germination assay suitable for high throughput screening. Using the subject germination assay, a screening of a 75,000-compound library yielded 108 germination-inhibiting compounds. Some of these compounds exhibited specific activity to inhibit germination of *Cryptococcus* spores (as contrasted to inhibiting vegetative cell growth). This indicates that germination itself is an effective target in developing antifungal drugs for prophylactic use in at-risk patients.

Thus, disclosed hererin is a method of testing compounds for activity to inhibit germination of spores. The method comprises providing bacterial, fungal, or plant spores transformed to contain and express a detectable marker, wherein the marker is operationally linked to a spore-specific or yeast-specific protein, in a medium and under environmental conditions in which the spores will germinate, and measuring a first signal output generated by the marker prior to the spores initiating germination. The spores are then contacted with a compound whose activity to inhibit germination of spores is to be measured. The spores are then incubated under environmental conditions and for a time wherein spores not treated with the compound will germinate. The extent of germination of the spores is determined by measuring a second signal output generated by the marker, wherein a difference between the first signal output and the second signal output is proportional to the extent of germination of the spores.

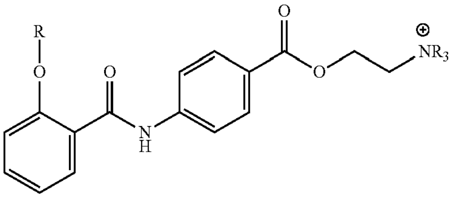
In certain versions of the method, the marker is operationally linked to a spore-specific protein selected from the group consisting of XP_567740.1 (SEQ. ID. NO: 2), XP_566791.1 (SEQ. ID. NO: 4), XP_570303.1 (SEQ. ID. NO: 6), XP_571089.1 (SEQ. ID. NO: 8), XP_571997.1 (SEQ. ID. NO: 10), XP_569295.1 (SEQ. ID. NO: 12), XP_569173.1 (SEQ. ID. NO: 14), XP_569068.1 (SEQ. ID. NO: 16), XP_569336.1 (SEQ. ID. NO: 18), XP_567136.1 (SEQ. ID. NO: 20), XP_568990.1 (SEQ. ID. NO: 22), XP_570610.1 (SEQ. ID. NO: 24), XP_571921.1 (SEQ. ID. NO: 26), XP_572925.1 (SEQ. ID. NO: 28), XP_570796.1 (SEQ. ID. NO: 30), XP_571548.1 (SEQ. ID. NO: 32), XP_570447.1 (SEQ. ID. NO: 34), and XP_571343.1 (SEQ. ID. NO: 36).

Another version of the method comprises the steps described previously, and further comprising plotting the area and aspect ratio of the spores and any germinated cells after the incubation of step (c). Because spores tend to be smaller and have a more oblong aspect ratio than do germinated, vegetative cells, the extent of germination can be determined by measuring the distribution of the cells' area versus aspect ratio. Again, in this version of the method, the marker, if present, is operationally linked to a spore-specific protein selected from the group consisting of XP_567740.1 (SEQ. ID. NO: 2), XP_566791.1 (SEQ. ID. NO: 4), XP_570303.1 (SEQ. ID. NO: 6), XP_571089.1 (SEQ. ID. NO: 8), XP_571997.1 (SEQ. ID. NO: 10), XP_569295.1 (SEQ. ID. NO: 12), XP_569173.1 (SEQ. ID. NO: 14), XP_569068.1 (SEQ. ID. NO: 16), XP_569336.1 (SEQ. ID. NO: 18), XP_567136.1 (SEQ. ID. NO: 20), XP_568990.1 (SEQ. ID. NO: 22), XP_570610.1 (SEQ. ID. NO: 24), XP_571921.1 (SEQ. ID. NO: 26), XP_572925.1 (SEQ. ID. NO: 28), XP_570796.1 (SEQ. ID. NO: 30), XP_571548.1 (SEQ. ID. NO: 32), XP_570447.1 (SEQ. ID. NO: 34), and XP_571343.1 (SEQ. ID. NO: 36),

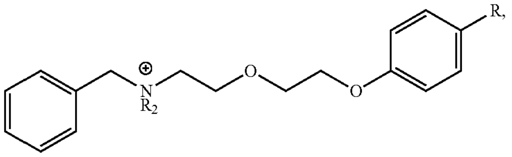
Also disclosed herein are antifungal compositions and method of using them as topical and systemic fungicides for industrial, agricultural, and pharmaceutical uses. Disclosed herein is a composition of matter for inhibiting germination of fungal spores, the composition comprising a spore germination-inhibiting concentration of a compound selected from the group consisting of



-continued

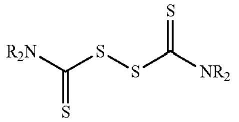


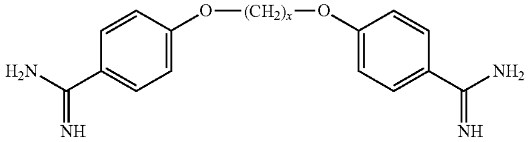
and

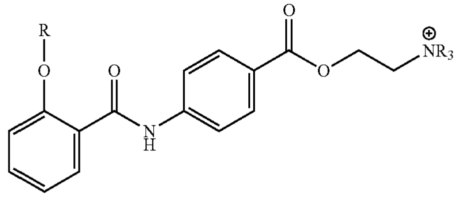


and salts thereof, in combination with a vehicle.

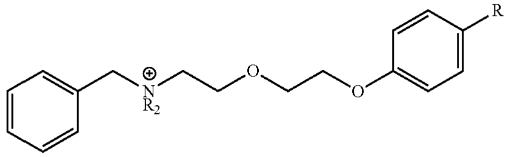
Also disclosed herein is a pharmaceutical composition for inhibiting fungal infection in mammals (as well as the corresponding method of inhibiting topical or systemic fungal infections in mammals, including humans), the composition comprising a spore germination-inhibiting amount of a compound selected from the group consisting of:







and



wherein R is linear or branched C_{1-12} alkyl and "x" is an integer of from 1 to 12, and salts thereof, in combination with a pharmaceutically suitable vehicle.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. **1** is a graph showing that *C. neoformans* var. grubii spores are pathogenic in a murine model of cryptococcosis. Groups of eight AJ/Cr mice were infected with *C. neoformans* var. grubii spores (10^5) or yeast (10^5) via intranasal inhalation. See Giles et al. *Infect. Immun.* 2009, 77(8):3491. Time post-infection (in days) is shown in the X-axis; percent of surviving mice is shown on the Y-axis.

FIG. **2**A is a series of scanning electron micrographs showing morphological transitions during germination. The germinating spore is false-colored green; the emerging yeast wall is false-colored yellow, and the resulting daughter cell is false-colored orange. Bar=1 μm for 0, 4, and 8 Hr; bar=2 μm for 12 Hr.

FIG. **2**B is a series of micrographs analogous to those in FIG. **2**A using transmission electron microscopy rather than scanning electron microscopy. Bars=500 nm.

FIG. **3**A is a schematic diagram of a screening assay for an uninhibited germination reporter strain as it undergoes germination (left-hand panel) and graphs depicting germination as reported by NanoLuciferase (NL) activity (top right, NanoLuc®-brand luciferace, Promega Corporation, Madison, Wis.), and as measured by optical density (OD) (bottom right). The schematic pictures below show the morphology and number of cells over time. This example depicts a yeast-specific protein.

FIG. **3**B is a schematic diagram showing the workflow for the screening assay.

FIG. **3**C shows representative plates from the screening assay described in FIGS. **3**A and **3**B, showing wells that contain germination-inhibiting compounds in red.

FIG. **3**D is a schematic diagram of the transformation construct containing a marker, in this case a gene encoding luciferase ("Nano-Luc").

FIG. **4** is a flow chart showing the workflow of a high-throughput screening assay according to the present disclosure.

FIG. **5**A shows schematic views of a microliter-scale well device and how it operates. The microfluidic device includes an input port connected to a culture well connected to an output port. Each microfluidic chamber is built upon a transparent support, such as a glass microscope slide. The microfluidic device is dimensioned and configured to culture and image non-adherent cells, such as spores and germinated fungi, yeast, and the like. The top panel of FIG. **5**A shows a perspective view of a single microfluidic culturing device. The middle panel of FIG. **5**A shows six (6) such devices disposed on a glass slide. Each of the six devices shown is filled with 10 μL of blue dye. The bottom panel of FIG. **5**A shows a front elevation cutaway of the device shown in the top panel.

FIG. **5**B depicts representative raw images of the fungal cells (spores and germinated cells) in the device shown in FIG. **5**A. Image processing steps are then applied to the raw images to discriminate between spores and germinated cells. These process steps may include, without limitation, applying a density threshold to the raw images and then automatically detecting and measuring the cells 2-D area and aspect ratio.

FIG. **6** depicts how photos of germinating spores in the micro-device depicted in FIG. **5**A were analyzed for the size and shape of the cells and the aspect ratio calculated. This was done using modified algorithms of ImageJ, a public domain, open-source, Java-based image processing program, which was developed originally by Wayne Rasband at the Research Services Branch of the National Institutes of Health. ImageJ can be downloaded free of charge at https://imagej.nih.gov/ij/download.html. The images of the cells are then plotted based on their 2-D area (X-axis) versus their aspect ratio (Y-axis) as shown in the right-hand panels of FIG. **6**. Spores, because they are more oblong and smaller in area, plot to the bottom left-hand side of the histogram; germinated cells, because they are more spherical and larger in area, plot to the upper right quadrant of the plots.

FIG. **7**A depicts a series of photographic analyses showing that germination in microscale devices as described herein can be determined by cell area versus aspect ratio.

Thus, each panel in FIG. **7**A depicts the germination dynamics of spores visualized by 2D histograms of cell area vs. aspect ratio. Data are also shown as a stacked bar plot of the population composition over time (at lower right). Colors are normalized on each plot such that yellow represents the area and aspect ratio combination with the most cells observed and dark blue represents area and aspect ratio combinations that were not observed. Cells in the lower left quadrant are defined as spores; cells in the upper right quadrant as yeast; all remaining cells are classified as intermediates.

FIG. **7**B shows 2D histograms as in FIG. **7**A, but for a 16-hour germination of *Cryptococcus* spores using PBS as a control (no germination), synthetic dextrose growth medium (SD) alone (full germination in the absence of compounds), and fluconazole (16 mg/mL) in the presence of growth medium.

FIGS. **8**A and **8**B show that pentamidine treatment lowers fungal burden in mouse lung. FIG. **8**A is a graph showing lung colony-forming units quantified for each mouse infected with JEC20×JEC21 yeast. The test group of mice were treated with 4 mg/kg/day pentamidine; the control group of mice were treated with 1×PBS; $^*p<0.05$ for two-tailed paired t-test.

FIG. **8**B is a graph depicting lung colony-forming units quantified for each mouse infected with JEC20×JEC21. Again, the test mice were treated with 4 mg/kg/day pentamidine; the control mice were given 1×PBS; $^{**}p<0.01$ for two-tailed paired t-test.

FIG. **9** is a graph showing that pentamidine prophylactically inhibits fungal spore germination in vivo. FIG. **9** depicts lung colony-forming units quantified for each mouse infected with JEC20×JEC21 spores. The test group of mice were treated with 4 mg/kg/day pentamidine; the control group of mice were treated with 1×PBS. $^{**}p<0.01$ for two-tailed paired t-test. See Examples for complete details.

DETAILED DESCRIPTION

Abbreviations and Definitions:

The term "pharmaceutically-suitable salt" refers to any acid or base addition salt whose counter-ions are non-toxic to the patient in pharmaceutical doses of the salts, so that the beneficial inhibitory effects inherent in the free base or free acid are not vitiated by side effects ascribable to the counter-ions. A host of pharmaceutically-suitable salts are well known in the art. For basic active ingredients, all acid addition salts are useful as sources of the free base form even if the particular salt, per se, is desired only as an intermediate product as, for example, when the salt is formed only for purposes of purification, and identification, or when it is used as intermediate in preparing a pharmaceutically-suitable salt by ion exchange procedures. Pharmaceutically-suitable salts include, without limitation, those derived from mineral acids and organic acids, explicitly including hydrohalides, e.g., hydrochlorides and hydrobromides, sulphates, phosphates, nitrates, sulphamates, acetates, citrates, lactates, tartrates, malonates, oxalates, salicylates, propionates, succinates, fumarates, maleates, gentisates, isethionates, di-p-toluoyltartrates, methane sulphonates, ethanesulphonates, benzenesulphonates, p-toluenesulphonates, cyclohexylsulphamates, quinates, and the like. Base addition salts include those derived from alkali or alkaline earth metal bases or conventional organic bases, such as triethylamine, pyridine, piperidine, morpholine, N-methylmorpholine, and the like. See, for example, "Handbook of Pharmaceutical Salts, Properties, Selection, and Use," P. H. Stahl and C. G. Wermuch, Eds., © 2008, Wiley-VCH (Zurich, Switzerland), ISBN: 978-3-90639-058-1.

"Spore-specific molecule" refers to any molecule, moiety, or protein that is highly overrepresented in abundance in spores relative to yeast. Conversely, "Yeast-specific molecule" refers to any molecule, moiety, or protein that is highly overrepresented in abundance in yeast relative to spores. Specifically included in the terms are the proteins identified in Huang M, Hebert A S, Coon J J, Hull C M (2015) "Protein Composition of Infectious Spores Reveals Novel Sexual Development and Germination Factors in *Cryptococcus*, PLoS Genet 11(8): e1005490 (https://doi.org/10.1371/journal.pgen.1005490). These spore-specific proteins were repeatedly identified by mass spectrometry in spore samples and never in yeast samples and are encoded by the following genes:

TABLE 1

Genes encoding spore-specific proteins.

Gene	JEC21 ID	Predicted functions/domains	Deletion phenotype(s)
		Group 1: Replication and Chromosome Biology	
TOP1	CNI03280	topoisomerase1	sporulation defects
IRR1	CNA07890	nuclear cohesion complex component	inviable
		Group 2: Transcription and Splicing	
RSC9	CNB00580	chromatin remodeling complex component	cell fusion defect
DST1	CNF01160	general transcription elongation factor TFIIS	sporulation defect
PRP31	CNB05520	U4/U6-U5 snRNP complex component	inviable
PRP11	CND02290	SF3a splicing factor complex component	inviable
		Group 3: Cellular Transport	
BCH1	CNG02530	specialized cargo export from Golgi	filamentation defect
SFH5	CNE04320	non-classical phosphatidylinositol transfer protein	no phenotype
DDI1	CNC00460	vSNARE binding protein	sporulation defect
EMC3	CNF02470	protein folding in the ER	decreased spore yield
		Group 4: Carbohydrate Metabolism	
GRE202	CNG01830	D-lactaldehyde dehydrogenase	decreased spore yield
ISP1[a]	CNB02490	conserved in fungi/short chain dehydrogenase	filamentation defect

TABLE 1-continued

Genes encoding spore-specific proteins.

Gene	JEC21 ID	Predicted functions/domains	Deletion phenotype(s)
ISP3	CND04560	conserved in fungi/mannose-6-phosphate isomerase	no phenotype
ISP4	CNK01510	conserved in fungi/glycosyl hydrolase	no phenotype
		Group 5: Proteins of Unknown Function	
ISP2	CNE01730	*Cryptococcus*-specific/no conserved domains	increased sporulation; slow germination
ISP5	CNB04980	conserved in fungi/ferritin-like superfamily domain	no phenotype
ISP6	CNA04360	*Cryptococcus*-specific/transmembrane domain	no phenotype
ISP7	CND00650	*Cryptococcus*-specific/no conserved domains	no phenotype

[a]Genes encoding proteins with no obvious homologs were named ISP for identified Spore Protein.

dDoi: 10.1371/journal.pgen. 1005490.t003

The spore-specific genes and proteins identified in the above table have the nucleotide and amino acid sequences and protein ID's shown in the Sequence Listing at SEQ. ID. NOS 1-36.

Yeast-specific proteins include, but are not limited to, CND06170, XP_570090.1 (SEQ. ID. NOS. 37 and 38); CND01050, XP_570422.1 (SEQ. ID. NOS. 39 and 40); CNH01340, XP_572322.1 (SEQ. ID. NOS. 41 and 42); CNN02360, XP_568723.1 (SEQ. ID. NOS. 43 and 44); CNB01440, XP_568816.1 (SEQ. ID. NOS. 45 and 46); CNG00410, XP_571739.1 (SEQ. ID. NOS. 47 and 48); CNH02740, XP_572447.1 (SEQ. ID. NOS. 49 and 50); CNJ01750, XP_567350.1 (SEQ. ID. NOS. 51 and 52); CNI02030, XP_572658.1 (SEQ. ID. NOS. 53 and 54); CNB05750, XP_569316.1 (SEQ. ID. NOS. 55 and 56); CNI03560, XP_572607.1 (SEQ. ID. NOS. 57 and 58); CNK01820, XP_567661.1 (SEQ. ID. NOS. 59 and 60); CNI00900, XP_572819.1 (SEQ. ID. NOS. 61 and 62); CNK02880, XP_567883.1 (SEQ. ID. NOS. 63 and 64); CNF00610, XP_571239.1 (SEQ. ID. NOS. 65 and 66); and CNI00870, XP_572850.1 (SEQ. ID. NOS. 66 and 67). These yeast-specific proteins, which are shown in the Sequence Listing, can be utilized as markers of germination.

The gene and encoded protein encoded by CNK01510 (SEQ. ID. NOS. 1 and 2, respectively) is the preferred spore-specific molecule to be labeled in accordance with the assay disclosed herein.

The terms "label," "marker," "probe," "reporter," and "tag" are used interchangeable and mean a molecular moiety or probe of any structure or configuration, that can be detected by any means, now known or developed in the future, by which a vegetative cell, spore, or molecule bearing such a "label," "marker," "probe," "reporter," or "tag" can be distinguished from cells, spores, or molecules not bearing such a "label," "marker," "probe," "reporter," or "tag." The terms include, without limitation, radioactive labels, fluorescent labels, chromophoric labels, affinity-based labels (such as antibody-type markers), chemiluminescent labels, and the like. Conventional radioactive isotopes used for detection include, without limitation, ^{32}P, ^{2}H and many others. A huge number of fluorescent and chromophoric probes are known in the art and commercially available from numerous worldwide suppliers, including Life Technologies (Carlsbad, Calif., USA), Enzo Life Sciences (Farmingdale, N.Y., USA), and Sigma-Aldrich (St. Louis, Mo., USA). Luciferase is the preferred marker. Complete kits for accomplishing luciferase labeling to a desired substrate are commercially available from several suppliers, including Promega Corporation, Madison, Wis. (e.g., Promega's NanoLuc®-brand vectors and NanoGlo®-brand luciferase assay systems).

The term "operationally linked" or "operationally connected" when referring to joined polynucleotide sequences denotes that the sequences are in the same reading frame and upstream regulatory sequences will perform as such in relation to downstream structural sequences. Polynucleotide sequences which are operationally linked are not necessarily physically linked directly to one another but may be separated by intervening nucleotides which do not interfere with the operational relationship of the linked sequences. Similarly, when referring to joined polypeptide sequences, operationally linked means that the functionality of the individual joined segments are substantially identical as compared to their functionality prior to being operationally linked. For example, a fluorescent protein or chemiluminescent protein can be fused to a polypeptide of interest and in the fused state retain its fluorescence or chemiluminscence, while the fused polypeptide of interest also retains its original biological activity.

All strains used in the working examples were of the serotype D background (*Cryptococcus neoformans* var. *neoformans* strains JEC20 (ATCC 96909) and JEC21 (ATCC 96910 and ATCC MYA-565). See Kwon-Chung K J, Edman J C, Wickes B L (1992) "Genetic association of mating types and virulence in *Cryptococcus neoformans,*" *Infect Immun.* 60:602-605 (pmid:1730495) and Moore T D, Edman J C (1993) "The alpha-mating type locus of *Cryptococcus neoformans* contains a peptide pheromone gene," *Mol Cell Biol.* 13:1962-1970 (pmid:8441425). All were handled using standard techniques and media as described in Sherman F. (2002) "Getting started with yeast," *Methods Enzymol.* 350:3-41(pmid:12073320) and Alspaugh J A, Perfect J R, Heitman J. (1998) "Signal transduction pathways regulating differentiation and pathogenicity of *Cryptococcus neoformans,*" *Fungal Genet Biol.* 25:1-14 (pmid:9806801).

Numerical ranges as used herein are intended to include every number and subset of numbers contained within that range, whether specifically disclosed or not. Further, these numerical ranges should be construed as providing support for a claim directed to any number or subset of numbers in that range. For example, a disclosure of from 1 to 10 should be construed as supporting a range of from 2 to 8, from 3 to 7, from 1 to 9, from 3.6 to 4.6, from 3.5 to 9.9, and so forth.

All references to singular characteristics or limitations of the present invention shall include the corresponding plural characteristic or limitation, and vice-versa, unless otherwise specified or clearly implied to the contrary by the context in which the reference is made. The indefinite articles “a” and “an” mean “one or more” unless explicitly stated otherwise.

All combinations of method or process steps as used herein can be performed in any order, unless otherwise specified or clearly implied to the contrary by the context in which the referenced combination is made.

The methods disclosed herein can comprise, consist of, or consist essentially of the essential elements and limitations of the method described, as well as any additional or optional ingredients, components, or limitations described herein or otherwise useful in microbiology, biochemistry, and/or mycology.

The Method:

At the core of the present invention is the realization that targeting a cellular process that is specific to organisms that sporulate—namely, spore germination—is likely to yield highly effective antifungal compositions that exhibit fewer side-effects than conventional antifungal drugs when used in humans. (Organisms that produce spores include fungi, bacteria, protists, plant seeds, ferns, and the like.) What then is needed then is a high-throughput assay that can evaluate compounds for their ability to inhibit fungal spore germination. As shown in FIG. **1**, it is known that spores are infectious agents. FIG. **1** is a graph showing survivability in a widely accepted mouse model of cryptococcosis. See Giles et al. *Infect. Immun.* 2009, 77(8):3491. Here, mice were infected with spores or yeast of *C. neoformans* var. grubii. Spores (10^5) or yeast (10^5) were administered to the test animals via intranasal inhalation. Mice infected with spores are shown in black circles; mice infected with yeast are shown in white circles. As can be seen in FIG. **1**, the mice died at virtually identical rates. In other words, *Cryptococcus* spores are just as virulent as the yeast form.

The method functions on two principles. The first principle is that the vegetative form of organisms, especially fungi, are very different, morphologically than their corresponding spores. This is shown quite convincingly in FIGS. **2**A and **2**B. FIG. **2**A is a series of scanning electron micrographs showing the morphological transitions that take place during germination of *C. neoformans* spores. A *C. neoformans* spore is shown in the far left photo. The germinating spore is false-colored green. The emerging yeast wall is false-colored yellow. This can been seen initially in the photo second from the left and then in a much more pronounced fashion in the third photo of the series. The daughter cell is false-colored orange and is seen clearly in the far right photo. A simple visual comparison between the far left and far right photos in FIG. **2**A illustrates the significant morphological differences between a spore of *C. neoformans* (on the left) and a yeast (vegetative form, on the right). As can be seen from FIG. **2**A, the spore is roughly cylindrical and clearly has a major axis that is much longer than its minor axis. The vegetative yeast form, in contrast is more nearly spherical or globular. Its major and minor axes are much closer in physical length. FIG. **2**B shows the same phenomenon using using transmission electron microscopy rather than scanning electron microscopy. Spores are quantitatively smaller and more oblong than yeast.

The second principle is that the inventors have identified 18 proteins that are expressed at far greater levels in the spore form as contrasted to the yeast form. Thus, by affixing a marker to one or more of these spore-specific proteins, the extent of germination can be tracked by following changes in the signal generated by the marker as the spore-specific protein is degraded during the germination process.

The first step of the method is to provide bacterial, fungal, or plant spores transformed to contain and express a detectable marker, wherein the marker is operationally linked to a spore-specific or a yeast-specific protein. The marker is preferably a protein fluorophore or protein chemiluminescent marker, such as luciferase, fluorescent protein A, green fluorescent protein, etc. The marker protein is incorporated into spores or yeast by fusing the gene encoding the marker protein to a spore-specific or yeast-specific target gene. The spore then produces the spore-specific protein with the marker attached. (Or the yeast then produces the yeast-specific protein with the marker attached.) The marker will thus generate a first signal associated with the spores. That first signal remains unchanged for as long as the spores remain intact. However, when the spore germinates, the spore-specific protein and its attached marker are degraded, which then alters the signal generated by the attached marker (or the yeast-specific marker is increased). A second signal measurement taken after germination is thus proportional to the extent of germination.

This process is shown schematically in FIG. **3**A. As shown in the left-hand side of the figure, the yeast form of the organism (in this case *C. neoformans*) was transformed to contain a fusion construct comprising a spore-specific protein fused to a luciferase gene. The transformed yeast were cultured to yield a population of propogating yeast that include the fusion construct. The yeast were then induced to sporulate. A first measure of the signal generated by the luciferase marker generated by the fusion construct is taken. This is shown at Time=0 in the two right-hand graphs depicted in FIG. **3**A. The upper graph show the signal generated by the reporter as the spore germinate. The lower graph shows the optical density of the culture solution at 600 nm (OD_{600}) over the same time period. As can be seen from the two graphs, as the spore germinate and multiply, the optical density increases (as the number of cells increases). In a corresponding fashion, the signal generated by the marker displays a proportional rise. The schematic pictures below show the morphology and number of cells over time.

The assay can be implemented in a massively redundant, massively high-throughput format that is easily automated using conventional multiwall plates and robotic equipment. (Laboratory robotics for handling multiwall culture plates are available from a host of international commercial suppliers, including Agilent Technologies (Santa Clara, Calif.), Beckman Coulter (Grants Pass, Oreg.), Hudson Robotics (Springfield, N.J.), and many others.) For a non-limiting example, see FIG. **3**B, which is a schematic diagram showing the workflow for a high-throughput screening assay according to the present disclosure. As shown in FIG. **3**B, the method can be implemented using conventional 384-well incubation plates. Spores to be studied are modified to contain a suitable marker, as described earlier. The spores are then incubated in a multiwall plate in a suitable germination medium. For many fungi, yeast extract-peptone-dextrose growth medium (YPD or YEPD) is suitable. (YPD is a well known medium for fungal germination and contains roughly 2% w/v bacto-peptone, 1% w/v yeast extract, and 2% w/v dextrose. A 1 L batch is made by combining 20 g bacto-peptone, 10 g yeast extract, and 20 g dextrose, adding water to 1 L and then autoclaving before use.)

A first signal from each well of the multiwall plate is then taken at the start of the incubation period. The contents of each well can be arranged in any suitably logical fashion, with positive and negative control wells, and wells containing compounds to be tested for their ability to inhibit germination of the spores, perhaps in appropriate serial dilutions of the compounds. The entire multiwall plate is then cultured for a time, temperature, humidity, etc. that is conducive to germination of the spores. After a set time, and OD600 measurement may optionally be taken to confirm that in the control wells the spores responded appropriately. The cells are then lysed, luciferase substrate is added, and a second measurement of the signal generated by the marker is taken. The extent of germination can then be determined by comparing the first signal to the second.

FIG. **3**C shows a representative multiwall plate from the resulting from the method just described. Positve and negative control wells are in columns 23 and 24, respectively. Wells that contain germination-inhibiting compounds in various shades of pink/red, with the darker red hues indicating great inhibitory activity. The signals can be gathered, digitized, recorded, and compared using a photomultiplier tube, in conventional fashion. Thus, wells H11, K11, C15, M16, and C21 all appear to contain very effective germination-inhibiting compounds.

FIG. **3**D shows a schematic diagram of a vector used to transform a spore so that it includes a marker responsive to germination

An exemplary protocol, using luciferase as the marker, can be accomplished using commercial kits and largely following the manufacture's instructions on how to use the kit. A preferred kit for is Promega's Nano-Luc®-brand vectors and Nano-Glo®-brand luciferase assay system.

Briefly, homologous recombination is utilized to tag spore proteins with luciferase under their endogenous promoters. See FIG. **3**D. In this fashion, their expression levels in the spores will remain undisturbed by tagging. As illustrated in FIG. **3**D, the transformation construct contains three parts (A, B, and, C). Part A includes the sequence that encodes ISP4 but without a stop codon. Part B includes NanoLuc sequence (GeneBank sequence number KM359770) and *C. neoformans* URAS gene (GenBank sequence number AE017347.1), the latter of which serves as a selection marker for cell transformation. Part C includes the 3' UTR of ISP4, so that together with Part A, the transformation construct will be more favorably integrated into the genome through homologous recombination. Individual parts were generated by regular PCR and the full-length transformation construct was created using fusion PCR. See Davidson R C, Blankenship J R, Kraus P R, de J Berrios M, Hull C M, D'Souza C, et al. A PCR-based strategy to generate integrative targeting alleles with large regions of homology. *Microbiology.* 2002; 148: 2607-2615. PMID: 12177355. The construct was transformed into cells by biolistic transformation before selection. See Toffaletti D L, Rude T H, Johnston S A, Durack D T, Perfect J R. Gene transfer in *Cryptococcus neoformans* by use of biolistic delivery of DNA. *J Bacteriol.* 1993; 175: 1405-1411. PMID: 8444802.

The present inventors have identified a signicant number of proteins in *C. neoformans* that were detected in spores only. Thus, these proteins are all candidates for labelling in the present invention. In *C. neoformans* and in other fungi where the correspnding genes are conserved, one or more of the following proteins can be labelled with the marker: XP_567740.1 (SEQ. ID. NO: 2), XP_566791.1 (SEQ. ID. NO: 4), XP_570303.1 (SEQ. ID. NO: 6), XP_571089.1 (SEQ. ID. NO: 8), XP_571997.1 (SEQ. ID. NO: 10), XP_569295.1 (SEQ. ID. NO: 12), XP_569173.1 (SEQ. ID. NO: 14), XP_569068.1 (SEQ. ID. NO: 16), XP_569336.1 (SEQ. ID. NO: 18), XP_567136.1 (SEQ. ID. NO: 20), XP_568990.1 (SEQ. ID. NO: 22), XP_570610.1 (SEQ. ID. NO: 24), XP_571921.1 (SEQ. ID. NO: 26), XP_572925.1 (SEQ. ID. NO: 28), XP_570796.1 (SEQ. ID. NO: 30), XP_571548.1 (SEQ. ID. NO: 32), XP_570447.1 (SEQ. ID. NO: 34), XP_571343.1 (SEQ. ID. NO: 36).

FIG. **4** is a flow chart showing the workflow of a high-throughput screening assay according to the present disclosure. Here, the figure shows how a large library of 75,000 compounds was screened using the present method set up in high-throughput format. As shown on the left-hand side of the figure, the full library was first subjected to a primary screening comprising a 10-hour germination, followed by evaluating which compounds showed initial interested as germination inhibitors. This yielded 2,100 putative "hits," i.e., compounds that at least initially showed promise as germination inhibitors. These 2,100 hits were then re-screened and the upper 900 best performing inhibitors were tested further. These 900 compounds were then re-screened using longer germination and yeast growth incubation times. This resulted in 270 compounds being advanced for further study. This group of 270 compounds was then studied using the method described herein to determine if any of the compounds inhibited spore germation and/or fungal growth in a dose-dependent fashion. This final screen yielded 108 compounds from the original 75,000 compounds that inhibited fungal spore germination and/or yeast grown in a dose-depedent fashion.

As shown in the middle panel of FIG. **4**, the 108 compounds that were "hits" were then clustered by structural similarity and further tested to see if their anti-fungal properties were germination specific (i.e., primarily germination inhibitory), non-specific, or primarily growth specific. As shown in the right-hand graphs of FIG. **4**, 37 of the compounds specifically inhibited germination in a dose-dependent manner; 52 of the compounds were non-specific, dose-dependent inhibitors; and 19 of the compounds specifically inhibited vegetative fungal growh in a dose-dependent manner.

As shown in FIGS. **5**A and **5**B, the method described herein can also be formatted for continuous studies using a microfluidic test bed. The test bed, depicted schematically in FIG. **5**A, comprises a microliter-scale culture well having an input port and an output port. That is, the device includes an input port operationally linked in fluid connection to to a culture well which is operationally linked in fluid connection to an output port. Each microfluidic chamber is built upon a transparent support, such as a glass microscope slide. The microfluidic device is dimensioned and configured to culture and image non-adherent cells, such as spores and germinated fungi, yeast, and the like. The top panel of FIG. **5**A shows a perspective view of a single microfluidic culturing device. The middle panel of FIG. **5**A shows six (6) such devices disposed on a glass slide. These six devices held 10 μL blue dye. The bottom panel of FIG. **5**A shows a front elevation cutaway of the device shown in the top panel. In this bottom panel, fluid flow is depicted as moving from left-to-right. Non-adherent cells are retained within the culture well, while the medium gently flows above them. Compounds to be tested are introduced through the input port, where they then flow to the culture well to interact with the cells therein. When built on an optically transparent substrate, the cells can be visualized and photographed in real time, as shown in the photos in FIG. **5**B.

FIG. **5**B depicts representative raw images of the fungal cells (spores, germinating cells, and yeast) in the device shown in FIG. **5**A. Various imaging processing steps, described in detail below, are then applied to the raw images to discriminate among spores, germinating cells, and yeast. These process steps may include, without limitation, applying a density threshold to the raw images and then automatically detecting and measuring the cells' 2-D area and aspect ratio.

FIG. **6** shows how computer processing can be brought to bear to automatically discriminate between ungerminated spores and vegetative yeast after a culture period has been completed. The left-hand side of FIG. **6** shows the three raw photographs from FIG. **5**B. These are raw photographs of the germinating spores in the microfluidic device showin in FIG. **5**A. The photos are digitized from the outset. The digitized images were analyzed for the size and shape of each cell in each image. The area of each cell, as well as its aspect ratio can be determined using a public domain, open-source, Java-based image processing program called ImageJ. Several other commercial image processing software packages can also accomplish this task. For example, Stream-brand image analysis sotware from Olympus Corporation (Waltham, Mass.) and PAX-it brand image analysis software from MIS, Inc. (Villa Park, Ill.). The images of the cells are then plotted based on their 2-D area (X-axis) versus their aspect ratio (Y-axis) as shown in the right-hand panels of FIG. **6**. As can be seen from the plots in FIG. **6**, the spores (upper plot) cluster in a distinctly different location and with a distinctly different distribution as compared to the vegetative yeast (lower plot). This is because spores, being more oblong and smaller in area, plot to the left-hand side of the histogram—indicating smaller average area and ovoid nature in the photographs. Spores tend to toward a wider distribution of their aspect ratios and areas. This may be due to the fact that the spores settle in the device at many angles. When photographed, spore aspect ratios and sizes are are more variable than in reality. Yeast, because they are more spherical and larger in area regardless of the position from which they are photographed, plot in a tight cluster in the upper right quadrant of the histograms.

Futher examples of how spores, germinating cells, and yeast can be compared is shown in FIGS. **7**A and **7**B. FIG. **7**A depicts a series of photographic analyses further demonstrating that germination in microscale devices as described herein can be determined by cell area versus aspect ratio. Each panel in FIG. **7**A depicts the germination dynamics of spores visualized by 2D histograms of cell area vs aspect ratio, as well as a stacked bar plot of the population composition over time (at lower right). Colors are normalized on each plot such that yellow represents the area and aspect ratio combination with the most cells observed and dark blue represents area and aspect ratio combinations that were not observed. Cells in the lower left quadrant are defined as spores; cells in the upper right quadrant as yeast; all remaining cells are classified as intermediates undergoing germination. FIG. **7**B shows 2D histograms as in FIG. **7**A, but for a 16-hour germination of *Cryptococcus* spores using PBS as a control (no germination), synthetic dextrose growth medium (SD) alone (full germination in the absence of compounds), and the antifungal compound fluconazole (16 mg/mL) in the presence of growth medium. In this study, we demonstrate that spore germination is a viable target for antifungal development by identifying and characterizing FDA approved drugs able to inhibit both spore germination and yeast replication. These inhibitors have the potential of becoming tools to probe the essential fungal process of spore germination, or repurposed into antifungal therapies. Importantly, we determined that one of the drugs, Pentamidine, was effective at lowering fungal burden in vivo and could be repurposed as a prophylactic treatment against *Cryptococcus* pathogens.

Germination Provides a Suitable Target for the Development of Novel Antifungals:

Limited therapies exist to combat fungal disease. Humans and fungi share many biological processes due to their eukaryotic nature. Because fungi-specific drug targets are difficult to find, potent antifungal agents often have toxic side-effects in humans. In the quest to find novel fungal-specific targets, the field has mainly focused on the cell membrane processes (ergosterol biosynthesis), and the fungal cell wall (β(1,3)-glucan synthesis). While these targets have been effective in the discovery of antifungals in the past; the lack of novel antifungal therapies is an indication that these targets currently have limited success. It is critical that novel fungi-specific targets are identified for the development of new antifungals. This requires identifying new cell processes to probe that are unique to fungi. Fungal spore germination provides one of these novel targets.

Fungal spore germination has been previously suggested to be a modified cell cycle. Recently discovered evidence suggests otherwise. In previous studies we identified and characterized spore-enriched proteins. One of these proteins (Isp2) was found to stall germination for two hours prior to initiating vegetative growth. Isp2 showed no apparent phenotype in vegetatively growing yeast. Isp2, along with other spore germination-specific results, indicate that it is unlikely that germination is simply a modified cell cycle. Spore germination in not only a unique fungal process but is also unlike any process defined in humans. The uniqueness of fungal spore germination makes it a prime process to probe in the effort to develop novel antifungals. The examples below show that using germination inhibition as a signal can identify drugs that could be repurposed in the treatment of invasive fungal diseases.

Targeting Hermination Provides a Mechanism for Prevention:

In addition to providing a fungal-specific drug targets, targeting germination provides a unique opportunity for preventing fungal disease. Spores are stress-resistant cell types that are known infectious particles of many fungal pathogens, and have distinct phenotypes compared to yeast when interacting with hosts. Developing antifungals that target all potential infectious particles could be used to protect against fungal pathogens through prophylaxis treatment. If a low toxicity antifungal is found, prophylactic treatment could be administered to immunocompromised individuals, the population most at risk of developing invasive fungal infections.

Screening Characterized Drugs Allows for the Potential Development of Tools:

The screening of already approved FDA drugs provides a unique opportunity to screen drugs that often have known targets. By screening compounds with known inhibition targets, pathways can be identified that could be potentially important to fungal spore germination. These compounds can be used to probe fungal spore germination to help understand this critical fungal differentiation process. One of the clearest examples of a potential tool in this study was alexidine hydrochloride, which had strong antifungal activity and was a potent inhibitor of fungal spore germination. See the Examples section. This drug has previously been reported to inhibit phospholipases of *Cryptococcus* (Ganendren et al., 2004). This may suggest that phospholipases are important for viability of fungal spores. The ability of alexidine to inhibit other fungal processes, however, is unclear. In the future, we will use alexidine as a tool to probe the molecular events of phospholipid biosynthesis in fungal spore germination.

Pentamidine, a Potential Antifungal Prophylactic Against *Cryptococcus* Infection:

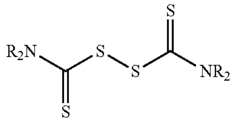
Screening FDA-approved drugs has the benefit of potential repurposing as these drugs could reach patients in need sooner than novel compounds. The Examples section shows that pentamidine has huge promise in repurposing for a variety of reasons. Pentamidine, an antiparasitic, is only approved for use against one fungal pathogen, Pneumocystis. Pentamidine is approved for use in immunocompromised individuals, which is the primary group of individuals infected by *Cryptococcus* pathogens. Pentamidine already exists in an aerosolized formulation which allows for the drug to build up in the lung, which is the main site where *Cryptococcus* pathogens establish infections. Finally, this drug is already approved for use prophylactically against Pneumocystis, which would suggest that pentamidine could be used to protect immunocompromised individuals from cryptococcosis.

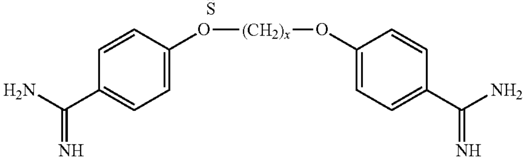
The Examples section shows that pentamidine was able to inhibit *Cryptococcus* infectious particles in vitro, was effective at lowering fungal burden in a mouse model of infection and, when used prophylactically, was able to inhibit spore germination in vivo, suggesting that pentamidine can build up in the lung sufficiently to inhibit this stress resistant cell type. The ability to inhibit both cell types, and the nature of this drug, suggest that it could make an ideal prophylactic against *Cryptococcus* pathogens which cause hundreds of thousands of deaths per year in immunocompromised individuals. While pentamidine is often not the first choice for prophylaxis against Pneumocystis, the data presented herein shows that pentamidine can be used to protect patients against other fungal pathogens generally and *Cryptococcus*. spp. specifically.

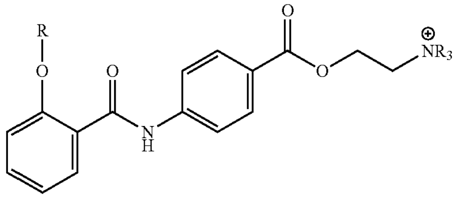
Pharmaceutical Compositions:

Using the method disclosed herein, the inventors identified four (4) FDA-approved compounds with germination-inhibiting properties that are effective antifungal therapeutics. These four compounds are disulfiram, pentamidine, otilonium bromide, and benzethonium chloride.

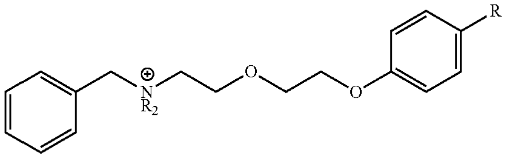
Thus, also disclosed herein are pharmaceutical compositions for inhibiting topical and systemic fungal infection in mammals. The compositions comprise a spore germination-inhibiting amount of a compound selected from the group consisting of:







and



wherein R is linear or branched C_{1-12} alkyl and "x" is an integer of from 1 to 12, and pharmaceutically suitable salts thereof, in combination with a pharmaceutically suitable vehicle.

The active ingredients may be used in combination with a standard, well-known, non-toxic pharmaceutically suitable carrier, adjuvant or vehicle such as, for example, phosphate buffered saline, water, ethanol, polyols, vegetable oils, a wetting agent or an emulsion such as a water/oil emulsion. The composition may be in either a liquid, solid or semi-solid form. For example, the composition may be in the form of a tablet, capsule, ingestible liquid or powder, injectible, suppository, or topical ointment or cream. Proper fluidity can be maintained, for example, by maintaining appropriate particle size in the case of dispersions and by the use of surfactants. It may also be desirable to include isotonic agents, for example, sugars, sodium chloride, and the like. Besides such inert diluents, the composition may also include adjuvants, such as wetting agents, emulsifying and suspending agents, sweetening agents, flavoring agents, perfuming agents, and the like.

Suspensions, in addition to the active compounds, may comprise suspending agents such as, for example, ethoxylated isostearyl alcohols, polyoxyethylene sorbitol and sorbitan esters, microcrystalline cellulose, aluminum metahydroxide, bentonite, agar-agar and tragacanth or mixtures of these substances.

Solid dosage forms such as tablets and capsules can be prepared using techniques well known in the art of pharmacy. For example, compounds as described herein can be tableted with conventional tablet bases such as lactose, sucrose, and cornstarch in combination with binders such as acacia, cornstarch or gelatin, disintegrating agents such as potato starch or alginic acid, and a lubricant such as stearic acid or magnesium stearate. Capsules can be prepared by incorporating these excipients into a gelatin capsule along with antioxidants and the relevant active agent.

For intravenous administration, the compounds may be incorporated into commercial formulations such as Intralipid©-brand fat emulsions for intravenous injection. ("Intralipid" is a registered trademark of Fresenius Kabi AB, Uppsalla, Sweden.) Where desired, the individual components of the formulations may be provided individually, in kit form, for single or multiple use. A typical intravenous dosage of a representative compound as described herein is from about 0.1 mg to 100 mg daily and is preferably from 0.5 mg to 3.0 mg daily. Dosages above and below these stated ranges are specifically within the scope of the claims.

Possible routes of administration of the pharmaceutical compositions include, for example, enteral (e.g., oral and rectal) and parenteral. For example, a liquid preparation may be administered, for example, orally or rectally. Additionally, a homogenous mixture can be completely dispersed in water, admixed under sterile conditions with physiologically acceptable diluents, preservatives, buffers or propellants in order to form a spray or inhalant. The route of administration will, of course, depend upon the desired effect and the medical state of the subject being treated. The dosage of the composition to be administered to the patient may be determined by one of ordinary skill in the art and depends upon various factors such as weight of the patient, age of the patient, immune status of the patient, etc., and is ultimately at the discretion of the medical professional administering the treatment.

With respect to form, the composition may be, for example, a solution, a dispersion, a suspension, an emulsion or a sterile powder which is then reconstituted. The composition may be administered in a single daily dose or multiple doses.

The present disclosure also includes treating fungal infections (topical and systemic) in mammals, including humans, by administering a spore germination-inhibiting amount of one or more compounds described herein. In particular, the compositions of the present invention may be used to treat fungal infections of any and all description.

The above-described pharmaceutical compositions may be utilized in connection with non-human animals, both domestic and non-domestic, as well as humans.

EXAMPLES

The following examples are included to provide a more complete description of the methods and compositions disclosed and claimed herein. The examples are not intended to limit the scope of the claims in any fashion.

Strain Manipulation, Media and Spore Isolation:

The following strains were used and handled using standard techniques and media as previously described. (Sherman et al., 1987). *Cryptococcus neoformans* serotype D: JEC20, JEC21, JEC20-GFP, JEC21-GFP (Walsh et al. 2018), serotype A: H99, *Candida albicans*: SC5314 and *Aspergillus fumigatus*: AF293. Spores were isolated from cultures as previously described. (Botts et al., 2009). Briefly, yeast of both mating types (JEC20 and JEC21) were grown on YPD for 2 days at 30° C. combined in phosphate buffered saline (PBS) mixed to a 1:1 ratio and spotted onto V8 pH 7 agar plates. Plates were incubated for 5 days at 25° C. and spots were resuspended in 70% Percoll in 1×PBS. Spores were counted using a hemocytometer.

MIC/MFC Experiments:

All minimum inhibitory concentration (MIC) experiments were based on EUCAST methodology. (European Committee on Antimicrobial Susceptibility Testing, a standards-setting committee of the European Society of Clinical Microbiology and Infectious Diseases; EUCAST Development Laboratory for fungi, Statens Serum Institut, Building 211, Artillerivej 5, DK-2300 Copenhagen, Denmark; www.eucast.org.) Yeast cells were grown overnight in liquid YPD and used to inoculate fresh YPD. After 6-hour incubation, yeast cells were washed in 1×PBS and quantified using a hemocytometer. For each drug, 1.25×10^5 yeast cells were incubated in RPMI, and 0.33M MOPS, pH 7 at varying concentrations of inhibitors, with a final volume of 200 μL. *Cryptococcus neoformans* cells were incubated for 2 days at 30° C. while *Candida albicans* strains were incubated for 2 days at 35° C. OD_{600} readings were used to assess the MIC values for each drug. To determine minimum fungicidal concentrations (MFC) values, 3 μL per well were plated on YPD and allowed to grow for 2 days. Spinning down of 96-well plates and washing did not alter the read outs of the MFC experiment.

For *Aspergillus fumigatus* MIC, conidia were collected using 0.01% Tween 80 in PBS after 3 days of growth on glucose medium media plates. Conidia at a final concentration of 2×10^4 cells were incubated in RPMI, 0.33 M MOPS, and 2% glucose at pH 7 at varying concentrations of inhibitors, with a final volume of 200 μL. MIC values were assessed based on the lowest concentration of drug that had complete absence of germ tubes or hyphae.

Quantitative Germination Assay:

All germination assays are based on Barkal et al., 2016. Briefly, microfluidic devices were loaded with 1×10^5 spores, and at 0 hours, SD media with drug of interest, were added to the sample. Spores were allowed to germinated at 30° C. in a humidified chamber and cells were monitored every two (2) hours for 16 hours. Each assay was performed in two (2) individual wells with three (3) field of views acquired from each well. All images were analyzed as previously described based on cell shape and size. Population ratio of spores, intermediate, and yeast cells were determined. Error bars in plots are based on variation between all fields of view acquired. All experiments were able to be reproduced independently. After the 16-hour experiment, samples were plated on YPD and allowed to grow at 30° C. to determine if drugs were completely germicidal or not based on lack of growth. If assays were unable to be performed in microfluidic devices, the 2×10^5 spores were incubated in identical conditions outside of PDMS devices and only loaded into devices for image acquisition.

Fungal Burden Animal Studies:

All yeast cells were cultured overnight in YPD, washed and diluted to 5×10^6 cells. For JEC20 and JEC21, 2.5×10^6 cells of each were combined. Spores were cultured as previously described and diluted to 2×10^6 cells. All experiments were performed on 8- to 10-week old C57BL/6J (Jackson Laboratory, Bar Harbor, Me., USA) female mice (5 mice per group). All mice were infected intranasally with a total of 50 μL. All dosing was performed with 4 mg/kg/day or 1×PBS for three (3) days either prior to infection or 1-day post-infection. Mice were sacked day-4 post-infection and lungs were collected, processed, and fungal burden was assessed.

In Vivo Germination:

Female mice, 8- to 10-week-old C57BL/6J (Jackson Laboratory) female mice (3 mice per group) were used. Mice were dosed with either 4mg/kg/day or 1×PBS (50 μL) for three (3) consecutive days. Mice were intranasally infected with 2×10^6 JEC20-GFPxJEC21-GFP spores, strains described in Walsh et al., 2018. After 8 hours post-infection, mice were sacked and lavaged with 0.05% TirtonX in 1×PBS. Lavage suspension underwent a series of treatments and washes, in order: red blood cell lysis (ACK lysing buffer, 2 mL, 5 minutes), formaldehyde fixation (4%, 500 μL, 30 minutes) and calcofluor white staining (25 μg/mL, 20 μL for 1 minute). Cells (50-100 per mouse) were imaged, and identified as *Cryptococcus neoformans* cells based on green fluorescent signal or cyan staining from calcofluor staining. Cells surface area and aspect ratio were measured in ImageJ and cells were classified as spores, intermediates, or yeast based on size and shapes parameters used in the quantitative germination assay.

Identifying Inhibitors of Germination and Growth

To identify inhibitors of *Cryptococcus neoformans* spore germination, a high throughput screen was developed that utilizes a nanoluciferase construct to monitor whether spores germinate in the presence of inhibitor. Briefly a protein luciferase construct was created resulting in a low luciferase signal for non-germinated spores and a high signal from germinated and replicating cells. The screen was coupled with OD_{600} readings to monitor the ability of compounds to inhibit yeast replication. The examples focused on FDA-approved drugs, as these drugs have the potential of being repurposed into antifungal therapeutics. To determine whether any FDA-approved drugs were able to inhibit *Cryptococcus neoformans* spore germination and yeast replication, the aforementioned high throughput screen was performed on the L1300 Selleck FDA-Approved Drug Library containing an array of 1108 compounds. This library of compounds is available commercially from Selleck Chemicals, 14408 W Sylvanfield Drive, Houston, Tex. 77014, USA.

The screening was successful at identifying known antifungal drugs as inhibitors of yeast replication as indicated by an OD_{600} signal of less than 75% of the negative control (Table 2). For the purpose of these examples, antifungal drugs were defined as any FDA-approved drug used in the treatment of fungal infections. Of these 23 known antifungal drugs, only six (6) were identified as inhibitors of spore germination, indicated by a luciferase signal of less than 30% of the negative control. These germination inhibitors demonstrated normal nanoluciferase signal dose response curves (data not shown).

TABLE 2

Antifungal drugs used to treat fungal infections and their ability to inhibit *Cryptococcus neoformans* spore germination (based on luciferase signal) and yeast replication (based on OD_{600}).

	Drugs	Germination Percent Luciferase Signal	Replication Percent OD_{600}
Inhibitors of Germination (6) Less than 30% Luciferase Signal	Pentamidine HCl	6.5	38.3
	Bifonazole	13.6	33.4
	Econazole nitrate	16.1	33.1
	Isoconazole nitrate	16.8	37.0
	Tioconazoie	25.0	36.8
	Miconazole nitrate	25.5	38.2
Non-inhibitors of Germination (17)	Butoconazole nitrate	41.5	33.4
	Fenticonazole nitrate	49.1	36.4
	Naftifine HCl	55.5	34.5
	Sulconazole nitrate	57.8	40.9
	Butenafine HCl	57.5	32.9
	Tolnaftate	60.2	47.3
	Liranaftate	64.8	37.6
	Clotrimazole	65.9	34.1
	Fluconazole	84.0	72.2
	Amphotericin B	84.6	45.7
	Amorolfine HCl	88.6	41.4
	Caspofungin acetate	89.7	48.5
	Climbazole	151.5	38.9
	Ketoconazole	154.8	35.4
	Itraconazole	159.6	58.9
	Posaconazole	167.2	46.7
	Voriconazole	173.9	35.8

In addition to the antifungal drugs from the screen, 60 other inhibitors of yeast replication were identified, 16 of which were also inhibitors of spore germination (Table 3). These inhibitors have a wide range of clinical functions, including quaternary ammonium compounds ("QACs") and mammalian target of rapamycin ("mTOR" inhibitors (i.e.,) which are known to have broad effects on eukaryotic processes. Some drugs used in treating neurological diseases were also identified. Finally, antimicrobial and antihelminth drugs were also identified to inhibit germination. All compounds, with the exception of doxercalciferol, demonstrated appropriate nanoluciferase dose response curves (data not shown). Only a handful of compounds were pursued further in the examples due to limited availability of certain drugs. Representatives from each group, however, were selected for further characterization. Finally, five inhibitors of only germination were identified (see below).

TABLE 3

FDA-approved drugs able to inhibit spore germination and yeast replication. List of drugs, their ability to inhibit *Cryptococcus neoformans* spore germination (based on luciferase signal) and yeast replication (based on OD600), as well as their function as listed by L1300 Selleck FDA Approved Drug Library.

		Germination Percent Luciferase Signal	Replication Percent OD_{600}	Function
Germination and Growth Inhibitors	Cetylpyridinium chloride	4.2	31.9	Infection
	Domiphen bromide	4.4	63.9	Infection
	Cetrimonium bromide	4.4	63.2	Infection
	Alexidine Hcl	4.6	29.6	
	Otilonium bromide	6.9	29.0	Cardiovascular Disease
	Benzethonium chloride	6.9	30.3	Neurological Disease
	Niclosamide	7.8	43.4	
	PCI-32765	10.6	70.3	Neurological Disease
	Everolimus	15.7	67.7	Cancer
	Doxercalciferol	17.1	55.2	Endocrinology
	Rapamycin	18.5	61.8	Immunology
	Temsirolimus	21.3	59.2	Cancer
	Ezetimibe	22.0	51.3	Cardiovascular Disease
	Dequalinium chloride	22.3	47.9	
	Disulfiram	22.7	65.6	Neurological Disease
	Biperiden HCl	23.4	56.6	Neurological Disease

Together these results give a set of compounds that are germination inhibitors and replication inhibitors that can be further investigated as potential targets for repurposing or to elucidate germination processes. Inhibitors of both germination and yeast replication were prioritized for further study.

Antifungal Drugs are Inhibitors of Fungal Pathogen Vegetative Growth:

To confirm the ability of the known antifungals to inhibit yeast replication, minimum inhibitory concentration (MIC) and minimum fungicidal concentration (MFC) testing was performed on the top three germination inhibition hits. All three antifungal compounds inhibited replication of *Cryptococcus neoformans* yeast of both serotype A and D, while being less potent against *Candida albicans* (Table 4). All of the antifungal drugs were fungicidal with the exception of bifonazole against H99.

TABLE 4

Ability to inhibit fungal pathogens of antifungal drug germination-inhibitor hits. MIC/MFC values of top three germination inhibitors against prominent human fungal pathogens.

	Cryptococcus neoformans (JEC21)		*Cryptococcus neoformans* (H99)	
	MIC (µg/mL)	MFC (µg/mL)	MIC (µg/mL)	MFC (µg/mL)
Pentamidine isethionate	1.56	3.13	6.25	6.25
Bifonazole	6.25	6.25	6.25	>100
Econazole nitrate	<0.78	6.25	<0.78	6.25

	Candida albicans (SC5314)		*Aspergillus Fumigatus* (AF293)
	MIC (µg/mL)	MFC (µg/mL)	MIC (µg/mL)
Pentamidine isethionate	50	50	>100
Bifonazole	>100	>100	>100
Econazole nitrate	6.25	12.5	3.13

Pentamidine and bifonazole were unable to inhibit *Aspergillus fumigatus* while econazole nitrate was able to inhibit its growth. It is important to note the *Aspergillus fumigatus* inhibition testing is performed on conidia, their asexual spore (Table 4). Together these results confirm the ability of these antifungals to inhibit fungal growth in a fungicidal manner.

Antifungal Drugs are Inhibitors of Fungal Spore Germination:

Once yeast replication inhibition was confirmed, the ability of the drugs to inhibit spore germination was characterized using a quantified microfluidics-based germination assay where the changes in size and morphology are monitored as small ovoid spores germinate into large circular yeast.

Pentamidine isethionate was able to successfully inhibit spore germination as seen by a decrease in morphology transition (data not shown). While germination is not completely halted, the spores were only able to circularize partially and unable to transition into the yeast state. It is important to note that all of the spores were inhibited, indicating that none of the ~10,000 spores showed inherent resistance and escape from inhibition. Due to the hydrophobic nature of bifonazole and econazole nitrate, the PDMS devices resulted in sequestration of the compounds and the assays could not be performed in the microfluidic devices.

To determine if these compounds had an effect on spore germination, the assay was performed outside of the microfluidic device and imaged at 0 and 16 hours. Both econazole nitrate and bifonazole were able to inhibit spore germination effectively with spore escape apparent in bifonazole-treated spores as determined by a yeast population increase. None of these drugs were fully germicidal at these concentrations. These assays confirm that the high throughput screen identified antifungal drugs that are potent inhibitors of spore germination.

FDA Drug Hits are Inhibitors of Fungal Pathogen Vegetative Growth:

To determine the ability of the 16 non-antifungal drugs to inhibit yeast growth, MIC and MFC testing was performed on nine of the 16 drugs. The nine drugs were selected based on dose response curves, drug availability and ensuring that all classes of inhibitors were tested. Seven inhibitors were able to inhibit yeast replication to varying degrees (Table 5) while biperiden HCl and ezetimibe, were unable to inhibit yeast growth (data not shown). All drugs were tested against *Aspergillus fumigatus* with varying degrees of success. Notably alexidine was extremely potent against *A. fumigatus*. Additionally, cetylpyridinium bromide, otilonium bromide, benzethonium chloride and disulfiram were all able to inhibit *A. fumigatus*. (Table 5)

TABLE 5

Ability to inhibit fungal pathogens of FDA drugs germination-inhibitor hits. MIC/MFC values of germination inhibitors against prominent human fungal pathogens.

	Cryptococcus neoformans (JEC21)		*Cryptococcus neoformans* (H99)	
	MIC (µg/mL)	MFC (µg/mL)	MIC (µg/mL)	MFC (µg/mL)
Cetylpyridinium chloride	<0.78	<0.78	<0.78	<0.78
Alexidine HCl	<0.78	<0.78	<0.78	<0.78
Otilonium bromide	3.13	3.13	3.13	3.13
Benzelthonium chloride	3.13	3.13	3.13	3.13
Niclosamide	<0.78	1.56	1.56	>100
Temsirolimus	6.25	6.25	6.25	6.25
Disulfiram	3.13	3.13	6.25	6.25

	Candida albicans (SC5314)		*Aspergillus Fumigatus* (AF293)
	MIC (µg/mL)	MFC (µg/mL)	MIC (µg/mL)
Cetylpyridinium chloride	1.56	3.13	1.56
Alexidine HCl	<0.78	<0.78	<0.78
Otilonium bromide	3.13	3.13	6.25
Benzelthonium chloride	6.25	12.5	12.5
Niclosamide	>100	>100	>100
Temsirolimus	1.56	1.56	>100
Disulfiram	6.25	12.5	25

These results indicate that these FDA-approved drugs have the ability to inhibit fungal pathogen vegetative growth and kill fungal cells. While some of these drugs have previously been shown to have antifungal activities, some have not.

FDA Drug Hits are Inhibitors of Fungal Spore Germination:

To determine the ability of these seven drugs, which inhibit fungal vegetative growth, to inhibit spore germination; germination assays were performed on the drugs at a concentration of 25 μg/mL. All seven of these drugs were able to inhibit germination to different extents (data not shown).

Five of the seven drugs were tested in microfluidic devices. Alexidine hydrochloride, an antimicrobial, and otilonium bromide, an antimuscarinic used to treat irritable bowel syndrome, were both able to completely inhibit spore germination, as seen by the lack of change in morphology. Both of these drugs were fully germicidal. Niclosamide, an antihelminth that inhibits oxidative phosphorylation, was also able to completely inhibit germination, but was not fully germicidal. Temsirolimus, an mTOR inhibitor used in some cancer treatments, was able to partially inhibit germination and appeared to stall germination strongly between 6 and 8 hours. When spores were exposed to temsirolimus they were able to circularize but appeared to have difficulty growing in size. Finally, disulfiram, an alcohol dehydrogenase inhibitor used in the treatment of alcoholism, was a weak inhibitor of germination leading to about a 2-hour stall in germination overall at this concentration. At higher concentrations, a similar stall to that observed with temsirolimus was observed (data not shown). Neither temsirolimus nor disulfiram were germicidal.

Cetylpyridinium chloride and benzethonium chloride, both quaternary ammonium salts, were unable to be tested in the microfluidic devices due to their viscosity and were therefore tested in outside the devices and imaged at 0 and 16 hours. Both drugs were able to inhibit spore germination completely and were fully germicidal at this concentration. These assays confirm that the method discloed herein has utility to identify a variety of non-antifungal, FDA-approved drugs that are able to inhibit fungal spore germination to varying degrees. These results also start to elucidate potential molecular processes crucial for fungal spore germination.

Pentamidine Ubiquitously Slows Germination:

Pentamidine was selected for further study due to many factors that make it a good candidate for repurposing. A range of concentrations of pentamidine isethionate was tested in a germination assay. As concentrations of pentamidine increased, spore germination became slower. However, no individual spores were able to escape inhibition, as seen by the lack of spores in the yeast state at higher concentrations. While pentamidine was not germicidal at lower concentration, at 50 μg/mL pentamidine showed germicidal activity. These results suggest that pentamidine slows the germination of spores ubiquitously and at high enough concentrations is sporicidal.

Pentamidine Treatment Lowers Fungal Burden in Mouse Lung:

Pentamidine is a successful inhibitor of *Cryptococcus neoformans* yeast replication in vitro. For repurposing potential, it is important to determine drug efficacy in vivo. For this purpose, the ability of pentamidine to lower the fungal burden in mouse lungs infected by both spores and yeast was determined. One-day post-infection intranasal dosing was begun at 4 mg/kg/day and the mice were treated for three consecutive days. On the fourth day post-infection, lungs were collected and fungal burden was determined. Pentamidine-treated mice had significantly lower fungal burdens in the lung than PBS-treated mice, in both yeast- and spore-infected mice. See FIG. **8**A and FIG. **8**B, respectively. These results indicate that pentamidine is able to inhibit yeast replication in vivo.

Prophylactic Pentamidine Inhibits Spore Germination In Vivo:

Pentamidine is a successful inhibitor of spore germination in vitro. It is important, though, to determine drug efficacy in vivo. Therefore, the ability of pentamidine to inhibit germination of spores in mouse lungs was determined. To determine if prophylactic pentamidine had an effect on fungal lung burden, mice were treated with 4 mg/kg/day of pentamidine or 1×PBS for three consecutive days. After three days of infection, mice were infected with JEC20×JEC21 spores and 4-days post infection, mouse lungs were collected and lung fungal burden was determined. The results are shown in FIG. **9**. As evidenced by data in FIG. **9**, pentamidine prophylaxis was successful in decreasing spore-mediated lung burden. These results indicate that spore germination was inhibited in vivo.

In vivo spore germination has never been characterized mainly due to technical hurdles. Using a novel assay, *Cryptococcus neoformans* cells were recovered from prophylactically treated, spore-infected mouse lungs 8 hours post infection. This was an early enough time point where no budding yeast were recovered from mouse lungs, ensuring that all cells were spore derived and not budding derived. Based on size and shape of the cells, the level of in vivo spore germination was quantified. Prophylactic pentamidine was able to inhibit spore germination as indicated by a higher spore percent and a lower yeast percent in pentamidine-treated mice. Together these results demonstrate that prophylactic pentamidine has in vivo activity against *Cryptococcus neoformans* spores, indicating it is useful to prophylactically treat (i.e., prevent) fungal infection.

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cct ctg gtg ccg gag acc tct gac gac ctt gag att gac gca gaa ttt      192
Pro Leu Val Pro Glu Thr Ser Asp Asp Leu Glu Ile Asp Ala Glu Phe
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gtg ccc atg atc tgg tca ccc caa tct tta gat gat ggt tgc gac ttg      240
Val Pro Met Ile Trp Ser Pro Gln Ser Leu Asp Asp Gly Cys Asp Leu
65                  70                  75                  80

caa gaa gga tgg aat ctt ctc ttg ggt ttc aac gag cct gac ctc gac      288
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aac gaa gct gtt gca agc cat cgc tct ccg cag gaa gct gca gac gcg      336
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gtt tcc ccc gct gta gca tcc aac gtg gaa tgg ctt aaa gag ttc ctc      432
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aac gag ttt gga ttg cct att atc ttg act gaa ttc tgc atg cag agt      576
Asn Glu Phe Gly Leu Pro Ile Ile Leu Thr Glu Phe Cys Met Gln Ser
            180                 185                 190

tgg gac gaa ggt gtt cca ggc cca gag gac cag cag caa gtc cat gat      624
Trp Asp Glu Gly Val Pro Gly Pro Glu Asp Gln Gln Gln Val His Asp
        195                 200                 205

tac atg ggc caa aca aca aaa tgg ctt gat gaa act gac tat gtt att      672
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Lys Tyr Cys Trp Phe Gly Ala Val Arg Asp Thr Ala Asn Leu His Asp
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Gln Glu Gly Trp Asn Leu Leu Leu Gly Phe Asn Glu Pro Asp Leu Asp
                85                  90                  95

Asn Glu Ala Val Ala Ser His Arg Ser Pro Gln Glu Ala Ala Asp Ala
            100                 105                 110

Trp Ile Gln Leu Ala Gln Leu Arg Thr Asp Pro Asp Asn Gln His Leu
        115                 120                 125

Val Ser Pro Ala Val Ala Ser Asn Val Glu Trp Leu Lys Glu Phe Leu
    130                 135                 140

Ser Leu Ile Pro Glu Asp Thr Tyr Pro Ala Tyr Leu Ala Val His Leu
145                 150                 155                 160

Tyr Thr Thr Thr Phe Asp Asp Phe Val Gly Lys Met Glu Met Tyr His
                165                 170                 175

Asn Glu Phe Gly Leu Pro Ile Ile Leu Thr Glu Phe Cys Met Gln Ser
            180                 185                 190

Trp Asp Glu Gly Val Pro Gly Pro Glu Asp Gln Gln Gln Val His Asp
        195                 200                 205

Tyr Met Gly Gln Thr Thr Lys Trp Leu Asp Glu Thr Asp Tyr Val Ile
    210                 215                 220

Lys Tyr Cys Trp Phe Gly Ala Val Arg Asp Thr Ala Asn Leu His Asp
225                 230                 235                 240

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

cat ccc gcc gca atc ggc tct caa tac ctt tat att ggc ggt ccc cgc      144
His Pro Ala Ala Ile Gly Ser Gln Tyr Leu Tyr Ile Gly Gly Pro Arg
        35                  40                  45

agc gcc tat cag gcc gcg aag gac aag tac gct ggc ttg tcc aaa gtc      192
Ser Ala Tyr Gln Ala Ala Lys Asp Lys Tyr Ala Gly Leu Ser Lys Val
    50                  55                  60

aag aaa ggt ctc ctc gct ctt gcc gtt gtt tgg ttc ggt ctt gtc gtt      240
Lys Lys Gly Leu Leu Ala Leu Ala Val Val Trp Phe Gly Leu Val Val
65                  70                  75                  80

ggc cat cag gct gcg cgt ctt gct ggc ggc aaa tgc cac cag gac gct      288
Gly His Gln Ala Ala Arg Leu Ala Gly Gly Lys Cys His Gln Asp Ala
                85                  90                  95

cat cat gct ccc gcc gaa ttt ggc gtg aag cag tgg aga gac cac tca      336
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Ser His Arg Phe Gly Gly Pro Ile Phe Leu Glu Asp Gly Pro Leu Asp
        115                 120                 125

tgt cat ggt ggc cgt aaa gac cgt gct cct gag gag ctt tct tcc gtt      432
Cys His Gly Gly Arg Lys Asp Arg Ala Pro Glu Glu Leu Ser Ser Val
    130                 135                 140

gcc act gtc tac gag tcc atc aac gtt gtc ggg agc aac gat gct acc      480
Ala Thr Val Tyr Glu Ser Ile Asn Val Val Gly Ser Asn Asp Ala Thr
145                 150                 155                 160

gac att ctc tcc gcc aac gcc tct ttc cct ctc aaa ctt ggc cgt ggc      528
Asp Ile Leu Ser Ala Asn Ala Ser Phe Pro Leu Lys Leu Gly Arg Gly
                165                 170                 175

aag cac ttt gat ctc acc ttc caa ggt gag ggt aac gtc atc atc tcg      576
Lys His Phe Asp Leu Thr Phe Gln Gly Glu Gly Asn Val Ile Ile Ser
            180                 185                 190

agg gct gag gag gag tct gaa gac tct act gtc aac gtt ttt gtt gag      624
Arg Ala Glu Glu Glu Ser Glu Asp Ser Thr Val Asn Val Phe Val Glu
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tct act tgg tcc ggt gag gag gct gaa ggg gtc aag atg ttg tct gga      672
Ser Thr Trp Ser Gly Glu Glu Ala Glu Gly Val Lys Met Leu Ser Gly
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aaa cac tct cac gct ctc tct gtt gct tct tct caa tcc tcg tct cat      720
Lys His Ser His Ala Leu Ser Val Ala Ser Ser Gln Ser Ser Ser His
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            340                 345                 350

gag cac aag aag ttt gac agc cgt cac gga gaa cac aat cac gag aag     1104
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aag cac ttc gga ggg cgt ttc cac tct gaa gaa gag cga cct tcc aag     1152
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cct ggt ggt cct gat ggt cct ggt ggt cct ggt ggt cct ggt ggc cct     1680
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gga ggt ccc ggt ggt ccc ggt ggt ccc ggt ggt ccc ggc ccc gac cac     1728
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ccc cgt ggt cct cct cct tgg gtt gtc ttc ccc ccc ggt cac tca gaa     1776
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            580                 585                 590

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        35                  40                  45

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Lys Lys Gly Leu Leu Ala Leu Ala Val Val Trp Phe Gly Leu Val Val
65                  70                  75                  80

Gly His Gln Ala Ala Arg Leu Ala Gly Gly Lys Cys His Gln Asp Ala
                85                  90                  95

His His Ala Pro Ala Glu Phe Gly Val Lys Gln Trp Arg Asp His Ser
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Arg Ala Glu Glu Glu Ser Glu Asp Ser Thr Val Asn Val Phe Val Glu
        195                 200                 205

Ser Thr Trp Ser Gly Glu Glu Ala Glu Gly Val Lys Met Leu Ser Gly
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Lys His Ser His Ala Leu Ser Val Ala Ser Ser Gln Ser Ser Ser His
225                 230                 235                 240

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                245                 250                 255

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Gln Asp Ile His Val Gly Lys Leu Ser Leu Lys Ser Glu Ser Gly Asp
        275                 280                 285

Ile Lys Leu Pro Thr Leu Ala Val Asn Lys Leu Val Ala Glu Thr Val
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Glu His Lys Lys Phe Asp Ser Arg His Gly Glu His Asn His Glu Lys
        355                 360                 365

Lys His Phe Gly Gly Arg Phe His Ser Glu Glu Glu Arg Pro Ser Lys
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Trp Ser Leu Asn Ile Phe Lys Ser Lys Lys Glu Asp Glu Pro Glu His
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                405                 410                 415

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

Val Phe Ser His Thr Gly Asp Val Asp Val Thr His Asp Lys Ser Phe
        435                 440                 445

His Gly Leu Tyr Glu Val Gly Ser Leu Lys Gly Thr Tyr Asp Val Val
    450                 455                 460

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465                 470                 475                 480

Glu Gly Gly Lys Gln Lys Gly Leu Ala Phe Val Pro Lys Asn Arg Lys
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Thr Glu Gly Ser His Glu Lys Arg His Phe Arg Asn Ala Glu Ser Val
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Asp Gly Glu Leu Pro Pro Pro Pro Pro Gly Lys Gly His Gly Pro Asp
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Pro Gly Gly Pro Asp Gly Pro Gly Gly Pro Gly Gly Pro Gly Gly Pro
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Val Phe Ala Ala Pro Phe Ala Glu Lys Asp Ser Ile Ala Ser Ser Pro
            20                  25                  30

gac ttg gtc aag aag gag gtt aac gtc ctc tct gtc gtc aat gaa gtc      144
Asp Leu Val Lys Lys Glu Val Asn Val Leu Ser Val Val Asn Glu Val
        35                  40                  45

cag tct agg gtt aat gct gct gcc gcc atg ccc cgc cag tct caa gcg      192
Gln Ser Arg Val Asn Ala Ala Ala Ala Met Pro Arg Gln Ser Gln Ala
    50                  55                  60

gat gtt gag gcc tgt ctc aac act gtc att gat gcc ttt aac tgg tgc      240
Asp Val Glu Ala Cys Leu Asn Thr Val Ile Asp Ala Phe Asn Trp Cys
65                  70                  75                  80

ggt ggc cag ctc ggt att gac gtt tcc gcc agc gcc agc gcc aat gcc      288
Gly Gly Gln Leu Gly Ile Asp Val Ser Ala Ser Ala Ser Ala Asn Ala
                85                  90                  95

ggt gct agc atc cat tac ttg cgt cgt gag att att gcc cgt gat gac      336
Gly Ala Ser Ile His Tyr Leu Arg Arg Glu Ile Ile Ala Arg Asp Asp
            100                 105                 110

gac aag gag gct gtt gct cag gca ctc tct agc gtt gtt cag acc gtt      384
Asp Lys Glu Ala Val Ala Gln Ala Leu Ser Ser Val Val Gln Thr Val
        115                 120                 125

aat gtc ggc atc gtc cag cag atc ccc agc caa ttc atc aac atc cct      432
Asn Val Gly Ile Val Gln Gln Ile Pro Ser Gln Phe Ile Asn Ile Pro
    130                 135                 140

ggc gtc tcc aac ctt gtt aac cag ctt gac att gct ctc agt ctc atc      480
Gly Val Ser Asn Leu Val Asn Gln Leu Asp Ile Ala Leu Ser Leu Ile
145                 150                 155                 160

ctt aag ggt gtt gac gct att ctc gcc ggt gtc ctc tac ctc gtc aag      528
Leu Lys Gly Val Asp Ala Ile Leu Ala Gly Val Leu Tyr Leu Val Lys
                165                 170                 175

gcc ctt ctc atc gat gtt ggc atc atc ctc gac tcg ctt ctc ggc ggt      576
Ala Leu Leu Ile Asp Val Gly Ile Ile Leu Asp Ser Leu Leu Gly Gly
            180                 185                 190

ctc ctt tcc atc ctt taa                                              594
Leu Leu Ser Ile Leu
        195


<210> SEQ ID NO 6
<211> LENGTH: 197
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans
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<400> SEQUENCE: 6

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

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

Asp Leu Val Lys Lys Glu Val Asn Val Leu Ser Val Val Asn Glu Val
        35                  40                  45

Gln Ser Arg Val Asn Ala Ala Ala Ala Met Pro Arg Gln Ser Gln Ala
    50                  55                  60

Asp Val Glu Ala Cys Leu Asn Thr Val Ile Asp Ala Phe Asn Trp Cys
65                  70                  75                  80

Gly Gly Gln Leu Gly Ile Asp Val Ser Ala Ser Ala Ser Ala Asn Ala
                85                  90                  95

Gly Ala Ser Ile His Tyr Leu Arg Arg Glu Ile Ile Ala Arg Asp Asp
            100                 105                 110

Asp Lys Glu Ala Val Ala Gln Ala Leu Ser Ser Val Val Gln Thr Val
        115                 120                 125

Asn Val Gly Ile Val Gln Gln Ile Pro Ser Gln Phe Ile Asn Ile Pro
    130                 135                 140

Gly Val Ser Asn Leu Val Asn Gln Leu Asp Ile Ala Leu Ser Leu Ile
145                 150                 155                 160

Leu Lys Gly Val Asp Ala Ile Leu Ala Gly Val Leu Tyr Leu Val Lys
                165                 170                 175

Ala Leu Leu Ile Asp Val Gly Ile Ile Leu Asp Ser Leu Leu Gly Gly
            180                 185                 190

Leu Leu Ser Ile Leu
        195


<210> SEQ ID NO 7
<211> LENGTH: 894
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(894)

<400> SEQUENCE: 7

atg tct gcc gtc gaa gca ccc tcc gcc tcg cag gcc atc tgg ccc gag       48
Met Ser Ala Val Glu Ala Pro Ser Ala Ser Gln Ala Ile Trp Pro Glu
1               5                   10                  15

ctc act gaa gac cac ccc ctt tcg cag ctc aac tct cgc ctc cct act       96
Leu Thr Glu Asp His Pro Leu Ser Gln Leu Asn Ser Arg Leu Pro Thr
            20                  25                  30

atc ctt tca gag gct ggt cac tcc caa atc tgg ggc gtt act ctt act      144
Ile Leu Ser Glu Ala Gly His Ser Gln Ile Trp Gly Val Thr Leu Thr
        35                  40                  45

tac tcc act ccc cca acc ttc tct agc ctt att att ctg caa aaa ttc      192
Tyr Ser Thr Pro Pro Thr Phe Ser Ser Leu Ile Ile Leu Gln Lys Phe
    50                  55                  60

ctt cgt tcc gtg gat aat aac gtg gat gag gct gcc acg gct cta ggc      240
Leu Arg Ser Val Asp Asn Asn Val Asp Glu Ala Ala Thr Ala Leu Gly
65                  70                  75                  80

aag aca ctc aag tgg cgg aag gac tgg gga ttg gac gcg cgg gcg gac      288
Lys Thr Leu Lys Trp Arg Lys Asp Trp Gly Leu Asp Ala Arg Ala Asp
                85                  90                  95

aaa aaa gag aag gaa aac ttt ggg ccc gat ttt gaa ggc tta gga tat      336
Lys Lys Glu Lys Glu Asn Phe Gly Pro Asp Phe Glu Gly Leu Gly Tyr
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            100                 105                 110

gtg acc aag atc aag aaa aat gat ggc gga gat gag atc gtg act tgg      384
Val Thr Lys Ile Lys Lys Asn Asp Gly Gly Asp Glu Ile Val Thr Trp
        115                 120                 125

aac gtt tat gga gct gtg aag gat ttg aaa tcg acc ttt ggg gat ctt      432
Asn Val Tyr Gly Ala Val Lys Asp Leu Lys Ser Thr Phe Gly Asp Leu
    130                 135                 140

gac cga ttc ctt cga tgg cgt gtc aat ctt atg gag gag gct atc gcc      480
Asp Arg Phe Leu Arg Trp Arg Val Asn Leu Met Glu Glu Ala Ile Ala
145                 150                 155                 160

cat ctt cat ctc gct acc acc tct act ccc atc cca gac ttt aac gcc      528
His Leu His Leu Ala Thr Thr Ser Thr Pro Ile Pro Asp Phe Asn Ala
                165                 170                 175

ggt att gat ccc cat cgc atg gca caa gtc cat cta tat gaa ggt gtc      576
Gly Ile Asp Pro His Arg Met Ala Gln Val His Leu Tyr Glu Gly Val
            180                 185                 190

tca ttc ctt cgc atg gat cct cat gtg aaa gct gcc tcc aag gca acc      624
Ser Phe Leu Arg Met Asp Pro His Val Lys Ala Ala Ser Lys Ala Thr
        195                 200                 205

att gag ctt atg gcg gcc aac tat ccc gaa ctt ctt tct cgc aaa ttc      672
Ile Glu Leu Met Ala Ala Asn Tyr Pro Glu Leu Leu Ser Arg Lys Phe
    210                 215                 220

ttt gtg ggc gtg cct ttg ata atg agc tgg atg ttt cag gcc gtg cga      720
Phe Val Gly Val Pro Leu Ile Met Ser Trp Met Phe Gln Ala Val Arg
225                 230                 235                 240

atg ttc gtt tcc gct gag act gcc aag aag ttt gtg gtc att agc tac      768
Met Phe Val Ser Ala Glu Thr Ala Lys Lys Phe Val Val Ile Ser Tyr
                245                 250                 255

aag gag aat ctg gcg aat gag ctg gga gaa ctt gaa ggt gtg ccc aag      816
Lys Glu Asn Leu Ala Asn Glu Leu Gly Glu Leu Glu Gly Val Pro Lys
            260                 265                 270

gag tat ggt gga aag ggt ctc agt ttg ggc gaa ctt cag aac cag ctg      864
Glu Tyr Gly Gly Lys Gly Leu Ser Leu Gly Glu Leu Gln Asn Gln Leu
        275                 280                 285

cga ggg gag gac gcg gtg act tct tcg taa                              894
Arg Gly Glu Asp Ala Val Thr Ser Ser
    290                 295


<210> SEQ ID NO 8
<211> LENGTH: 297
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 8

Met Ser Ala Val Glu Ala Pro Ser Ala Ser Gln Ala Ile Trp Pro Glu
1               5                   10                  15

Leu Thr Glu Asp His Pro Leu Ser Gln Leu Asn Ser Arg Leu Pro Thr
            20                  25                  30

Ile Leu Ser Glu Ala Gly His Ser Gln Ile Trp Gly Val Thr Leu Thr
        35                  40                  45

Tyr Ser Thr Pro Pro Thr Phe Ser Ser Leu Ile Ile Leu Gln Lys Phe
    50                  55                  60

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

Lys Thr Leu Lys Trp Arg Lys Asp Trp Gly Leu Asp Ala Arg Ala Asp
                85                  90                  95

Lys Lys Glu Lys Glu Asn Phe Gly Pro Asp Phe Glu Gly Leu Gly Tyr
            100                 105                 110
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Val Thr Lys Ile Lys Lys Asn Asp Gly Gly Asp Glu Ile Val Thr Trp
        115                 120                 125

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

Asp Arg Phe Leu Arg Trp Arg Val Asn Leu Met Glu Glu Ala Ile Ala
145                 150                 155                 160

His Leu His Leu Ala Thr Thr Ser Thr Pro Ile Pro Asp Phe Asn Ala
                165                 170                 175

Gly Ile Asp Pro His Arg Met Ala Gln Val His Leu Tyr Glu Gly Val
            180                 185                 190

Ser Phe Leu Arg Met Asp Pro His Val Lys Ala Ala Ser Lys Ala Thr
        195                 200                 205

Ile Glu Leu Met Ala Ala Asn Tyr Pro Glu Leu Leu Ser Arg Lys Phe
    210                 215                 220

Phe Val Gly Val Pro Leu Ile Met Ser Trp Met Phe Gln Ala Val Arg
225                 230                 235                 240

Met Phe Val Ser Ala Glu Thr Ala Lys Lys Phe Val Val Ile Ser Tyr
                245                 250                 255

Lys Glu Asn Leu Ala Asn Glu Leu Gly Glu Leu Glu Gly Val Pro Lys
            260                 265                 270

Glu Tyr Gly Gly Lys Gly Leu Ser Leu Gly Glu Leu Gln Asn Gln Leu
        275                 280                 285

Arg Gly Glu Asp Ala Val Thr Ser Ser
    290                 295


<210> SEQ ID NO 9
<211> LENGTH: 2094
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(2094)

<400> SEQUENCE: 9

atg tca gag cta ttc aag gac atc cca gag ttt gta gag acc gac atc       48
Met Ser Glu Leu Phe Lys Asp Ile Pro Glu Phe Val Glu Thr Asp Ile
1               5                   10                  15

gga gag agc ctt gca gcc aga acg gaa acc ctt ggc tcc ttc aga gaa       96
Gly Glu Ser Leu Ala Ala Arg Thr Glu Thr Leu Gly Ser Phe Arg Glu
            20                  25                  30

cta ggc cct cca gac ctc tgc cat gtt atg aaa gtt tat ggg aaa ccg      144
Leu Gly Pro Pro Asp Leu Cys His Val Met Lys Val Tyr Gly Lys Pro
        35                  40                  45

ccg act caa cga gag atc ggg tcc tat cac tac tgc tct gga ata gag      192
Pro Thr Gln Arg Glu Ile Gly Ser Tyr His Tyr Cys Ser Gly Ile Glu
    50                  55                  60

gct tcg tcc tct gcg tca ctc gct gcc tat ctc aac tct ttg cag ttt      240
Ala Ser Ser Ser Ala Ser Leu Ala Ala Tyr Leu Asn Ser Leu Gln Phe
65                  70                  75                  80

tca gtg gaa gat tcg tct gca tgg ttt ggc aag ggg tcg gca tgg aaa      288
Ser Val Glu Asp Ser Ser Ala Trp Phe Gly Lys Gly Ser Ala Trp Lys
                85                  90                  95

gtt cga agc ggg acg tat tgc tgc ttc aat gcc ttt tca cgg gta gat      336
Val Arg Ser Gly Thr Tyr Cys Cys Phe Asn Ala Phe Ser Arg Val Asp
            100                 105                 110

atg cgg gtg gaa gcc aat att ccc ggc ggt gtc gac gct ttt gtg gtt      384
Met Arg Val Glu Ala Asn Ile Pro Gly Gly Val Asp Ala Phe Val Val
        115                 120                 125
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gat ctt cac ggt caa aga cac cct gcg acc ccc gag ctc tgg caa gag      432
Asp Leu His Gly Gln Arg His Pro Ala Thr Pro Glu Leu Trp Gln Glu
    130                 135                 140

acg tac ctg tct gcg atc ctg cgt gct att aga tat gcg gac gat gcc      480
Thr Tyr Leu Ser Ala Ile Leu Arg Ala Ile Arg Tyr Ala Asp Asp Ala
145                 150                 155                 160

tcc tat agg ttg gca ggg tat aga aag ctg gat ccg atc aca acg cca      528
Ser Tyr Arg Leu Ala Gly Tyr Arg Lys Leu Asp Pro Ile Thr Thr Pro
                165                 170                 175

gaa gca gag gaa aga ttc ctc aaa gcc gcc gaa gcg ctg ttc ttc aag      576
Glu Ala Glu Glu Arg Phe Leu Lys Ala Ala Glu Ala Leu Phe Phe Lys
            180                 185                 190

ggc tgg cag ctt ggc tca gat ccc gaa ata cag gtc gcc aca gtt gtc      624
Gly Trp Gln Leu Gly Ser Asp Pro Glu Ile Gln Val Ala Thr Val Val
        195                 200                 205

acc aac cac ctg acc tct gcc att ctt aaa tac ttt tcc gac tct ttc      672
Thr Asn His Leu Thr Ser Ala Ile Leu Lys Tyr Phe Ser Asp Ser Phe
    210                 215                 220

aga ctt cat cga gcc gcc aac ctt ttc gaa agg atg atg gac aag gag      720
Arg Leu His Arg Ala Ala Asn Leu Phe Glu Arg Met Met Asp Lys Glu
225                 230                 235                 240

cca gag gta gcc gct cta gtg gcg aag agt tac atc ggc atg aac gag      768
Pro Glu Val Ala Ala Leu Val Ala Lys Ser Tyr Ile Gly Met Asn Glu
                245                 250                 255

gag atc aaa gct gtc aag atc atg aac gct gcc ctt gcc gcc aat cct      816
Glu Ile Lys Ala Val Lys Ile Met Asn Ala Ala Leu Ala Ala Asn Pro
            260                 265                 270

caa tcc tat ccc atc ctt cat gcc caa gtc gat ttc ctc ctt tcc aag      864
Gln Ser Tyr Pro Ile Leu His Ala Gln Val Asp Phe Leu Leu Ser Lys
        275                 280                 285

cac aaa tac gaa tgg gcc cag caa gtc gcc cag cag gcg gtc aat tct      912
His Lys Tyr Glu Trp Ala Gln Gln Val Ala Gln Gln Ala Val Asn Ser
    290                 295                 300

gca ccc agc gag ttc acg act tgg gcc aaa ctc acg gag acg tac atc      960
Ala Pro Ser Glu Phe Thr Thr Trp Ala Lys Leu Thr Glu Thr Tyr Ile
305                 310                 315                 320

gag ttg ggg caa ctc gac cag gct ttg ttg aca ctc aac tca tgt cca     1008
Glu Leu Gly Gln Leu Asp Gln Ala Leu Leu Thr Leu Asn Ser Cys Pro
                325                 330                 335

atg ttt act tat aac gaa aga gat ctc cat cgg atg cct acc cct gca     1056
Met Phe Thr Tyr Asn Glu Arg Asp Leu His Arg Met Pro Thr Pro Ala
            340                 345                 350

aag tcc aat atg cca gtc aag aag ttt atc gca gac tcc aat ttg gtg     1104
Lys Ser Asn Met Pro Val Lys Lys Phe Ile Ala Asp Ser Asn Leu Val
        355                 360                 365

gat gaa gat tcg tca cga gag aac gag gcc gat atc gct ctc ctc cgt     1152
Asp Glu Asp Ser Ser Arg Glu Asn Glu Ala Asp Ile Ala Leu Leu Arg
    370                 375                 380

ctc ccc gct ccc aac ctc cgc ggc aca ttc gcc aaa gcg tac tcc ctc     1200
Leu Pro Ala Pro Asn Leu Arg Gly Thr Phe Ala Lys Ala Tyr Ser Leu
385                 390                 395                 400

ctc act ctc ctt gtc tct aag att ggt tgg gat gag ctt ctc aaa att     1248
Leu Thr Leu Leu Val Ser Lys Ile Gly Trp Asp Glu Leu Leu Lys Ile
                405                 410                 415

aga tcc tcc gtc ttc gtc atg gaa gag gaa tat cgg ctg cat aaa acg     1296
Arg Ser Ser Val Phe Val Met Glu Glu Glu Tyr Arg Leu His Lys Thr
            420                 425                 430

aac gtt tct gtt gat atg aat ggc gaa gcg ggt gac ggc gcg tcc att     1344
Asn Val Ser Val Asp Met Asn Gly Glu Ala Gly Asp Gly Ala Ser Ile
        435                 440                 445
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gcg ggc ttg aag agg acc tcg tcc gaa gag gtc aac act ccc agc gat      1392
Ala Gly Leu Lys Arg Thr Ser Ser Glu Glu Val Asn Thr Pro Ser Asp
    450                 455                 460

ata cct acc atc agg ata tca agc gag tcg atg cgc act cct aat acg      1440
Ile Pro Thr Ile Arg Ile Ser Ser Glu Ser Met Arg Thr Pro Asn Thr
465                 470                 475                 480

gct cca gga cca ggg ttc agc gaa aag gca agt act cac aag ccc gct      1488
Ala Pro Gly Pro Gly Phe Ser Glu Lys Ala Ser Thr His Lys Pro Ala
                485                 490                 495

ctg gag aag ccc gag aca gca caa gcg aat gaa gat ccc aat tcg cct      1536
Leu Glu Lys Pro Glu Thr Ala Gln Ala Asn Glu Asp Pro Asn Ser Pro
            500                 505                 510

ttg ggg atg aag agt gaa ggg gaa cag ccg gtt tcg gcg ttt tct cat      1584
Leu Gly Met Lys Ser Glu Gly Glu Gln Pro Val Ser Ala Phe Ser His
        515                 520                 525

aag cga tta tgt gag aga tgg tta gat aac ctc ttt tta gtt ctg tat      1632
Lys Arg Leu Cys Glu Arg Trp Leu Asp Asn Leu Phe Leu Val Leu Tyr
    530                 535                 540

gaa gac ttg aga gtc tac acc att tgg aga gca gag ata tct cat ttc      1680
Glu Asp Leu Arg Val Tyr Thr Ile Trp Arg Ala Glu Ile Ser His Phe
545                 550                 555                 560

aaa acc cag cac atg tca tac cga aag act ggt acc gag tgg gag atc      1728
Lys Thr Gln His Met Ser Tyr Arg Lys Thr Gly Thr Glu Trp Glu Ile
                565                 570                 575

ctt ggt gaa ctt gcc aca cgt ttg cat cac aaa gaa gaa gcc aag gac      1776
Leu Gly Glu Leu Ala Thr Arg Leu His His Lys Glu Glu Ala Lys Asp
            580                 585                 590

gcg tac caa cgc tgt ctc gac tcc aaa ttc agc gca aaa gca ctt atg      1824
Ala Tyr Gln Arg Cys Leu Asp Ser Lys Phe Ser Ala Lys Ala Leu Met
        595                 600                 605

aag ctt ctt gaa acg tat gcg aat gag ggc gat ctt caa aag acc ttg      1872
Lys Leu Leu Glu Thr Tyr Ala Asn Glu Gly Asp Leu Gln Lys Thr Leu
    610                 615                 620

acg gcg gct gtg agg ctg aca acc tat cac cat cga tgg tat atg gac      1920
Thr Ala Ala Val Arg Leu Thr Thr Tyr His His Arg Trp Tyr Met Asp
625                 630                 635                 640

gcg tca tac ccg tcc atg gtc gcg cat tat ttg tac aag gtc gga ctc      1968
Ala Ser Tyr Pro Ser Met Val Ala His Tyr Leu Tyr Lys Val Gly Leu
                645                 650                 655

ata cat gga cat gcc aaa tta caa tac aca atg ctc agt atg aac ctg      2016
Ile His Gly His Ala Lys Leu Gln Tyr Thr Met Leu Ser Met Asn Leu
            660                 665                 670

ccg gtc ggg atc ttt gaa ata atg caa ggc tat atg aaa tac ggg gcg      2064
Pro Val Gly Ile Phe Glu Ile Met Gln Gly Tyr Met Lys Tyr Gly Ala
        675                 680                 685

acg ttc aac gtc gaa ggt tca gaa ttc tag                              2094
Thr Phe Asn Val Glu Gly Ser Glu Phe
    690                 695


<210> SEQ ID NO 10
<211> LENGTH: 697
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 10

Met Ser Glu Leu Phe Lys Asp Ile Pro Glu Phe Val Glu Thr Asp Ile
1               5                   10                  15

Gly Glu Ser Leu Ala Ala Arg Thr Glu Thr Leu Gly Ser Phe Arg Glu
            20                  25                  30
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Leu Gly Pro Pro Asp Leu Cys His Val Met Lys Val Tyr Gly Lys Pro
        35                  40                  45

Pro Thr Gln Arg Glu Ile Gly Ser Tyr His Tyr Cys Ser Gly Ile Glu
    50                  55                  60

Ala Ser Ser Ser Ala Ser Leu Ala Ala Tyr Leu Asn Ser Leu Gln Phe
65                  70                  75                  80

Ser Val Glu Asp Ser Ser Ala Trp Phe Gly Lys Gly Ser Ala Trp Lys
                85                  90                  95

Val Arg Ser Gly Thr Tyr Cys Cys Phe Asn Ala Phe Ser Arg Val Asp
            100                 105                 110

Met Arg Val Glu Ala Asn Ile Pro Gly Gly Val Asp Ala Phe Val Val
        115                 120                 125

Asp Leu His Gly Gln Arg His Pro Ala Thr Pro Glu Leu Trp Gln Glu
    130                 135                 140

Thr Tyr Leu Ser Ala Ile Leu Arg Ala Ile Arg Tyr Ala Asp Asp Ala
145                 150                 155                 160

Ser Tyr Arg Leu Ala Gly Tyr Arg Lys Leu Asp Pro Ile Thr Thr Pro
                165                 170                 175

Glu Ala Glu Glu Arg Phe Leu Lys Ala Ala Glu Ala Leu Phe Phe Lys
            180                 185                 190

Gly Trp Gln Leu Gly Ser Asp Pro Glu Ile Gln Val Ala Thr Val Val
        195                 200                 205

Thr Asn His Leu Thr Ser Ala Ile Leu Lys Tyr Phe Ser Asp Ser Phe
    210                 215                 220

Arg Leu His Arg Ala Ala Asn Leu Phe Glu Arg Met Met Asp Lys Glu
225                 230                 235                 240

Pro Glu Val Ala Ala Leu Val Ala Lys Ser Tyr Ile Gly Met Asn Glu
                245                 250                 255

Glu Ile Lys Ala Val Lys Ile Met Asn Ala Ala Leu Ala Ala Asn Pro
            260                 265                 270

Gln Ser Tyr Pro Ile Leu His Ala Gln Val Asp Phe Leu Leu Ser Lys
        275                 280                 285

His Lys Tyr Glu Trp Ala Gln Gln Val Ala Gln Gln Ala Val Asn Ser
    290                 295                 300

Ala Pro Ser Glu Phe Thr Thr Trp Ala Lys Leu Thr Glu Thr Tyr Ile
305                 310                 315                 320

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

Met Phe Thr Tyr Asn Glu Arg Asp Leu His Arg Met Pro Thr Pro Ala
            340                 345                 350

Lys Ser Asn Met Pro Val Lys Lys Phe Ile Ala Asp Ser Asn Leu Val
        355                 360                 365

Asp Glu Asp Ser Ser Arg Glu Asn Glu Ala Asp Ile Ala Leu Leu Arg
    370                 375                 380

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

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

Arg Ser Ser Val Phe Val Met Glu Glu Glu Tyr Arg Leu His Lys Thr
            420                 425                 430

Asn Val Ser Val Asp Met Asn Gly Glu Ala Gly Asp Gly Ala Ser Ile
        435                 440                 445

Ala Gly Leu Lys Arg Thr Ser Ser Glu Glu Val Asn Thr Pro Ser Asp
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    450                 455                 460

Ile Pro Thr Ile Arg Ile Ser Ser Glu Ser Met Arg Thr Pro Asn Thr
465                 470                 475                 480

Ala Pro Gly Pro Gly Phe Ser Glu Lys Ala Ser Thr His Lys Pro Ala
                485                 490                 495

Leu Glu Lys Pro Glu Thr Ala Gln Ala Asn Glu Asp Pro Asn Ser Pro
            500                 505                 510

Leu Gly Met Lys Ser Glu Gly Glu Gln Pro Val Ser Ala Phe Ser His
        515                 520                 525

Lys Arg Leu Cys Glu Arg Trp Leu Asp Asn Leu Phe Leu Val Leu Tyr
    530                 535                 540

Glu Asp Leu Arg Val Tyr Thr Ile Trp Arg Ala Glu Ile Ser His Phe
545                 550                 555                 560

Lys Thr Gln His Met Ser Tyr Arg Lys Thr Gly Thr Glu Trp Glu Ile
                565                 570                 575

Leu Gly Glu Leu Ala Thr Arg Leu His His Lys Glu Glu Ala Lys Asp
            580                 585                 590

Ala Tyr Gln Arg Cys Leu Asp Ser Lys Phe Ser Ala Lys Ala Leu Met
        595                 600                 605

Lys Leu Leu Glu Thr Tyr Ala Asn Glu Gly Asp Leu Gln Lys Thr Leu
    610                 615                 620

Thr Ala Ala Val Arg Leu Thr Thr Tyr His His Arg Trp Tyr Met Asp
625                 630                 635                 640

Ala Ser Tyr Pro Ser Met Val Ala His Tyr Leu Tyr Lys Val Gly Leu
                645                 650                 655

Ile His Gly His Ala Lys Leu Gln Tyr Thr Met Leu Ser Met Asn Leu
            660                 665                 670

Pro Val Gly Ile Phe Glu Ile Met Gln Gly Tyr Met Lys Tyr Gly Ala
        675                 680                 685

Thr Phe Asn Val Glu Gly Ser Glu Phe
    690                 695


<210> SEQ ID NO 11
<211> LENGTH: 1662
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1662)

<400> SEQUENCE: 11

atg tcg tta gcg gac gcc ctt ctg gca gac ctt gat ggt ctc tcg gat       48
Met Ser Leu Ala Asp Ala Leu Leu Ala Asp Leu Asp Gly Leu Ser Asp
1               5                   10                  15

gac gaa gct cga tct cct tct cct ggc ccc gag gcc tcc tcc tcg tca       96
Asp Glu Ala Arg Ser Pro Ser Pro Gly Pro Glu Ala Ser Ser Ser Ser
            20                  25                  30

atg ccg cct cct ggt ttg ccc aac aaa gga aaa cgt ccc gcc agc gct      144
Met Pro Pro Pro Gly Leu Pro Asn Lys Gly Lys Arg Pro Ala Ser Ala
        35                  40                  45

atg gaa gtc gat gat ggc gaa gga ggt gcg aat gaa gat gag gga gac      192
Met Glu Val Asp Asp Gly Glu Gly Gly Ala Asn Glu Asp Glu Gly Asp
    50                  55                  60

gat atg aag ctg gaa gac ggg acg agt gct gtg gga ttt gta cct gaa      240
Asp Met Lys Leu Glu Asp Gly Thr Ser Ala Val Gly Phe Val Pro Glu
65                  70                  75                  80

gga ggt gta agg cct gca gat gag ctg gac aag gag gaa gtg gaa aaa      288
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Gly Gly Val Arg Pro Ala Asp Glu Leu Asp Lys Glu Glu Val Glu Lys
                85                  90                  95

acc gat atg aag ggt gtc gag gat gtg aag aaa gta gcc agg ttg gca      336
Thr Asp Met Lys Gly Val Glu Asp Val Lys Lys Val Ala Arg Leu Ala
            100                 105                 110

gga agc cag aag ctt cga gat gtt ctg gca gat atc ata aaa tac acc      384
Gly Ser Gln Lys Leu Arg Asp Val Leu Ala Asp Ile Ile Lys Tyr Thr
        115                 120                 125

gag tct ccc acc gat atg tct tcg tct gcc ggt ccc ctc gag gag aat      432
Glu Ser Pro Thr Asp Met Ser Ser Ser Ala Gly Pro Leu Glu Glu Asn
    130                 135                 140

cca gag tac cat ctt gtt gtc act gcg aac aac atg tcc gtc gag gtt      480
Pro Glu Tyr His Leu Val Val Thr Ala Asn Asn Met Ser Val Glu Val
145                 150                 155                 160

gac aac gag att ctc atc gtg cac aaa ttc att cgt gac cac tat gct      528
Asp Asn Glu Ile Leu Ile Val His Lys Phe Ile Arg Asp His Tyr Ala
                165                 170                 175

cct cga ttt ccg gaa ctc gaa cag ctc att gcc gaa cct tgg aca tac      576
Pro Arg Phe Pro Glu Leu Glu Gln Leu Ile Ala Glu Pro Trp Thr Tyr
            180                 185                 190

att gcc gcc gtt aat gcc atc ggt cag tct gaa gat cta acg aag gtc      624
Ile Ala Ala Val Asn Ala Ile Gly Gln Ser Glu Asp Leu Thr Lys Val
        195                 200                 205

aca ttc ccc aac acc ctc cct gcg gct act gta ctc tct atc act ctt      672
Thr Phe Pro Asn Thr Leu Pro Ala Ala Thr Val Leu Ser Ile Thr Leu
    210                 215                 220

act gct acg act tcc cgt ggt cgg ccg ctc acg cct gca gag tgg gaa      720
Thr Ala Thr Thr Ser Arg Gly Arg Pro Leu Thr Pro Ala Glu Trp Glu
225                 230                 235                 240

aca att cag cgc gcc atc gct gtc gcc caa aat ctc cgt tcg gcg cga      768
Thr Ile Gln Arg Ala Ile Ala Val Ala Gln Asn Leu Arg Ser Ala Arg
                245                 250                 255

gaa caa att ttt tcc tac gtc gag tcc cgt atg gct gct gta gca cct      816
Glu Gln Ile Phe Ser Tyr Val Glu Ser Arg Met Ala Ala Val Ala Pro
            260                 265                 270

aat ttg tct gct att gtg ggc acc ggt atc gct gcc aaa tta ctt ggt      864
Asn Leu Ser Ala Ile Val Gly Thr Gly Ile Ala Ala Lys Leu Leu Gly
        275                 280                 285

tta gca ggt ggt ctc cat gcg ttt agt cga cag ccg agt tgt aat gtg      912
Leu Ala Gly Gly Leu His Ala Phe Ser Arg Gln Pro Ser Cys Asn Val
    290                 295                 300

atg ctt ttt ggc gcg atg aag aag act ttg gcc acc tct cat ctt tct      960
Met Leu Phe Gly Ala Met Lys Lys Thr Leu Ala Thr Ser His Leu Ser
305                 310                 315                 320

gct gcc tct cag caa cga cat acc ggc ttt atc ttc caa agc tct ata     1008
Ala Ala Ser Gln Gln Arg His Thr Gly Phe Ile Phe Gln Ser Ser Ile
                325                 330                 335

gta cag agt gcc cag cct gaa gat cga aga aga gct cag cga gcg gtg     1056
Val Gln Ser Ala Gln Pro Glu Asp Arg Arg Arg Ala Gln Arg Ala Val
            340                 345                 350

tct gcc aag tgt gct ctt gcg gcc agg atc gat gca gga aag ggg tct     1104
Ser Ala Lys Cys Ala Leu Ala Ala Arg Ile Asp Ala Gly Lys Gly Ser
        355                 360                 365

agg gac gga tct tat gga aga aag tgt ttg gcg gat ttg caa aag agg     1152
Arg Asp Gly Ser Tyr Gly Arg Lys Cys Leu Ala Asp Leu Gln Lys Arg
    370                 375                 380

att gaa aag atg gcg gaa cct cct ccc aac aag atg atc aag gcg ttg     1200
Ile Glu Lys Met Ala Glu Pro Pro Pro Asn Lys Met Ile Lys Ala Leu
385                 390                 395                 400
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cct atc cct cag gag act aac agg aag aag cgt ggt ggt aag aga gct      1248
Pro Ile Pro Gln Glu Thr Asn Arg Lys Lys Arg Gly Gly Lys Arg Ala
                405                 410                 415

cga aaa gcc aag gaa gcg tac gcc cag acc gaa ttg aga aag tta caa      1296
Arg Lys Ala Lys Glu Ala Tyr Ala Gln Thr Glu Leu Arg Lys Leu Gln
            420                 425                 430

aac cga atg gag ttt ggc aag gcg gaa gaa gag atc ggg gtg gac gac      1344
Asn Arg Met Glu Phe Gly Lys Ala Glu Glu Glu Ile Gly Val Asp Asp
        435                 440                 445

gag act gtt ggt ttg ggt atg atc ggt tcc gcc gga agg gtc cga ggc      1392
Glu Thr Val Gly Leu Gly Met Ile Gly Ser Ala Gly Arg Val Arg Gly
    450                 455                 460

gag atg gca gat gcg agg agt aaa gct aaa ctt tct cga gcc aac aaa      1440
Glu Met Ala Asp Ala Arg Ser Lys Ala Lys Leu Ser Arg Ala Asn Lys
465                 470                 475                 480

ctt cga act cag ctc ctt ggt cgc tca gtc aca tcc aac gac gct gcc      1488
Leu Arg Thr Gln Leu Leu Gly Arg Ser Val Thr Ser Asn Asp Ala Ala
                485                 490                 495

agc ggt atg gcc acc tcc tta tca ttc acg cct gtc caa ggt ctt gaa      1536
Ser Gly Met Ala Thr Ser Leu Ser Phe Thr Pro Val Gln Gly Leu Glu
            500                 505                 510

ata gtt aca ccc tcc ctc tct gca gcc cag aaa gta cag gct gcg aat      1584
Ile Val Thr Pro Ser Leu Ser Ala Ala Gln Lys Val Gln Ala Ala Asn
        515                 520                 525

gac aga tgg ttc tcc ggg ggt aca ttt acg cat gta agg aag ggg gga      1632
Asp Arg Trp Phe Ser Gly Gly Thr Phe Thr His Val Arg Lys Gly Gly
    530                 535                 540

agc agt att ccg gga cag gaa cag aaa tag                              1662
Ser Ser Ile Pro Gly Gln Glu Gln Lys
545                 550


<210> SEQ ID NO 12
<211> LENGTH: 553
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 12

Met Ser Leu Ala Asp Ala Leu Leu Ala Asp Leu Asp Gly Leu Ser Asp
1               5                   10                  15

Asp Glu Ala Arg Ser Pro Ser Pro Gly Pro Glu Ala Ser Ser Ser Ser
            20                  25                  30

Met Pro Pro Pro Gly Leu Pro Asn Lys Gly Lys Arg Pro Ala Ser Ala
        35                  40                  45

Met Glu Val Asp Asp Gly Glu Gly Gly Ala Asn Glu Asp Glu Gly Asp
    50                  55                  60

Asp Met Lys Leu Glu Asp Gly Thr Ser Ala Val Gly Phe Val Pro Glu
65                  70                  75                  80

Gly Gly Val Arg Pro Ala Asp Glu Leu Asp Lys Glu Glu Val Glu Lys
                85                  90                  95

Thr Asp Met Lys Gly Val Glu Asp Val Lys Lys Val Ala Arg Leu Ala
            100                 105                 110

Gly Ser Gln Lys Leu Arg Asp Val Leu Ala Asp Ile Ile Lys Tyr Thr
        115                 120                 125

Glu Ser Pro Thr Asp Met Ser Ser Ser Ala Gly Pro Leu Glu Glu Asn
    130                 135                 140

Pro Glu Tyr His Leu Val Val Thr Ala Asn Asn Met Ser Val Glu Val
145                 150                 155                 160

Asp Asn Glu Ile Leu Ile Val His Lys Phe Ile Arg Asp His Tyr Ala
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                165                 170                 175

Pro Arg Phe Pro Glu Leu Glu Gln Leu Ile Ala Glu Pro Trp Thr Tyr
            180                 185                 190

Ile Ala Ala Val Asn Ala Ile Gly Gln Ser Glu Asp Leu Thr Lys Val
        195                 200                 205

Thr Phe Pro Asn Thr Leu Pro Ala Ala Thr Val Leu Ser Ile Thr Leu
    210                 215                 220

Thr Ala Thr Thr Ser Arg Gly Arg Pro Leu Thr Pro Ala Glu Trp Glu
225                 230                 235                 240

Thr Ile Gln Arg Ala Ile Ala Val Ala Gln Asn Leu Arg Ser Ala Arg
                245                 250                 255

Glu Gln Ile Phe Ser Tyr Val Glu Ser Arg Met Ala Ala Val Ala Pro
            260                 265                 270

Asn Leu Ser Ala Ile Val Gly Thr Gly Ile Ala Ala Lys Leu Leu Gly
        275                 280                 285

Leu Ala Gly Gly Leu His Ala Phe Ser Arg Gln Pro Ser Cys Asn Val
    290                 295                 300

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

Ala Ala Ser Gln Gln Arg His Thr Gly Phe Ile Phe Gln Ser Ser Ile
                325                 330                 335

Val Gln Ser Ala Gln Pro Glu Asp Arg Arg Arg Ala Gln Arg Ala Val
            340                 345                 350

Ser Ala Lys Cys Ala Leu Ala Ala Arg Ile Asp Ala Gly Lys Gly Ser
        355                 360                 365

Arg Asp Gly Ser Tyr Gly Arg Lys Cys Leu Ala Asp Leu Gln Lys Arg
    370                 375                 380

Ile Glu Lys Met Ala Glu Pro Pro Pro Asn Lys Met Ile Lys Ala Leu
385                 390                 395                 400

Pro Ile Pro Gln Glu Thr Asn Arg Lys Lys Arg Gly Gly Lys Arg Ala
                405                 410                 415

Arg Lys Ala Lys Glu Ala Tyr Ala Gln Thr Glu Leu Arg Lys Leu Gln
            420                 425                 430

Asn Arg Met Glu Phe Gly Lys Ala Glu Glu Glu Ile Gly Val Asp Asp
        435                 440                 445

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

Glu Met Ala Asp Ala Arg Ser Lys Ala Lys Leu Ser Arg Ala Asn Lys
465                 470                 475                 480

Leu Arg Thr Gln Leu Leu Gly Arg Ser Val Thr Ser Asn Asp Ala Ala
                485                 490                 495

Ser Gly Met Ala Thr Ser Leu Ser Phe Thr Pro Val Gln Gly Leu Glu
            500                 505                 510

Ile Val Thr Pro Ser Leu Ser Ala Ala Gln Lys Val Gln Ala Ala Asn
        515                 520                 525

Asp Arg Trp Phe Ser Gly Gly Thr Phe Thr His Val Arg Lys Gly Gly
    530                 535                 540

Ser Ser Ile Pro Gly Gln Glu Gln Lys
545                 550


<210> SEQ ID NO 13
<211> LENGTH: 759
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
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<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(759)

<400> SEQUENCE: 13

atg tca tca act gat ctc gga ggc caa gct gcc gtc atc act ggc ggt       48
Met Ser Ser Thr Asp Leu Gly Gly Gln Ala Ala Val Ile Thr Gly Gly
1               5                   10                  15

ggt aag aat ctt ggt gct ttg att gcg aag act ctc gcc aag cag gga       96
Gly Lys Asn Leu Gly Ala Leu Ile Ala Lys Thr Leu Ala Lys Gln Gly
            20                  25                  30

gtc aac gtt gcg atc cat tac aac tcg gcc agt tcc aag tcc gag aca      144
Val Asn Val Ala Ile His Tyr Asn Ser Ala Ser Ser Lys Ser Glu Thr
        35                  40                  45

gaa gct aca ttg aag aca ctc gga tcg tat ggg gtc aaa gcc gct gct      192
Glu Ala Thr Leu Lys Thr Leu Gly Ser Tyr Gly Val Lys Ala Ala Ala
    50                  55                  60

ttc cag gcc aat ctt acc act gag gca tca gtt gag aaa ctc ttc tca      240
Phe Gln Ala Asn Leu Thr Thr Glu Ala Ser Val Glu Lys Leu Phe Ser
65                  70                  75                  80

gac gca gca gct gct ctt gga gtg tcc aag ttc gat atc gcc atc aat      288
Asp Ala Ala Ala Ala Leu Gly Val Ser Lys Phe Asp Ile Ala Ile Asn
                85                  90                  95

acg gtc ggt aag gtt ctt aaa aag cct atc gtt gaa aca aca gag caa      336
Thr Val Gly Lys Val Leu Lys Lys Pro Ile Val Glu Thr Thr Glu Gln
            100                 105                 110

gga ttc gac gac atg ttc cta gtc aac tca aag tgt gcc ttc ttt ttt      384
Gly Phe Asp Asp Met Phe Leu Val Asn Ser Lys Cys Ala Phe Phe Phe
        115                 120                 125

atc aag cat gcg gcc aag aat ctc aac gag ggg ggc acg att ata tca      432
Ile Lys His Ala Ala Lys Asn Leu Asn Glu Gly Gly Thr Ile Ile Ser
    130                 135                 140

ctc gtg act tca ctc ctt gga gca ttt gcg cct ggt tat tca act tat      480
Leu Val Thr Ser Leu Leu Gly Ala Phe Ala Pro Gly Tyr Ser Thr Tyr
145                 150                 155                 160

caa ggc agt aaa gct cct gta gag tgg ttc act aag tcg gct gcc aag      528
Gln Gly Ser Lys Ala Pro Val Glu Trp Phe Thr Lys Ser Ala Ala Lys
                165                 170                 175

gag ctt cag cct aag aat att agg gtc aac tgt gtg gct ccg ggg cca      576
Glu Leu Gln Pro Lys Asn Ile Arg Val Asn Cys Val Ala Pro Gly Pro
            180                 185                 190

atg gac act ccc ttc ttt tac ggg caa gag act gaa gat gcc gtt gct      624
Met Asp Thr Pro Phe Phe Tyr Gly Gln Glu Thr Glu Asp Ala Val Ala
        195                 200                 205

ttc cat aaa agc cag gcg ctc aca gga cgg ctc aca gat att aaa gat      672
Phe His Lys Ser Gln Ala Leu Thr Gly Arg Leu Thr Asp Ile Lys Asp
    210                 215                 220

att gca cca ttg gtg gag ttc ctt tgc aag gat aag tgg att acc gga      720
Ile Ala Pro Leu Val Glu Phe Leu Cys Lys Asp Lys Trp Ile Thr Gly
225                 230                 235                 240

caa gtc atc ttc tca aat gga ggt tac acg act cgc tga                  759
Gln Val Ile Phe Ser Asn Gly Gly Tyr Thr Thr Arg
                245                 250


<210> SEQ ID NO 14
<211> LENGTH: 252
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 14

Met Ser Ser Thr Asp Leu Gly Gly Gln Ala Ala Val Ile Thr Gly Gly
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1               5                   10                  15

Gly Lys Asn Leu Gly Ala Leu Ile Ala Lys Thr Leu Ala Lys Gln Gly
            20                  25                  30

Val Asn Val Ala Ile His Tyr Asn Ser Ala Ser Ser Lys Ser Glu Thr
        35                  40                  45

Glu Ala Thr Leu Lys Thr Leu Gly Ser Tyr Gly Val Lys Ala Ala Ala
    50                  55                  60

Phe Gln Ala Asn Leu Thr Thr Glu Ala Ser Val Glu Lys Leu Phe Ser
65                  70                  75                  80

Asp Ala Ala Ala Ala Leu Gly Val Ser Lys Phe Asp Ile Ala Ile Asn
                85                  90                  95

Thr Val Gly Lys Val Leu Lys Lys Pro Ile Val Glu Thr Thr Glu Gln
            100                 105                 110

Gly Phe Asp Asp Met Phe Leu Val Asn Ser Lys Cys Ala Phe Phe Phe
        115                 120                 125

Ile Lys His Ala Ala Lys Asn Leu Asn Glu Gly Gly Thr Ile Ile Ser
    130                 135                 140

Leu Val Thr Ser Leu Leu Gly Ala Phe Ala Pro Gly Tyr Ser Thr Tyr
145                 150                 155                 160

Gln Gly Ser Lys Ala Pro Val Glu Trp Phe Thr Lys Ser Ala Ala Lys
                165                 170                 175

Glu Leu Gln Pro Lys Asn Ile Arg Val Asn Cys Val Ala Pro Gly Pro
            180                 185                 190

Met Asp Thr Pro Phe Phe Tyr Gly Gln Glu Thr Glu Asp Ala Val Ala
        195                 200                 205

Phe His Lys Ser Gln Ala Leu Thr Gly Arg Leu Thr Asp Ile Lys Asp
    210                 215                 220

Ile Ala Pro Leu Val Glu Phe Leu Cys Lys Asp Lys Trp Ile Thr Gly
225                 230                 235                 240

Gln Val Ile Phe Ser Asn Gly Gly Tyr Thr Thr Arg
                245                 250


<210> SEQ ID NO 15
<211> LENGTH: 2199
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(2199)

<400> SEQUENCE: 15

atg cag cac cac ccc gcg gta gca gca cag ccg ggc cgc act att gcc       48
Met Gln His His Pro Ala Val Ala Ala Gln Pro Gly Arg Thr Ile Ala
1               5                   10                  15

cct atc ccg cac cac cgc cca cag caa ccc cgg atc act cct tac aca       96
Pro Ile Pro His His Arg Pro Gln Gln Pro Arg Ile Thr Pro Tyr Thr
            20                  25                  30

cca aac gta cgc gac ctc aac cca gga cct aag aac aga ctc atc ctc      144
Pro Asn Val Arg Asp Leu Asn Pro Gly Pro Lys Asn Arg Leu Ile Leu
        35                  40                  45

gcc ctc cgc tcc aac atc ccc ttt gaa gtc gac tgg gcg cta ccg cag      192
Ala Leu Arg Ser Asn Ile Pro Phe Glu Val Asp Trp Ala Leu Pro Gln
    50                  55                  60

ctt gtt gtc gca agt ttc gac cag tcg gac ggg ttc aag ctc gag gca      240
Leu Val Val Ala Ser Phe Asp Gln Ser Asp Gly Phe Lys Leu Glu Ala
65                  70                  75                  80

tgg cca gac agc att tgc gcg ttg aag gaa tgg ccg gcc aag tgg ctt      288
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Trp Pro Asp Ser Ile Cys Ala Leu Lys Glu Trp Pro Ala Lys Trp Leu
                85                  90                  95

gaa gga cta gaa agg gaa gct gca gtg ttt gag atg aaa gct ggg cga      336
Glu Gly Leu Glu Arg Glu Ala Ala Val Phe Glu Met Lys Ala Gly Arg
            100                 105                 110

ttg gat ttt gag ggg gac gag aat gat gaa gag ggg agg atg gca aag      384
Leu Asp Phe Glu Gly Asp Glu Asn Asp Glu Glu Gly Arg Met Ala Lys
        115                 120                 125

cgc aga aaa agg gat ctg gcg ctg ggg gcg gtg gta gag tgg gag aac      432
Arg Arg Lys Arg Asp Leu Ala Leu Gly Ala Val Val Glu Trp Glu Asn
    130                 135                 140

gat ctc aag gtg gaa caa cgg gcg acc aac tct ttg ctc gtc ctc aga      480
Asp Leu Lys Val Glu Gln Arg Ala Thr Asn Ser Leu Leu Val Leu Arg
145                 150                 155                 160

aac gca tcc ttc aac gca ccc aac gca aag atc ctc tca agc tca agc      528
Asn Ala Ser Phe Asn Ala Pro Asn Ala Lys Ile Leu Ser Ser Ser Ser
                165                 170                 175

ttc ctc gct ttt cta gcc gat ttc ttc tct ttg cct cta ccg ttt ctc      576
Phe Leu Ala Phe Leu Ala Asp Phe Phe Ser Leu Pro Leu Pro Phe Leu
            180                 185                 190

cag cat ctt tgc ctg aga acc cca gag cct ata cat cat atc ctc atc      624
Gln His Leu Cys Leu Arg Thr Pro Glu Pro Ile His His Ile Leu Ile
        195                 200                 205

att gtc cag tcc atc ttc ccc cat ttg cgc gtg gac atg cca ggt atc      672
Ile Val Gln Ser Ile Phe Pro His Leu Arg Val Asp Met Pro Gly Ile
    210                 215                 220

gac cgc atc aag cac atc ttt ggc gtc gtc ttc cct cag ctt ttt gtt      720
Asp Arg Ile Lys His Ile Phe Gly Val Val Phe Pro Gln Leu Phe Val
225                 230                 235                 240

gat acc cgc gat atc gca atg atg aac aac ctt atc cct ctc atg atg      768
Asp Thr Arg Asp Ile Ala Met Met Asn Asn Leu Ile Pro Leu Met Met
                245                 250                 255

atg ggc cag aca atc ccc aat aac cac cct cct ccg cct gaa ctc atc      816
Met Gly Gln Thr Ile Pro Asn Asn His Pro Pro Pro Pro Glu Leu Ile
            260                 265                 270

cct cat ctt ctc cag ctt ctc gtt ctc cgt cca gca ggc cca ctt ctc      864
Pro His Leu Leu Gln Leu Leu Val Leu Arg Pro Ala Gly Pro Leu Leu
        275                 280                 285

gat ttg act ctt gac atc ctc atc tcc ctc tcc aca aat ccc atc cac      912
Asp Leu Thr Leu Asp Ile Leu Ile Ser Leu Ser Thr Asn Pro Ile His
    290                 295                 300

tcc cgt gcc ata ctt tct cat act tct ttc ccg cat cat ctc aaa tcc      960
Ser Arg Ala Ile Leu Ser His Thr Ser Phe Pro His His Leu Lys Ser
305                 310                 315                 320

atc aca gcc tta ctc gaa cat caa gct cgt ccg gtg gtg aat gcc ctt     1008
Ile Thr Ala Leu Leu Glu His Gln Ala Arg Pro Val Val Asn Ala Leu
                325                 330                 335

gac cca ccg cct tct acg aga ggg aaa atg gtg cgt aac cca gcg gga     1056
Asp Pro Pro Pro Ser Thr Arg Gly Lys Met Val Arg Asn Pro Ala Gly
            340                 345                 350

ccg agt tgc aga gca gag gaa ctt aat caa agg cgg acg aag gaa cga     1104
Pro Ser Cys Arg Ala Glu Glu Leu Asn Gln Arg Arg Thr Lys Glu Arg
        355                 360                 365

gag gcc gca ttg gga cat atg gat ccc atg gct gga ggt aga ccg gtg     1152
Glu Ala Ala Leu Gly His Met Asp Pro Met Ala Gly Gly Arg Pro Val
    370                 375                 380

tac aat gag gta ggg gat aag cca ccg aca ttt agt ccg gcg acg aag     1200
Tyr Asn Glu Val Gly Asp Lys Pro Pro Thr Phe Ser Pro Ala Thr Lys
385                 390                 395                 400
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aag agg ctt ttc agg atg aaa gaa ccc gaa agg tct atc gag tgg atg     1248
Lys Arg Leu Phe Arg Met Lys Glu Pro Glu Arg Ser Ile Glu Trp Met
                405                 410                 415

cac cag gca ttc gtc tac tca tcg aca gcc caa gtc ctt caa gtg aca     1296
His Gln Ala Phe Val Tyr Ser Ser Thr Ala Gln Val Leu Gln Val Thr
            420                 425                 430

ttc tgg cac gcc tac cga gat ttc ttc acc aac cca gct tgc gta gaa     1344
Phe Trp His Ala Tyr Arg Asp Phe Phe Thr Asn Pro Ala Cys Val Glu
        435                 440                 445

cca atg ttg agt gca tct gat gtg atc aag aat gtc act gca gct ttc     1392
Pro Met Leu Ser Ala Ser Asp Val Ile Lys Asn Val Thr Ala Ala Phe
    450                 455                 460

cct gga gcg agc gca aaa gtt tgg acc gat gcg agt ggt gcg caa aag     1440
Pro Gly Ala Ser Ala Lys Val Trp Thr Asp Ala Ser Gly Ala Gln Lys
465                 470                 475                 480

ttt gtg att gct ggt gtc ggg ttc agg aag cga tca gat gac gat gaa     1488
Phe Val Ile Ala Gly Val Gly Phe Arg Lys Arg Ser Asp Asp Asp Glu
                485                 490                 495

agg ttt aca tgt tac tgg cat gca tgc acc caa cgg tac tca gct acc     1536
Arg Phe Thr Cys Tyr Trp His Ala Cys Thr Gln Arg Tyr Ser Ala Thr
            500                 505                 510

aac ccc gtc caa ctg ctc gaa cac att agc aac tac cat ctc caa acc     1584
Asn Pro Val Gln Leu Leu Glu His Ile Ser Asn Tyr His Leu Gln Thr
        515                 520                 525

ttt tct gca ccc caa tgc caa tgg ggc tca tgc gat cac aac ctc tgc     1632
Phe Ser Ala Pro Gln Cys Gln Trp Gly Ser Cys Asp His Asn Leu Cys
    530                 535                 540

acg tac tct cat ctc ctc acc cat atc ccc ctc ggc cag cct cca tcc     1680
Thr Tyr Ser His Leu Leu Thr His Ile Pro Leu Gly Gln Pro Pro Ser
545                 550                 555                 560

tcc atc tcc gtc cct gac gcc atc tct tgc cat atc gca gac cat agt     1728
Ser Ile Ser Val Pro Asp Ala Ile Ser Cys His Ile Ala Asp His Ser
                565                 570                 575

agc tcc gtc ttg cag cgc aag atc acc aat cgt acc gtc cct cct tta     1776
Ser Ser Val Leu Gln Arg Lys Ile Thr Asn Arg Thr Val Pro Pro Leu
            580                 585                 590

tcc agc gtt cgt cta gcc gtt cag ggg gca ttt acc cct gtc gac gct     1824
Ser Ser Val Arg Leu Ala Val Gln Gly Ala Phe Thr Pro Val Asp Ala
        595                 600                 605

cgt cga caa cct act ggc gcc gcc ctt ctc gcg gcg tta ctt atc cgt     1872
Arg Arg Gln Pro Thr Gly Ala Ala Leu Leu Ala Ala Leu Leu Ile Arg
    610                 615                 620

aac ctc gcc cgt acc ctc cgt gcc gag atc tcg ctc gcc gtg ccc gaa     1920
Asn Leu Ala Arg Thr Leu Arg Ala Glu Ile Ser Leu Ala Val Pro Glu
625                 630                 635                 640

ttg tct cat gct caa acg caa gaa acg gca gat gaa gct caa gcg aga     1968
Leu Ser His Ala Gln Thr Gln Glu Thr Ala Asp Glu Ala Gln Ala Arg
                645                 650                 655

aaa aaa cac ctt ctc gaa gag agg tat gga ttg cca atc ccg gat tcg     2016
Lys Lys His Leu Leu Glu Glu Arg Tyr Gly Leu Pro Ile Pro Asp Ser
            660                 665                 670

gtg ttg aaa gaa gaa gaa gag gag cag gcg aat gtg cag caa ggc caa     2064
Val Leu Lys Glu Glu Glu Glu Glu Gln Ala Asn Val Gln Gln Gly Gln
        675                 680                 685

gat tta gat atg agt gag gaa gag agg gag agg gcg aaa aag gcg ttt     2112
Asp Leu Asp Met Ser Glu Glu Glu Arg Glu Arg Ala Lys Lys Ala Phe
    690                 695                 700

gag aat gtg gag gag agg att atg aag gtc atg ttg gag aat gtt agt     2160
Glu Asn Val Glu Glu Arg Ile Met Lys Val Met Leu Glu Asn Val Ser
705                 710                 715                 720
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ggg ata acg cag tat ctt ggt gat gcg ctt ggg ctg tag                 2199
Gly Ile Thr Gln Tyr Leu Gly Asp Ala Leu Gly Leu
                725                 730


<210> SEQ ID NO 16
<211> LENGTH: 732
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 16

Met Gln His His Pro Ala Val Ala Ala Gln Pro Gly Arg Thr Ile Ala
1               5                   10                  15

Pro Ile Pro His His Arg Pro Gln Gln Pro Arg Ile Thr Pro Tyr Thr
            20                  25                  30

Pro Asn Val Arg Asp Leu Asn Pro Gly Pro Lys Asn Arg Leu Ile Leu
        35                  40                  45

Ala Leu Arg Ser Asn Ile Pro Phe Glu Val Asp Trp Ala Leu Pro Gln
    50                  55                  60

Leu Val Val Ala Ser Phe Asp Gln Ser Asp Gly Phe Lys Leu Glu Ala
65                  70                  75                  80

Trp Pro Asp Ser Ile Cys Ala Leu Lys Glu Trp Pro Ala Lys Trp Leu
                85                  90                  95

Glu Gly Leu Glu Arg Glu Ala Ala Val Phe Glu Met Lys Ala Gly Arg
            100                 105                 110

Leu Asp Phe Glu Gly Asp Glu Asn Asp Glu Glu Gly Arg Met Ala Lys
        115                 120                 125

Arg Arg Lys Arg Asp Leu Ala Leu Gly Ala Val Val Glu Trp Glu Asn
    130                 135                 140

Asp Leu Lys Val Glu Gln Arg Ala Thr Asn Ser Leu Leu Val Leu Arg
145                 150                 155                 160

Asn Ala Ser Phe Asn Ala Pro Asn Ala Lys Ile Leu Ser Ser Ser Ser
                165                 170                 175

Phe Leu Ala Phe Leu Ala Asp Phe Phe Ser Leu Pro Leu Pro Phe Leu
            180                 185                 190

Gln His Leu Cys Leu Arg Thr Pro Glu Pro Ile His His Ile Leu Ile
        195                 200                 205

Ile Val Gln Ser Ile Phe Pro His Leu Arg Val Asp Met Pro Gly Ile
    210                 215                 220

Asp Arg Ile Lys His Ile Phe Gly Val Val Phe Pro Gln Leu Phe Val
225                 230                 235                 240

Asp Thr Arg Asp Ile Ala Met Met Asn Asn Leu Ile Pro Leu Met Met
                245                 250                 255

Met Gly Gln Thr Ile Pro Asn Asn His Pro Pro Pro Pro Glu Leu Ile
            260                 265                 270

Pro His Leu Leu Gln Leu Leu Val Leu Arg Pro Ala Gly Pro Leu Leu
        275                 280                 285

Asp Leu Thr Leu Asp Ile Leu Ile Ser Leu Ser Thr Asn Pro Ile His
    290                 295                 300

Ser Arg Ala Ile Leu Ser His Thr Ser Phe Pro His His Leu Lys Ser
305                 310                 315                 320

Ile Thr Ala Leu Leu Glu His Gln Ala Arg Pro Val Val Asn Ala Leu
                325                 330                 335

Asp Pro Pro Pro Ser Thr Arg Gly Lys Met Val Arg Asn Pro Ala Gly
            340                 345                 350
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Pro Ser Cys Arg Ala Glu Glu Leu Asn Gln Arg Arg Thr Lys Glu Arg
        355                 360                 365

Glu Ala Ala Leu Gly His Met Asp Pro Met Ala Gly Gly Arg Pro Val
    370                 375                 380

Tyr Asn Glu Val Gly Asp Lys Pro Pro Thr Phe Ser Pro Ala Thr Lys
385                 390                 395                 400

Lys Arg Leu Phe Arg Met Lys Glu Pro Glu Arg Ser Ile Glu Trp Met
                405                 410                 415

His Gln Ala Phe Val Tyr Ser Ser Thr Ala Gln Val Leu Gln Val Thr
            420                 425                 430

Phe Trp His Ala Tyr Arg Asp Phe Phe Thr Asn Pro Ala Cys Val Glu
        435                 440                 445

Pro Met Leu Ser Ala Ser Asp Val Ile Lys Asn Val Thr Ala Ala Phe
    450                 455                 460

Pro Gly Ala Ser Ala Lys Val Trp Thr Asp Ala Ser Gly Ala Gln Lys
465                 470                 475                 480

Phe Val Ile Ala Gly Val Gly Phe Arg Lys Arg Ser Asp Asp Asp Glu
                485                 490                 495

Arg Phe Thr Cys Tyr Trp His Ala Cys Thr Gln Arg Tyr Ser Ala Thr
            500                 505                 510

Asn Pro Val Gln Leu Leu Glu His Ile Ser Asn Tyr His Leu Gln Thr
        515                 520                 525

Phe Ser Ala Pro Gln Cys Gln Trp Gly Ser Cys Asp His Asn Leu Cys
    530                 535                 540

Thr Tyr Ser His Leu Leu Thr His Ile Pro Leu Gly Gln Pro Pro Ser
545                 550                 555                 560

Ser Ile Ser Val Pro Asp Ala Ile Ser Cys His Ile Ala Asp His Ser
                565                 570                 575

Ser Ser Val Leu Gln Arg Lys Ile Thr Asn Arg Thr Val Pro Pro Leu
            580                 585                 590

Ser Ser Val Arg Leu Ala Val Gln Gly Ala Phe Thr Pro Val Asp Ala
        595                 600                 605

Arg Arg Gln Pro Thr Gly Ala Ala Leu Leu Ala Ala Leu Leu Ile Arg
    610                 615                 620

Asn Leu Ala Arg Thr Leu Arg Ala Glu Ile Ser Leu Ala Val Pro Glu
625                 630                 635                 640

Leu Ser His Ala Gln Thr Gln Glu Thr Ala Asp Glu Ala Gln Ala Arg
                645                 650                 655

Lys Lys His Leu Leu Glu Glu Arg Tyr Gly Leu Pro Ile Pro Asp Ser
            660                 665                 670

Val Leu Lys Glu Glu Glu Glu Glu Gln Ala Asn Val Gln Gln Gly Gln
        675                 680                 685

Asp Leu Asp Met Ser Glu Glu Glu Arg Glu Arg Ala Lys Lys Ala Phe
    690                 695                 700

Glu Asn Val Glu Glu Arg Ile Met Lys Val Met Leu Glu Asn Val Ser
705                 710                 715                 720

Gly Ile Thr Gln Tyr Leu Gly Asp Ala Leu Gly Leu
                725                 730


<210> SEQ ID NO 17
<211> LENGTH: 1305
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
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<222> LOCATION: (1)..(1305)

<400> SEQUENCE: 17

atg aga ctc acg att att gcc cca gac tcg gtt cat gag cac gaa gtg        48
Met Arg Leu Thr Ile Ile Ala Pro Asp Ser Val His Glu His Glu Val
1               5                   10                  15

tcc cct tcc ttg ctc atc caa gac atc atc aac atc gtt gag gca act        96
Ser Pro Ser Leu Leu Ile Gln Asp Ile Ile Asn Ile Val Glu Ala Thr
            20                  25                  30

gcc gac ctt ccc ccg gct gtt att gtt ctc aca agt gac gcc ggt aca       144
Ala Asp Leu Pro Pro Ala Val Ile Val Leu Thr Ser Asp Ala Gly Thr
        35                  40                  45

cca ctc acg gac ccc aca aga act ctc gaa agc tat ggg tta aat gga       192
Pro Leu Thr Asp Pro Thr Arg Thr Leu Glu Ser Tyr Gly Leu Asn Gly
    50                  55                  60

gag acc gcc acc atc ttc ctt aca cct aca gga cca ccc gtc gct tct       240
Glu Thr Ala Thr Ile Phe Leu Thr Pro Thr Gly Pro Pro Val Ala Ser
65                  70                  75                  80

tcg tct tcc att cca ttc cct gat gca gat gcc gac att gaa agg atg       288
Ser Ser Ser Ile Pro Phe Pro Asp Ala Asp Ala Asp Ile Glu Arg Met
                85                  90                  95

cgt tta caa gcg ctc gga aat cct tct ttg atg aat gat ttg cgt gag       336
Arg Leu Gln Ala Leu Gly Asn Pro Ser Leu Met Asn Asp Leu Arg Glu
            100                 105                 110

cgt gat ccg gaa acc ttt gcc gct att caa ggg ggt act caa agc ttc       384
Arg Asp Pro Glu Thr Phe Ala Ala Ile Gln Gly Gly Thr Gln Ser Phe
        115                 120                 125

aaa aaa gcc ctc caa ctg gcg caa tca aga caa aga gat gcc gaa ttc       432
Lys Lys Ala Leu Gln Leu Ala Gln Ser Arg Gln Arg Asp Ala Glu Phe
    130                 135                 140

gaa aag caa cgc cag att gaa gca ctc aat gcc gac cct tat gac att       480
Glu Lys Gln Arg Gln Ile Glu Ala Leu Asn Ala Asp Pro Tyr Asp Ile
145                 150                 155                 160

gaa gct cag aaa aag att gag gaa gca att cgg atg gag gcc gtt ttg       528
Glu Ala Gln Lys Lys Ile Glu Glu Ala Ile Arg Met Glu Ala Val Leu
                165                 170                 175

gag aat atg cag cac gct atg gaa tat tcc cct gag tcg ttt gga aac       576
Glu Asn Met Gln His Ala Met Glu Tyr Ser Pro Glu Ser Phe Gly Asn
            180                 185                 190

gtg acc atg ctg tat atc aat gtg gaa gta aat ggt cat cct gtt aag       624
Val Thr Met Leu Tyr Ile Asn Val Glu Val Asn Gly His Pro Val Lys
        195                 200                 205

gca ttc gtt gat tct ggt gca caa aca acg atc att tcc cct gaa tgt       672
Ala Phe Val Asp Ser Gly Ala Gln Thr Thr Ile Ile Ser Pro Glu Cys
    210                 215                 220

gcc gag caa tgt gga atc atg cgc ctg ctt gat act cgt ttc gcg ggt       720
Ala Glu Gln Cys Gly Ile Met Arg Leu Leu Asp Thr Arg Phe Ala Gly
225                 230                 235                 240

atg gcc gaa gga gta gga aca gct cgt atc ctc ggt cgt atc cac tct       768
Met Ala Glu Gly Val Gly Thr Ala Arg Ile Leu Gly Arg Ile His Ser
                245                 250                 255

gcc caa att aag ctc ggc tca ctc tac ctc cct tgt gca ttc tcc gtc       816
Ala Gln Ile Lys Leu Gly Ser Leu Tyr Leu Pro Cys Ala Phe Ser Val
            260                 265                 270

ctc gaa ggc cgt tct gtc gac ctc tta ttt ggt ctt gac atg ctt aaa       864
Leu Glu Gly Arg Ser Val Asp Leu Leu Phe Gly Leu Asp Met Leu Lys
        275                 280                 285

cgc cat caa tgc tgt atc gac ctc tcc acg aac acg ctc cgg ata aat       912
Arg His Gln Cys Cys Ile Asp Leu Ser Thr Asn Thr Leu Arg Ile Asn
    290                 295                 300
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aac act gaa gta ccc ttt ttg tcg gag cac gag ctg cct gac aag gcg      960
Asn Thr Glu Val Pro Phe Leu Ser Glu His Glu Leu Pro Asp Lys Ala
305                 310                 315                 320

aga aga cgt ggg gag gcg caa gtg gcc ggg gaa atg ggt gat gcg gca     1008
Arg Arg Arg Gly Glu Ala Gln Val Ala Gly Glu Met Gly Asp Ala Ala
                325                 330                 335

ggg caa ggc gtg aaa gcg ggt gtg gcg agt ccg aag att ggg aag aag     1056
Gly Gln Gly Val Lys Ala Gly Val Ala Ser Pro Lys Ile Gly Lys Lys
            340                 345                 350

acg ttt ccg gga gag ggg cat gcg ctt ggt gcg ggc agc tcg act gga     1104
Thr Phe Pro Gly Glu Gly His Ala Leu Gly Ala Gly Ser Ser Thr Gly
        355                 360                 365

cca ggg acg gct acg ggg agt gca agt gcg aca ggt gca agg act ggg     1152
Pro Gly Thr Ala Thr Gly Ser Ala Ser Ala Thr Gly Ala Arg Thr Gly
    370                 375                 380

ggg act gca agt gtc ccc tcg cct tca aat agg tgg aaa gag gac gat     1200
Gly Thr Ala Ser Val Pro Ser Pro Ser Asn Arg Trp Lys Glu Asp Asp
385                 390                 395                 400

att caa acg ctt gtg aac ctg ggt gcc cct cga gcg caa gct ata cag     1248
Ile Gln Thr Leu Val Asn Leu Gly Ala Pro Arg Ala Gln Ala Ile Gln
                405                 410                 415

cta ctt gaa gcg tca ggt gga aac gtg gat gtt gct gct tct atg ctc     1296
Leu Leu Glu Ala Ser Gly Gly Asn Val Asp Val Ala Ala Ser Met Leu
            420                 425                 430

ttt ggt tag                                                         1305
Phe Gly


<210> SEQ ID NO 18
<211> LENGTH: 434
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 18

Met Arg Leu Thr Ile Ile Ala Pro Asp Ser Val His Glu His Glu Val
1               5                   10                  15

Ser Pro Ser Leu Leu Ile Gln Asp Ile Ile Asn Ile Val Glu Ala Thr
            20                  25                  30

Ala Asp Leu Pro Pro Ala Val Ile Val Leu Thr Ser Asp Ala Gly Thr
        35                  40                  45

Pro Leu Thr Asp Pro Thr Arg Thr Leu Glu Ser Tyr Gly Leu Asn Gly
    50                  55                  60

Glu Thr Ala Thr Ile Phe Leu Thr Pro Thr Gly Pro Pro Val Ala Ser
65                  70                  75                  80

Ser Ser Ser Ile Pro Phe Pro Asp Ala Asp Ala Asp Ile Glu Arg Met
                85                  90                  95

Arg Leu Gln Ala Leu Gly Asn Pro Ser Leu Met Asn Asp Leu Arg Glu
            100                 105                 110

Arg Asp Pro Glu Thr Phe Ala Ala Ile Gln Gly Gly Thr Gln Ser Phe
        115                 120                 125

Lys Lys Ala Leu Gln Leu Ala Gln Ser Arg Gln Arg Asp Ala Glu Phe
    130                 135                 140

Glu Lys Gln Arg Gln Ile Glu Ala Leu Asn Ala Asp Pro Tyr Asp Ile
145                 150                 155                 160

Glu Ala Gln Lys Lys Ile Glu Glu Ala Ile Arg Met Glu Ala Val Leu
                165                 170                 175

Glu Asn Met Gln His Ala Met Glu Tyr Ser Pro Glu Ser Phe Gly Asn
            180                 185                 190
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Val Thr Met Leu Tyr Ile Asn Val Glu Val Asn Gly His Pro Val Lys
        195                 200                 205

Ala Phe Val Asp Ser Gly Ala Gln Thr Thr Ile Ile Ser Pro Glu Cys
    210                 215                 220

Ala Glu Gln Cys Gly Ile Met Arg Leu Leu Asp Thr Arg Phe Ala Gly
225                 230                 235                 240

Met Ala Glu Gly Val Gly Thr Ala Arg Ile Leu Gly Arg Ile His Ser
                245                 250                 255

Ala Gln Ile Lys Leu Gly Ser Leu Tyr Leu Pro Cys Ala Phe Ser Val
            260                 265                 270

Leu Glu Gly Arg Ser Val Asp Leu Leu Phe Gly Leu Asp Met Leu Lys
        275                 280                 285

Arg His Gln Cys Cys Ile Asp Leu Ser Thr Asn Thr Leu Arg Ile Asn
    290                 295                 300

Asn Thr Glu Val Pro Phe Leu Ser Glu His Glu Leu Pro Asp Lys Ala
305                 310                 315                 320

Arg Arg Arg Gly Glu Ala Gln Val Ala Gly Glu Met Gly Asp Ala Ala
                325                 330                 335

Gly Gln Gly Val Lys Ala Gly Val Ala Ser Pro Lys Ile Gly Lys Lys
            340                 345                 350

Thr Phe Pro Gly Glu Gly His Ala Leu Gly Ala Gly Ser Ser Thr Gly
        355                 360                 365

Pro Gly Thr Ala Thr Gly Ser Ala Ser Ala Thr Gly Ala Arg Thr Gly
    370                 375                 380

Gly Thr Ala Ser Val Pro Ser Pro Ser Asn Arg Trp Lys Glu Asp Asp
385                 390                 395                 400

Ile Gln Thr Leu Val Asn Leu Gly Ala Pro Arg Ala Gln Ala Ile Gln
                405                 410                 415

Leu Leu Glu Ala Ser Gly Gly Asn Val Asp Val Ala Ala Ser Met Leu
            420                 425                 430

Phe Gly


<210> SEQ ID NO 19
<211> LENGTH: 3555
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(3555)

<400> SEQUENCE: 19

atg tct tcg cca gaa cca gag gag cct cgc aga ggt gca agg gtc agg       48
Met Ser Ser Pro Glu Pro Glu Glu Pro Arg Arg Gly Ala Arg Val Arg
1               5                   10                  15

aag cag gtt aat aag ttt gat gct agc cag cag aac ggg agg ggc aag       96
Lys Gln Val Asn Lys Phe Asp Ala Ser Gln Gln Asn Gly Arg Gly Lys
            20                  25                  30

aga aag cac att gaa gac agg gag gac gac gac cag gag ggt ttg ata      144
Arg Lys His Ile Glu Asp Arg Glu Asp Asp Asp Gln Glu Gly Leu Ile
        35                  40                  45

cca gac ccg gaa gac gag tct gat cac gaa cca act ccc aag aag aag      192
Pro Asp Pro Glu Asp Glu Ser Asp His Glu Pro Thr Pro Lys Lys Lys
    50                  55                  60

aag ccg gcg gca cca cga aaa tct cga gct tct gcg ggt act acc aag      240
Lys Pro Ala Ala Pro Arg Lys Ser Arg Ala Ser Ala Gly Thr Thr Lys
65                  70                  75                  80
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aag gac gga cca aag aca aaa aca aag cct gca gct gaa ggc gtg agc       288
Lys Asp Gly Pro Lys Thr Lys Thr Lys Pro Ala Ala Glu Gly Val Ser
                85                  90                  95

gaa atc gta gaa aag act gat tcg cct tta ttt aat gct ctc cag caa       336
Glu Ile Val Glu Lys Thr Asp Ser Pro Leu Phe Asn Ala Leu Gln Gln
            100                 105                 110

ccc gat atc gcc ctt caa cct ctg att gat gag tgg atc gag acc tac       384
Pro Asp Ile Ala Leu Gln Pro Leu Ile Asp Glu Trp Ile Glu Thr Tyr
        115                 120                 125

caa caa gcc gct ggt gat gaa ata tca gag cag aaa tcc att cac gaa       432
Gln Gln Ala Ala Gly Asp Glu Ile Ser Glu Gln Lys Ser Ile His Glu
    130                 135                 140

ctg gtt gtc ttc ttc att cga tgt tgc ggt atg act acc gag atc gag       480
Leu Val Val Phe Phe Ile Arg Cys Cys Gly Met Thr Thr Glu Ile Glu
145                 150                 155                 160

caa gct gaa gca acg gat gac gat ggt atc ccc gat gtc atc gag cga       528
Gln Ala Glu Ala Thr Asp Asp Asp Gly Ile Pro Asp Val Ile Glu Arg
                165                 170                 175

gtg cag gat gaa agc gtt cgc gta gcg ttg gcg act tat ccc tta att       576
Val Gln Asp Glu Ser Val Arg Val Ala Leu Ala Thr Tyr Pro Leu Ile
            180                 185                 190

tcc aaa gca aag aat ttt aag ccc ttc aag tcc aat ttg aac gag ttc       624
Ser Lys Ala Lys Asn Phe Lys Pro Phe Lys Ser Asn Leu Asn Glu Phe
        195                 200                 205

att tca cac ttt att tca tcg ctc gct ctc aca cct atc ctc ttt cac       672
Ile Ser His Phe Ile Ser Ser Leu Ala Leu Thr Pro Ile Leu Phe His
    210                 215                 220

act gcc gac aat act cct cac tca tct ctg ctc atc cca ctt ctc ctc       720
Thr Ala Asp Asn Thr Pro His Ser Ser Leu Leu Ile Pro Leu Leu Leu
225                 230                 235                 240

aac tgg ctg atg tgt atg tca tca tca act ctt cga ccc atc cgt cat       768
Asn Trp Leu Met Cys Met Ser Ser Ser Thr Leu Arg Pro Ile Arg His
                245                 250                 255

acc tca aca tac gtg acg ctc agg atg aac tcg gct ttg tgt gac gtt       816
Thr Ser Thr Tyr Val Thr Leu Arg Met Asn Ser Ala Leu Cys Asp Val
            260                 265                 270

gct gcg gat gtg agc aaa gac ctg agc gtt aag caa agg cag cga gat       864
Ala Ala Asp Val Ser Lys Asp Leu Ser Val Lys Gln Arg Gln Arg Asp
        275                 280                 285

gca gaa gtc aga aaa gct gga gct aca aat gca gcg cag aag aga gtg       912
Ala Glu Val Arg Lys Ala Gly Ala Thr Asn Ala Ala Gln Lys Arg Val
    290                 295                 300

aag gct gcc gag gac agg gtc aag gaa gtg caa gaa aga aag caa act       960
Lys Ala Ala Glu Asp Arg Val Lys Glu Val Gln Glu Arg Lys Gln Thr
305                 310                 315                 320

tta gaa gag ttg atg cag gag atc ttt gat gtg atg ttc gtc cac cga      1008
Leu Glu Glu Leu Met Gln Glu Ile Phe Asp Val Met Phe Val His Arg
                325                 330                 335

gtt cgc gat gcc gat ccc aac att cga acc gat tgt ctg cgt gaa tta      1056
Val Arg Asp Ala Asp Pro Asn Ile Arg Thr Asp Cys Leu Arg Glu Leu
            340                 345                 350

ggt ctg tgg gcc aaa aaa cac cca gag tac tac gtt tcg act tct tat      1104
Gly Leu Trp Ala Lys Lys His Pro Glu Tyr Tyr Val Ser Thr Ser Tyr
        355                 360                 365

ctc tcc tac ttc acc cgt ggc tgt aac gat acc cac gct cat gcc cga      1152
Leu Ser Tyr Phe Thr Arg Gly Cys Asn Asp Thr His Ala His Ala Arg
    370                 375                 380

ctt gag act gtc aag gct ctt gcc aac ctc tac atc cga gaa acc ttt      1200
Leu Glu Thr Val Lys Ala Leu Ala Asn Leu Tyr Ile Arg Glu Thr Phe
385                 390                 395                 400
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atc agt aac gct cga acc ttg acg atg cgt tta gcg cct agg gtg att      1248
Ile Ser Asn Ala Arg Thr Leu Thr Met Arg Leu Ala Pro Arg Val Ile
                405                 410                 415

gag atg gcc acc agg gat gtg gat ttg aat gtg agg gta gtg gct ttg      1296
Glu Met Ala Thr Arg Asp Val Asp Leu Asn Val Arg Val Val Ala Leu
            420                 425                 430

cag gtg att aca ctt ata gac aag acg ggt att ctg caa gac gag gag      1344
Gln Val Ile Thr Leu Ile Asp Lys Thr Gly Ile Leu Gln Asp Glu Glu
        435                 440                 445

gac gag gaa aga gat aag gtg gcg aag ctt gtt ttc gac cag gag cct      1392
Asp Glu Glu Arg Asp Lys Val Ala Lys Leu Val Phe Asp Gln Glu Pro
    450                 455                 460

cga att cga aaa gct gca ggg gcg ttc atc ctt ggt ttg tgg gaa gag      1440
Arg Ile Arg Lys Ala Ala Gly Ala Phe Ile Leu Gly Leu Trp Glu Glu
465                 470                 475                 480

agg aaa gaa ggc ctc aaa gca gtc tgg tcg ggt ctg aga gcg aac aaa      1488
Arg Lys Glu Gly Leu Lys Ala Val Trp Ser Gly Leu Arg Ala Asn Lys
                485                 490                 495

aag aag cgt gca gca aac atc acc gaa gac gaa atg tcc aac tac ctc      1536
Lys Lys Arg Ala Ala Asn Ile Thr Glu Asp Glu Met Ser Asn Tyr Leu
            500                 505                 510

aac tgg aaa tcc ctc gct gca gtt ctc ctc tac acc tct aaa tcc ctg      1584
Asn Trp Lys Ser Leu Ala Ala Val Leu Leu Tyr Thr Ser Lys Ser Leu
        515                 520                 525

gac gac gac cct tct gga caa ccc tct gcc ctc aaa cca agc cta ctc      1632
Asp Asp Asp Pro Ser Gly Gln Pro Ser Ala Leu Lys Pro Ser Leu Leu
    530                 535                 540

att ccg tct tta ccc aat aca cag atg aca agg gcg act gct gcc gtc      1680
Ile Pro Ser Leu Pro Asn Thr Gln Met Thr Arg Ala Thr Ala Ala Val
545                 550                 555                 560

gag tct atc ggt gct gag cat gag ctg tgg aaa gac tgg gag agc ttg      1728
Glu Ser Ile Gly Ala Glu His Glu Leu Trp Lys Asp Trp Glu Ser Leu
                565                 570                 575

gtg gac tat ctt ttg gtg gat cac tcg act aac gaa gaa gat atg tgg      1776
Val Asp Tyr Leu Leu Val Asp His Ser Thr Asn Glu Glu Asp Met Trp
            580                 585                 590

ctg ctc cgt gaa gat gag gaa act ttc atg ttg cag gtg ctt ttg gct      1824
Leu Leu Arg Glu Asp Glu Glu Thr Phe Met Leu Gln Val Leu Leu Ala
        595                 600                 605

tgt att aag cgg gaa gaa aat gaa gag gat gag ccg gat agg acc aaa      1872
Cys Ile Lys Arg Glu Glu Asn Glu Glu Asp Glu Pro Asp Arg Thr Lys
    610                 615                 620

acg ttg ata aag gtt ttg cct cgg tta ttt gcc aag cat cag gct gat      1920
Thr Leu Ile Lys Val Leu Pro Arg Leu Phe Ala Lys His Gln Ala Asp
625                 630                 635                 640

gtt ggt cga atg act ggg att tta tct gtt ccc gga cac atg aag ctc      1968
Val Gly Arg Met Thr Gly Ile Leu Ser Val Pro Gly His Met Lys Leu
                645                 650                 655

agt ctc tat ctc gac atg cgc atg tcc tct gcc tac gag tcc ctc tgg      2016
Ser Leu Tyr Leu Asp Met Arg Met Ser Ser Ala Tyr Glu Ser Leu Trp
            660                 665                 670

gat gac atc agc aaa cag ttc cta aaa tac act tcc cct acc atc ctc      2064
Asp Asp Ile Ser Lys Gln Phe Leu Lys Tyr Thr Ser Pro Thr Ile Leu
        675                 680                 685

aca gca tcc att tct gcg atc agc cat ctc gtc ggc aac tcg tcc ctt      2112
Thr Ala Ser Ile Ser Ala Ile Ser His Leu Val Gly Asn Ser Ser Leu
    690                 695                 700

tca tcc atc aat gaa acc aag ctt tct gag ctg cac gag tct ctc ttc      2160
Ser Ser Ile Asn Glu Thr Lys Leu Ser Glu Leu His Glu Ser Leu Phe
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705                 710                 715                 720

gct tct cta aga gat gcg att ggc tct gaa gat gtt gcg ctt gtc act     2208
Ala Ser Leu Arg Asp Ala Ile Gly Ser Glu Asp Val Ala Leu Val Thr
                725                 730                 735

ttg gag gac gag cag atc agc cag ctg gaa gca atc atg ctg agg ata     2256
Leu Glu Asp Glu Gln Ile Ser Gln Leu Glu Ala Ile Met Leu Arg Ile
            740                 745                 750

acg tta ctg cag aga agt atg gat ttg gta gat gtc atg gag gat gag     2304
Thr Leu Leu Gln Arg Ser Met Asp Leu Val Asp Val Met Glu Asp Glu
        755                 760                 765

gaa ggg cag cag agt agc ggc tgg gac att atc tgt gcg ttt gct gat     2352
Glu Gly Gln Gln Ser Ser Gly Trp Asp Ile Ile Cys Ala Phe Ala Asp
    770                 775                 780

agg ggc aaa ttg ggg tac aag gag gaa gct act atg gta gac tat gct     2400
Arg Gly Lys Leu Gly Tyr Lys Glu Glu Ala Thr Met Val Asp Tyr Ala
785                 790                 795                 800

gtt caa atc atc ttc ctc cac atc act tgg ctc ttc aag cgg ttc acc     2448
Val Gln Ile Ile Phe Leu His Ile Thr Trp Leu Phe Lys Arg Phe Thr
                805                 810                 815

aag gaa gat gcg caa gat gcc acc aag att gat ctc ctt tcc acc cga     2496
Lys Glu Asp Ala Gln Asp Ala Thr Lys Ile Asp Leu Leu Ser Thr Arg
            820                 825                 830

cgc gat acc gcc ctt cag aca ttt aac cag ctt ttc ctc gga gaa acg     2544
Arg Asp Thr Ala Leu Gln Thr Phe Asn Gln Leu Phe Leu Gly Glu Thr
        835                 840                 845

acc aat acc gcc agt gct gta cga cgt caa gcc ttc atc tct ttc atc     2592
Thr Asn Thr Ala Ser Ala Val Arg Arg Gln Ala Phe Ile Ser Phe Ile
    850                 855                 860

aat acg tac gta ttg ttc gcc aaa cgt gca gag ggt agg gga gga gct     2640
Asn Thr Tyr Val Leu Phe Ala Lys Arg Ala Glu Gly Arg Gly Gly Ala
865                 870                 875                 880

cca gcg agc gac gtt tgt tct gtg acg atg ccg gaa gaa gta cag cat     2688
Pro Ala Ser Asp Val Cys Ser Val Thr Met Pro Glu Glu Val Gln His
                885                 890                 895

aga ctg gga ggg gcg ttc caa gcg gtg att gag agg tat gct tcc gtc     2736
Arg Leu Gly Gly Ala Phe Gln Ala Val Ile Glu Arg Tyr Ala Ser Val
            900                 905                 910

gtg gag act aga tca gca gga cgg gaa gag agt cag cag ccc ccc gaa     2784
Val Glu Thr Arg Ser Ala Gly Arg Glu Glu Ser Gln Gln Pro Pro Glu
        915                 920                 925

ctc act cct gat gag atg cac gag gat ttc cag ttt ttc caa ctc gtt     2832
Leu Thr Pro Asp Glu Met His Glu Asp Phe Gln Phe Phe Gln Leu Val
    930                 935                 940

tcc gtt ttt gtc ggt gcc atc cga tgt ggt gtc ctc gag gtt gaa cat     2880
Ser Val Phe Val Gly Ala Ile Arg Cys Gly Val Leu Glu Val Glu His
945                 950                 955                 960

gcc aag gaa cct ctt gcc cat tac agt cgt ttt ggt cca acg tac gat     2928
Ala Lys Glu Pro Leu Ala His Tyr Ser Arg Phe Gly Pro Thr Tyr Asp
                965                 970                 975

gcg atc gtc aag aag ctc gtt gat gta ctt cga gat gag ggt atc tac     2976
Ala Ile Val Lys Lys Leu Val Asp Val Leu Arg Asp Glu Gly Ile Tyr
            980                 985                 990

aat agg gag gca gat gcg gtg cag  cat gtt gcg gga agc  gcc ttg cag   3024
Asn Arg Glu Ala Asp Ala Val Gln  His Val Ala Gly Ser  Ala Leu Gln
        995                 1000                 1005

caa tcg  ttc aac atc ttc ctc  gac tct gag gaa gac  gaa cca act      3069
Gln Ser  Phe Asn Ile Phe Leu  Asp Ser Glu Glu Asp  Glu Pro Thr
    1010                 1015                 1020

gct cct  ctg gcc ctt gcc cgt  gtt att gca act gcg  ttc gtc atc      3114
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Ala Pro  Leu Ala Leu Ala Arg  Val Ile Ala Thr Ala  Phe Val Ile
    1025                 1030                 1035

cat ggt  tcc caa ttc gct atc  cta aga caa ttg cat  cca tct gat      3159
His Gly  Ser Gln Phe Ala Ile  Leu Arg Gln Leu His  Pro Ser Asp
    1040                 1045                 1050

gtt tgc  gat ttc cac ctc gaa  gcg ctt gac ttt gtt  tct ctc aaa      3204
Val Cys  Asp Phe His Leu Glu  Ala Leu Asp Phe Val  Ser Leu Lys
    1055                 1060                 1065

gtc tca  acg att gtc aaa caa  gaa gga aat gca agg  aac aag gag      3249
Val Ser  Thr Ile Val Lys Gln  Glu Gly Asn Ala Arg  Asn Lys Glu
    1070                 1075                 1080

caa aaa  tcc aga cta aca agg  aaa aag tgg gca gtg  ctc aca ttc      3294
Gln Lys  Ser Arg Leu Thr Arg  Lys Lys Trp Ala Val  Leu Thr Phe
    1085                 1090                 1095

ttc aag  gtg ctc gtc cct ctt  ctc gcg cct gtc aca  ggt aga gat      3339
Phe Lys  Val Leu Val Pro Leu  Leu Ala Pro Val Thr  Gly Arg Asp
    1100                 1105                 1110

gct ctc  aag atc aag gct cat  ctc gaa gat gta atc  gac tct tct      3384
Ala Leu  Lys Ile Lys Ala His  Leu Glu Asp Val Ile  Asp Ser Ser
    1115                 1120                 1125

ggg gtg  caa ctg aca acc aac  aag ggt tgg gat ggc  tac cga gcg      3429
Gly Val  Gln Leu Thr Thr Asn  Lys Gly Trp Asp Gly  Tyr Arg Ala
    1130                 1135                 1140

tac gaa  aag aga tta gta ggg  atc gca agc aag gac  ccg aat gtg      3474
Tyr Glu  Lys Arg Leu Val Gly  Ile Ala Ser Lys Asp  Pro Asn Val
    1145                 1150                 1155

aaa atg  atg gct agc aag aag  gtt gta gaa agg gag  gat act gaa      3519
Lys Met  Met Ala Ser Lys Lys  Val Val Glu Arg Glu  Asp Thr Glu
    1160                 1165                 1170

cag ggt  gat gaa gac aat gtc  ttt gca agg caa tga                  3555
Gln Gly  Asp Glu Asp Asn Val  Phe Ala Arg Gln
    1175                 1180


<210> SEQ ID NO 20
<211> LENGTH: 1184
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 20

Met Ser Ser Pro Glu Pro Glu Glu Pro Arg Arg Gly Ala Arg Val Arg
1               5                   10                  15

Lys Gln Val Asn Lys Phe Asp Ala Ser Gln Gln Asn Gly Arg Gly Lys
            20                  25                  30

Arg Lys His Ile Glu Asp Arg Glu Asp Asp Asp Gln Glu Gly Leu Ile
        35                  40                  45

Pro Asp Pro Glu Asp Glu Ser Asp His Glu Pro Thr Pro Lys Lys Lys
    50                  55                  60

Lys Pro Ala Ala Pro Arg Lys Ser Arg Ala Ser Ala Gly Thr Thr Lys
65                  70                  75                  80

Lys Asp Gly Pro Lys Thr Lys Thr Lys Pro Ala Ala Glu Gly Val Ser
                85                  90                  95

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

Pro Asp Ile Ala Leu Gln Pro Leu Ile Asp Glu Trp Ile Glu Thr Tyr
        115                 120                 125

Gln Gln Ala Ala Gly Asp Glu Ile Ser Glu Gln Lys Ser Ile His Glu
    130                 135                 140

Leu Val Val Phe Phe Ile Arg Cys Cys Gly Met Thr Thr Glu Ile Glu
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145                 150                 155                 160

Gln Ala Glu Ala Thr Asp Asp Asp Gly Ile Pro Asp Val Ile Glu Arg
                165                 170                 175

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

Ser Lys Ala Lys Asn Phe Lys Pro Phe Lys Ser Asn Leu Asn Glu Phe
        195                 200                 205

Ile Ser His Phe Ile Ser Ser Leu Ala Leu Thr Pro Ile Leu Phe His
    210                 215                 220

Thr Ala Asp Asn Thr Pro His Ser Ser Leu Leu Ile Pro Leu Leu Leu
225                 230                 235                 240

Asn Trp Leu Met Cys Met Ser Ser Ser Thr Leu Arg Pro Ile Arg His
                245                 250                 255

Thr Ser Thr Tyr Val Thr Leu Arg Met Asn Ser Ala Leu Cys Asp Val
            260                 265                 270

Ala Ala Asp Val Ser Lys Asp Leu Ser Val Lys Gln Arg Gln Arg Asp
        275                 280                 285

Ala Glu Val Arg Lys Ala Gly Ala Thr Asn Ala Ala Gln Lys Arg Val
    290                 295                 300

Lys Ala Ala Glu Asp Arg Val Lys Glu Val Gln Glu Arg Lys Gln Thr
305                 310                 315                 320

Leu Glu Glu Leu Met Gln Glu Ile Phe Asp Val Met Phe Val His Arg
                325                 330                 335

Val Arg Asp Ala Asp Pro Asn Ile Arg Thr Asp Cys Leu Arg Glu Leu
            340                 345                 350

Gly Leu Trp Ala Lys Lys His Pro Glu Tyr Tyr Val Ser Thr Ser Tyr
        355                 360                 365

Leu Ser Tyr Phe Thr Arg Gly Cys Asn Asp Thr His Ala His Ala Arg
    370                 375                 380

Leu Glu Thr Val Lys Ala Leu Ala Asn Leu Tyr Ile Arg Glu Thr Phe
385                 390                 395                 400

Ile Ser Asn Ala Arg Thr Leu Thr Met Arg Leu Ala Pro Arg Val Ile
                405                 410                 415

Glu Met Ala Thr Arg Asp Val Asp Leu Asn Val Arg Val Val Ala Leu
            420                 425                 430

Gln Val Ile Thr Leu Ile Asp Lys Thr Gly Ile Leu Gln Asp Glu Glu
        435                 440                 445

Asp Glu Glu Arg Asp Lys Val Ala Lys Leu Val Phe Asp Gln Glu Pro
    450                 455                 460

Arg Ile Arg Lys Ala Ala Gly Ala Phe Ile Leu Gly Leu Trp Glu Glu
465                 470                 475                 480

Arg Lys Glu Gly Leu Lys Ala Val Trp Ser Gly Leu Arg Ala Asn Lys
                485                 490                 495

Lys Lys Arg Ala Ala Asn Ile Thr Glu Asp Glu Met Ser Asn Tyr Leu
            500                 505                 510

Asn Trp Lys Ser Leu Ala Ala Val Leu Leu Tyr Thr Ser Lys Ser Leu
        515                 520                 525

Asp Asp Asp Pro Ser Gly Gln Pro Ser Ala Leu Lys Pro Ser Leu Leu
    530                 535                 540

Ile Pro Ser Leu Pro Asn Thr Gln Met Thr Arg Ala Thr Ala Ala Val
545                 550                 555                 560

Glu Ser Ile Gly Ala Glu His Glu Leu Trp Lys Asp Trp Glu Ser Leu
                565                 570                 575
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Val Asp Tyr Leu Leu Val Asp His Ser Thr Asn Glu Glu Asp Met Trp
            580                 585                 590

Leu Leu Arg Glu Asp Glu Glu Thr Phe Met Leu Gln Val Leu Leu Ala
        595                 600                 605

Cys Ile Lys Arg Glu Glu Asn Glu Glu Asp Glu Pro Asp Arg Thr Lys
    610                 615                 620

Thr Leu Ile Lys Val Leu Pro Arg Leu Phe Ala Lys His Gln Ala Asp
625                 630                 635                 640

Val Gly Arg Met Thr Gly Ile Leu Ser Val Pro Gly His Met Lys Leu
                645                 650                 655

Ser Leu Tyr Leu Asp Met Arg Met Ser Ser Ala Tyr Glu Ser Leu Trp
            660                 665                 670

Asp Asp Ile Ser Lys Gln Phe Leu Lys Tyr Thr Ser Pro Thr Ile Leu
        675                 680                 685

Thr Ala Ser Ile Ser Ala Ile Ser His Leu Val Gly Asn Ser Ser Leu
    690                 695                 700

Ser Ser Ile Asn Glu Thr Lys Leu Ser Glu Leu His Glu Ser Leu Phe
705                 710                 715                 720

Ala Ser Leu Arg Asp Ala Ile Gly Ser Glu Asp Val Ala Leu Val Thr
                725                 730                 735

Leu Glu Asp Glu Gln Ile Ser Gln Leu Glu Ala Ile Met Leu Arg Ile
            740                 745                 750

Thr Leu Leu Gln Arg Ser Met Asp Leu Val Asp Val Met Glu Asp Glu
        755                 760                 765

Glu Gly Gln Gln Ser Ser Gly Trp Asp Ile Ile Cys Ala Phe Ala Asp
    770                 775                 780

Arg Gly Lys Leu Gly Tyr Lys Glu Glu Ala Thr Met Val Asp Tyr Ala
785                 790                 795                 800

Val Gln Ile Ile Phe Leu His Ile Thr Trp Leu Phe Lys Arg Phe Thr
                805                 810                 815

Lys Glu Asp Ala Gln Asp Ala Thr Lys Ile Asp Leu Leu Ser Thr Arg
            820                 825                 830

Arg Asp Thr Ala Leu Gln Thr Phe Asn Gln Leu Phe Leu Gly Glu Thr
        835                 840                 845

Thr Asn Thr Ala Ser Ala Val Arg Arg Gln Ala Phe Ile Ser Phe Ile
    850                 855                 860

Asn Thr Tyr Val Leu Phe Ala Lys Arg Ala Glu Gly Arg Gly Gly Ala
865                 870                 875                 880

Pro Ala Ser Asp Val Cys Ser Val Thr Met Pro Glu Glu Val Gln His
                885                 890                 895

Arg Leu Gly Gly Ala Phe Gln Ala Val Ile Glu Arg Tyr Ala Ser Val
            900                 905                 910

Val Glu Thr Arg Ser Ala Gly Arg Glu Glu Ser Gln Gln Pro Pro Glu
        915                 920                 925

Leu Thr Pro Asp Glu Met His Glu Asp Phe Gln Phe Phe Gln Leu Val
    930                 935                 940

Ser Val Phe Val Gly Ala Ile Arg Cys Gly Val Leu Glu Val Glu His
945                 950                 955                 960

Ala Lys Glu Pro Leu Ala His Tyr Ser Arg Phe Gly Pro Thr Tyr Asp
                965                 970                 975

Ala Ile Val Lys Lys Leu Val Asp Val Leu Arg Asp Glu Gly Ile Tyr
            980                 985                 990
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Asn Arg Glu Ala Asp Ala Val Gln  His Val Ala Gly Ser  Ala Leu Gln
        995                 1000                 1005

Gln Ser  Phe Asn Ile Phe Leu  Asp Ser Glu Glu Asp  Glu Pro Thr
    1010                 1015                 1020

Ala Pro  Leu Ala Leu Ala Arg  Val Ile Ala Thr Ala  Phe Val Ile
    1025                 1030                 1035

His Gly  Ser Gln Phe Ala Ile  Leu Arg Gln Leu His  Pro Ser Asp
    1040                 1045                 1050

Val Cys  Asp Phe His Leu Glu  Ala Leu Asp Phe Val  Ser Leu Lys
    1055                 1060                 1065

Val Ser  Thr Ile Val Lys Gln  Glu Gly Asn Ala Arg  Asn Lys Glu
    1070                 1075                 1080

Gln Lys  Ser Arg Leu Thr Arg  Lys Lys Trp Ala Val  Leu Thr Phe
    1085                 1090                 1095

Phe Lys  Val Leu Val Pro Leu  Leu Ala Pro Val Thr  Gly Arg Asp
    1100                 1105                 1110

Ala Leu  Lys Ile Lys Ala His  Leu Glu Asp Val Ile  Asp Ser Ser
    1115                 1120                 1125

Gly Val  Gln Leu Thr Thr Asn  Lys Gly Trp Asp Gly  Tyr Arg Ala
    1130                 1135                 1140

Tyr Glu  Lys Arg Leu Val Gly  Ile Ala Ser Lys Asp  Pro Asn Val
    1145                 1150                 1155

Lys Met  Met Ala Ser Lys Lys  Val Val Glu Arg Glu  Asp Thr Glu
    1160                 1165                 1170

Gln Gly  Asp Glu Asp Asn Val  Phe Ala Arg Gln
    1175                 1180


<210> SEQ ID NO 21
<211> LENGTH: 897
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(897)

<400> SEQUENCE: 21

atg aag tac tct gct acc gca gtc gcc gtt atg ggt gcc ctc gcc att           48
Met Lys Tyr Ser Ala Thr Ala Val Ala Val Met Gly Ala Leu Ala Ile
1               5                   10                  15

caa gcc acc cca atc aag aga gat gct tac acc cca acc gac att gat           96
Gln Ala Thr Pro Ile Lys Arg Asp Ala Tyr Thr Pro Thr Asp Ile Asp
            20                  25                  30

atc cta cag tat gcg ttg act ctc gag cac ctg gag aac aac ttc tac          144
Ile Leu Gln Tyr Ala Leu Thr Leu Glu His Leu Glu Asn Asn Phe Tyr
        35                  40                  45

tcc tgc gcc ctc aac aac atg gac gct caa gcg ttc gcc gat gcc gga          192
Ser Cys Ala Leu Asn Asn Met Asp Ala Gln Ala Phe Ala Asp Ala Gly
    50                  55                  60

ttc cca gcc tgg gta cgg aac agg ttt gag cag att gcc gct cac gag          240
Phe Pro Ala Trp Val Arg Asn Arg Phe Glu Gln Ile Ala Ala His Glu
65                  70                  75                  80

gcc tcc cac gtc gcc gtt ctc tcc gat gcc ctc ggc gct gac gcc acc          288
Ala Ser His Val Ala Val Leu Ser Asp Ala Leu Gly Ala Asp Ala Thr
                85                  90                  95

aag cca tgc gag tac tcc ttc cca tac acc gac gcc aaa tcg ttc acc          336
Lys Pro Cys Glu Tyr Ser Phe Pro Tyr Thr Asp Ala Lys Ser Phe Thr
            100                 105                 110

gct ctc gct cag gtc att gag aat gtt ggt gtt tct gct tac ctc ggt          384
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Ala Leu Ala Gln Val Ile Glu Asn Val Gly Val Ser Ala Tyr Leu Gly
        115                 120                 125

gcc gcc ggt ttc atc atg gac aag acc tac ttg acc gtt gct ggt tcc          432
Ala Ala Gly Phe Ile Met Asp Lys Thr Tyr Leu Thr Val Ala Gly Ser
    130                 135                 140

att ctc acc acc gag gcc cgc cac cag gcc tgg atc gct tcc gcc gtt          480
Ile Leu Thr Thr Glu Ala Arg His Gln Ala Trp Ile Ala Ser Ala Val
145                 150                 155                 160

aac aag cag aac cca tgg tcc ggc cca tac gac act cct ctc ggt ctc          528
Asn Lys Gln Asn Pro Trp Ser Gly Pro Tyr Asp Thr Pro Leu Gly Leu
                165                 170                 175

tcc gat gtc tac tcc att gcc gct gcc ttc atc acc agc tgt cca tcc          576
Ser Asp Val Tyr Ser Ile Ala Ala Ala Phe Ile Thr Ser Cys Pro Ser
            180                 185                 190

tcc aac cca act ctc cca gtc aag gca ttc cca gct ctc act ctc tct          624
Ser Asn Pro Thr Leu Pro Val Lys Ala Phe Pro Ala Leu Thr Leu Ser
        195                 200                 205

tgc gac tcc gcc ggt tcg act gcc acc ctc aac tat acc ggc gct gat          672
Cys Asp Ser Ala Gly Ser Thr Ala Thr Leu Asn Tyr Thr Gly Ala Asp
    210                 215                 220

tca tcc gac acc ctt att ctc tac tct ggc ctc acg acc ctc gct ctc          720
Ser Ser Asp Thr Leu Ile Leu Tyr Ser Gly Leu Thr Thr Leu Ala Leu
225                 230                 235                 240

ccc atc acc gac atg atg gtc acc atc cca tcc tct ctt cag ggc att          768
Pro Ile Thr Asp Met Met Val Thr Ile Pro Ser Ser Leu Gln Gly Ile
                245                 250                 255

gct tac gca gtc gtg tct tca acg tct aac acc acc atg gtt gac gac          816
Ala Tyr Ala Val Val Ser Ser Thr Ser Asn Thr Thr Met Val Asp Asp
            260                 265                 270

tct aac acc att gcc ggc cca gcc atc att gac ctt cct ttc gct tct          864
Ser Asn Thr Ile Ala Gly Pro Ala Ile Ile Asp Leu Pro Phe Ala Ser
        275                 280                 285

tcc gcc agc aac ccc aac ttc act ggt atg taa                              897
Ser Ala Ser Asn Pro Asn Phe Thr Gly Met
    290                 295


<210> SEQ ID NO 22
<211> LENGTH: 298
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 22

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

Gln Ala Thr Pro Ile Lys Arg Asp Ala Tyr Thr Pro Thr Asp Ile Asp
            20                  25                  30

Ile Leu Gln Tyr Ala Leu Thr Leu Glu His Leu Glu Asn Asn Phe Tyr
        35                  40                  45

Ser Cys Ala Leu Asn Asn Met Asp Ala Gln Ala Phe Ala Asp Ala Gly
    50                  55                  60

Phe Pro Ala Trp Val Arg Asn Arg Phe Glu Gln Ile Ala Ala His Glu
65                  70                  75                  80

Ala Ser His Val Ala Val Leu Ser Asp Ala Leu Gly Ala Asp Ala Thr
                85                  90                  95

Lys Pro Cys Glu Tyr Ser Phe Pro Tyr Thr Asp Ala Lys Ser Phe Thr
            100                 105                 110

Ala Leu Ala Gln Val Ile Glu Asn Val Gly Val Ser Ala Tyr Leu Gly
        115                 120                 125
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Ala Ala Gly Phe Ile Met Asp Lys Thr Tyr Leu Thr Val Ala Gly Ser
    130                 135                 140

Ile Leu Thr Thr Glu Ala Arg His Gln Ala Trp Ile Ala Ser Ala Val
145                 150                 155                 160

Asn Lys Gln Asn Pro Trp Ser Gly Pro Tyr Asp Thr Pro Leu Gly Leu
                165                 170                 175

Ser Asp Val Tyr Ser Ile Ala Ala Ala Phe Ile Thr Ser Cys Pro Ser
            180                 185                 190

Ser Asn Pro Thr Leu Pro Val Lys Ala Phe Pro Ala Leu Thr Leu Ser
        195                 200                 205

Cys Asp Ser Ala Gly Ser Thr Ala Thr Leu Asn Tyr Thr Gly Ala Asp
    210                 215                 220

Ser Ser Asp Thr Leu Ile Leu Tyr Ser Gly Leu Thr Thr Leu Ala Leu
225                 230                 235                 240

Pro Ile Thr Asp Met Met Val Thr Ile Pro Ser Ser Leu Gln Gly Ile
                245                 250                 255

Ala Tyr Ala Val Val Ser Ser Thr Ser Asn Thr Thr Met Val Asp Asp
            260                 265                 270

Ser Asn Thr Ile Ala Gly Pro Ala Ile Ile Asp Leu Pro Phe Ala Ser
        275                 280                 285

Ser Ala Ser Asn Pro Asn Phe Thr Gly Met
    290                 295


<210> SEQ ID NO 23
<211> LENGTH: 534
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(534)

<400> SEQUENCE: 23

atg tct cta act agt gtc act cgc gtc gta tcc aaa tcc atc ctc ggc        48
Met Ser Leu Thr Ser Val Thr Arg Val Val Ser Lys Ser Ile Leu Gly
1           5                       10                  15

gct tcc ttt act agc aca act cgc agg ctt acc act acc gtt ccc aga        96
Ala Ser Phe Thr Ser Thr Thr Arg Arg Leu Thr Thr Thr Val Pro Arg
            20                  25                  30

ttt ggt aga atg cct cct cct gct cac aag atg gcc cac ttc ccg agg       144
Phe Gly Arg Met Pro Pro Pro Ala His Lys Met Ala His Phe Pro Arg
        35                  40                  45

atc aca tcc tct ctt ccc tca gaa cac tct gag ttt aga aca gtg atg       192
Ile Thr Ser Ser Leu Pro Ser Glu His Ser Glu Phe Arg Thr Val Met
    50                  55                  60

tgg acg ggc gag agc agt caa ctt gtc ctc atg act atc cct gtc gga       240
Trp Thr Gly Glu Ser Ser Gln Leu Val Leu Met Thr Ile Pro Val Gly
65                  70                  75                  80

gga gaa ata ggg gaa gaa att cac cat gtt gac caa cac ttg gtt ttc       288
Gly Glu Ile Gly Glu Glu Ile His His Val Asp Gln His Leu Val Phe
                85                  90                  95

acc tct ggt act gcc aag gcc att gtt gga gga gaa gaa aaa gag atc       336
Thr Ser Gly Thr Ala Lys Ala Ile Val Gly Gly Glu Glu Lys Glu Ile
            100                 105                 110

aag gct gga gat ctt gtc atc gtt cct cag ggt acc aag cat aac ttc       384
Lys Ala Gly Asp Leu Val Ile Val Pro Gln Gly Thr Lys His Asn Phe
        115                 120                 125

gtc aat acg ggc cct acc cct ctt tgc ctt ttt act gta tat gct ccg       432
Val Asn Thr Gly Pro Thr Pro Leu Cys Leu Phe Thr Val Tyr Ala Pro
    130                 135                 140
```

```
gcc gag cat gcc gag aca aca gtc aac aaa acg aag gag gaa ggg gat      480
Ala Glu His Ala Glu Thr Thr Val Asn Lys Thr Lys Glu Glu Gly Asp
145                 150                 155                 160

aaa ttg gaa gac gag ggc aag gat gag cct cca aag tgg gca gtt agg      528
Lys Leu Glu Asp Glu Gly Lys Asp Glu Pro Pro Lys Trp Ala Val Arg
                165                 170                 175

aag tag                                                              534
Lys


<210> SEQ ID NO 24
<211> LENGTH: 177
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 24

Met Ser Leu Thr Ser Val Thr Arg Val Val Ser Lys Ser Ile Leu Gly
1               5                   10                  15

Ala Ser Phe Thr Ser Thr Thr Arg Arg Leu Thr Thr Thr Val Pro Arg
            20                  25                  30

Phe Gly Arg Met Pro Pro Pro Ala His Lys Met Ala His Phe Pro Arg
        35                  40                  45

Ile Thr Ser Ser Leu Pro Ser Glu His Ser Glu Phe Arg Thr Val Met
    50                  55                  60

Trp Thr Gly Glu Ser Ser Gln Leu Val Leu Met Thr Ile Pro Val Gly
65                  70                  75                  80

Gly Glu Ile Gly Glu Glu Ile His His Val Asp Gln His Leu Val Phe
                85                  90                  95

Thr Ser Gly Thr Ala Lys Ala Ile Val Gly Gly Glu Glu Lys Glu Ile
            100                 105                 110

Lys Ala Gly Asp Leu Val Ile Val Pro Gln Gly Thr Lys His Asn Phe
        115                 120                 125

Val Asn Thr Gly Pro Thr Pro Leu Cys Leu Phe Thr Val Tyr Ala Pro
    130                 135                 140

Ala Glu His Ala Glu Thr Thr Val Asn Lys Thr Lys Glu Glu Gly Asp
145                 150                 155                 160

Lys Leu Glu Asp Glu Gly Lys Asp Glu Pro Pro Lys Trp Ala Val Arg
                165                 170                 175

Lys


<210> SEQ ID NO 25
<211> LENGTH: 1074
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1074)

<400> SEQUENCE: 25

atg cca act gta ctc ctc aca ggt atc acg gga ttt ctg tct gcg cac       48
Met Pro Thr Val Leu Leu Thr Gly Ile Thr Gly Phe Leu Ser Ala His
1               5                   10                  15

gtc gcc cat acc ttc ctg aag cat gac tgg ata gtg cac ggc aca ctt       96
Val Ala His Thr Phe Leu Lys His Asp Trp Ile Val His Gly Thr Leu
            20                  25                  30

cgg tcc agc tcg aag gta gcg tta atc gaa gtt att cct gaa tac tct      144
Arg Ser Ser Ser Lys Val Ala Leu Ile Glu Val Ile Pro Glu Tyr Ser
        35                  40                  45

cct tat att tcg tca ggc aaa cta aaa ctc ttc gtt gtc gga cct ctt      192
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Pro Tyr Ile Ser Ser Gly Lys Leu Lys Leu Phe Val Val Gly Pro Leu
    50                  55                  60

gag aat gcc gat tac act gaa gcc atg aaa ggc gtt gat gct gtg gtc      240
Glu Asn Ala Asp Tyr Thr Glu Ala Met Lys Gly Val Asp Ala Val Val
65                  70                  75                  80

cac act gcg tct ccg gta gag ttt ggt gga gac aat ttt aga gag agc      288
His Thr Ala Ser Pro Val Glu Phe Gly Gly Asp Asn Phe Arg Glu Ser
                85                  90                  95

cat ttg aaa cct gct ttg gaa gga aca agg ggt gtc ctc aga gct gta      336
His Leu Lys Pro Ala Leu Glu Gly Thr Arg Gly Val Leu Arg Ala Val
            100                 105                 110

gcc aaa gag aag aat gta aag tcc gtc gtc tac act agt act ttt gga      384
Ala Lys Glu Lys Asn Val Lys Ser Val Val Tyr Thr Ser Thr Phe Gly
        115                 120                 125

gcc gtt ggt gat cat agg tat cat ccc act gag atc aaa ggc aaa gtt      432
Ala Val Gly Asp His Arg Tyr His Pro Thr Glu Ile Lys Gly Lys Val
    130                 135                 140

atc act gag gat aac tgg aac ccg tat acc ttg gaa gag ctg gat aag      480
Ile Thr Glu Asp Asn Trp Asn Pro Tyr Thr Leu Glu Glu Leu Asp Lys
145                 150                 155                 160

atg gtg gaa tct gga gag tca ggc aac ccc aca ttt cct cca gga tat      528
Met Val Glu Ser Gly Glu Ser Gly Asn Pro Thr Phe Pro Pro Gly Tyr
                165                 170                 175

ctg ttc tat aaa gga gcc aag aag tac gcg gaa ctc gct gct tgg gaa      576
Leu Phe Tyr Lys Gly Ala Lys Lys Tyr Ala Glu Leu Ala Ala Trp Glu
            180                 185                 190

tgc cag aaa gaa gcg aga gaa cag ggt gct gaa tgg tct ttg gcc acg      624
Cys Gln Lys Glu Ala Arg Glu Gln Gly Ala Glu Trp Ser Leu Ala Thr
        195                 200                 205

atg aac tgt gtg atg atc tgg ggg cct cca att caa cct ctc aca tca      672
Met Asn Cys Val Met Ile Trp Gly Pro Pro Ile Gln Pro Leu Thr Ser
    210                 215                 220

ctc agt cat ggg ggc atg tcg acc gag ttc ctt tgg atg ctt gca gga      720
Leu Ser His Gly Gly Met Ser Thr Glu Phe Leu Trp Met Leu Ala Gly
225                 230                 235                 240

ggg aaa gat gcc cat atc atg gac agt ctc tat ccc tat tac gtc gat      768
Gly Lys Asp Ala His Ile Met Asp Ser Leu Tyr Pro Tyr Tyr Val Asp
                245                 250                 255

gtt cgg gat gct gct gaa gca cac tat caa gcc acc gtc cgt aga gcg      816
Val Arg Asp Ala Ala Glu Ala His Tyr Gln Ala Thr Val Arg Arg Ala
            260                 265                 270

caa gga agg ttt atc atc tct gcc ggc cct tat gat ttc caa gag ttc      864
Gln Gly Arg Phe Ile Ile Ser Ala Gly Pro Tyr Asp Phe Gln Glu Phe
        275                 280                 285

gca gac atg ctt agg gag ctt tat cct gag caa aaa gaa cga ttc gcc      912
Ala Asp Met Leu Arg Glu Leu Tyr Pro Glu Gln Lys Glu Arg Phe Ala
    290                 295                 300

ctt ggt gct ccc ggc aaa tat atg tac aga gat cca gga gtg tac gtg      960
Leu Gly Ala Pro Gly Lys Tyr Met Tyr Arg Asp Pro Gly Val Tyr Val
305                 310                 315                 320

ctc aca aat gaa aag agt caa agg gaa ctt ggt att act tac cgt cca     1008
Leu Thr Asn Glu Lys Ser Gln Arg Glu Leu Gly Ile Thr Tyr Arg Pro
                325                 330                 335

aaa caa gag act ctc aaa gat gca ttt gac agg ttt ttc gct ttg gag     1056
Lys Gln Glu Thr Leu Lys Asp Ala Phe Asp Arg Phe Phe Ala Leu Glu
            340                 345                 350

aaa caa gga ttg aag taa                                             1074
Lys Gln Gly Leu Lys
        355
```

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<210> SEQ ID NO 26
<211> LENGTH: 357
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 26

Met Pro Thr Val Leu Leu Thr Gly Ile Thr Gly Phe Leu Ser Ala His
1               5                   10                  15

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

Arg Ser Ser Ser Lys Val Ala Leu Ile Glu Val Ile Pro Glu Tyr Ser
        35                  40                  45

Pro Tyr Ile Ser Ser Gly Lys Leu Lys Leu Phe Val Val Gly Pro Leu
    50                  55                  60

Glu Asn Ala Asp Tyr Thr Glu Ala Met Lys Gly Val Asp Ala Val Val
65                  70                  75                  80

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

His Leu Lys Pro Ala Leu Glu Gly Thr Arg Gly Val Leu Arg Ala Val
            100                 105                 110

Ala Lys Glu Lys Asn Val Lys Ser Val Val Tyr Thr Ser Thr Phe Gly
        115                 120                 125

Ala Val Gly Asp His Arg Tyr His Pro Thr Glu Ile Lys Gly Lys Val
    130                 135                 140

Ile Thr Glu Asp Asn Trp Asn Pro Tyr Thr Leu Glu Glu Leu Asp Lys
145                 150                 155                 160

Met Val Glu Ser Gly Glu Ser Gly Asn Pro Thr Phe Pro Pro Gly Tyr
                165                 170                 175

Leu Phe Tyr Lys Gly Ala Lys Lys Tyr Ala Glu Leu Ala Ala Trp Glu
            180                 185                 190

Cys Gln Lys Glu Ala Arg Glu Gln Gly Ala Glu Trp Ser Leu Ala Thr
        195                 200                 205

Met Asn Cys Val Met Ile Trp Gly Pro Pro Ile Gln Pro Leu Thr Ser
    210                 215                 220

Leu Ser His Gly Gly Met Ser Thr Glu Phe Leu Trp Met Leu Ala Gly
225                 230                 235                 240

Gly Lys Asp Ala His Ile Met Asp Ser Leu Tyr Pro Tyr Tyr Val Asp
                245                 250                 255

Val Arg Asp Ala Ala Glu Ala His Tyr Gln Ala Thr Val Arg Arg Ala
            260                 265                 270

Gln Gly Arg Phe Ile Ile Ser Ala Gly Pro Tyr Asp Phe Gln Glu Phe
        275                 280                 285

Ala Asp Met Leu Arg Glu Leu Tyr Pro Glu Gln Lys Glu Arg Phe Ala
    290                 295                 300

Leu Gly Ala Pro Gly Lys Tyr Met Tyr Arg Asp Pro Gly Val Tyr Val
305                 310                 315                 320

Leu Thr Asn Glu Lys Ser Gln Arg Glu Leu Gly Ile Thr Tyr Arg Pro
                325                 330                 335

Lys Gln Glu Thr Leu Lys Asp Ala Phe Asp Arg Phe Phe Ala Leu Glu
            340                 345                 350

Lys Gln Gly Leu Lys
        355


<210> SEQ ID NO 27
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```
<211> LENGTH: 2781
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(2781)

<400> SEQUENCE: 27

atg ttt agg aag aga att ctt tat ctt tct tct ttt tca atc cct ttg       48
Met Phe Arg Lys Arg Ile Leu Tyr Leu Ser Ser Phe Ser Ile Pro Leu
1               5                   10                  15

tac aca gtc cca gcc cac agt tat tcc tgt act ttt cag acc aac cag       96
Tyr Thr Val Pro Ala His Ser Tyr Ser Cys Thr Phe Gln Thr Asn Gln
            20                  25                  30

cgc cct tct act ctc ctc aaa cgc gta cat tcg ctc gct atg tcc ttc      144
Arg Pro Ser Thr Leu Leu Lys Arg Val His Ser Leu Ala Met Ser Phe
        35                  40                  45

ccg cca gtg cag ccc gcc gac aat ggc atg gcg gtc gtt gct ccc aat      192
Pro Pro Val Gln Pro Ala Asp Asn Gly Met Ala Val Val Ala Pro Asn
    50                  55                  60

ctc gag tct aac cct acc act gtt gcg tcc cac gcc cca caa att gcc      240
Leu Glu Ser Asn Pro Thr Thr Val Ala Ser His Ala Pro Gln Ile Ala
65                  70                  75                  80

gtc aag gat gaa aat gat agt atg agc gag gat gag cag cct ttg gcg      288
Val Lys Asp Glu Asn Asp Ser Met Ser Glu Asp Glu Gln Pro Leu Ala
                85                  90                  95

aaa agc aaa gcg aat gga gcg agg aag aga gtc gaa aac agc agt gac      336
Lys Ser Lys Ala Asn Gly Ala Arg Lys Arg Val Glu Asn Ser Ser Asp
            100                 105                 110

gag gaa gag aaa cct ctc agc aaa aag ccc aga gcc aat ggt gtc aac      384
Glu Glu Glu Lys Pro Leu Ser Lys Lys Pro Arg Ala Asn Gly Val Asn
        115                 120                 125

aag aaa agg gtc gtc gcc agc agt gat gaa gaa agc gat gtt tca cct      432
Lys Lys Arg Val Val Ala Ser Ser Asp Glu Glu Ser Asp Val Ser Pro
    130                 135                 140

cct gct aag agg cct gtt tcc aag caa tcc aaa cct gcc acc ccc gat      480
Pro Ala Lys Arg Pro Val Ser Lys Gln Ser Lys Pro Ala Thr Pro Asp
145                 150                 155                 160

tct gaa tct gat gac gat caa cct ctc gcc aag aag gct aac gga ctg      528
Ser Glu Ser Asp Asp Asp Gln Pro Leu Ala Lys Lys Ala Asn Gly Leu
                165                 170                 175

gcc gca tcc aaa cgt cag gct aaa aaa gcg gag gaa tta tca gaa gaa      576
Ala Ala Ser Lys Arg Gln Ala Lys Lys Ala Glu Glu Leu Ser Glu Glu
            180                 185                 190

agc tcg gag gaa gaa aag cct ctt gcg aag gtt gcc aag agg gta tca      624
Ser Ser Glu Glu Glu Lys Pro Leu Ala Lys Val Ala Lys Arg Val Ser
        195                 200                 205

gca aag aag atg aag agc gag act gag gac tct gag gaa gac cgg cct      672
Ala Lys Lys Met Lys Ser Glu Thr Glu Asp Ser Glu Glu Asp Arg Pro
    210                 215                 220

ctt gca aag aag aag gct cct gtt aag cgt gct cca gca aag aaa tcg      720
Leu Ala Lys Lys Lys Ala Pro Val Lys Arg Ala Pro Ala Lys Lys Ser
225                 230                 235                 240

gcg aag aag gaa cct agt gag agt gaa gag gat gag aag cct tta gcg      768
Ala Lys Lys Glu Pro Ser Glu Ser Glu Glu Asp Glu Lys Pro Leu Ala
                245                 250                 255

aag aac gct aga ggg aag gcc aag gcg gcg acg gtg aag gaa gag aaa      816
Lys Asn Ala Arg Gly Lys Ala Lys Ala Ala Thr Val Lys Glu Glu Lys
            260                 265                 270

ggt aag aag aca aag aag gag aaa gaa gag gaa gaa gag gag gaa agg      864
Gly Lys Lys Thr Lys Lys Glu Lys Glu Glu Glu Glu Glu Glu Glu Arg
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        275                 280                 285

tac aag tgg tgg gaa cag gat gct ttg ggt gat ggg tca tcc aag tgg          912
Tyr Lys Trp Trp Glu Gln Asp Ala Leu Gly Asp Gly Ser Ser Lys Trp
    290                 295                 300

acg gtc ctt gag cac aac gct gtt ctc ttc cct cct cct tat gtt cct          960
Thr Val Leu Glu His Asn Ala Val Leu Phe Pro Pro Pro Tyr Val Pro
305                 310                 315                 320

tta ccc aag aac gtg aaa atg aag tac gat ggc gtc tca ctt acc ctc         1008
Leu Pro Lys Asn Val Lys Met Lys Tyr Asp Gly Val Ser Leu Thr Leu
                325                 330                 335

cct ccc gag tct gaa gaa gtc gcc ggt ttc ttc ggt gcc ctc ctt gaa         1056
Pro Pro Glu Ser Glu Glu Val Ala Gly Phe Phe Gly Ala Leu Leu Glu
            340                 345                 350

acc gac tat gct caa gat gcc aaa ttc cgt gaa aac ttt ttc cga gac         1104
Thr Asp Tyr Ala Gln Asp Ala Lys Phe Arg Glu Asn Phe Phe Arg Asp
        355                 360                 365

ttt aag gct atc gtc gaa aaa tat cca ccc aag gag gac gtc aag gtt         1152
Phe Lys Ala Ile Val Glu Lys Tyr Pro Pro Lys Glu Asp Val Lys Val
    370                 375                 380

aag aag ttg gaa aag tgc gat ttt aga ccg atg ttt gag tac ttt gaa         1200
Lys Lys Leu Glu Lys Cys Asp Phe Arg Pro Met Phe Glu Tyr Phe Glu
385                 390                 395                 400

aag gag aag gag aag aag aag gcg ttg act aag gaa gag aaa aag gcg         1248
Lys Glu Lys Glu Lys Lys Lys Ala Leu Thr Lys Glu Glu Lys Lys Ala
                405                 410                 415

att aaa gcg gag aag gac aag ctt gaa gca ccg tat ctc tat gcg aat         1296
Ile Lys Ala Glu Lys Asp Lys Leu Glu Ala Pro Tyr Leu Tyr Ala Asn
            420                 425                 430

gtt gat gga agg aag gaa aag gtc ggc aac ttc cgt gca gaa cct cct         1344
Val Asp Gly Arg Lys Glu Lys Val Gly Asn Phe Arg Ala Glu Pro Pro
        435                 440                 445

gga ttg ttc aag ggt cgt ggt gaa cat ccc aag aag ggt act gtc aag         1392
Gly Leu Phe Lys Gly Arg Gly Glu His Pro Lys Lys Gly Thr Val Lys
    450                 455                 460

aac cgt ctc cga cct gaa gat atc att atc aac att ggc aaa gaa gct         1440
Asn Arg Leu Arg Pro Glu Asp Ile Ile Ile Asn Ile Gly Lys Glu Ala
465                 470                 475                 480

cct atc cct gtg ccc aac att ccc ggt cag tgg aag ggt atc cag cat         1488
Pro Ile Pro Val Pro Asn Ile Pro Gly Gln Trp Lys Gly Ile Gln His
                485                 490                 495

gat aac aca gtg act tgg ctc gct cat tgg aag gag aat gtc aac ggt         1536
Asp Asn Thr Val Thr Trp Leu Ala His Trp Lys Glu Asn Val Asn Gly
            500                 505                 510

aac gcc aaa tac gtc ttc ttg agc gct ggt agt gcg tgg aaa ggt caa         1584
Asn Ala Lys Tyr Val Phe Leu Ser Ala Gly Ser Ala Trp Lys Gly Gln
        515                 520                 525

agt gat cgt gcc aag ttt gaa aag gcc cgt gag ctt atc aaa cat gtc         1632
Ser Asp Arg Ala Lys Phe Glu Lys Ala Arg Glu Leu Ile Lys His Val
    530                 535                 540

gac aaa att cga aaa gac tac act gcc gac ctc aaa tcc aaa gtc atg         1680
Asp Lys Ile Arg Lys Asp Tyr Thr Ala Asp Leu Lys Ser Lys Val Met
545                 550                 555                 560

gct gac cga caa cgt gcc acc gcc ctg tac ttt atc gat cgt ctg gct         1728
Ala Asp Arg Gln Arg Ala Thr Ala Leu Tyr Phe Ile Asp Arg Leu Ala
                565                 570                 575

ctg cga gcg ggt aat gaa aag ggt gaa gat gaa gcg gat act gtc ggc         1776
Leu Arg Ala Gly Asn Glu Lys Gly Glu Asp Glu Ala Asp Thr Val Gly
            580                 585                 590

tgt tgt tct ctg cga tac gaa cac gtg acg ctc tct cca ccg aat act         1824
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Cys Cys Ser Leu Arg Tyr Glu His Val Thr Leu Ser Pro Pro Asn Thr
        595                 600                 605

atc atc ttt gat ttc ctc ggt aag gac tcg atg agg ttc cat cag gaa     1872
Ile Ile Phe Asp Phe Leu Gly Lys Asp Ser Met Arg Phe His Gln Glu
    610                 615                 620

gtc gag gtc gat ccg caa gtg ttc aag aac ata aaa ctg ttt aag gct     1920
Val Glu Val Asp Pro Gln Val Phe Lys Asn Ile Lys Leu Phe Lys Ala
625                 630                 635                 640

gat ccg aag aag aag ggt gac gat atc ttt gac cga ctg acc acc act     1968
Asp Pro Lys Lys Lys Gly Asp Asp Ile Phe Asp Arg Leu Thr Thr Thr
                645                 650                 655

ctt ctt aac aag cac ctc aac agc atg atg cct ggt ctt acc gcc aag     2016
Leu Leu Asn Lys His Leu Asn Ser Met Met Pro Gly Leu Thr Ala Lys
            660                 665                 670

gtt ttc cgt acc tac aac gcc tca tgg act ttc caa gaa caa ctc aaa     2064
Val Phe Arg Thr Tyr Asn Ala Ser Trp Thr Phe Gln Glu Gln Leu Lys
        675                 680                 685

aac aca cct aag aac gga act gta gcc gag aag att gcg gcg tac aac     2112
Asn Thr Pro Lys Asn Gly Thr Val Ala Glu Lys Ile Ala Ala Tyr Asn
    690                 695                 700

act gcc aat agg gat gtt gcc atc ttg tgt aat cac caa aag agt gtc     2160
Thr Ala Asn Arg Asp Val Ala Ile Leu Cys Asn His Gln Lys Ser Val
705                 710                 715                 720

agc aag ggt ttt gag ggc agt ttt gcc aaa gcc gag gat aag att cgt     2208
Ser Lys Gly Phe Glu Gly Ser Phe Ala Lys Ala Glu Asp Lys Ile Arg
                725                 730                 735

gcc ctc aag tat cag cgt ctc aag ctt cgt ctc caa ctt ttt tct ctt     2256
Ala Leu Lys Tyr Gln Arg Leu Lys Leu Arg Leu Gln Leu Phe Ser Leu
            740                 745                 750

aac ccc aag att aag aag aag cat ccc gag ctt gcg gag gat gag tct     2304
Asn Pro Lys Ile Lys Lys Lys His Pro Glu Leu Ala Glu Asp Glu Ser
        755                 760                 765

gat gtg gat gac gaa ttt atg gag cgc cac gaa gcc gaa tta ctc gaa     2352
Asp Val Asp Asp Glu Phe Met Glu Arg His Glu Ala Glu Leu Leu Glu
    770                 775                 780

aaa gct ttg gag aac gca aag aag aaa tgg gat acg gat aat gtc aag     2400
Lys Ala Leu Glu Asn Ala Lys Lys Lys Trp Asp Thr Asp Asn Val Lys
785                 790                 795                 800

ctt gaa ggg gat ggg aag aaa aag aag acg aag gga gag ttg gat gag     2448
Leu Glu Gly Asp Gly Lys Lys Lys Lys Thr Lys Gly Glu Leu Asp Glu
                805                 810                 815

agg ttg agt gag atc aag gca gag ttt aag gag ttg aag aag gag agg     2496
Arg Leu Ser Glu Ile Lys Ala Glu Phe Lys Glu Leu Lys Lys Glu Arg
            820                 825                 830

aag gct aaa aag att gat gcc aag aga gga gcc acg gag gag aaa ctt     2544
Lys Ala Lys Lys Ile Asp Ala Lys Arg Gly Ala Thr Glu Glu Lys Leu
        835                 840                 845

ctt gct cag gtc gcc agg atc gac gaa cgt atc gct acc gcc aaa gtc     2592
Leu Ala Gln Val Ala Arg Ile Asp Glu Arg Ile Ala Thr Ala Lys Val
    850                 855                 860

cag ctt caa gat cga gac aag ctc aag gat gtt gct ttg ggc aca tcc     2640
Gln Leu Gln Asp Arg Asp Lys Leu Lys Asp Val Ala Leu Gly Thr Ser
865                 870                 875                 880

aag att aac tat atc gat cca aga cta act gtc gcg tgg gcg aag aag     2688
Lys Ile Asn Tyr Ile Asp Pro Arg Leu Thr Val Ala Trp Ala Lys Lys
                885                 890                 895

ttt gat gtt cct ctc gaa aaa ctg ttc tcc aaa acc ctg cga gaa aag     2736
Phe Asp Val Pro Leu Glu Lys Leu Phe Ser Lys Thr Leu Arg Glu Lys
            900                 905                 910
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ttc cct tgg gct gag gcg gag gct gga ccg gac tgg gtt ttc tag         2781
Phe Pro Trp Ala Glu Ala Glu Ala Gly Pro Asp Trp Val Phe
        915                 920                 925


<210> SEQ ID NO 28
<211> LENGTH: 926
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 28

Met Phe Arg Lys Arg Ile Leu Tyr Leu Ser Ser Phe Ser Ile Pro Leu
1               5                   10                  15

Tyr Thr Val Pro Ala His Ser Tyr Ser Cys Thr Phe Gln Thr Asn Gln
            20                  25                  30

Arg Pro Ser Thr Leu Leu Lys Arg Val His Ser Leu Ala Met Ser Phe
        35                  40                  45

Pro Pro Val Gln Pro Ala Asp Asn Gly Met Ala Val Val Ala Pro Asn
    50                  55                  60

Leu Glu Ser Asn Pro Thr Thr Val Ala Ser His Ala Pro Gln Ile Ala
65                  70                  75                  80

Val Lys Asp Glu Asn Asp Ser Met Ser Glu Asp Glu Gln Pro Leu Ala
                85                  90                  95

Lys Ser Lys Ala Asn Gly Ala Arg Lys Arg Val Glu Asn Ser Ser Asp
            100                 105                 110

Glu Glu Glu Lys Pro Leu Ser Lys Lys Pro Arg Ala Asn Gly Val Asn
        115                 120                 125

Lys Lys Arg Val Val Ala Ser Ser Asp Glu Glu Ser Asp Val Ser Pro
    130                 135                 140

Pro Ala Lys Arg Pro Val Ser Lys Gln Ser Lys Pro Ala Thr Pro Asp
145                 150                 155                 160

Ser Glu Ser Asp Asp Asp Gln Pro Leu Ala Lys Lys Ala Asn Gly Leu
                165                 170                 175

Ala Ala Ser Lys Arg Gln Ala Lys Lys Ala Glu Glu Leu Ser Glu Glu
            180                 185                 190

Ser Ser Glu Glu Glu Lys Pro Leu Ala Lys Val Ala Lys Arg Val Ser
        195                 200                 205

Ala Lys Lys Met Lys Ser Glu Thr Glu Asp Ser Glu Glu Asp Arg Pro
    210                 215                 220

Leu Ala Lys Lys Lys Ala Pro Val Lys Arg Ala Pro Ala Lys Lys Ser
225                 230                 235                 240

Ala Lys Lys Glu Pro Ser Glu Ser Glu Glu Asp Glu Lys Pro Leu Ala
                245                 250                 255

Lys Asn Ala Arg Gly Lys Ala Lys Ala Ala Thr Val Lys Glu Glu Lys
            260                 265                 270

Gly Lys Lys Thr Lys Lys Glu Lys Glu Glu Glu Glu Glu Glu Glu Arg
        275                 280                 285

Tyr Lys Trp Trp Glu Gln Asp Ala Leu Gly Asp Gly Ser Ser Lys Trp
    290                 295                 300

Thr Val Leu Glu His Asn Ala Val Leu Phe Pro Pro Pro Tyr Val Pro
305                 310                 315                 320

Leu Pro Lys Asn Val Lys Met Lys Tyr Asp Gly Val Ser Leu Thr Leu
                325                 330                 335

Pro Pro Glu Ser Glu Glu Val Ala Gly Phe Phe Gly Ala Leu Leu Glu
            340                 345                 350

Thr Asp Tyr Ala Gln Asp Ala Lys Phe Arg Glu Asn Phe Phe Arg Asp
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        355                 360                 365

Phe Lys Ala Ile Val Glu Lys Tyr Pro Pro Lys Glu Asp Val Lys Val
    370                 375                 380

Lys Lys Leu Glu Lys Cys Asp Phe Arg Pro Met Phe Glu Tyr Phe Glu
385                 390                 395                 400

Lys Glu Lys Glu Lys Lys Lys Ala Leu Thr Lys Glu Glu Lys Lys Ala
                405                 410                 415

Ile Lys Ala Glu Lys Asp Lys Leu Glu Ala Pro Tyr Leu Tyr Ala Asn
            420                 425                 430

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

Gly Leu Phe Lys Gly Arg Gly Glu His Pro Lys Lys Gly Thr Val Lys
    450                 455                 460

Asn Arg Leu Arg Pro Glu Asp Ile Ile Ile Asn Ile Gly Lys Glu Ala
465                 470                 475                 480

Pro Ile Pro Val Pro Asn Ile Pro Gly Gln Trp Lys Gly Ile Gln His
                485                 490                 495

Asp Asn Thr Val Thr Trp Leu Ala His Trp Lys Glu Asn Val Asn Gly
            500                 505                 510

Asn Ala Lys Tyr Val Phe Leu Ser Ala Gly Ser Ala Trp Lys Gly Gln
        515                 520                 525

Ser Asp Arg Ala Lys Phe Glu Lys Ala Arg Glu Leu Ile Lys His Val
    530                 535                 540

Asp Lys Ile Arg Lys Asp Tyr Thr Ala Asp Leu Lys Ser Lys Val Met
545                 550                 555                 560

Ala Asp Arg Gln Arg Ala Thr Ala Leu Tyr Phe Ile Asp Arg Leu Ala
                565                 570                 575

Leu Arg Ala Gly Asn Glu Lys Gly Glu Asp Glu Ala Asp Thr Val Gly
            580                 585                 590

Cys Cys Ser Leu Arg Tyr Glu His Val Thr Leu Ser Pro Pro Asn Thr
        595                 600                 605

Ile Ile Phe Asp Phe Leu Gly Lys Asp Ser Met Arg Phe His Gln Glu
    610                 615                 620

Val Glu Val Asp Pro Gln Val Phe Lys Asn Ile Lys Leu Phe Lys Ala
625                 630                 635                 640

Asp Pro Lys Lys Lys Gly Asp Asp Ile Phe Asp Arg Leu Thr Thr Thr
                645                 650                 655

Leu Leu Asn Lys His Leu Asn Ser Met Met Pro Gly Leu Thr Ala Lys
            660                 665                 670

Val Phe Arg Thr Tyr Asn Ala Ser Trp Thr Phe Gln Glu Gln Leu Lys
        675                 680                 685

Asn Thr Pro Lys Asn Gly Thr Val Ala Glu Lys Ile Ala Ala Tyr Asn
    690                 695                 700

Thr Ala Asn Arg Asp Val Ala Ile Leu Cys Asn His Gln Lys Ser Val
705                 710                 715                 720

Ser Lys Gly Phe Glu Gly Ser Phe Ala Lys Ala Glu Asp Lys Ile Arg
                725                 730                 735

Ala Leu Lys Tyr Gln Arg Leu Lys Leu Arg Leu Gln Leu Phe Ser Leu
            740                 745                 750

Asn Pro Lys Ile Lys Lys Lys His Pro Glu Leu Ala Glu Asp Glu Ser
        755                 760                 765

Asp Val Asp Asp Glu Phe Met Glu Arg His Glu Ala Glu Leu Leu Glu
    770                 775                 780
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Lys Ala Leu Glu Asn Ala Lys Lys Lys Trp Asp Thr Asp Asn Val Lys
785                 790                 795                 800

Leu Glu Gly Asp Gly Lys Lys Lys Lys Thr Lys Gly Glu Leu Asp Glu
                805                 810                 815

Arg Leu Ser Glu Ile Lys Ala Glu Phe Lys Glu Leu Lys Lys Glu Arg
            820                 825                 830

Lys Ala Lys Lys Ile Asp Ala Lys Arg Gly Ala Thr Glu Glu Lys Leu
        835                 840                 845

Leu Ala Gln Val Ala Arg Ile Asp Glu Arg Ile Ala Thr Ala Lys Val
    850                 855                 860

Gln Leu Gln Asp Arg Asp Lys Leu Lys Asp Val Ala Leu Gly Thr Ser
865                 870                 875                 880

Lys Ile Asn Tyr Ile Asp Pro Arg Leu Thr Val Ala Trp Ala Lys Lys
                885                 890                 895

Phe Asp Val Pro Leu Glu Lys Leu Phe Ser Lys Thr Leu Arg Glu Lys
            900                 905                 910

Phe Pro Trp Ala Glu Ala Glu Ala Gly Pro Asp Trp Val Phe
        915                 920                 925


<210> SEQ ID NO 29
<211> LENGTH: 1125
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1125)

<400> SEQUENCE: 29

atg gcc cac cac cac ttc gta ggc ata aac ccg gca ggc ctc tcc ttc       48
Met Ala His His His Phe Val Gly Ile Asn Pro Ala Gly Leu Ser Phe
1               5                   10                  15

tcc cat ccc acc ccg cca gca gac cac ccc gcg ccc ccc tcc tcg ggc       96
Ser His Pro Thr Pro Pro Ala Asp His Pro Ala Pro Pro Ser Ser Gly
            20                  25                  30

agc atc cac acc cca gca aac ttc gcc agc att caa gaa ccc atc aca      144
Ser Ile His Thr Pro Ala Asn Phe Ala Ser Ile Gln Glu Pro Ile Thr
        35                  40                  45

gac cca tcc gct gtc gcc gcc cgc cga cgc ggt cgt cct tcc aca agg      192
Asp Pro Ser Ala Val Ala Ala Arg Arg Arg Gly Arg Pro Ser Thr Arg
    50                  55                  60

ggc gaa gct ggc gtc act ccg ccc cca gag atc gga tgg tgg gag gac      240
Gly Glu Ala Gly Val Thr Pro Pro Pro Glu Ile Gly Trp Trp Glu Asp
65                  70                  75                  80

cgt gcg ccc agc tgg cac aag gat gcc atg cag ggc ggc aag tct tct      288
Arg Ala Pro Ser Trp His Lys Asp Ala Met Gln Gly Gly Lys Ser Ser
                85                  90                  95

atg gag ctc ctg atg gaa tgg tca gag gag atg aag aat caa ggc cac      336
Met Glu Leu Leu Met Glu Trp Ser Glu Glu Met Lys Asn Gln Gly His
            100                 105                 110

tac tac tgg atg ggc gtc agg gat ggc ggc aat ctg cat caa ggt gct      384
Tyr Tyr Trp Met Gly Val Arg Asp Gly Gly Asn Leu His Gln Gly Ala
        115                 120                 125

tcg cgt ttt agg gac tac tta tat gcc cag cat ggt cct att agg cgg      432
Ser Arg Phe Arg Asp Tyr Leu Tyr Ala Gln His Gly Pro Ile Arg Arg
    130                 135                 140

tca agt aag gct atc aga aat aaa gtg gag aat att aag caa aag ttc      480
Ser Ser Lys Ala Ile Arg Asn Lys Val Glu Asn Ile Lys Gln Lys Phe
145                 150                 155                 160
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ttt gaa gcc cag gaa tgg ctc aag gat ccc aat ggg gac cat acc acc      528
Phe Glu Ala Gln Glu Trp Leu Lys Asp Pro Asn Gly Asp His Thr Thr
                165                 170                 175

atg acc att ccg gac gtc gaa aaa aaa ctc aac aag atc tgt cgc aac      576
Met Thr Ile Pro Asp Val Glu Lys Lys Leu Asn Lys Ile Cys Arg Asn
            180                 185                 190

tac cgc ttc tgg gaa acc atc ttc gta gag ctt cct cca gtt gac cac      624
Tyr Arg Phe Trp Glu Thr Ile Phe Val Glu Leu Pro Pro Val Asp His
        195                 200                 205

gaa gct ggc cag aat gcc gaa ggg tct tca tcc aac cag act ctt cag      672
Glu Ala Gly Gln Asn Ala Glu Gly Ser Ser Ser Asn Gln Thr Leu Gln
    210                 215                 220

tct gct tct caa act gcc gtt cga cag ggt aat ggg ccc ctc atc cgc      720
Ser Ala Ser Gln Thr Ala Val Arg Gln Gly Asn Gly Pro Leu Ile Arg
225                 230                 235                 240

ggt att cct gtt ccg gaa atg gga cag gca gcg gcc gat gat gcg cag      768
Gly Ile Pro Val Pro Glu Met Gly Gln Ala Ala Ala Asp Asp Ala Gln
                245                 250                 255

cga aat gtc cgc cga cgc ctt aat gat ggc agc tct gcc act att cct      816
Arg Asn Val Arg Arg Arg Leu Asn Asp Gly Ser Ser Ala Thr Ile Pro
            260                 265                 270

tcc gac tca tct ttg gtt ggt cgc gtg ctc cct gct agc tac ctc gaa      864
Ser Asp Ser Ser Leu Val Gly Arg Val Leu Pro Ala Ser Tyr Leu Glu
        275                 280                 285

cgc acc cgt gaa gaa cgc gat cgc gaa aag cat gaa tta gcg aaa aag      912
Arg Thr Arg Glu Glu Arg Asp Arg Glu Lys His Glu Leu Ala Lys Lys
    290                 295                 300

cag caa gcc ctc aac agg gaa caa tat gaa ctc gag cag aag aaa gat      960
Gln Gln Ala Leu Asn Arg Glu Gln Tyr Glu Leu Glu Gln Lys Lys Asp
305                 310                 315                 320

gag aga gat cag aag aga ttt gag tgg gag cag act aag cat ctg gtg     1008
Glu Arg Asp Gln Lys Arg Phe Glu Trp Glu Gln Thr Lys His Leu Val
                325                 330                 335

gag acg gct tta aaa atc cga gaa ttg gat atc att ccg ttg gaa gcg     1056
Glu Thr Ala Leu Lys Ile Arg Glu Leu Asp Ile Ile Pro Leu Glu Ala
            340                 345                 350

gcg atg atc aaa gct aga gct ctt tat ggc cag gcg cga gag gaa gat     1104
Ala Met Ile Lys Ala Arg Ala Leu Tyr Gly Gln Ala Arg Glu Glu Asp
        355                 360                 365

caa gct gaa gct act ctt taa                                         1125
Gln Ala Glu Ala Thr Leu
    370


<210> SEQ ID NO 30
<211> LENGTH: 374
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 30

Met Ala His His His Phe Val Gly Ile Asn Pro Ala Gly Leu Ser Phe
1               5                   10                  15

Ser His Pro Thr Pro Pro Ala Asp His Pro Ala Pro Pro Ser Ser Gly
            20                  25                  30

Ser Ile His Thr Pro Ala Asn Phe Ala Ser Ile Gln Glu Pro Ile Thr
        35                  40                  45

Asp Pro Ser Ala Val Ala Ala Arg Arg Arg Gly Arg Pro Ser Thr Arg
    50                  55                  60

Gly Glu Ala Gly Val Thr Pro Pro Pro Glu Ile Gly Trp Trp Glu Asp
65                  70                  75                  80
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Arg Ala Pro Ser Trp His Lys Asp Ala Met Gln Gly Gly Lys Ser Ser
                85                  90                  95

Met Glu Leu Leu Met Glu Trp Ser Glu Glu Met Lys Asn Gln Gly His
            100                 105                 110

Tyr Tyr Trp Met Gly Val Arg Asp Gly Gly Asn Leu His Gln Gly Ala
        115                 120                 125

Ser Arg Phe Arg Asp Tyr Leu Tyr Ala Gln His Gly Pro Ile Arg Arg
    130                 135                 140

Ser Ser Lys Ala Ile Arg Asn Lys Val Glu Asn Ile Lys Gln Lys Phe
145                 150                 155                 160

Phe Glu Ala Gln Glu Trp Leu Lys Asp Pro Asn Gly Asp His Thr Thr
                165                 170                 175

Met Thr Ile Pro Asp Val Glu Lys Lys Leu Asn Lys Ile Cys Arg Asn
            180                 185                 190

Tyr Arg Phe Trp Glu Thr Ile Phe Val Glu Leu Pro Pro Val Asp His
        195                 200                 205

Glu Ala Gly Gln Asn Ala Glu Gly Ser Ser Ser Asn Gln Thr Leu Gln
    210                 215                 220

Ser Ala Ser Gln Thr Ala Val Arg Gln Gly Asn Gly Pro Leu Ile Arg
225                 230                 235                 240

Gly Ile Pro Val Pro Glu Met Gly Gln Ala Ala Ala Asp Asp Ala Gln
                245                 250                 255

Arg Asn Val Arg Arg Arg Leu Asn Asp Gly Ser Ser Ala Thr Ile Pro
            260                 265                 270

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

Arg Thr Arg Glu Glu Arg Asp Arg Glu Lys His Glu Leu Ala Lys Lys
    290                 295                 300

Gln Gln Ala Leu Asn Arg Glu Gln Tyr Glu Leu Glu Gln Lys Lys Asp
305                 310                 315                 320

Glu Arg Asp Gln Lys Arg Phe Glu Trp Glu Gln Thr Lys His Leu Val
                325                 330                 335

Glu Thr Ala Leu Lys Ile Arg Glu Leu Asp Ile Ile Pro Leu Glu Ala
            340                 345                 350

Ala Met Ile Lys Ala Arg Ala Leu Tyr Gly Gln Ala Arg Glu Glu Asp
        355                 360                 365

Gln Ala Glu Ala Thr Leu
    370


<210> SEQ ID NO 31
<211> LENGTH: 1251
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1251)

<400> SEQUENCE: 31

atg gac gcc acc act ctt aca ggg cac gtc aag gag ctc aat gct gca       48
Met Asp Ala Thr Thr Leu Thr Gly His Val Lys Glu Leu Asn Ala Ala
1               5                   10                  15

aac caa gcg gga aaa tca gat gaa gtt atc tct ctg ctc aag aaa ctt       96
Asn Gln Ala Gly Lys Ser Asp Glu Val Ile Ser Leu Leu Lys Lys Leu
            20                  25                  30

cag gct gag gtt gtt cct aca gaa gat ctc ctt cga tca tcg aaa gct      144
Gln Ala Glu Val Val Pro Thr Glu Asp Leu Leu Arg Ser Ser Lys Ala
        35                  40                  45
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ggt gtc gca gtc ggc aag ctt cgt acc cac gcc aca cca tca gtc tca      192
Gly Val Ala Val Gly Lys Leu Arg Thr His Ala Thr Pro Ser Val Ser
    50                  55                  60

agt ctt gcc aag gag ata gtt aag aag tgg aga gat gcg gtc gag gag      240
Ser Leu Ala Lys Glu Ile Val Lys Lys Trp Arg Asp Ala Val Glu Glu
65                  70                  75                  80

aca aag aag aag aga aaa aga gca gaa ggt gat gaa gga aaa gat gta      288
Thr Lys Lys Lys Arg Lys Arg Ala Glu Gly Asp Glu Gly Lys Asp Val
                85                  90                  95

aag aag gag aag gag gaa ggg aac ggg aaa cga gtc aag gcg gaa acg      336
Lys Lys Glu Lys Glu Glu Gly Asn Gly Lys Arg Val Lys Ala Glu Thr
            100                 105                 110

ggg tca tta gcg gcg aca cca tca gct agc aca ccc gcc tcg gcc tct      384
Gly Ser Leu Ala Ala Thr Pro Ser Ala Ser Thr Pro Ala Ser Ala Ser
        115                 120                 125

aca ccc gat gtc aaa gcg acc tcc cct cct gtc cgt caa cct ctt tca      432
Thr Pro Asp Val Lys Ala Thr Ser Pro Pro Val Arg Gln Pro Leu Ser
    130                 135                 140

acc att gac tca tca cgc act acg cct cga acc gcc aaa agc gat gga      480
Thr Ile Asp Ser Ser Arg Thr Thr Pro Arg Thr Ala Lys Ser Asp Gly
145                 150                 155                 160

gtg gcc gac agc ctg aga gct gat tcg agc gaa gga ggc agt gta gat      528
Val Ala Asp Ser Leu Arg Ala Asp Ser Ser Glu Gly Gly Ser Val Asp
                165                 170                 175

agc gtg agg gac aag tgt gtg atc atg att tat gac gca ttg gcg ttg      576
Ser Val Arg Asp Lys Cys Val Ile Met Ile Tyr Asp Ala Leu Ala Leu
            180                 185                 190

gat agc acg gct gaa ata aag att ttg aaa gag cgc gcc att gga att      624
Asp Ser Thr Ala Glu Ile Lys Ile Leu Lys Glu Arg Ala Ile Gly Ile
        195                 200                 205

gag cgc gca gcg aat aaa gct atg aac ttc tca aca gga aac gat tat      672
Glu Arg Ala Ala Asn Lys Ala Met Asn Phe Ser Thr Gly Asn Asp Tyr
    210                 215                 220

cgc gct aaa atg aga tca cta ttc ctc aac ttg aaa gac aag ggt aat      720
Arg Ala Lys Met Arg Ser Leu Phe Leu Asn Leu Lys Asp Lys Gly Asn
225                 230                 235                 240

ccc gct ttg aga aac gag att gtc ttg ggc tac gtc agc acc gaa aaa      768
Pro Ala Leu Arg Asn Glu Ile Val Leu Gly Tyr Val Ser Thr Glu Lys
                245                 250                 255

gtc gct agc atg tcc aaa gat gaa atg gcc tct gaa agc gtt cga atg      816
Val Ala Ser Met Ser Lys Asp Glu Met Ala Ser Glu Ser Val Arg Met
            260                 265                 270

cta aag gag aag att gcg agt gac aac ttg ttc aag gcc aag gct gtc      864
Leu Lys Glu Lys Ile Ala Ser Asp Asn Leu Phe Lys Ala Lys Ala Val
        275                 280                 285

gga gtc acc caa gct gag aca gac gcg ttc aag tgc gga cgg tgt cac      912
Gly Val Thr Gln Ala Glu Thr Asp Ala Phe Lys Cys Gly Arg Cys His
    290                 295                 300

cag agg aaa tgt act tat tac cag atg cag aca aga agc gcg gat gaa      960
Gln Arg Lys Cys Thr Tyr Tyr Gln Met Gln Thr Arg Ser Ala Asp Glu
305                 310                 315                 320

cct atg act act ttt gtt acg tat gtg tct gac ctg act cca aaa gaa     1008
Pro Met Thr Thr Phe Val Thr Tyr Val Ser Asp Leu Thr Pro Lys Glu
                325                 330                 335

tca ttg ctg act acg tgt acg act tgc tct ttt tat tca gat gta cta     1056
Ser Leu Leu Thr Thr Cys Thr Thr Cys Ser Phe Tyr Ser Asp Val Leu
            340                 345                 350

att gta aca aca ggt gga aat tca gct agt ttc gga ttt tgc ctc tgg     1104
Ile Val Thr Thr Gly Gly Asn Ser Ala Ser Phe Gly Phe Cys Leu Trp
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        355                 360                 365

gga gca ttg tat ctt tcg ggt ttt ttg tca cgt cgt cta tgc agc cag     1152
Gly Ala Leu Tyr Leu Ser Gly Phe Leu Ser Arg Arg Leu Cys Ser Gln
    370                 375                 380

tat att tac gag gcg tat cgt tgt gat ttg cgt gtc aat gtc aca aag     1200
Tyr Ile Tyr Glu Ala Tyr Arg Cys Asp Leu Arg Val Asn Val Thr Lys
385                 390                 395                 400

cca tta agt gcc gta aat atg cct ttt tgc agt gtt ctg aaa ttc aaa     1248
Pro Leu Ser Ala Val Asn Met Pro Phe Cys Ser Val Leu Lys Phe Lys
                405                 410                 415

tga                                                                 1251


<210> SEQ ID NO 32
<211> LENGTH: 416
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 32

Met Asp Ala Thr Thr Leu Thr Gly His Val Lys Glu Leu Asn Ala Ala
1               5                   10                  15

Asn Gln Ala Gly Lys Ser Asp Glu Val Ile Ser Leu Leu Lys Lys Leu
            20                  25                  30

Gln Ala Glu Val Val Pro Thr Glu Asp Leu Leu Arg Ser Ser Lys Ala
        35                  40                  45

Gly Val Ala Val Gly Lys Leu Arg Thr His Ala Thr Pro Ser Val Ser
    50                  55                  60

Ser Leu Ala Lys Glu Ile Val Lys Lys Trp Arg Asp Ala Val Glu Glu
65                  70                  75                  80

Thr Lys Lys Lys Arg Lys Arg Ala Glu Gly Asp Glu Gly Lys Asp Val
                85                  90                  95

Lys Lys Glu Lys Glu Glu Gly Asn Gly Lys Arg Val Lys Ala Glu Thr
            100                 105                 110

Gly Ser Leu Ala Ala Thr Pro Ser Ala Ser Thr Pro Ala Ser Ala Ser
        115                 120                 125

Thr Pro Asp Val Lys Ala Thr Ser Pro Pro Val Arg Gln Pro Leu Ser
    130                 135                 140

Thr Ile Asp Ser Ser Arg Thr Thr Pro Arg Thr Ala Lys Ser Asp Gly
145                 150                 155                 160

Val Ala Asp Ser Leu Arg Ala Asp Ser Ser Glu Gly Gly Ser Val Asp
                165                 170                 175

Ser Val Arg Asp Lys Cys Val Ile Met Ile Tyr Asp Ala Leu Ala Leu
            180                 185                 190

Asp Ser Thr Ala Glu Ile Lys Ile Leu Lys Glu Arg Ala Ile Gly Ile
        195                 200                 205

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

Arg Ala Lys Met Arg Ser Leu Phe Leu Asn Leu Lys Asp Lys Gly Asn
225                 230                 235                 240

Pro Ala Leu Arg Asn Glu Ile Val Leu Gly Tyr Val Ser Thr Glu Lys
                245                 250                 255

Val Ala Ser Met Ser Lys Asp Glu Met Ala Ser Glu Ser Val Arg Met
            260                 265                 270

Leu Lys Glu Lys Ile Ala Ser Asp Asn Leu Phe Lys Ala Lys Ala Val
        275                 280                 285

Gly Val Thr Gln Ala Glu Thr Asp Ala Phe Lys Cys Gly Arg Cys His
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    290                 295                 300

Gln Arg Lys Cys Thr Tyr Tyr Gln Met Gln Thr Arg Ser Ala Asp Glu
305                 310                 315                 320

Pro Met Thr Thr Phe Val Thr Tyr Val Ser Asp Leu Thr Pro Lys Glu
                325                 330                 335

Ser Leu Leu Thr Thr Cys Thr Thr Cys Ser Phe Tyr Ser Asp Val Leu
            340                 345                 350

Ile Val Thr Thr Gly Gly Asn Ser Ala Ser Phe Gly Phe Cys Leu Trp
        355                 360                 365

Gly Ala Leu Tyr Leu Ser Gly Phe Leu Ser Arg Arg Leu Cys Ser Gln
    370                 375                 380

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

Pro Leu Ser Ala Val Asn Met Pro Phe Cys Ser Val Leu Lys Phe Lys
                405                 410                 415


<210> SEQ ID NO 33
<211> LENGTH: 657
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(657)

<400> SEQUENCE: 33

atg gat tac caa aat cga gca ggt gca aac aag ggt agt ggt ggt gtc       48
Met Asp Tyr Gln Asn Arg Ala Gly Ala Asn Lys Gly Ser Gly Gly Val
1               5                   10                  15

gct ggt gca tcc gag aca gca gtg gac agg aga gaa cgt ctt cga aaa       96
Ala Gly Ala Ser Glu Thr Ala Val Asp Arg Arg Glu Arg Leu Arg Lys
            20                  25                  30

ctt gct ttg gag act att gac ttg gcc aaa gat ccc tat atc ctt agg      144
Leu Ala Leu Glu Thr Ile Asp Leu Ala Lys Asp Pro Tyr Ile Leu Arg
        35                  40                  45

acc cat ctc ggt aca tta gaa tgc cgt ctt tgt ctc act ctt cac gtc      192
Thr His Leu Gly Thr Leu Glu Cys Arg Leu Cys Leu Thr Leu His Val
    50                  55                  60

aac gag ggt tct tac ctt gcc cac act caa gga aag aaa cat caa aca      240
Asn Glu Gly Ser Tyr Leu Ala His Thr Gln Gly Lys Lys His Gln Thr
65                  70                  75                  80

aac ctt gct agg cgt gca gcc aag gac aac aag gat cag aca tta atg      288
Asn Leu Ala Arg Arg Ala Ala Lys Asp Asn Lys Asp Gln Thr Leu Met
                85                  90                  95

atc caa gct ccc aca gcc gcg caa caa gtg aag aag aaa gtg ttt gtt      336
Ile Gln Ala Pro Thr Ala Ala Gln Gln Val Lys Lys Lys Val Phe Val
            100                 105                 110

aag att gga aga cct gga tac aaa atc atc aaa att cga gag cct gtc      384
Lys Ile Gly Arg Pro Gly Tyr Lys Ile Ile Lys Ile Arg Glu Pro Val
        115                 120                 125

agt caa agg atg ggt tta tta ttc act gtg tct tta cct gag ata aaa      432
Ser Gln Arg Met Gly Leu Leu Phe Thr Val Ser Leu Pro Glu Ile Lys
    130                 135                 140

gcg gga gag agg cca aga agg agg ttc atg tct gct ttt gaa caa cgg      480
Ala Gly Glu Arg Pro Arg Arg Arg Phe Met Ser Ala Phe Glu Gln Arg
145                 150                 155                 160

cga gag att ccc aat aaa gct ttc cag tac tta gtt ttg gca gcc gag      528
Arg Glu Ile Pro Asn Lys Ala Phe Gln Tyr Leu Val Leu Ala Ala Glu
                165                 170                 175

cca tac gag acc ata gca ttt gcc atc ccc tca aaa gag atg gtt gac      576
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Pro Tyr Glu Thr Ile Ala Phe Ala Ile Pro Ser Lys Glu Met Val Asp
            180                 185                 190

gtt gat gaa gac ccg gag tcg aca tgg gag cac tgg gat gcc gac gag      624
Val Asp Glu Asp Pro Glu Ser Thr Trp Glu His Trp Asp Ala Asp Glu
        195                 200                 205

aag gtt tac agt tgt caa ttc ttg tat aaa taa                          657
Lys Val Tyr Ser Cys Gln Phe Leu Tyr Lys
    210                 215


<210> SEQ ID NO 34
<211> LENGTH: 218
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 34

Met Asp Tyr Gln Asn Arg Ala Gly Ala Asn Lys Gly Ser Gly Gly Val
1               5                   10                  15

Ala Gly Ala Ser Glu Thr Ala Val Asp Arg Arg Glu Arg Leu Arg Lys
            20                  25                  30

Leu Ala Leu Glu Thr Ile Asp Leu Ala Lys Asp Pro Tyr Ile Leu Arg
        35                  40                  45

Thr His Leu Gly Thr Leu Glu Cys Arg Leu Cys Leu Thr Leu His Val
    50                  55                  60

Asn Glu Gly Ser Tyr Leu Ala His Thr Gln Gly Lys Lys His Gln Thr
65                  70                  75                  80

Asn Leu Ala Arg Arg Ala Ala Lys Asp Asn Lys Asp Gln Thr Leu Met
                85                  90                  95

Ile Gln Ala Pro Thr Ala Ala Gln Gln Val Lys Lys Lys Val Phe Val
            100                 105                 110

Lys Ile Gly Arg Pro Gly Tyr Lys Ile Ile Lys Ile Arg Glu Pro Val
        115                 120                 125

Ser Gln Arg Met Gly Leu Leu Phe Thr Val Ser Leu Pro Glu Ile Lys
    130                 135                 140

Ala Gly Glu Arg Pro Arg Arg Arg Phe Met Ser Ala Phe Glu Gln Arg
145                 150                 155                 160

Arg Glu Ile Pro Asn Lys Ala Phe Gln Tyr Leu Val Leu Ala Ala Glu
                165                 170                 175

Pro Tyr Glu Thr Ile Ala Phe Ala Ile Pro Ser Lys Glu Met Val Asp
            180                 185                 190

Val Asp Glu Asp Pro Glu Ser Thr Trp Glu His Trp Asp Ala Asp Glu
        195                 200                 205

Lys Val Tyr Ser Cys Gln Phe Leu Tyr Lys
    210                 215


<210> SEQ ID NO 35
<211> LENGTH: 813
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(813)

<400> SEQUENCE: 35

atg aca gtc aag gca gag caa gat ctc tat ctt gac ccc tcc att cgg       48
Met Thr Val Lys Ala Glu Gln Asp Leu Tyr Leu Asp Pro Ser Ile Arg
1               5                   10                  15

gat tgg gtc ctt atc cct atc acc cta atc atg cta ctc gtc ggt gtg       96
Asp Trp Val Leu Ile Pro Ile Thr Leu Ile Met Leu Leu Val Gly Val
            20                  25                  30
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tta aga cac tac atc acg caa ttc ctt aac tct gca cca aaa aaa caa      144
Leu Arg His Tyr Ile Thr Gln Phe Leu Asn Ser Ala Pro Lys Lys Gln
        35                  40                  45

aca gca gct gcc gtt cgc gaa caa cgc gca ctt ggt cgc tca gct ctg      192
Thr Ala Ala Ala Val Arg Glu Gln Arg Ala Leu Gly Arg Ser Ala Leu
    50                  55                  60

ctt cgg gca act gcg act ctg tcc ccc ctt ccg cct gcc tct tac aag      240
Leu Arg Ala Thr Ala Thr Leu Ser Pro Leu Pro Pro Ala Ser Tyr Lys
65                  70                  75                  80

gct ctc tcg gga tcc ctt gct gct tca ctt tct act ggt gag tat atc      288
Ala Leu Ser Gly Ser Leu Ala Ala Ser Leu Ser Thr Gly Glu Tyr Ile
                85                  90                  95

aag ccc gcc cca gag tca aag ggg gat gct tct ccc gcc aat cct ctc      336
Lys Pro Ala Pro Glu Ser Lys Gly Asp Ala Ser Pro Ala Asn Pro Leu
            100                 105                 110

gaa ggt gct ggg atg gaa aat gcg atg gac ggt atg aaa aag cag gcc      384
Glu Gly Ala Gly Met Glu Asn Ala Met Asp Gly Met Lys Lys Gln Ala
        115                 120                 125

gta atg atg gta ccc aac atg gtt atc atg cag tat atc aac gtc ttt      432
Val Met Met Val Pro Asn Met Val Ile Met Gln Tyr Ile Asn Val Phe
    130                 135                 140

ttt tcc gga ttt atc ctt atg cgt ctg cca ttt cct tta acc gca ggc      480
Phe Ser Gly Phe Ile Leu Met Arg Leu Pro Phe Pro Leu Thr Ala Gly
145                 150                 155                 160

ttt aag tcg ttg ctg tca agg gat att ccc atg gct gat ctc gat gtg      528
Phe Lys Ser Leu Leu Ser Arg Asp Ile Pro Met Ala Asp Leu Asp Val
                165                 170                 175

cga tgg gtt tcc gct ttg tcc tgg tat ttt ctc aac ttg ttt ggc ttg      576
Arg Trp Val Ser Ala Leu Ser Trp Tyr Phe Leu Asn Leu Phe Gly Leu
            180                 185                 190

aac ggt gtt ttc aaa cta att ctt gga gct gag aat gct gct gta gac      624
Asn Gly Val Phe Lys Leu Ile Leu Gly Ala Glu Asn Ala Ala Val Asp
        195                 200                 205

agc cgt gac ctc acc tcg ctg tct gca ctt tct ggg gca gga ggc cct      672
Ser Arg Asp Leu Thr Ser Leu Ser Ala Leu Ser Gly Ala Gly Gly Pro
    210                 215                 220

atg ccc ggc ccc ggc ggt cca cca gac atg gtc aag ctt ttc aag gcc      720
Met Pro Gly Pro Gly Gly Pro Pro Asp Met Val Lys Leu Phe Lys Ala
225                 230                 235                 240

gag gtt gag aac ttg gca ttg gca gaa agt tca tac aag tgg gtc ggc      768
Glu Val Glu Asn Leu Ala Leu Ala Glu Ser Ser Tyr Lys Trp Val Gly
                245                 250                 255

gac gga gta gaa gat aga gtt ttg aga gct tgg ggc aaa gtt taa          813
Asp Gly Val Glu Asp Arg Val Leu Arg Ala Trp Gly Lys Val
            260                 265                 270


<210> SEQ ID NO 36
<211> LENGTH: 270
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 36

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

Asp Trp Val Leu Ile Pro Ile Thr Leu Ile Met Leu Leu Val Gly Val
            20                  25                  30

Leu Arg His Tyr Ile Thr Gln Phe Leu Asn Ser Ala Pro Lys Lys Gln
        35                  40                  45

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

Leu Arg Ala Thr Ala Thr Leu Ser Pro Leu Pro Pro Ala Ser Tyr Lys
65                  70                  75                  80

Ala Leu Ser Gly Ser Leu Ala Ala Ser Leu Ser Thr Gly Glu Tyr Ile
                85                  90                  95

Lys Pro Ala Pro Glu Ser Lys Gly Asp Ala Ser Pro Ala Asn Pro Leu
            100                 105                 110

Glu Gly Ala Gly Met Glu Asn Ala Met Asp Gly Met Lys Lys Gln Ala
        115                 120                 125

Val Met Met Val Pro Asn Met Val Ile Met Gln Tyr Ile Asn Val Phe
    130                 135                 140

Phe Ser Gly Phe Ile Leu Met Arg Leu Pro Phe Pro Leu Thr Ala Gly
145                 150                 155                 160

Phe Lys Ser Leu Leu Ser Arg Asp Ile Pro Met Ala Asp Leu Asp Val
                165                 170                 175

Arg Trp Val Ser Ala Leu Ser Trp Tyr Phe Leu Asn Leu Phe Gly Leu
            180                 185                 190

Asn Gly Val Phe Lys Leu Ile Leu Gly Ala Glu Asn Ala Ala Val Asp
        195                 200                 205

Ser Arg Asp Leu Thr Ser Leu Ser Ala Leu Ser Gly Ala Gly Gly Pro
    210                 215                 220

Met Pro Gly Pro Gly Gly Pro Pro Asp Met Val Lys Leu Phe Lys Ala
225                 230                 235                 240

Glu Val Glu Asn Leu Ala Leu Ala Glu Ser Ser Tyr Lys Trp Val Gly
                245                 250                 255

Asp Gly Val Glu Asp Arg Val Leu Arg Ala Trp Gly Lys Val
            260                 265                 270


<210> SEQ ID NO 37
<211> LENGTH: 1365
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1365)

<400> SEQUENCE: 37

atg acc gcg gtg aac agc aac cag ggc acc ggc aaa ctg agc ggc cgc        48
Met Thr Ala Val Asn Ser Asn Gln Gly Thr Gly Lys Leu Ser Gly Arg
1               5                   10                  15

gtg ggc att gtg ggc acc ggc cat cgc gcg cgc ctg tat acc acc gcg        96
Val Gly Ile Val Gly Thr Gly His Arg Ala Arg Leu Tyr Thr Thr Ala
            20                  25                  30

gtg gcg agc cgc gcg aac acc agc ctg gtg gcg ctg tgc gat acc aac       144
Val Ala Ser Arg Ala Asn Thr Ser Leu Val Ala Leu Cys Asp Thr Asn
        35                  40                  45

gat gcg cgc atg gat tgg cat aac aaa atg ctg cgc gaa gcg ggc cgc       192
Asp Ala Arg Met Asp Trp His Asn Lys Met Leu Arg Glu Ala Gly Arg
    50                  55                  60

ccg gaa gcg aaa aaa tat gcg gcg gaa gat ttt cgc aaa atg ctg gaa       240
Pro Glu Ala Lys Lys Tyr Ala Ala Glu Asp Phe Arg Lys Met Leu Glu
65                  70                  75                  80

cag gaa aaa ctg gat gtg ctg gtg gtg acc acc att gat tat acc cat       288
Gln Glu Lys Leu Asp Val Leu Val Val Thr Thr Ile Asp Tyr Thr His
                85                  90                  95

gat atg tat att att ccg gcg ctg aaa gcg ggc att aaa gtg ctg agc       336
Asp Met Tyr Ile Ile Pro Ala Leu Lys Ala Gly Ile Lys Val Leu Ser
            100                 105                 110
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gaa aaa ccg atg acc acc aac gtg gat aaa tgc aaa gcg att ctg aac      384
Glu Lys Pro Met Thr Thr Asn Val Asp Lys Cys Lys Ala Ile Leu Asn
        115                 120                 125

gcg gtg aac gaa agc aaa ggc agc ctg acc gtg ctg ttt aac tat cgc      432
Ala Val Asn Glu Ser Lys Gly Ser Leu Thr Val Leu Phe Asn Tyr Arg
    130                 135                 140

tat aac ccg att cat tgg aaa gtg gcg gaa gtg att gcg aaa ggc gaa      480
Tyr Asn Pro Ile His Trp Lys Val Ala Glu Val Ile Ala Lys Gly Glu
145                 150                 155                 160

att ggc gaa gtg aaa agc gtg cat ttt gaa tgg ctg ctg gat acc gtg      528
Ile Gly Glu Val Lys Ser Val His Phe Glu Trp Leu Leu Asp Thr Val
                165                 170                 175

cat ggc gcg gat tat ttt cgc cgc tgg cat cgc tat aaa gat cgc agc      576
His Gly Ala Asp Tyr Phe Arg Arg Trp His Arg Tyr Lys Asp Arg Ser
            180                 185                 190

ggc ggc ctg atg att cat aaa agc agc cat cat ttt gat ctg gtg aac      624
Gly Gly Leu Met Ile His Lys Ser Ser His His Phe Asp Leu Val Asn
        195                 200                 205

ttt tgg att cag agc gtg ccg cag agc gtg ttt ggc atg ggc agc ctg      672
Phe Trp Ile Gln Ser Val Pro Gln Ser Val Phe Gly Met Gly Ser Leu
    210                 215                 220

gcg ttt tat ggc aaa gaa aac ggc aaa aaa agc ggc tgg ggc aaa aac      720
Ala Phe Tyr Gly Lys Glu Asn Gly Lys Lys Ser Gly Trp Gly Lys Asn
225                 230                 235                 240

tat gaa cgc gcg cgc gat gcg aaa gaa gcg gaa aac gat ccg ttt gcg      768
Tyr Glu Arg Ala Arg Asp Ala Lys Glu Ala Glu Asn Asp Pro Phe Ala
                245                 250                 255

att cat ctg ggc gat gaa gaa ggc ctg aaa ggc ctg tat ttt gat gcg      816
Ile His Leu Gly Asp Glu Glu Gly Leu Lys Gly Leu Tyr Phe Asp Ala
            260                 265                 270

gaa cat att gat ggc tat cat cgc gat atg aac gtg ttt gcg gat gat      864
Glu His Ile Asp Gly Tyr His Arg Asp Met Asn Val Phe Ala Asp Asp
        275                 280                 285

att acc att gaa gat gat atg agc gtg ctg gtg cat tat gaa agc ggc      912
Ile Thr Ile Glu Asp Asp Met Ser Val Leu Val His Tyr Glu Ser Gly
    290                 295                 300

gtg aac atg acc tat cat ctg acc gcg tat agc ccg tgg gaa ggc tat      960
Val Asn Met Thr Tyr His Leu Thr Ala Tyr Ser Pro Trp Glu Gly Tyr
305                 310                 315                 320

cgc gtg atg ttt aac ggc acc cat ggc cgc ctg gaa ctg gaa gtg gtg     1008
Arg Val Met Phe Asn Gly Thr His Gly Arg Leu Glu Leu Glu Val Val
                325                 330                 335

gaa aac gcg ttt cgc ctg ccg att ccg aaa ggc agc aac aac gcg agc     1056
Glu Asn Ala Phe Arg Leu Pro Ile Pro Lys Gly Ser Asn Asn Ala Ser
            340                 345                 350

gaa cat gtg cat ggc gat agc gcg ctg ccg aac gaa ggc cat agc aaa     1104
Glu His Val His Gly Asp Ser Ala Leu Pro Asn Glu Gly His Ser Lys
        355                 360                 365

att acc ctg cat aaa ctg tgg cag cag ccg gtg aac gtg ccg tat cag     1152
Ile Thr Leu His Lys Leu Trp Gln Gln Pro Val Asn Val Pro Tyr Gln
    370                 375                 380

gaa gcg aaa ggc ggc cat ggc ggc ggc gat gaa gcg atg ctg gat gaa     1200
Glu Ala Lys Gly Gly His Gly Gly Gly Asp Glu Ala Met Leu Asp Glu
385                 390                 395                 400

att ttt ggc ccg aaa gaa ggc gaa gaa gaa cgc aaa tgc ccg gtg aac     1248
Ile Phe Gly Pro Lys Glu Gly Glu Glu Glu Arg Lys Cys Pro Val Asn
                405                 410                 415

ggc ctg agc gcg gat cag aaa gat ggc gcg ctg gcg atg gcg gtg ggc     1296
Gly Leu Ser Ala Asp Gln Lys Asp Gly Ala Leu Ala Met Ala Val Gly
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            420                 425                 430

ctg gcg gcg aac gaa agc ttt aaa aac ggc aaa cag gtg ttt att aaa         1344
Leu Ala Ala Asn Glu Ser Phe Lys Asn Gly Lys Gln Val Phe Ile Lys
        435                 440                 445

gaa ctg ctg ggc ggc acc ctg                                             1365
Glu Leu Leu Gly Gly Thr Leu
    450                 455


<210> SEQ ID NO 38
<211> LENGTH: 455
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 38

Met Thr Ala Val Asn Ser Asn Gln Gly Thr Gly Lys Leu Ser Gly Arg
1               5                   10                  15

Val Gly Ile Val Gly Thr Gly His Arg Ala Arg Leu Tyr Thr Thr Ala
            20                  25                  30

Val Ala Ser Arg Ala Asn Thr Ser Leu Val Ala Leu Cys Asp Thr Asn
        35                  40                  45

Asp Ala Arg Met Asp Trp His Asn Lys Met Leu Arg Glu Ala Gly Arg
    50                  55                  60

Pro Glu Ala Lys Lys Tyr Ala Ala Glu Asp Phe Arg Lys Met Leu Glu
65                  70                  75                  80

Gln Glu Lys Leu Asp Val Leu Val Val Thr Thr Ile Asp Tyr Thr His
                85                  90                  95

Asp Met Tyr Ile Ile Pro Ala Leu Lys Ala Gly Ile Lys Val Leu Ser
            100                 105                 110

Glu Lys Pro Met Thr Thr Asn Val Asp Lys Cys Lys Ala Ile Leu Asn
        115                 120                 125

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

Tyr Asn Pro Ile His Trp Lys Val Ala Glu Val Ile Ala Lys Gly Glu
145                 150                 155                 160

Ile Gly Glu Val Lys Ser Val His Phe Glu Trp Leu Leu Asp Thr Val
                165                 170                 175

His Gly Ala Asp Tyr Phe Arg Arg Trp His Arg Tyr Lys Asp Arg Ser
            180                 185                 190

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

Phe Trp Ile Gln Ser Val Pro Gln Ser Val Phe Gly Met Gly Ser Leu
    210                 215                 220

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

Tyr Glu Arg Ala Arg Asp Ala Lys Glu Ala Glu Asn Asp Pro Phe Ala
                245                 250                 255

Ile His Leu Gly Asp Glu Glu Gly Leu Lys Gly Leu Tyr Phe Asp Ala
            260                 265                 270

Glu His Ile Asp Gly Tyr His Arg Asp Met Asn Val Phe Ala Asp Asp
        275                 280                 285

Ile Thr Ile Glu Asp Asp Met Ser Val Leu Val His Tyr Glu Ser Gly
    290                 295                 300

Val Asn Met Thr Tyr His Leu Thr Ala Tyr Ser Pro Trp Glu Gly Tyr
305                 310                 315                 320

Arg Val Met Phe Asn Gly Thr His Gly Arg Leu Glu Leu Glu Val Val
```

```
                325                 330                 335

Glu Asn Ala Phe Arg Leu Pro Ile Pro Lys Gly Ser Asn Asn Ala Ser
            340                 345                 350

Glu His Val His Gly Asp Ser Ala Leu Pro Asn Glu Gly His Ser Lys
        355                 360                 365

Ile Thr Leu His Lys Leu Trp Gln Gln Pro Val Asn Val Pro Tyr Gln
    370                 375                 380

Glu Ala Lys Gly Gly His Gly Gly Gly Asp Glu Ala Met Leu Asp Glu
385                 390                 395                 400

Ile Phe Gly Pro Lys Glu Gly Glu Glu Glu Arg Lys Cys Pro Val Asn
                405                 410                 415

Gly Leu Ser Ala Asp Gln Lys Asp Gly Ala Leu Ala Met Ala Val Gly
            420                 425                 430

Leu Ala Ala Asn Glu Ser Phe Lys Asn Gly Lys Gln Val Phe Ile Lys
        435                 440                 445

Glu Leu Leu Gly Gly Thr Leu
    450                 455


<210> SEQ ID NO 39
<211> LENGTH: 1338
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1338)

<400> SEQUENCE: 39

atg agc gcg att cgc gcg ctg aac atg cgc aaa acc gcg agc gcg ctg       48
Met Ser Ala Ile Arg Ala Leu Asn Met Arg Lys Thr Ala Ser Ala Leu
1               5                   10                  15

aaa gcg ccg gtg gcg ttt aaa cgc acc ctg gcg acc ccg gtg aac agc       96
Lys Ala Pro Val Ala Phe Lys Arg Thr Leu Ala Thr Pro Val Asn Ser
            20                  25                  30

ctg tat acc agc gtg ctg ccg gcg aaa att ccg gcg gcg ctg cat ctg      144
Leu Tyr Thr Ser Val Leu Pro Ala Lys Ile Pro Ala Ala Leu His Leu
        35                  40                  45

aaa agc ggc cag agc tat ttt ggc agc agc ttt ggc agc gaa aac agc      192
Lys Ser Gly Gln Ser Tyr Phe Gly Ser Ser Phe Gly Ser Glu Asn Ser
    50                  55                  60

aaa ttt ggc gaa acc gtg ttt agc acc agc att acc agc tat acc gat      240
Lys Phe Gly Glu Thr Val Phe Ser Thr Ser Ile Thr Ser Tyr Thr Asp
65                  70                  75                  80

agc atg acc gat ccg agc tat ctg ggc cag att ctg gtg ttt acc agc      288
Ser Met Thr Asp Pro Ser Tyr Leu Gly Gln Ile Leu Val Phe Thr Ser
                85                  90                  95

ccg atg att ggc aac tat ggc gtg ccg agc aac acc agc agc cag ttt      336
Pro Met Ile Gly Asn Tyr Gly Val Pro Ser Asn Thr Ser Ser Gln Phe
            100                 105                 110

ccg ggc att ccg ttt ctg gaa agc gaa aaa att cag tgc acc ggc gtg      384
Pro Gly Ile Pro Phe Leu Glu Ser Glu Lys Ile Gln Cys Thr Gly Val
        115                 120                 125

gtg gtg agc gat gtg gcg ctg aaa tat agc cat tat cag gcg gtg gaa      432
Val Val Ser Asp Val Ala Leu Lys Tyr Ser His Tyr Gln Ala Val Glu
    130                 135                 140

agc ctg cat gaa tgg tgc aaa cgc tat gat gtg ccg ggc att acc ggc      480
Ser Leu His Glu Trp Cys Lys Arg Tyr Asp Val Pro Gly Ile Thr Gly
145                 150                 155                 160

gtg gat acc cgc gcg att acc agc ctg ctg cgc gat cag ggc acc acc      528
Val Asp Thr Arg Ala Ile Thr Ser Leu Leu Arg Asp Gln Gly Thr Thr
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                165                 170                 175

ctg ggc cgc ctg gcg gtg ggc gat gaa gcg ggc aaa ccg gcg ccg cag      576
Leu Gly Arg Leu Ala Val Gly Asp Glu Ala Gly Lys Pro Ala Pro Gln
            180                 185                 190

gaa gcg gaa tat tgg gat ccg agc aaa gaa aac ctg gtg gcg cag gcg      624
Glu Ala Glu Tyr Trp Asp Pro Ser Lys Glu Asn Leu Val Ala Gln Ala
        195                 200                 205

agc acc aaa aaa gcg tat gtg ctg aac gaa aaa ggc agc ggc ccg cgc      672
Ser Thr Lys Lys Ala Tyr Val Leu Asn Glu Lys Gly Ser Gly Pro Arg
    210                 215                 220

att gcg gtg ctg gat ttt ggc acc aaa gcg aac att ctg cgc agc ctg      720
Ile Ala Val Leu Asp Phe Gly Thr Lys Ala Asn Ile Leu Arg Ser Leu
225                 230                 235                 240

att cgc cgc gat gcg gtg gtg acc gtg ctg ccg tgg gat ttt gat ttt      768
Ile Arg Arg Asp Ala Val Val Thr Val Leu Pro Trp Asp Phe Asp Phe
                245                 250                 255

aac acc gtg cgc gat cag ttt gat ggc ctg ttt ctg agc aac ggc ccg      816
Asn Thr Val Arg Asp Gln Phe Asp Gly Leu Phe Leu Ser Asn Gly Pro
            260                 265                 270

ggc gat ccg aaa atg att atg gat agc gcg atg cgc gtg cgc cag acc      864
Gly Asp Pro Lys Met Ile Met Asp Ser Ala Met Arg Val Arg Gln Thr
        275                 280                 285

att aac gaa tgg aac aaa ccg att ttt ggc att tgc atg ggc cat cag      912
Ile Asn Glu Trp Asn Lys Pro Ile Phe Gly Ile Cys Met Gly His Gln
    290                 295                 300

gtg ctg ggc ctg gcg gcg ggc ctg gaa gcg tat cgc atg acc ttt ggc      960
Val Leu Gly Leu Ala Ala Gly Leu Glu Ala Tyr Arg Met Thr Phe Gly
305                 310                 315                 320

aac cgc ggc cat aac cag ccg gtg ctg gcg ctg gcg agc agc ggc agc     1008
Asn Arg Gly His Asn Gln Pro Val Leu Ala Leu Ala Ser Ser Gly Ser
                325                 330                 335

att aaa gcg ggc cgc gtg tat gtg acc agc cag aac cat cag tat gcg     1056
Ile Lys Ala Gly Arg Val Tyr Val Thr Ser Gln Asn His Gln Tyr Ala
            340                 345                 350

ctg cgc ctg acc gaa gat ttt ccg gaa ggc tgg gcg ccg ttt ttt att     1104
Leu Arg Leu Thr Glu Asp Phe Pro Glu Gly Trp Ala Pro Phe Phe Ile
        355                 360                 365

aac tgc aac gat agc agc gtg gaa ggc att att agc acc ccg gaa agc     1152
Asn Cys Asn Asp Ser Ser Val Glu Gly Ile Ile Ser Thr Pro Glu Ser
    370                 375                 380

ggc aaa cgc att tgg ggc gtg cag ttt cat ccg gaa agc gcg ggc ggc     1200
Gly Lys Arg Ile Trp Gly Val Gln Phe His Pro Glu Ser Ala Gly Gly
385                 390                 395                 400

ccg ctg gat acc att gaa atg ttt acc gat ttt gtg aac gaa tgc gat     1248
Pro Leu Asp Thr Ile Glu Met Phe Thr Asp Phe Val Asn Glu Cys Asp
                405                 410                 415

gtg agc cgc aaa ggc ttt agc ggc agc gcg atg att gcg aac gaa gtg     1296
Val Ser Arg Lys Gly Phe Ser Gly Ser Ala Met Ile Ala Asn Glu Val
            420                 425                 430

aaa gtg gat ggc cat gcg gcg aaa gcg gcg agc gtg agc gcg             1338
Lys Val Asp Gly His Ala Ala Lys Ala Ala Ser Val Ser Ala
        435                 440                 445


<210> SEQ ID NO 40
<211> LENGTH: 446
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 40

Met Ser Ala Ile Arg Ala Leu Asn Met Arg Lys Thr Ala Ser Ala Leu
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1               5                   10                  15

Lys Ala Pro Val Ala Phe Lys Arg Thr Leu Ala Thr Pro Val Asn Ser
            20                  25                  30

Leu Tyr Thr Ser Val Leu Pro Ala Lys Ile Pro Ala Ala Leu His Leu
        35                  40                  45

Lys Ser Gly Gln Ser Tyr Phe Gly Ser Ser Phe Gly Ser Glu Asn Ser
    50                  55                  60

Lys Phe Gly Glu Thr Val Phe Ser Thr Ser Ile Thr Ser Tyr Thr Asp
65                  70                  75                  80

Ser Met Thr Asp Pro Ser Tyr Leu Gly Gln Ile Leu Val Phe Thr Ser
                85                  90                  95

Pro Met Ile Gly Asn Tyr Gly Val Pro Ser Asn Thr Ser Ser Gln Phe
            100                 105                 110

Pro Gly Ile Pro Phe Leu Glu Ser Glu Lys Ile Gln Cys Thr Gly Val
        115                 120                 125

Val Val Ser Asp Val Ala Leu Lys Tyr Ser His Tyr Gln Ala Val Glu
    130                 135                 140

Ser Leu His Glu Trp Cys Lys Arg Tyr Asp Val Pro Gly Ile Thr Gly
145                 150                 155                 160

Val Asp Thr Arg Ala Ile Thr Ser Leu Leu Arg Asp Gln Gly Thr Thr
                165                 170                 175

Leu Gly Arg Leu Ala Val Gly Asp Glu Ala Gly Lys Pro Ala Pro Gln
            180                 185                 190

Glu Ala Glu Tyr Trp Asp Pro Ser Lys Glu Asn Leu Val Ala Gln Ala
        195                 200                 205

Ser Thr Lys Lys Ala Tyr Val Leu Asn Glu Lys Gly Ser Gly Pro Arg
    210                 215                 220

Ile Ala Val Leu Asp Phe Gly Thr Lys Ala Asn Ile Leu Arg Ser Leu
225                 230                 235                 240

Ile Arg Arg Asp Ala Val Val Thr Val Leu Pro Trp Asp Phe Asp Phe
                245                 250                 255

Asn Thr Val Arg Asp Gln Phe Asp Gly Leu Phe Leu Ser Asn Gly Pro
            260                 265                 270

Gly Asp Pro Lys Met Ile Met Asp Ser Ala Met Arg Val Arg Gln Thr
        275                 280                 285

Ile Asn Glu Trp Asn Lys Pro Ile Phe Gly Ile Cys Met Gly His Gln
    290                 295                 300

Val Leu Gly Leu Ala Ala Gly Leu Glu Ala Tyr Arg Met Thr Phe Gly
305                 310                 315                 320

Asn Arg Gly His Asn Gln Pro Val Leu Ala Leu Ala Ser Ser Gly Ser
                325                 330                 335

Ile Lys Ala Gly Arg Val Tyr Val Thr Ser Gln Asn His Gln Tyr Ala
            340                 345                 350

Leu Arg Leu Thr Glu Asp Phe Pro Glu Gly Trp Ala Pro Phe Phe Ile
        355                 360                 365

Asn Cys Asn Asp Ser Ser Val Glu Gly Ile Ile Ser Thr Pro Glu Ser
    370                 375                 380

Gly Lys Arg Ile Trp Gly Val Gln Phe His Pro Glu Ser Ala Gly Gly
385                 390                 395                 400

Pro Leu Asp Thr Ile Glu Met Phe Thr Asp Phe Val Asn Glu Cys Asp
                405                 410                 415

Val Ser Arg Lys Gly Phe Ser Gly Ser Ala Met Ile Ala Asn Glu Val
            420                 425                 430
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Lys Val Asp Gly His Ala Ala Lys Ala Ala Ser Val Ser Ala
        435                 440                 445


<210> SEQ ID NO 41
<211> LENGTH: 843
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(843)

<400> SEQUENCE: 41

atg agc gtg ccg agc ctg aaa agc gcg ctg aaa aaa ccg acc aaa agc       48
Met Ser Val Pro Ser Leu Lys Ser Ala Leu Lys Lys Pro Thr Lys Ser
1               5                   10                  15

ttt gat acc ccg ccg gcg ggc ccg agc aaa ctg agc gtg gcg gcg gcg       96
Phe Asp Thr Pro Pro Ala Gly Pro Ser Lys Leu Ser Val Ala Ala Ala
            20                  25                  30

gtg ccg gaa aaa agc aaa gcg aaa gcg aaa cag agc gtg agc att gcg      144
Val Pro Glu Lys Ser Lys Ala Lys Ala Lys Gln Ser Val Ser Ile Ala
        35                  40                  45

gaa aaa ccg cag cgc ctg cgc ggc ccg gat ctg gaa agc gaa agc gaa      192
Glu Lys Pro Gln Arg Leu Arg Gly Pro Asp Leu Glu Ser Glu Ser Glu
    50                  55                  60

ggc aac gcg agc ggc ttt gaa gat gaa agc gcg agc gaa gtg gaa gtg      240
Gly Asn Ala Ser Gly Phe Glu Asp Glu Ser Ala Ser Glu Val Glu Val
65                  70                  75                  80

gat gaa gat gaa gaa atg aac acc gat gaa gaa att gaa aaa gcg aaa      288
Asp Glu Asp Glu Glu Met Asn Thr Asp Glu Glu Ile Glu Lys Ala Lys
                85                  90                  95

gaa ggc aaa ccg aaa aaa agc acc aaa cgc aaa aaa gcg ccg acc acc      336
Glu Gly Lys Pro Lys Lys Ser Thr Lys Arg Lys Lys Ala Pro Thr Thr
            100                 105                 110

gcg gcg gat ttt ggc gcg acc ctg acc agc ctg ctg gcg gat ccg ctg      384
Ala Ala Asp Phe Gly Ala Thr Leu Thr Ser Leu Leu Ala Asp Pro Leu
        115                 120                 125

acc aaa agc aac aaa aaa gcg aaa acc gcg gat agc acc aaa aaa gcg      432
Thr Lys Ser Asn Lys Lys Ala Lys Thr Ala Asp Ser Thr Lys Lys Ala
    130                 135                 140

gcg gcg gcg ccg att ctg gcg ctg agc gcg cat aaa ctg ccg acc aaa      480
Ala Ala Ala Pro Ile Leu Ala Leu Ser Ala His Lys Leu Pro Thr Lys
145                 150                 155                 160

gcg agc gtg agc ctg gaa gcg aaa gcg aaa cgc cag ctg aaa gcg gaa      528
Ala Ser Val Ser Leu Glu Ala Lys Ala Lys Arg Gln Leu Lys Ala Glu
                165                 170                 175

aaa gaa gaa aaa gaa gat cgc gcg cgc gtg cag aac gtg ctg gaa ggc      576
Lys Glu Glu Lys Glu Asp Arg Ala Arg Val Gln Asn Val Leu Glu Gly
            180                 185                 190

tgg agc ggc gat ggc gtg gtg ggc ggc cag gaa ttt gaa cgc aac ctg      624
Trp Ser Gly Asp Gly Val Val Gly Gly Gln Glu Phe Glu Arg Asn Leu
        195                 200                 205

cgc aaa acc gcg cag aaa ggc gtg gtg aaa ctg ttt aac gcg att ctg      672
Arg Lys Thr Ala Gln Lys Gly Val Val Lys Leu Phe Asn Ala Ile Leu
    210                 215                 220

gtg gcg agc aaa aac gcg gaa gcg gcg cag acc acc ctg agc gaa aaa      720
Val Ala Ser Lys Asn Ala Glu Ala Ala Gln Thr Thr Leu Ser Glu Lys
225                 230                 235                 240

gcg cgc ctg aaa ccg gaa gcg gcg aaa aaa aaa gaa aaa gat aac att      768
Ala Arg Leu Lys Pro Glu Ala Ala Lys Lys Lys Glu Lys Asp Asn Ile
                245                 250                 255
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ctg ggc cgc ggc ggc aaa gaa gat gtg ctg acc aaa gaa agc ttt ctg      816
Leu Gly Arg Gly Gly Lys Glu Asp Val Leu Thr Lys Glu Ser Phe Leu
            260                 265                 270

gaa atg gtg cgc aaa ggc agc agc aaa                                  843
Glu Met Val Arg Lys Gly Ser Ser Lys
        275                 280


<210> SEQ ID NO 42
<211> LENGTH: 281
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 42

Met Ser Val Pro Ser Leu Lys Ser Ala Leu Lys Lys Pro Thr Lys Ser
1               5                   10                  15

Phe Asp Thr Pro Pro Ala Gly Pro Ser Lys Leu Ser Val Ala Ala Ala
            20                  25                  30

Val Pro Glu Lys Ser Lys Ala Lys Ala Lys Gln Ser Val Ser Ile Ala
        35                  40                  45

Glu Lys Pro Gln Arg Leu Arg Gly Pro Asp Leu Glu Ser Glu Ser Glu
    50                  55                  60

Gly Asn Ala Ser Gly Phe Glu Asp Glu Ser Ala Ser Glu Val Glu Val
65                  70                  75                  80

Asp Glu Asp Glu Glu Met Asn Thr Asp Glu Glu Ile Glu Lys Ala Lys
                85                  90                  95

Glu Gly Lys Pro Lys Lys Ser Thr Lys Arg Lys Lys Ala Pro Thr Thr
            100                 105                 110

Ala Ala Asp Phe Gly Ala Thr Leu Thr Ser Leu Leu Ala Asp Pro Leu
        115                 120                 125

Thr Lys Ser Asn Lys Lys Ala Lys Thr Ala Asp Ser Thr Lys Lys Ala
    130                 135                 140

Ala Ala Ala Pro Ile Leu Ala Leu Ser Ala His Lys Leu Pro Thr Lys
145                 150                 155                 160

Ala Ser Val Ser Leu Glu Ala Lys Ala Lys Arg Gln Leu Lys Ala Glu
                165                 170                 175

Lys Glu Glu Lys Glu Asp Arg Ala Arg Val Gln Asn Val Leu Glu Gly
            180                 185                 190

Trp Ser Gly Asp Gly Val Val Gly Gly Gln Glu Phe Glu Arg Asn Leu
        195                 200                 205

Arg Lys Thr Ala Gln Lys Gly Val Val Lys Leu Phe Asn Ala Ile Leu
    210                 215                 220

Val Ala Ser Lys Asn Ala Glu Ala Ala Gln Thr Thr Leu Ser Glu Lys
225                 230                 235                 240

Ala Arg Leu Lys Pro Glu Ala Ala Lys Lys Lys Glu Lys Asp Asn Ile
                245                 250                 255

Leu Gly Arg Gly Gly Lys Glu Asp Val Leu Thr Lys Glu Ser Phe Leu
            260                 265                 270

Glu Met Val Arg Lys Gly Ser Ser Lys
        275                 280


<210> SEQ ID NO 43
<211> LENGTH: 600
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(600)
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<400> SEQUENCE: 43

atg acc tgc gcg ctg att ccg ctg ctg cgc aaa agc gat ctg cgc agc       48
Met Thr Cys Ala Leu Ile Pro Leu Leu Arg Lys Ser Asp Leu Arg Ser
1               5                   10                  15

gtg gtg att att gcg agc att gcg ggc ctg gcg aac cag cgc gcg acc       96
Val Val Ile Ile Ala Ser Ile Ala Gly Leu Ala Asn Gln Arg Ala Thr
            20                  25                  30

ggc agc gtg agc tat ggc gtg agc aaa gcg gcg gcg att cat ctg ggc      144
Gly Ser Val Ser Tyr Gly Val Ser Lys Ala Ala Ala Ile His Leu Gly
        35                  40                  45

aaa ctg ctg gcg ggc cgc ctg cat ccg ctg aaa att cgc gtg aac acc      192
Lys Leu Leu Ala Gly Arg Leu His Pro Leu Lys Ile Arg Val Asn Thr
    50                  55                  60

att tgc ccg ggc att ttt ccg agc gaa atg acc ggc aaa aac gat gcg      240
Ile Cys Pro Gly Ile Phe Pro Ser Glu Met Thr Gly Lys Asn Asp Ala
65              70                  75                      80

ggc cag ggc ctg gaa tat gat att ggc gaa att ccg acc aaa gcg gcg      288
Gly Gln Gly Leu Glu Tyr Asp Ile Gly Glu Ile Pro Thr Lys Ala Ala
                85                  90                  95

aaa cgc agc acc gtg ggc cgc ccg ggc ctg ccg gaa gaa att gtg ggc      336
Lys Arg Ser Thr Val Gly Arg Pro Gly Leu Pro Glu Glu Ile Val Gly
            100                 105                 110

ccg gtg ctg ctg ctg agc agc aaa gcg ggc ggc tat ttt gat ggc gcg      384
Pro Val Leu Leu Leu Ser Ser Lys Ala Gly Gly Tyr Phe Asp Gly Ala
        115                 120                 125

atg ctg acc gtg gat ggc ggc cgc ctg atg gtg agc ggc ccg ttt tgc      432
Met Leu Thr Val Asp Gly Gly Arg Leu Met Val Ser Gly Pro Phe Cys
    130                 135                 140

ttt gtg ttt agc ccg agc agc ctg ccg gtg gat aac ctg cgc tgc ttt      480
Phe Val Phe Ser Pro Ser Ser Leu Pro Val Asp Asn Leu Arg Cys Phe
145             150                 155                     160

ctg ctg ctg acc acc gtg ggc aac cgc gtg ccg gcg ttt atg atg gtg      528
Leu Leu Leu Thr Thr Val Gly Asn Arg Val Pro Ala Phe Met Met Val
                165                 170                 175

agc gat tgc ctg cgc att cgc att ttt gaa ctg aac gaa cag cgc aaa      576
Ser Asp Cys Leu Arg Ile Arg Ile Phe Glu Leu Asn Glu Gln Arg Lys
            180                 185                 190

aac gaa acc gat gtg gaa atg ggc                                      600
Asn Glu Thr Asp Val Glu Met Gly
        195                 200


<210> SEQ ID NO 44
<211> LENGTH: 200
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 44

Met Thr Cys Ala Leu Ile Pro Leu Leu Arg Lys Ser Asp Leu Arg Ser
1               5                   10                  15

Val Val Ile Ile Ala Ser Ile Ala Gly Leu Ala Asn Gln Arg Ala Thr
            20                  25                  30

Gly Ser Val Ser Tyr Gly Val Ser Lys Ala Ala Ala Ile His Leu Gly
        35                  40                  45

Lys Leu Leu Ala Gly Arg Leu His Pro Leu Lys Ile Arg Val Asn Thr
    50                  55                  60

Ile Cys Pro Gly Ile Phe Pro Ser Glu Met Thr Gly Lys Asn Asp Ala
65              70                  75                      80

Gly Gln Gly Leu Glu Tyr Asp Ile Gly Glu Ile Pro Thr Lys Ala Ala
                85                  90                  95
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Lys Arg Ser Thr Val Gly Arg Pro Gly Leu Pro Glu Glu Ile Val Gly
            100                 105                 110

Pro Val Leu Leu Leu Ser Ser Lys Ala Gly Gly Tyr Phe Asp Gly Ala
        115                 120                 125

Met Leu Thr Val Asp Gly Gly Arg Leu Met Val Ser Gly Pro Phe Cys
    130                 135                 140

Phe Val Phe Ser Pro Ser Ser Leu Pro Val Asp Asn Leu Arg Cys Phe
145                 150                 155                 160

Leu Leu Leu Thr Thr Val Gly Asn Arg Val Pro Ala Phe Met Met Val
                165                 170                 175

Ser Asp Cys Leu Arg Ile Arg Ile Phe Glu Leu Asn Glu Gln Arg Lys
            180                 185                 190

Asn Glu Thr Asp Val Glu Met Gly
        195                 200


<210> SEQ ID NO 45
<211> LENGTH: 1440
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1440)

<400> SEQUENCE: 45

atg ctg gtg aac agc agc agc atg ctg gtg acc cgc acc cat ggc ctg       48
Met Leu Val Asn Ser Ser Ser Met Leu Val Thr Arg Thr His Gly Leu
1               5                   10                  15

atg ggc gat gaa gcg tgg aaa gaa ctg gcg aaa tat ggc ctg acc cgc       96
Met Gly Asp Glu Ala Trp Lys Glu Leu Ala Lys Tyr Gly Leu Thr Arg
            20                  25                  30

tgg agc gat gat ggc gcg ttt ctg acc gtg ccg gcg cgc ggc tgc agc      144
Trp Ser Asp Asp Gly Ala Phe Leu Thr Val Pro Ala Arg Gly Cys Ser
        35                  40                  45

atg tgc gaa gtg gat ccg gtg ctg tgc gaa gaa att ggc gaa gat aac      192
Met Cys Glu Val Asp Pro Val Leu Cys Glu Glu Ile Gly Glu Asp Asn
    50                  55                  60

ctg aaa cgc agc ctg gcg ttt agc ggc acc aac cgc cgc ctg aaa cgc      240
Leu Lys Arg Ser Leu Ala Phe Ser Gly Thr Asn Arg Arg Leu Lys Arg
65                  70                  75                  80

gtg ctg gcg aaa ctg cgc cgc ggc gaa acc att aac gtg ggc gcg att      288
Val Leu Ala Lys Leu Arg Arg Gly Glu Thr Ile Asn Val Gly Ala Ile
                85                  90                  95

ggc ggc agc gtg acc aaa ggc tat ggc ctg aac cgc tat aac gaa ccg      336
Gly Gly Ser Val Thr Lys Gly Tyr Gly Leu Asn Arg Tyr Asn Glu Pro
            100                 105                 110

tat tat ccg gat acc ccg acc aac ctg cat cgc att att ttt gat cat      384
Tyr Tyr Pro Asp Thr Pro Thr Asn Leu His Arg Ile Ile Phe Asp His
        115                 120                 125

ctg gtg agc ctg tat ccg gcg ccg aac ggc gtg aaa acc gat gat agc      432
Leu Val Ser Leu Tyr Pro Ala Pro Asn Gly Val Lys Thr Asp Asp Ser
    130                 135                 140

ggc cgc aaa gaa ggc aaa cat ggc tat att aac ggc ggc cag ggc gcg      480
Gly Arg Lys Glu Gly Lys His Gly Tyr Ile Asn Gly Gly Gln Gly Ala
145                 150                 155                 160

acc ggc acc ggc tat ttt agc tat tgc tgg gaa gaa cat gtg ccg gcg      528
Thr Gly Thr Gly Tyr Phe Ser Tyr Cys Trp Glu Glu His Val Pro Ala
                165                 170                 175

gat ctg gat ctg att ttt ctg gaa cag gcg att aac gat gaa ctg ctg      576
Asp Leu Asp Leu Ile Phe Leu Glu Gln Ala Ile Asn Asp Glu Leu Leu
```

```
            180                 185                 190

ctg cgc aac att gat agc tat gaa ctg ctg gtg cgc agc ctg ctg gat      624
Leu Arg Asn Ile Asp Ser Tyr Glu Leu Leu Val Arg Ser Leu Leu Asp
        195                 200                 205

ctg ccg acc agc ccg gcg att gtg aac ctg cat gtg ttt gcg ctg atg      672
Leu Pro Thr Ser Pro Ala Ile Val Asn Leu His Val Phe Ala Leu Met
    210                 215                 220

ttt aac agc att acc ctg ggc ggc gat ctg cat cag agc att gcg cag      720
Phe Asn Ser Ile Thr Leu Gly Gly Asp Leu His Gln Ser Ile Ala Gln
225                 230                 235                 240

ttt tat gat ctg ccg gtg ctg agc ctg cgc aac gcg ctg ctg aac gat      768
Phe Tyr Asp Leu Pro Val Leu Ser Leu Arg Asn Ala Leu Leu Asn Asp
                245                 250                 255

atg ctg aaa aac gaa agc ctg att agc gaa tat ttt ttt gtg cat ccg      816
Met Leu Lys Asn Glu Ser Leu Ile Ser Glu Tyr Phe Phe Val His Pro
            260                 265                 270

gaa ggc gat att gat ctg cgc cat att agc cgc aaa ggc cat aac gtg      864
Glu Gly Asp Ile Asp Leu Arg His Ile Ser Arg Lys Gly His Asn Val
        275                 280                 285

atg ggc cgc att ggc gcg gcg tat atg gat agc cag att tgc gaa atg      912
Met Gly Arg Ile Gly Ala Ala Tyr Met Asp Ser Gln Ile Cys Glu Met
    290                 295                 300

gat aaa tat gaa cag ggc att ccg ggc gcg gat agc atg agc att gat      960
Asp Lys Tyr Glu Gln Gly Ile Pro Gly Ala Asp Ser Met Ser Ile Asp
305                 310                 315                 320

cag ctg tat ccg gtg gaa ccg att ccg cgc atg cag att aac atg aaa     1008
Gln Leu Tyr Pro Val Glu Pro Ile Pro Arg Met Gln Ile Asn Met Lys
                325                 330                 335

tat gat aaa gat ctg gtg ctg ccg acc att aaa ccg cag tgc ttt agc     1056
Tyr Asp Lys Asp Leu Val Leu Pro Thr Ile Lys Pro Gln Cys Phe Ser
            340                 345                 350

gcg aac agc gaa aaa cat ccg ctg gtg ccg gtg gaa aac aac ggc tgg     1104
Ala Asn Ser Glu Lys His Pro Leu Val Pro Val Glu Asn Asn Gly Trp
        355                 360                 365

cgc aaa tgg aac tgg aaa gaa aaa cat tat ctg gtg gcg gat gtg ccg     1152
Arg Lys Trp Asn Trp Lys Glu Lys His Tyr Leu Val Ala Asp Val Pro
    370                 375                 380

ggc agc cgc gtg agc ttt aaa ctg aaa acc aac atg ggc aaa att gaa     1200
Gly Ser Arg Val Ser Phe Lys Leu Lys Thr Asn Met Gly Lys Ile Glu
385                 390                 395                 400

gtg cag tat ctg cgc agc tat cag tat cat cag ggc agc gcg aaa tgc     1248
Val Gln Tyr Leu Arg Ser Tyr Gln Tyr His Gln Gly Ser Ala Lys Cys
                405                 410                 415

tgg gtg gat gaa gaa gtg gaa aaa gcg att aaa ctg gat ggc tat tgg     1296
Trp Val Asp Glu Glu Val Glu Lys Ala Ile Lys Leu Asp Gly Tyr Trp
            420                 425                 430

aaa gaa ccg tat aac att ggc cgc gcg gtg acc att cgc gaa ggc ctg     1344
Lys Glu Pro Tyr Asn Ile Gly Arg Ala Val Thr Ile Arg Glu Gly Leu
        435                 440                 445

gaa ccg ggc gaa cat acc ctg acc tgc gaa ctg ctg aaa cag acc gcg     1392
Glu Pro Gly Glu His Thr Leu Thr Cys Glu Leu Leu Lys Gln Thr Ala
    450                 455                 460

gat ccg gaa ggc ggc ctg gaa ttt cgc ctg att agc att atg agc att     1440
Asp Pro Glu Gly Gly Leu Glu Phe Arg Leu Ile Ser Ile Met Ser Ile
465                 470                 475                 480


<210> SEQ ID NO 46
<211> LENGTH: 480
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans
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<400> SEQUENCE: 46

Met Leu Val Asn Ser Ser Ser Met Leu Val Thr Arg Thr His Gly Leu
1               5                   10                  15

Met Gly Asp Glu Ala Trp Lys Glu Leu Ala Lys Tyr Gly Leu Thr Arg
            20                  25                  30

Trp Ser Asp Asp Gly Ala Phe Leu Thr Val Pro Ala Arg Gly Cys Ser
        35                  40                  45

Met Cys Glu Val Asp Pro Val Leu Cys Glu Glu Ile Gly Glu Asp Asn
    50                  55                  60

Leu Lys Arg Ser Leu Ala Phe Ser Gly Thr Asn Arg Arg Leu Lys Arg
65                  70                  75                  80

Val Leu Ala Lys Leu Arg Arg Gly Glu Thr Ile Asn Val Gly Ala Ile
                85                  90                  95

Gly Gly Ser Val Thr Lys Gly Tyr Gly Leu Asn Arg Tyr Asn Glu Pro
            100                 105                 110

Tyr Tyr Pro Asp Thr Pro Thr Asn Leu His Arg Ile Ile Phe Asp His
        115                 120                 125

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

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

Thr Gly Thr Gly Tyr Phe Ser Tyr Cys Trp Glu Glu His Val Pro Ala
                165                 170                 175

Asp Leu Asp Leu Ile Phe Leu Glu Gln Ala Ile Asn Asp Glu Leu Leu
            180                 185                 190

Leu Arg Asn Ile Asp Ser Tyr Glu Leu Leu Val Arg Ser Leu Leu Asp
        195                 200                 205

Leu Pro Thr Ser Pro Ala Ile Val Asn Leu His Val Phe Ala Leu Met
    210                 215                 220

Phe Asn Ser Ile Thr Leu Gly Gly Asp Leu His Gln Ser Ile Ala Gln
225                 230                 235                 240

Phe Tyr Asp Leu Pro Val Leu Ser Leu Arg Asn Ala Leu Leu Asn Asp
                245                 250                 255

Met Leu Lys Asn Glu Ser Leu Ile Ser Glu Tyr Phe Phe Val His Pro
            260                 265                 270

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

Met Gly Arg Ile Gly Ala Ala Tyr Met Asp Ser Gln Ile Cys Glu Met
    290                 295                 300

Asp Lys Tyr Glu Gln Gly Ile Pro Gly Ala Asp Ser Met Ser Ile Asp
305                 310                 315                 320

Gln Leu Tyr Pro Val Glu Pro Ile Pro Arg Met Gln Ile Asn Met Lys
                325                 330                 335

Tyr Asp Lys Asp Leu Val Leu Pro Thr Ile Lys Pro Gln Cys Phe Ser
            340                 345                 350

Ala Asn Ser Glu Lys His Pro Leu Val Pro Val Glu Asn Asn Gly Trp
        355                 360                 365

Arg Lys Trp Asn Trp Lys Glu Lys His Tyr Leu Val Ala Asp Val Pro
    370                 375                 380

Gly Ser Arg Val Ser Phe Lys Leu Lys Thr Asn Met Gly Lys Ile Glu
385                 390                 395                 400

Val Gln Tyr Leu Arg Ser Tyr Gln Tyr His Gln Gly Ser Ala Lys Cys
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                405                 410                 415

Trp Val Asp Glu Glu Val Glu Lys Ala Ile Lys Leu Asp Gly Tyr Trp
            420                 425                 430

Lys Glu Pro Tyr Asn Ile Gly Arg Ala Val Thr Ile Arg Glu Gly Leu
        435                 440                 445

Glu Pro Gly Glu His Thr Leu Thr Cys Glu Leu Leu Lys Gln Thr Ala
    450                 455                 460

Asp Pro Glu Gly Gly Leu Glu Phe Arg Leu Ile Ser Ile Met Ser Ile
465                 470                 475                 480


<210> SEQ ID NO 47
<211> LENGTH: 1176
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1176)

<400> SEQUENCE: 47

atg agc ttt gat gcg gtg gtg att ggc agc ggc gtg att ggc ctg agc       48
Met Ser Phe Asp Ala Val Val Ile Gly Ser Gly Val Ile Gly Leu Ser
1               5                   10                  15

att gcg cgc gaa ctg cat aac cgc ggc ctg aaa gtg gcg att gtg gcg       96
Ile Ala Arg Glu Leu His Asn Arg Gly Leu Lys Val Ala Ile Val Ala
            20                  25                  30

cgc gat ctg gcg gaa gat agc att agc gtg ggc ttt gcg agc ccg tgg      144
Arg Asp Leu Ala Glu Asp Ser Ile Ser Val Gly Phe Ala Ser Pro Trp
        35                  40                  45

gcg ggc tgc aac tgg ttt agc ttt gcg gaa ggc ggc acc ccg gcg gcg      192
Ala Gly Cys Asn Trp Phe Ser Phe Ala Glu Gly Gly Thr Pro Ala Ala
    50                  55                  60

gaa tgg gat acc att acc ttt ggc aaa ctg gcg aaa ctg gcg aaa gat      240
Glu Trp Asp Thr Ile Thr Phe Gly Lys Leu Ala Lys Leu Ala Lys Asp
65                  70                  75                  80

cat ccg cat att tgc cag aaa att ccg ttt tgc agc gtg tgg gat ctg      288
His Pro His Ile Cys Gln Lys Ile Pro Phe Cys Ser Val Trp Asp Leu
                85                  90                  95

ccg aaa agc gat gcg gaa agc gaa ccg tgg ttt aaa gat ctg gtg ttt      336
Pro Lys Ser Asp Ala Glu Ser Glu Pro Trp Phe Lys Asp Leu Val Phe
            100                 105                 110

gat tat aaa aac ctg aaa agc acc ccg ggc cag ccg ctg ccg ggc ggc      384
Asp Tyr Lys Asn Leu Lys Ser Thr Pro Gly Gln Pro Leu Pro Gly Gly
        115                 120                 125

aaa aaa ttt ggc cat agc ttt gcg agc tat gtg ctg cat gcg ccg aac      432
Lys Lys Phe Gly His Ser Phe Ala Ser Tyr Val Leu His Ala Pro Asn
    130                 135                 140

tat att cgc cat ctg agc agc gaa acc cgc gcg ctg ggc att ccg gtg      480
Tyr Ile Arg His Leu Ser Ser Glu Thr Arg Ala Leu Gly Ile Pro Val
145                 150                 155                 160

cat cgc tat cgc ctg agc agc ctg gat gaa gcg tat aac ctg agc ggc      528
His Arg Tyr Arg Leu Ser Ser Leu Asp Glu Ala Tyr Asn Leu Ser Gly
                165                 170                 175

att ggc aaa gtg agc ctg gtg gtg aac gcg agc ggc ctg ggc gcg aaa      576
Ile Gly Lys Val Ser Leu Val Val Asn Ala Ser Gly Leu Gly Ala Lys
            180                 185                 190

gcg ctg att ggc gtg gaa gat gaa aaa gtg tat ccg ggc cgc ggc cag      624
Ala Leu Ile Gly Val Glu Asp Glu Lys Val Tyr Pro Gly Arg Gly Gln
        195                 200                 205

acc gtg ctg gtg cgc gcg ccg ggc ttt aaa gcg tgc att atg cat acc      672
Thr Val Leu Val Arg Ala Pro Gly Phe Lys Ala Cys Ile Met His Thr
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    210                 215                 220

gaa ggc ttt tat gcg gat ctg gat gaa agc ggc cgc gaa gtg acc ccg      720
Glu Gly Phe Tyr Ala Asp Leu Asp Glu Ser Gly Arg Glu Val Thr Pro
225                 230                 235                 240

ccg ccg ccg gcg tat att att ccg cgc ccg ggc ccg gaa ggc cat gtg      768
Pro Pro Pro Ala Tyr Ile Ile Pro Arg Pro Gly Pro Glu Gly His Val
                245                 250                 255

gtg ctg ggc ggc gtg tat cag cgc gat aac tgg agc acc ctg ccg gat      816
Val Leu Gly Gly Val Tyr Gln Arg Asp Asn Trp Ser Thr Leu Pro Asp
            260                 265                 270

ctg aaa gaa gcg gaa cgc att ctg aaa gat tgc tat aac ctg gcg ccg      864
Leu Lys Glu Ala Glu Arg Ile Leu Lys Asp Cys Tyr Asn Leu Ala Pro
        275                 280                 285

gaa ctg gcg ggc ccg aac ggc aaa acc tgg aaa gat att gaa att att      912
Glu Leu Ala Gly Pro Asn Gly Lys Thr Trp Lys Asp Ile Glu Ile Ile
    290                 295                 300

agc cat aac gtg ggc ctg cgc ccg gcg cgc gaa ggc ggc ccg cgc ctg      960
Ser His Asn Val Gly Leu Arg Pro Ala Arg Glu Gly Gly Pro Arg Leu
305                 310                 315                 320

gaa att gaa gaa cgc gaa gtg ggc acc ggc gcg aac gaa ggc aac gcg     1008
Glu Ile Glu Glu Arg Glu Val Gly Thr Gly Ala Asn Glu Gly Asn Ala
                325                 330                 335

tat gat gtg gcg ccg atg att ggc cgc att ggc gaa cgc cgc aaa gtg     1056
Tyr Asp Val Ala Pro Met Ile Gly Arg Ile Gly Glu Arg Arg Lys Val
            340                 345                 350

gcg gtg gtg cat gcg tat ggc att ggc agc gcg ggc ttt cag gcg agc     1104
Ala Val Val His Ala Tyr Gly Ile Gly Ser Ala Gly Phe Gln Ala Ser
        355                 360                 365

ctg ggc atg gcg gaa aaa gcg agc gat ctg acc gtg aaa tat ctg agc     1152
Leu Gly Met Ala Glu Lys Ala Ser Asp Leu Thr Val Lys Tyr Leu Ser
    370                 375                 380

ggc aaa cgc agc ccg gcg cgc ctg                                     1176
Gly Lys Arg Ser Pro Ala Arg Leu
385                 390


<210> SEQ ID NO 48
<211> LENGTH: 392
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 48

Met Ser Phe Asp Ala Val Val Ile Gly Ser Gly Val Ile Gly Leu Ser
1               5                   10                  15

Ile Ala Arg Glu Leu His Asn Arg Gly Leu Lys Val Ala Ile Val Ala
            20                  25                  30

Arg Asp Leu Ala Glu Asp Ser Ile Ser Val Gly Phe Ala Ser Pro Trp
        35                  40                  45

Ala Gly Cys Asn Trp Phe Ser Phe Ala Glu Gly Gly Thr Pro Ala Ala
    50                  55                  60

Glu Trp Asp Thr Ile Thr Phe Gly Lys Leu Ala Lys Leu Ala Lys Asp
65                  70                  75                  80

His Pro His Ile Cys Gln Lys Ile Pro Phe Cys Ser Val Trp Asp Leu
                85                  90                  95

Pro Lys Ser Asp Ala Glu Ser Glu Pro Trp Phe Lys Asp Leu Val Phe
            100                 105                 110

Asp Tyr Lys Asn Leu Lys Ser Thr Pro Gly Gln Pro Leu Pro Gly Gly
        115                 120                 125

Lys Lys Phe Gly His Ser Phe Ala Ser Tyr Val Leu His Ala Pro Asn
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    130                 135                 140

Tyr Ile Arg His Leu Ser Ser Glu Thr Arg Ala Leu Gly Ile Pro Val
145                 150                 155                 160

His Arg Tyr Arg Leu Ser Ser Leu Asp Glu Ala Tyr Asn Leu Ser Gly
                165                 170                 175

Ile Gly Lys Val Ser Leu Val Val Asn Ala Ser Gly Leu Gly Ala Lys
            180                 185                 190

Ala Leu Ile Gly Val Glu Asp Glu Lys Val Tyr Pro Gly Arg Gly Gln
        195                 200                 205

Thr Val Leu Val Arg Ala Pro Gly Phe Lys Ala Cys Ile Met His Thr
    210                 215                 220

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

Pro Pro Pro Ala Tyr Ile Ile Pro Arg Pro Gly Pro Glu Gly His Val
                245                 250                 255

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

Leu Lys Glu Ala Glu Arg Ile Leu Lys Asp Cys Tyr Asn Leu Ala Pro
        275                 280                 285

Glu Leu Ala Gly Pro Asn Gly Lys Thr Trp Lys Asp Ile Glu Ile Ile
    290                 295                 300

Ser His Asn Val Gly Leu Arg Pro Ala Arg Glu Gly Gly Pro Arg Leu
305                 310                 315                 320

Glu Ile Glu Glu Arg Glu Val Gly Thr Gly Ala Asn Glu Gly Asn Ala
                325                 330                 335

Tyr Asp Val Ala Pro Met Ile Gly Arg Ile Gly Glu Arg Arg Lys Val
            340                 345                 350

Ala Val Val His Ala Tyr Gly Ile Gly Ser Ala Gly Phe Gln Ala Ser
        355                 360                 365

Leu Gly Met Ala Glu Lys Ala Ser Asp Leu Thr Val Lys Tyr Leu Ser
    370                 375                 380

Gly Lys Arg Ser Pro Ala Arg Leu
385                 390


<210> SEQ ID NO 49
<211> LENGTH: 198
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(198)

<400> SEQUENCE: 49

atg ccg ggc ttt cag gat gtg att tat aac acc ttt ttt cgc cgc aac       48
Met Pro Gly Phe Gln Asp Val Ile Tyr Asn Thr Phe Phe Arg Arg Asn
1               5                   10                  15

agc gtg ttt gtg gcg acc acc ttt att gcg gcg ttt agc ttt agc atg       96
Ser Val Phe Val Ala Thr Thr Phe Ile Ala Ala Phe Ser Phe Ser Met
            20                  25                  30

ggc ttt gat ctg gcg acc acc gcg ttt tgg gat agc cat aac cgc ggc      144
Gly Phe Asp Leu Ala Thr Thr Ala Phe Trp Asp Ser His Asn Arg Gly
        35                  40                  45

aaa cag tgg aaa gat att cgc cat aaa tat att gaa gcg gcg ggc gat      192
Lys Gln Trp Lys Asp Ile Arg His Lys Tyr Ile Glu Ala Ala Gly Asp
    50                  55                  60

gat gaa                                                              198
Asp Glu
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65


<210> SEQ ID NO 50
<211> LENGTH: 66
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 50

Met Pro Gly Phe Gln Asp Val Ile Tyr Asn Thr Phe Phe Arg Arg Asn
1               5                   10                  15

Ser Val Phe Val Ala Thr Thr Phe Ile Ala Ala Phe Ser Phe Ser Met
            20                  25                  30

Gly Phe Asp Leu Ala Thr Thr Ala Phe Trp Asp Ser His Asn Arg Gly
        35                  40                  45

Lys Gln Trp Lys Asp Ile Arg His Lys Tyr Ile Glu Ala Ala Gly Asp
    50                  55                  60

Asp Glu
65


<210> SEQ ID NO 51
<211> LENGTH: 1368
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1368)

<400> SEQUENCE: 51

atg agc agc ggc aac gtg ccg aaa att gaa cgc ctg agc tgc gtg ccg       48
Met Ser Ser Gly Asn Val Pro Lys Ile Glu Arg Leu Ser Cys Val Pro
1               5                   10                  15

aac gat tat ccg tgg ggc gaa gtg ggc aac gat agc ctg gcg gcg cgc       96
Asn Asp Tyr Pro Trp Gly Glu Val Gly Asn Asp Ser Leu Ala Ala Arg
            20                  25                  30

ctg gcg agc aaa aac ggc gcg gtg agc ttt gat ctg aaa ccg gaa cag      144
Leu Ala Ser Lys Asn Gly Ala Val Ser Phe Asp Leu Lys Pro Glu Gln
        35                  40                  45

gcg tat gcg gaa ctg tgg atg ggc acc cat ccg aac aac ccg gcg cat      192
Ala Tyr Ala Glu Leu Trp Met Gly Thr His Pro Asn Asn Pro Ala His
    50                  55                  60

ctg ttt agc agc ccg gat acc ctg ctg agc acc cat ctg aaa aaa aac      240
Leu Phe Ser Ser Pro Asp Thr Leu Leu Ser Thr His Leu Lys Lys Asn
65                  70                  75                  80

ccg agc ctg ctg ggc gcg gcg aac cgc ttt agc ccg ccg ttt acc ggc      288
Pro Ser Leu Leu Gly Ala Ala Asn Arg Phe Ser Pro Pro Phe Thr Gly
                85                  90                  95

gcg aaa ggc agc ggc gcg gaa ggc cag gaa gaa ggc cat gtg ccg ttt      336
Ala Lys Gly Ser Gly Ala Glu Gly Gln Glu Glu Gly His Val Pro Phe
            100                 105                 110

ctg ttt aaa gtg ctg acc tgc aaa cag gcg ctg ccg ctg cag att cat      384
Leu Phe Lys Val Leu Thr Cys Lys Gln Ala Leu Pro Leu Gln Ile His
        115                 120                 125

ccg gat aaa gcg ctg gcg aaa aaa ctg cat gaa gaa aac ccg aaa cag      432
Pro Asp Lys Ala Leu Ala Lys Lys Leu His Glu Glu Asn Pro Lys Gln
    130                 135                 140

ttt ggc gat att aac cat aaa ccg gaa att gcg gtg tgc ctg agc gat      480
Phe Gly Asp Ile Asn His Lys Pro Glu Ile Ala Val Cys Leu Ser Asp
145                 150                 155                 160

cgc ttt ctg ggc ttt gcg agc ttt cgc ccg tat gat aaa att gcg agc      528
Arg Phe Leu Gly Phe Ala Ser Phe Arg Pro Tyr Asp Lys Ile Ala Ser
                165                 170                 175
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ctg ctg aaa agc gtg cag gaa att agc ctg ctg ccg agc ctg ctg cag      576
Leu Leu Lys Ser Val Gln Glu Ile Ser Leu Leu Pro Ser Leu Leu Gln
            180                 185                 190

aaa agc att aaa agc ttt att agc gcg ccg agc gcg gaa acc ctg cag      624
Lys Ser Ile Lys Ser Phe Ile Ser Ala Pro Ser Ala Glu Thr Leu Gln
        195                 200                 205

ccg acc tgg gaa ggc ttt att aaa ctg ggc gat aac gaa gaa agc gtg      672
Pro Thr Trp Glu Gly Phe Ile Lys Leu Gly Asp Asn Glu Glu Ser Val
    210                 215                 220

aaa aaa ttt agc gat cgc gtg ctg agc cag ggc ctg aaa gcg ttt gat      720
Lys Lys Phe Ser Asp Arg Val Leu Ser Gln Gly Leu Lys Ala Phe Asp
225                 230                 235                 240

agc gtg gat att gaa gat gaa gat aaa aac cgc ctg gtg cgc gcg gtg      768
Ser Val Asp Ile Glu Asp Glu Asp Lys Asn Arg Leu Val Arg Ala Val
                245                 250                 255

gaa ctg ggc aaa aaa tat aac ccg ggc gat gcg ggc ctg ttt agc agc      816
Glu Leu Gly Lys Lys Tyr Asn Pro Gly Asp Ala Gly Leu Phe Ser Ser
            260                 265                 270

ctg ctg ttt ctg aac ctg att gaa ctg aaa aaa gat cag ggc atg tat      864
Leu Leu Phe Leu Asn Leu Ile Glu Leu Lys Lys Asp Gln Gly Met Tyr
        275                 280                 285

gtg ggc gcg gat ggc ccg cat gcg tgg ctg gaa ggc gaa att gtg gaa      912
Val Gly Ala Asp Gly Pro His Ala Trp Leu Glu Gly Glu Ile Val Glu
    290                 295                 300

ctg atg gcg att agc gat aac gtg ctg aac gtg ggc ttt acc agc gat      960
Leu Met Ala Ile Ser Asp Asn Val Leu Asn Val Gly Phe Thr Ser Asp
305                 310                 315                 320

gat agc aaa gat gat ccg agc ctg gtg gcg aaa gcg gtg acc tgc acc     1008
Asp Ser Lys Asp Asp Pro Ser Leu Val Ala Lys Ala Val Thr Cys Thr
                325                 330                 335

ccg aaa gcg att aaa gat ctg ctg ctg gat gcg agc aaa tat agc aaa     1056
Pro Lys Ala Ile Lys Asp Leu Leu Leu Asp Ala Ser Lys Tyr Ser Lys
            340                 345                 350

agc cag aac ggc cgc acc acc gtg tat agc acc ccg ttt gaa gaa ttt     1104
Ser Gln Asn Gly Arg Thr Thr Val Tyr Ser Thr Pro Phe Glu Glu Phe
        355                 360                 365

agc att atg aaa att gcg ggc gat gaa att ctg agc ccg ctg gat ggc     1152
Ser Ile Met Lys Ile Ala Gly Asp Glu Ile Leu Ser Pro Leu Asp Gly
    370                 375                 380

gcg ggc gtg gcg gtg gtg ctg gaa ggc gaa tgg acc gtg gaa gat cag     1200
Ala Gly Val Ala Val Val Leu Glu Gly Glu Trp Thr Val Glu Asp Gln
385                 390                 395                 400

gaa ggc acc aaa cgc ggc ggc gaa ggc acc gat ggc gaa ggc ggc gaa     1248
Glu Gly Thr Lys Arg Gly Gly Glu Gly Thr Asp Gly Glu Gly Gly Glu
                405                 410                 415

ggc acc att tgg ttt att ggc agc gcg acc gaa acc aaa tgg acc gcg     1296
Gly Thr Ile Trp Phe Ile Gly Ser Ala Thr Glu Thr Lys Trp Thr Ala
            420                 425                 430

aaa ggc ggc aaa ggc cag att tgg att gcg ttt tat gat aaa acc gcg     1344
Lys Gly Gly Lys Gly Gln Ile Trp Ile Ala Phe Tyr Asp Lys Thr Ala
        435                 440                 445

aaa aaa gat gat gtg ggc aaa aaa                                     1368
Lys Lys Asp Asp Val Gly Lys Lys
    450                 455
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<210> SEQ ID NO 52
<211> LENGTH: 456
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

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<400> SEQUENCE: 52

Met Ser Ser Gly Asn Val Pro Lys Ile Glu Arg Leu Ser Cys Val Pro
1               5                   10                  15

Asn Asp Tyr Pro Trp Gly Glu Val Gly Asn Asp Ser Leu Ala Ala Arg
            20                  25                  30

Leu Ala Ser Lys Asn Gly Ala Val Ser Phe Asp Leu Lys Pro Glu Gln
        35                  40                  45

Ala Tyr Ala Glu Leu Trp Met Gly Thr His Pro Asn Asn Pro Ala His
    50                  55                  60

Leu Phe Ser Ser Pro Asp Thr Leu Leu Ser Thr His Leu Lys Lys Asn
65                  70                  75                  80

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

Ala Lys Gly Ser Gly Ala Glu Gly Gln Glu Glu Gly His Val Pro Phe
            100                 105                 110

Leu Phe Lys Val Leu Thr Cys Lys Gln Ala Leu Pro Leu Gln Ile His
        115                 120                 125

Pro Asp Lys Ala Leu Ala Lys Lys Leu His Glu Glu Asn Pro Lys Gln
    130                 135                 140

Phe Gly Asp Ile Asn His Lys Pro Glu Ile Ala Val Cys Leu Ser Asp
145                 150                 155                 160

Arg Phe Leu Gly Phe Ala Ser Phe Arg Pro Tyr Asp Lys Ile Ala Ser
                165                 170                 175

Leu Leu Lys Ser Val Gln Glu Ile Ser Leu Leu Pro Ser Leu Leu Gln
            180                 185                 190

Lys Ser Ile Lys Ser Phe Ile Ser Ala Pro Ser Ala Glu Thr Leu Gln
        195                 200                 205

Pro Thr Trp Glu Gly Phe Ile Lys Leu Gly Asp Asn Glu Glu Ser Val
    210                 215                 220

Lys Lys Phe Ser Asp Arg Val Leu Ser Gln Gly Leu Lys Ala Phe Asp
225                 230                 235                 240

Ser Val Asp Ile Glu Asp Glu Asp Lys Asn Arg Leu Val Arg Ala Val
                245                 250                 255

Glu Leu Gly Lys Lys Tyr Asn Pro Gly Asp Ala Gly Leu Phe Ser Ser
            260                 265                 270

Leu Leu Phe Leu Asn Leu Ile Glu Leu Lys Lys Asp Gln Gly Met Tyr
        275                 280                 285

Val Gly Ala Asp Gly Pro His Ala Trp Leu Glu Gly Glu Ile Val Glu
    290                 295                 300

Leu Met Ala Ile Ser Asp Asn Val Leu Asn Val Gly Phe Thr Ser Asp
305                 310                 315                 320

Asp Ser Lys Asp Asp Pro Ser Leu Val Ala Lys Ala Val Thr Cys Thr
                325                 330                 335

Pro Lys Ala Ile Lys Asp Leu Leu Leu Asp Ala Ser Lys Tyr Ser Lys
            340                 345                 350

Ser Gln Asn Gly Arg Thr Thr Val Tyr Ser Thr Pro Phe Glu Glu Phe
        355                 360                 365

Ser Ile Met Lys Ile Ala Gly Asp Glu Ile Leu Ser Pro Leu Asp Gly
    370                 375                 380

Ala Gly Val Ala Val Val Leu Glu Gly Glu Trp Thr Val Glu Asp Gln
385                 390                 395                 400

Glu Gly Thr Lys Arg Gly Gly Glu Gly Thr Asp Gly Glu Gly Gly Glu
                405                 410                 415
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Gly Thr Ile Trp Phe Ile Gly Ser Ala Thr Glu Thr Lys Trp Thr Ala
            420                 425                 430

Lys Gly Gly Lys Gly Gln Ile Trp Ile Ala Phe Tyr Asp Lys Thr Ala
        435                 440                 445

Lys Lys Asp Asp Val Gly Lys Lys
    450                 455


<210> SEQ ID NO 53
<211> LENGTH: 1962
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1962)

<400> SEQUENCE: 53

atg acc cgc gat ttt gat agc ctg ttt ttt acc ggc ccg att ttt gtg           48
Met Thr Arg Asp Phe Asp Ser Leu Phe Phe Thr Gly Pro Ile Phe Val
1               5                   10                  15

gat tat agc ttt acc gcg cgc cat ctg gaa agc ttt ctg agc agc ttt           96
Asp Tyr Ser Phe Thr Ala Arg His Leu Glu Ser Phe Leu Ser Ser Phe
            20                  25                  30

ccg ccg cag gtg agc cat gcg atg agc agc gcg agc acc ccg acc gcg          144
Pro Pro Gln Val Ser His Ala Met Ser Ser Ala Ser Thr Pro Thr Ala
        35                  40                  45

ccg tat ctg gaa gat ctg gtg cgc aac agc ctg gat cag acc ctg ccg          192
Pro Tyr Leu Glu Asp Leu Val Arg Asn Ser Leu Asp Gln Thr Leu Pro
    50                  55                  60

tgg gtg gtg cag aaa tat ggc ggc acc agc gtg ggc aaa agc ctg gat          240
Trp Val Val Gln Lys Tyr Gly Gly Thr Ser Val Gly Lys Ser Leu Asp
65                  70                  75                  80

aac att acc aaa att gtg ggc agc tat att gat aac ggc agc aaa gtg          288
Asn Ile Thr Lys Ile Val Gly Ser Tyr Ile Asp Asn Gly Ser Lys Val
                85                  90                  95

gcg att gtg tgc agc gcg cgc agc acc cag acc aaa agc ctg ggc acc          336
Ala Ile Val Cys Ser Ala Arg Ser Thr Gln Thr Lys Ser Leu Gly Thr
            100                 105                 110

acc aac ctg ctg ctg cag gcg agc cgc gaa gcg ctg cag ccg gcg ctg          384
Thr Asn Leu Leu Leu Gln Ala Ser Arg Glu Ala Leu Gln Pro Ala Leu
        115                 120                 125

agc agc agc ggc gat ggc cgc agc ggc agc atg agc ggc acc gcg acc          432
Ser Ser Ser Gly Asp Gly Arg Ser Gly Ser Met Ser Gly Thr Ala Thr
    130                 135                 140

ccg ttt tat ccg aaa cgc gtg ggc agc ggc ttt ttt ggc aaa gat cag          480
Pro Phe Tyr Pro Lys Arg Val Gly Ser Gly Phe Phe Gly Lys Asp Gln
145                 150                 155                 160

agc acc agc atg gtg agc agc gtg agc agc ctg agc cag ctg gaa ccg          528
Ser Thr Ser Met Val Ser Ser Val Ser Ser Leu Ser Gln Leu Glu Pro
                165                 170                 175

cag ctg ggc cgc agc ggc agc ccg agc ccg ttt cag agc agc agc agc          576
Gln Leu Gly Arg Ser Gly Ser Pro Ser Pro Phe Gln Ser Ser Ser Ser
            180                 185                 190

cgc agc ccg ccg cgc agc ccg gcg acc ccg agc cag gat agc agc gtg          624
Arg Ser Pro Pro Arg Ser Pro Ala Thr Pro Ser Gln Asp Ser Ser Val
        195                 200                 205

agc cag gaa ccg gcg ttt cat gcg acc gtg gat ctg att aaa aaa ggc          672
Ser Gln Glu Pro Ala Phe His Ala Thr Val Asp Leu Ile Lys Lys Gly
    210                 215                 220

cat ctg gaa gcg gcg cgc gcg agc ctg aaa gaa ggc ccg ctg cgc gat          720
His Leu Glu Ala Ala Arg Ala Ser Leu Lys Glu Gly Pro Leu Arg Asp
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225                 230                 235                 240

gaa ctg gaa gaa gaa att gaa cgc gat tgc gaa agc ctg cgc agc ttt      768
Glu Leu Glu Glu Glu Ile Glu Arg Asp Cys Glu Ser Leu Arg Ser Phe
                245                 250                 255

ctg tat gcg gcg cag att att gat gaa att agc ccg cgc agc cag gat      816
Leu Tyr Ala Ala Gln Ile Ile Asp Glu Ile Ser Pro Arg Ser Gln Asp
            260                 265                 270

agc att gtg ggc acc ggc gaa cgc ctg gcg tgc aaa att gtg gcg gcg      864
Ser Ile Val Gly Thr Gly Glu Arg Leu Ala Cys Lys Ile Val Ala Ala
        275                 280                 285

gcg ctg cgc gat cgc ggc gtg gat agc gaa ctg gtg gtg ctg gat aac      912
Ala Leu Arg Asp Arg Gly Val Asp Ser Glu Leu Val Val Leu Asp Asn
    290                 295                 300

att gtg gat gcg agc atg agc gcg gcg agc gaa gcg att agc gtg gat      960
Ile Val Asp Ala Ser Met Ser Ala Ala Ser Glu Ala Ile Ser Val Asp
305                 310                 315                 320

gcg ggc gat cag ggc gtg gcg cag ctg ggc cag gaa ttt tat gat cag     1008
Ala Gly Asp Gln Gly Val Ala Gln Leu Gly Gln Glu Phe Tyr Asp Gln
                325                 330                 335

ctg agc ttt cgc ctg ggc gaa cgc ctg cgc gaa tgc ggc cag cgc gtg     1056
Leu Ser Phe Arg Leu Gly Glu Arg Leu Arg Glu Cys Gly Gln Arg Val
            340                 345                 350

ccg gtg gtg acc ggc tat ttt ggc ccg gtg ccg ggc agc ctg ctg gcg     1104
Pro Val Val Thr Gly Tyr Phe Gly Pro Val Pro Gly Ser Leu Leu Ala
        355                 360                 365

cag att ggc cgc ggc tat acc gat ctg tgc gcg gcg ctg tgc gcg gtg     1152
Gln Ile Gly Arg Gly Tyr Thr Asp Leu Cys Ala Ala Leu Cys Ala Val
    370                 375                 380

ggc ctg aaa gcg agc gaa ctg cag gtg tgg aaa gaa gtg gat ggc att     1200
Gly Leu Lys Ala Ser Glu Leu Gln Val Trp Lys Glu Val Asp Gly Ile
385                 390                 395                 400

ttt acc gcg gat ccg cgc aaa gtg ccg agc gcg cgc ctg gtg ccg att     1248
Phe Thr Ala Asp Pro Arg Lys Val Pro Ser Ala Arg Leu Val Pro Ile
                405                 410                 415

att acc ccg gat gaa gcg gcg gaa ctg acc tat tat ggc agc gaa gtg     1296
Ile Thr Pro Asp Glu Ala Ala Glu Leu Thr Tyr Tyr Gly Ser Glu Val
            420                 425                 430

att cat ccg ttt acc atg gaa cag gtg att cgc gcg cgc att ccg att     1344
Ile His Pro Phe Thr Met Glu Gln Val Ile Arg Ala Arg Ile Pro Ile
        435                 440                 445

cgc att aaa aac gtg gaa aac ccg agc ggc gcg ggc acc gtg att tat     1392
Arg Ile Lys Asn Val Glu Asn Pro Ser Gly Ala Gly Thr Val Ile Tyr
    450                 455                 460

ccg gat ctg ggc ttt ccg cgc ggc ctg gat acc gaa ccg ccg aaa gcg     1440
Pro Asp Leu Gly Phe Pro Arg Gly Leu Asp Thr Glu Pro Pro Lys Ala
465                 470                 475                 480

gaa cgc att gtg gaa ggc gtg gat gaa cgc atg ccg acc gcg gtg acc     1488
Glu Arg Ile Val Glu Gly Val Asp Glu Arg Met Pro Thr Ala Val Thr
                485                 490                 495

att aaa gat gaa att att gtg ctg aac att cat agc aac cgc aaa acc     1536
Ile Lys Asp Glu Ile Ile Val Leu Asn Ile His Ser Asn Arg Lys Thr
            500                 505                 510

ctg agc cat ggc ttt ctg gcg cgc att ttt ggc acc ctg gat cgc gcg     1584
Leu Ser His Gly Phe Leu Ala Arg Ile Phe Gly Thr Leu Asp Arg Ala
        515                 520                 525

ggc gtg gtg gtg gat ctg att agc acc agc gaa gtg cat gtg agc atg     1632
Gly Val Val Val Asp Leu Ile Ser Thr Ser Glu Val His Val Ser Met
    530                 535                 540

gcg atg cag gat ttt ctg aac cgc aaa cgc ctg gaa cgc ctg gtg aaa     1680
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Ala Met Gln Asp Phe Leu Asn Arg Lys Arg Leu Glu Arg Leu Val Lys
545                 550                 555                 560

gat ctg gaa aaa att ggc gaa gtg acc gtg agc aaa gat atg gcg att     1728
Asp Leu Glu Lys Ile Gly Glu Val Thr Val Ser Lys Asp Met Ala Ile
                565                 570                 575

ctg agc ctg gtg ggc cgc aac atg cgc aac gcg att ggc agc gcg ggc     1776
Leu Ser Leu Val Gly Arg Asn Met Arg Asn Ala Ile Gly Ser Ala Gly
            580                 585                 590

ctg atg ttt gcg agc ctg gcg cgc gcg atg att aac att gaa atg att     1824
Leu Met Phe Ala Ser Leu Ala Arg Ala Met Ile Asn Ile Glu Met Ile
        595                 600                 605

agc cag ggc gcg agc gaa att aac att agc tgc gtg att gaa aac aaa     1872
Ser Gln Gly Ala Ser Glu Ile Asn Ile Ser Cys Val Ile Glu Asn Lys
    610                 615                 620

gat gcg att aaa gcg ctg aac gtg att cat gaa agc tgc ctg agc tat     1920
Asp Ala Ile Lys Ala Leu Asn Val Ile His Glu Ser Cys Leu Ser Tyr
625                 630                 635                 640

ccg cgc agc ccg gcg acc gaa atg gcg ggc ctg cag ctg cag             1962
Pro Arg Ser Pro Ala Thr Glu Met Ala Gly Leu Gln Leu Gln
                645                 650


<210> SEQ ID NO 54
<211> LENGTH: 654
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 54

Met Thr Arg Asp Phe Asp Ser Leu Phe Phe Thr Gly Pro Ile Phe Val
1               5                   10                  15

Asp Tyr Ser Phe Thr Ala Arg His Leu Glu Ser Phe Leu Ser Ser Phe
            20                  25                  30

Pro Pro Gln Val Ser His Ala Met Ser Ser Ala Ser Thr Pro Thr Ala
        35                  40                  45

Pro Tyr Leu Glu Asp Leu Val Arg Asn Ser Leu Asp Gln Thr Leu Pro
    50                  55                  60

Trp Val Val Gln Lys Tyr Gly Gly Thr Ser Val Gly Lys Ser Leu Asp
65                  70                  75                  80

Asn Ile Thr Lys Ile Val Gly Ser Tyr Ile Asp Asn Gly Ser Lys Val
                85                  90                  95

Ala Ile Val Cys Ser Ala Arg Ser Thr Gln Thr Lys Ser Leu Gly Thr
            100                 105                 110

Thr Asn Leu Leu Leu Gln Ala Ser Arg Glu Ala Leu Gln Pro Ala Leu
        115                 120                 125

Ser Ser Ser Gly Asp Gly Arg Ser Gly Ser Met Ser Gly Thr Ala Thr
    130                 135                 140

Pro Phe Tyr Pro Lys Arg Val Gly Ser Gly Phe Phe Gly Lys Asp Gln
145                 150                 155                 160

Ser Thr Ser Met Val Ser Ser Val Ser Ser Leu Ser Gln Leu Glu Pro
                165                 170                 175

Gln Leu Gly Arg Ser Gly Ser Pro Ser Pro Phe Gln Ser Ser Ser Ser
            180                 185                 190

Arg Ser Pro Pro Arg Ser Pro Ala Thr Pro Ser Gln Asp Ser Ser Val
        195                 200                 205

Ser Gln Glu Pro Ala Phe His Ala Thr Val Asp Leu Ile Lys Lys Gly
    210                 215                 220

His Leu Glu Ala Ala Arg Ala Ser Leu Lys Glu Gly Pro Leu Arg Asp
225                 230                 235                 240
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Glu Leu Glu Glu Glu Ile Glu Arg Asp Cys Glu Ser Leu Arg Ser Phe
                245                 250                 255

Leu Tyr Ala Ala Gln Ile Ile Asp Glu Ile Ser Pro Arg Ser Gln Asp
            260                 265                 270

Ser Ile Val Gly Thr Gly Glu Arg Leu Ala Cys Lys Ile Val Ala Ala
        275                 280                 285

Ala Leu Arg Asp Arg Gly Val Asp Ser Glu Leu Val Val Leu Asp Asn
    290                 295                 300

Ile Val Asp Ala Ser Met Ser Ala Ala Ser Glu Ala Ile Ser Val Asp
305                 310                 315                 320

Ala Gly Asp Gln Gly Val Ala Gln Leu Gly Gln Glu Phe Tyr Asp Gln
                325                 330                 335

Leu Ser Phe Arg Leu Gly Glu Arg Leu Arg Glu Cys Gly Gln Arg Val
            340                 345                 350

Pro Val Val Thr Gly Tyr Phe Gly Pro Val Pro Gly Ser Leu Leu Ala
        355                 360                 365

Gln Ile Gly Arg Gly Tyr Thr Asp Leu Cys Ala Ala Leu Cys Ala Val
    370                 375                 380

Gly Leu Lys Ala Ser Glu Leu Gln Val Trp Lys Glu Val Asp Gly Ile
385                 390                 395                 400

Phe Thr Ala Asp Pro Arg Lys Val Pro Ser Ala Arg Leu Val Pro Ile
                405                 410                 415

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

Ile His Pro Phe Thr Met Glu Gln Val Ile Arg Ala Arg Ile Pro Ile
        435                 440                 445

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

Pro Asp Leu Gly Phe Pro Arg Gly Leu Asp Thr Glu Pro Pro Lys Ala
465                 470                 475                 480

Glu Arg Ile Val Glu Gly Val Asp Glu Arg Met Pro Thr Ala Val Thr
                485                 490                 495

Ile Lys Asp Glu Ile Ile Val Leu Asn Ile His Ser Asn Arg Lys Thr
            500                 505                 510

Leu Ser His Gly Phe Leu Ala Arg Ile Phe Gly Thr Leu Asp Arg Ala
        515                 520                 525

Gly Val Val Val Asp Leu Ile Ser Thr Ser Glu Val His Val Ser Met
    530                 535                 540

Ala Met Gln Asp Phe Leu Asn Arg Lys Arg Leu Glu Arg Leu Val Lys
545                 550                 555                 560

Asp Leu Glu Lys Ile Gly Glu Val Thr Val Ser Lys Asp Met Ala Ile
                565                 570                 575

Leu Ser Leu Val Gly Arg Asn Met Arg Asn Ala Ile Gly Ser Ala Gly
            580                 585                 590

Leu Met Phe Ala Ser Leu Ala Arg Ala Met Ile Asn Ile Glu Met Ile
        595                 600                 605

Ser Gln Gly Ala Ser Glu Ile Asn Ile Ser Cys Val Ile Glu Asn Lys
    610                 615                 620

Asp Ala Ile Lys Ala Leu Asn Val Ile His Glu Ser Cys Leu Ser Tyr
625                 630                 635                 640

Pro Arg Ser Pro Ala Thr Glu Met Ala Gly Leu Gln Leu Gln
                645                 650
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<210> SEQ ID NO 55
<211> LENGTH: 1269
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1269)

<400> SEQUENCE: 55

atg ccg aaa cag tgg ccg acc att gtg aaa ctg gaa acc ttt att ccg        48
Met Pro Lys Gln Trp Pro Thr Ile Val Lys Leu Glu Thr Phe Ile Pro
1               5                   10                  15

agc gcg cat ggc agc ggc ggc gat tat cat cgc cag ggc ggc gat cat        96
Ser Ala His Gly Ser Gly Gly Asp Tyr His Arg Gln Gly Gly Asp His
            20                  25                  30

tgg att gtg cag ggc aac att agc tgc ccg atg cat aaa tat gaa gaa       144
Trp Ile Val Gln Gly Asn Ile Ser Cys Pro Met His Lys Tyr Glu Glu
        35                  40                  45

tat aaa gtg agc cgc acc agc tgg ggc att ggc gtg ctg ggc agc att       192
Tyr Lys Val Ser Arg Thr Ser Trp Gly Ile Gly Val Leu Gly Ser Ile
    50                  55                  60

ttt gtg aaa gtg cat gcg agc gat ggc acc gtg ggc tat gcg acc ggc       240
Phe Val Lys Val His Ala Ser Asp Gly Thr Val Gly Tyr Ala Thr Gly
65                  70                  75                  80

ttt ggc ggc ccg ccg gcg tgc tgg ctg att gaa gaa cat ttt aaa cgc       288
Phe Gly Gly Pro Pro Ala Cys Trp Leu Ile Glu Glu His Phe Lys Arg
                85                  90                  95

ttt att gtg ggc cag gat ccg cgc gat acc aac aaa atg tgg gat cag       336
Phe Ile Val Gly Gln Asp Pro Arg Asp Thr Asn Lys Met Trp Asp Gln
            100                 105                 110

atg ttt cgc gcg agc atg ttt tat ggc cgc aaa ggc ctg ccg ctg gcg       384
Met Phe Arg Ala Ser Met Phe Tyr Gly Arg Lys Gly Leu Pro Leu Ala
        115                 120                 125

gcg att agc gtg gtg gat ctg gcg att tgg gat ctg ctg ggc aaa att       432
Ala Ile Ser Val Val Asp Leu Ala Ile Trp Asp Leu Leu Gly Lys Ile
    130                 135                 140

cgc ggc gaa ccg att tat aaa atg att ggc ggc cgc acc aaa aaa gat       480
Arg Gly Glu Pro Ile Tyr Lys Met Ile Gly Gly Arg Thr Lys Lys Asp
145                 150                 155                 160

att ccg ctg tat ctg acc ggc ccg cgc ccg gaa gtg gcg aaa aaa ctg       528
Ile Pro Leu Tyr Leu Thr Gly Pro Arg Pro Glu Val Ala Lys Lys Leu
                165                 170                 175

ggc ttt tgg ggc agc aaa gtg gcg ctg ccg cat ggc ccg ccg gat ggc       576
Gly Phe Trp Gly Ser Lys Val Ala Leu Pro His Gly Pro Pro Asp Gly
            180                 185                 190

cat gaa ggc att cgc aaa aac gtg gaa tat ctg aaa gcg tgc aaa gaa       624
His Glu Gly Ile Arg Lys Asn Val Glu Tyr Leu Lys Ala Cys Lys Glu
        195                 200                 205

gcg gtg ggc ccg gat tat ccg gtg cag gtg gat tgc tat atg agc ctg       672
Ala Val Gly Pro Asp Tyr Pro Val Gln Val Asp Cys Tyr Met Ser Leu
    210                 215                 220

gat gtg ccg tat acc att gcg ctg gtg aaa gcg tgc gaa aaa gcg ggc       720
Asp Val Pro Tyr Thr Ile Ala Leu Val Lys Ala Cys Glu Lys Ala Gly
225                 230                 235                 240

gtg gaa att aac tgg tgg gaa gaa gtg ctg cat ccg gat gat ttt gat       768
Val Glu Ile Asn Trp Trp Glu Glu Val Leu His Pro Asp Asp Phe Asp
                245                 250                 255

ggc cat att aaa ctg aaa gaa gcg ctg ccg tat gtg aaa ttt acc acc       816
Gly His Ile Lys Leu Lys Glu Ala Leu Pro Tyr Val Lys Phe Thr Thr
            260                 265                 270
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ggc gaa cat gaa tat agc aaa tat ggc ttt cgc aaa ctg att gaa aac       864
Gly Glu His Glu Tyr Ser Lys Tyr Gly Phe Arg Lys Leu Ile Glu Asn
        275                 280                 285

cgc gcg gtg gat att att cag ccg gat gtg atg tgg ctg ggc ggc ctg       912
Arg Ala Val Asp Ile Ile Gln Pro Asp Val Met Trp Leu Gly Gly Leu
    290                 295                 300

acc gaa ctg att aaa gtg gcg gcg atg gcg gcg gcg tat gat att ccg       960
Thr Glu Leu Ile Lys Val Ala Ala Met Ala Ala Ala Tyr Asp Ile Pro
305                 310                 315                 320

gtg gtg ccg cat ggc agc ggc ccg tat agc ttt cag gcg att atg agc      1008
Val Val Pro His Gly Ser Gly Pro Tyr Ser Phe Gln Ala Ile Met Ser
                325                 330                 335

ttt ccg aac agc gat ttt tgc gaa tat att gcg aac agc ccg gat ggc      1056
Phe Pro Asn Ser Asp Phe Cys Glu Tyr Ile Ala Asn Ser Pro Asp Gly
            340                 345                 350

aaa agc att gaa ccg agc ttt ggc aac ctg ttt ctg aac gaa gtg ctg      1104
Lys Ser Ile Glu Pro Ser Phe Gly Asn Leu Phe Leu Asn Glu Val Leu
        355                 360                 365

ccg cgc aac ggc cgc gtg gat ctg acc gat gaa ccg ggc ttt ggc ctg      1152
Pro Arg Asn Gly Arg Val Asp Leu Thr Asp Glu Pro Gly Phe Gly Leu
    370                 375                 380

gaa ctg aac ccg agc gcg gaa ctg gtg ccg tat aaa agc ttt ttt acc      1200
Glu Leu Asn Pro Ser Ala Glu Leu Val Pro Tyr Lys Ser Phe Phe Thr
385                 390                 395                 400

ccg agc aaa agc ctg ggc gcg gcg ggc gaa gtg gaa gat gat ggc aaa      1248
Pro Ser Lys Ser Leu Gly Ala Ala Gly Glu Val Glu Asp Asp Gly Lys
                405                 410                 415

gcg aaa gtg aac ggc aaa cat                                          1269
Ala Lys Val Asn Gly Lys His
            420


<210> SEQ ID NO 56
<211> LENGTH: 423
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 56

Met Pro Lys Gln Trp Pro Thr Ile Val Lys Leu Glu Thr Phe Ile Pro
1               5                   10                  15

Ser Ala His Gly Ser Gly Gly Asp Tyr His Arg Gln Gly Gly Asp His
            20                  25                  30

Trp Ile Val Gln Gly Asn Ile Ser Cys Pro Met His Lys Tyr Glu Glu
        35                  40                  45

Tyr Lys Val Ser Arg Thr Ser Trp Gly Ile Gly Val Leu Gly Ser Ile
    50                  55                  60

Phe Val Lys Val His Ala Ser Asp Gly Thr Val Gly Tyr Ala Thr Gly
65                  70                  75                  80

Phe Gly Gly Pro Pro Ala Cys Trp Leu Ile Glu Glu His Phe Lys Arg
                85                  90                  95

Phe Ile Val Gly Gln Asp Pro Arg Asp Thr Asn Lys Met Trp Asp Gln
            100                 105                 110

Met Phe Arg Ala Ser Met Phe Tyr Gly Arg Lys Gly Leu Pro Leu Ala
        115                 120                 125

Ala Ile Ser Val Val Asp Leu Ala Ile Trp Asp Leu Leu Gly Lys Ile
    130                 135                 140

Arg Gly Glu Pro Ile Tyr Lys Met Ile Gly Gly Arg Thr Lys Lys Asp
145                 150                 155                 160

Ile Pro Leu Tyr Leu Thr Gly Pro Arg Pro Glu Val Ala Lys Lys Leu
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                165                 170                 175

Gly Phe Trp Gly Ser Lys Val Ala Leu Pro His Gly Pro Pro Asp Gly
            180                 185                 190

His Glu Gly Ile Arg Lys Asn Val Glu Tyr Leu Lys Ala Cys Lys Glu
        195                 200                 205

Ala Val Gly Pro Asp Tyr Pro Val Gln Val Asp Cys Tyr Met Ser Leu
    210                 215                 220

Asp Val Pro Tyr Thr Ile Ala Leu Val Lys Ala Cys Glu Lys Ala Gly
225                 230                 235                 240

Val Glu Ile Asn Trp Trp Glu Glu Val Leu His Pro Asp Asp Phe Asp
                245                 250                 255

Gly His Ile Lys Leu Lys Glu Ala Leu Pro Tyr Val Lys Phe Thr Thr
            260                 265                 270

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

Arg Ala Val Asp Ile Ile Gln Pro Asp Val Met Trp Leu Gly Gly Leu
    290                 295                 300

Thr Glu Leu Ile Lys Val Ala Ala Met Ala Ala Ala Tyr Asp Ile Pro
305                 310                 315                 320

Val Val Pro His Gly Ser Gly Pro Tyr Ser Phe Gln Ala Ile Met Ser
                325                 330                 335

Phe Pro Asn Ser Asp Phe Cys Glu Tyr Ile Ala Asn Ser Pro Asp Gly
            340                 345                 350

Lys Ser Ile Glu Pro Ser Phe Gly Asn Leu Phe Leu Asn Glu Val Leu
        355                 360                 365

Pro Arg Asn Gly Arg Val Asp Leu Thr Asp Glu Pro Gly Phe Gly Leu
    370                 375                 380

Glu Leu Asn Pro Ser Ala Glu Leu Val Pro Tyr Lys Ser Phe Phe Thr
385                 390                 395                 400

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

Ala Lys Val Asn Gly Lys His
            420


<210> SEQ ID NO 57
<211> LENGTH: 1743
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1743)

<400> SEQUENCE: 57

atg gcg aac gcg ccg cat ggc ggc gtg ctg aaa gat ctg ctg gtg cgc       48
Met Ala Asn Ala Pro His Gly Gly Val Leu Lys Asp Leu Leu Val Arg
1               5                   10                  15

gat gcg gcg ctg cat gat agc ctg ctg cag gaa gcg cgc agc ctg aac       96
Asp Ala Ala Leu His Asp Ser Leu Leu Gln Glu Ala Arg Ser Leu Asn
            20                  25                  30

gat att ttt ctg acc gaa cgc cag ctg tgc gat ctg gaa ctg att ctg      144
Asp Ile Phe Leu Thr Glu Arg Gln Leu Cys Asp Leu Glu Leu Ile Leu
        35                  40                  45

aac ggc ggc ttt agc ccg ctg gaa ggc ttt atg aac gaa cgc gat tat      192
Asn Gly Gly Phe Ser Pro Leu Glu Gly Phe Met Asn Glu Arg Asp Tyr
    50                  55                  60

acc agc gtg gtg gaa acc ctg cgc ctg gcg ccg tat aac ggc cag aaa      240
Thr Ser Val Val Glu Thr Leu Arg Leu Ala Pro Tyr Asn Gly Gln Lys
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65                  70                  75                  80

cat ggc gat gtg ttt ccg att ccg att acc ctg gat gtg agc cag gaa      288
His Gly Asp Val Phe Pro Ile Pro Ile Thr Leu Asp Val Ser Gln Glu
                85                  90                  95

gat att aac acc ctg ggc ctg aaa cag ggc ggc cgc gtg gcg ctg cgc      336
Asp Ile Asn Thr Leu Gly Leu Lys Gln Gly Gly Arg Val Ala Leu Arg
            100                 105                 110

gat ccg cgc gat gat gcg gcg ctg gcg att ctg acc gtg agc gat att      384
Asp Pro Arg Asp Asp Ala Ala Leu Ala Ile Leu Thr Val Ser Asp Ile
        115                 120                 125

tat cgc ccg aac aaa gcg att gaa gcg gaa aaa gtg atg ggc gcg gat      432
Tyr Arg Pro Asn Lys Ala Ile Glu Ala Glu Lys Val Met Gly Ala Asp
    130                 135                 140

gat att gcg cat ccg agc gtg gcg tat ctg cgc aac aac gtg aaa gaa      480
Asp Ile Ala His Pro Ser Val Ala Tyr Leu Arg Asn Asn Val Lys Glu
145                 150                 155                 160

ttt tat gtg ggc ggc aaa gtg cag gcg att cag gcg ccg acc cat ttt      528
Phe Tyr Val Gly Gly Lys Val Gln Ala Ile Gln Ala Pro Thr His Phe
                165                 170                 175

gat tat gtg ccg ctg cgc ttt acc ccg gcg gaa ctg cgc gcg cat ttt      576
Asp Tyr Val Pro Leu Arg Phe Thr Pro Ala Glu Leu Arg Ala His Phe
            180                 185                 190

cat aaa ctg gcg tgg cgc aaa gtg gtg gcg ttt cag acc cgc aac ccg      624
His Lys Leu Ala Trp Arg Lys Val Val Ala Phe Gln Thr Arg Asn Pro
        195                 200                 205

atg cat cgc gcg cat cgc gaa ctg acc gtg cgc gcg gcg cgc cag cgc      672
Met His Arg Ala His Arg Glu Leu Thr Val Arg Ala Ala Arg Gln Arg
    210                 215                 220

cgc gcg aac gtg ctg att cat ccg gtg gtg ggc ctg acc aaa ccg ggc      720
Arg Ala Asn Val Leu Ile His Pro Val Val Gly Leu Thr Lys Pro Gly
225                 230                 235                 240

gat gtg gat cat tat acc cgc gtg cgc gcg tat cag gcg ctg atg ccg      768
Asp Val Asp His Tyr Thr Arg Val Arg Ala Tyr Gln Ala Leu Met Pro
                245                 250                 255

agc tat ccg gaa ggc atg gcg cat ctg gcg ctg ctg ccg ctg gcg atg      816
Ser Tyr Pro Glu Gly Met Ala His Leu Ala Leu Leu Pro Leu Ala Met
            260                 265                 270

cgc atg gcg ggc ccg cgc gaa gcg gtg tgg cat gcg gtg att cgc aaa      864
Arg Met Ala Gly Pro Arg Glu Ala Val Trp His Ala Val Ile Arg Lys
        275                 280                 285

aac ttt ggc gcg acc cat ttt att gtg ggc cgc gat cat gcg ggc ccg      912
Asn Phe Gly Ala Thr His Phe Ile Val Gly Arg Asp His Ala Gly Pro
    290                 295                 300

ggc aaa aac agc cag ggc cag gat ttt tat ggc ccg tat gat gcg cag      960
Gly Lys Asn Ser Gln Gly Gln Asp Phe Tyr Gly Pro Tyr Asp Ala Gln
305                 310                 315                 320

gaa ctg gtg acc cag ttt aaa gat gaa ctg cag att gaa atg gtg ccg     1008
Glu Leu Val Thr Gln Phe Lys Asp Glu Leu Gln Ile Glu Met Val Pro
                325                 330                 335

ttt cag gcg atg acc tat ctg ccg ggc agc gat gaa tat cag ccg gtg     1056
Phe Gln Ala Met Thr Tyr Leu Pro Gly Ser Asp Glu Tyr Gln Pro Val
            340                 345                 350

gat gaa gtg ccg aaa ggc acc ccg acc gcg gat att agc ggc acc gaa     1104
Asp Glu Val Pro Lys Gly Thr Pro Thr Ala Asp Ile Ser Gly Thr Glu
        355                 360                 365

ctg cgc aaa cgc ctg cgc acc ggc gcg agc att ccg gat tgg ttt agc     1152
Leu Arg Lys Arg Leu Arg Thr Gly Ala Ser Ile Pro Asp Trp Phe Ser
    370                 375                 380

tat acc ggc gtg gtg aaa gtg ctg cgc gaa agc tat ccg ccg cgc ccg     1200
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Tyr Thr Gly Val Val Lys Val Leu Arg Glu Ser Tyr Pro Pro Arg Pro
385                 390                 395                 400

cag cag ggc ttt acc att ctg ctg acc ggc ctg cat aac agc ggc aaa     1248
Gln Gln Gly Phe Thr Ile Leu Leu Thr Gly Leu His Asn Ser Gly Lys
                405                 410                 415

gat acc att gcg cgc gcg ctg cag gtg acc ctg cag cag cag ggc agc     1296
Asp Thr Ile Ala Arg Ala Leu Gln Val Thr Leu Gln Gln Gln Gly Ser
            420                 425                 430

cgc agc gtg agc ctg ctg ctg ggc gaa gaa ctg cgc agc gat ctg gat     1344
Arg Ser Val Ser Leu Leu Leu Gly Glu Glu Leu Arg Ser Asp Leu Asp
        435                 440                 445

ccg cag att ggc cgc gcg att acc ccg gaa cag aaa cat att aac ctg     1392
Pro Gln Ile Gly Arg Ala Ile Thr Pro Glu Gln Lys His Ile Asn Leu
    450                 455                 460

gaa cgc att ggc ttt gtg gcg ggc gaa ctg acc aaa gcg ggc gcg gcg     1440
Glu Arg Ile Gly Phe Val Ala Gly Glu Leu Thr Lys Ala Gly Ala Ala
465                 470                 475                 480

gtg att gcg gcg ccg acc gcg ccg tat gaa cgc agc cgc cag gcg ttt     1488
Val Ile Ala Ala Pro Thr Ala Pro Tyr Glu Arg Ser Arg Gln Ala Phe
                485                 490                 495

aaa aaa cag gtg gtg ggc agc ggc ggc ggc aac tat ttt ctg gtg cat     1536
Lys Lys Gln Val Val Gly Ser Gly Gly Gly Asn Tyr Phe Leu Val His
            500                 505                 510

gtg gcg acc ccg ctg gaa tgg tgc gaa aaa gtg gat cgc cgc ggc ctg     1584
Val Ala Thr Pro Leu Glu Trp Cys Glu Lys Val Asp Arg Arg Gly Leu
        515                 520                 525

tat aaa gcg gcg cgc gcg ggc gaa att aaa aac ctg acc ggc gtg gat     1632
Tyr Lys Ala Ala Arg Ala Gly Glu Ile Lys Asn Leu Thr Gly Val Asp
    530                 535                 540

gat gtg tat gaa gcg ccg gaa gat gcg gat ctg gtg tgc gat ctg cgc     1680
Asp Val Tyr Glu Ala Pro Glu Asp Ala Asp Leu Val Cys Asp Leu Arg
545                 550                 555                 560

aac gat acc gtg ccg gaa att gtg cat agc att att atg att ctg gaa     1728
Asn Asp Thr Val Pro Glu Ile Val His Ser Ile Ile Met Ile Leu Glu
                565                 570                 575

agc cag aac ctg gtg                                                 1743
Ser Gln Asn Leu Val
            580
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<210> SEQ ID NO 58
<211> LENGTH: 581
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 58

```
Met Ala Asn Ala Pro His Gly Gly Val Leu Lys Asp Leu Leu Val Arg
1               5                   10                  15

Asp Ala Ala Leu His Asp Ser Leu Leu Gln Glu Ala Arg Ser Leu Asn
            20                  25                  30

Asp Ile Phe Leu Thr Glu Arg Gln Leu Cys Asp Leu Glu Leu Ile Leu
        35                  40                  45

Asn Gly Gly Phe Ser Pro Leu Glu Gly Phe Met Asn Glu Arg Asp Tyr
    50                  55                  60

Thr Ser Val Val Glu Thr Leu Arg Leu Ala Pro Tyr Asn Gly Gln Lys
65                  70                  75                  80

His Gly Asp Val Phe Pro Ile Pro Ile Thr Leu Asp Val Ser Gln Glu
                85                  90                  95

Asp Ile Asn Thr Leu Gly Leu Lys Gln Gly Gly Arg Val Ala Leu Arg
            100                 105                 110
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Asp Pro Arg Asp Asp Ala Ala Leu Ala Ile Leu Thr Val Ser Asp Ile
        115                 120                 125

Tyr Arg Pro Asn Lys Ala Ile Glu Ala Glu Lys Val Met Gly Ala Asp
    130                 135                 140

Asp Ile Ala His Pro Ser Val Ala Tyr Leu Arg Asn Asn Val Lys Glu
145                 150                 155                 160

Phe Tyr Val Gly Gly Lys Val Gln Ala Ile Gln Ala Pro Thr His Phe
                165                 170                 175

Asp Tyr Val Pro Leu Arg Phe Thr Pro Ala Glu Leu Arg Ala His Phe
            180                 185                 190

His Lys Leu Ala Trp Arg Lys Val Val Ala Phe Gln Thr Arg Asn Pro
        195                 200                 205

Met His Arg Ala His Arg Glu Leu Thr Val Arg Ala Ala Arg Gln Arg
    210                 215                 220

Arg Ala Asn Val Leu Ile His Pro Val Val Gly Leu Thr Lys Pro Gly
225                 230                 235                 240

Asp Val Asp His Tyr Thr Arg Val Arg Ala Tyr Gln Ala Leu Met Pro
                245                 250                 255

Ser Tyr Pro Glu Gly Met Ala His Leu Ala Leu Leu Pro Leu Ala Met
            260                 265                 270

Arg Met Ala Gly Pro Arg Glu Ala Val Trp His Ala Val Ile Arg Lys
        275                 280                 285

Asn Phe Gly Ala Thr His Phe Ile Val Gly Arg Asp His Ala Gly Pro
    290                 295                 300

Gly Lys Asn Ser Gln Gly Gln Asp Phe Tyr Gly Pro Tyr Asp Ala Gln
305                 310                 315                 320

Glu Leu Val Thr Gln Phe Lys Asp Glu Leu Gln Ile Glu Met Val Pro
                325                 330                 335

Phe Gln Ala Met Thr Tyr Leu Pro Gly Ser Asp Glu Tyr Gln Pro Val
            340                 345                 350

Asp Glu Val Pro Lys Gly Thr Pro Thr Ala Asp Ile Ser Gly Thr Glu
        355                 360                 365

Leu Arg Lys Arg Leu Arg Thr Gly Ala Ser Ile Pro Asp Trp Phe Ser
    370                 375                 380

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

Gln Gln Gly Phe Thr Ile Leu Leu Thr Gly Leu His Asn Ser Gly Lys
                405                 410                 415

Asp Thr Ile Ala Arg Ala Leu Gln Val Thr Leu Gln Gln Gln Gly Ser
            420                 425                 430

Arg Ser Val Ser Leu Leu Leu Gly Glu Glu Leu Arg Ser Asp Leu Asp
        435                 440                 445

Pro Gln Ile Gly Arg Ala Ile Thr Pro Glu Gln Lys His Ile Asn Leu
    450                 455                 460

Glu Arg Ile Gly Phe Val Ala Gly Glu Leu Thr Lys Ala Gly Ala Ala
465                 470                 475                 480

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

Lys Lys Gln Val Val Gly Ser Gly Gly Gly Asn Tyr Phe Leu Val His
            500                 505                 510

Val Ala Thr Pro Leu Glu Trp Cys Glu Lys Val Asp Arg Arg Gly Leu
        515                 520                 525
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Tyr Lys Ala Ala Arg Ala Gly Glu Ile Lys Asn Leu Thr Gly Val Asp
    530                 535                 540

Asp Val Tyr Glu Ala Pro Glu Asp Ala Asp Leu Val Cys Asp Leu Arg
545                 550                 555                 560

Asn Asp Thr Val Pro Glu Ile Val His Ser Ile Ile Met Ile Leu Glu
                565                 570                 575

Ser Gln Asn Leu Val
            580


<210> SEQ ID NO 59
<211> LENGTH: 1716
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1716)

<400> SEQUENCE: 59

atg cac atc gca tac att ctc ggc ctc gta ccc ctc gct ttc gcc ggt       48
Met His Ile Ala Tyr Ile Leu Gly Leu Val Pro Leu Ala Phe Ala Gly
1               5                   10                  15

gtc atc aag cac gac cct ccc aag ttc cag cct att cag tct acc agg       96
Val Ile Lys His Asp Pro Pro Lys Phe Gln Pro Ile Gln Ser Thr Arg
            20                  25                  30

att gtg cgg ctg cac cca aac ggg gac aaa agc aag tgc gtt gac ctc      144
Ile Val Arg Leu His Pro Asn Gly Asp Lys Ser Lys Cys Val Asp Leu
        35                  40                  45

ctg ggt aat act cgc cag gat ggt cag ccc gtg cag att tgc gac tgc      192
Leu Gly Asn Thr Arg Gln Asp Gly Gln Pro Val Gln Ile Cys Asp Cys
    50                  55                  60

gac ggt acc ccg gct cag gac tgg gtc ctc aat gcc ggc cgc ggt cag      240
Asp Gly Thr Pro Ala Gln Asp Trp Val Leu Asn Ala Gly Arg Gly Gln
65                  70                  75                  80

acc aag gtc cag ctc gcc ggc acc agt ttc tgt ctc gat gcc acc cac      288
Thr Lys Val Gln Leu Ala Gly Thr Ser Phe Cys Leu Asp Ala Thr His
                85                  90                  95

cct tac gca gcc gac ggg acc aac atg aag atc tgg aag tgc ttg gac      336
Pro Tyr Ala Ala Asp Gly Thr Asn Met Lys Ile Trp Lys Cys Leu Asp
            100                 105                 110

gtc caa cag caa gac tgg tat tgg acg agt gat aac aga atc gtt ctc      384
Val Gln Gln Gln Asp Trp Tyr Trp Thr Ser Asp Asn Arg Ile Val Leu
        115                 120                 125

cgc gac cag ggc aag tgc ctc gac tgg gcc act ggg gat cgg tct gat      432
Arg Asp Gln Gly Lys Cys Leu Asp Trp Ala Thr Gly Asp Arg Ser Asp
    130                 135                 140

ttc aac cag ctg cag gtc tgg cgg tgc agc acg gat aac aac aat cag      480
Phe Asn Gln Leu Gln Val Trp Arg Cys Ser Thr Asp Asn Asn Asn Gln
145                 150                 155                 160

gtc tgg aca acg gga ccg gac tac ggt ggg aac cat ggg ggt gat gct      528
Val Trp Thr Thr Gly Pro Asp Tyr Gly Gly Asn His Gly Gly Asp Ala
                165                 170                 175

ggt ggg aac ccc gga ggt aat caa ggc gat gat tca aga ggc aaa acc      576
Gly Gly Asn Pro Gly Gly Asn Gln Gly Asp Asp Ser Arg Gly Lys Thr
            180                 185                 190

aat act ggt gga aac ccc gga ggt aat caa ggt ggt gat tca gga ggg      624
Asn Thr Gly Gly Asn Pro Gly Gly Asn Gln Gly Gly Asp Ser Gly Gly
        195                 200                 205

aaa acc aat cac atc att ccc gac ccc cca ggg cca gac ccc aac agc      672
Lys Thr Asn His Ile Ile Pro Asp Pro Pro Gly Pro Asp Pro Asn Ser
    210                 215                 220
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gag ccc ctc aac ccc gcc ctt gaa gcc att gtt aac gtc acc gag gca       720
Glu Pro Leu Asn Pro Ala Leu Glu Ala Ile Val Asn Val Thr Glu Ala
225                 230                 235                 240

gct gga ccc tgg ccg ccc atg atc aac ttc gac ggc gat tac agc aat       768
Ala Gly Pro Trp Pro Pro Met Ile Asn Phe Asp Gly Asp Tyr Ser Asn
                245                 250                 255

gac gac gtg acc gta tcg gac caa gta ccg ttc gac tac tgt atc ggg       816
Asp Asp Val Thr Val Ser Asp Gln Val Pro Phe Asp Tyr Cys Ile Gly
            260                 265                 270

gag ggg tct ggt aac ccg acg gat gat gaa gga cag cag caa gga caa       864
Glu Gly Ser Gly Asn Pro Thr Asp Asp Glu Gly Gln Gln Gln Gly Gln
        275                 280                 285

aac ttc aca gca aat gta gct ggg ata ggg aga gac ttc tgc ctg gac       912
Asn Phe Thr Ala Asn Val Ala Gly Ile Gly Arg Asp Phe Cys Leu Asp
    290                 295                 300

aat ttt ggc aat cct gac att cgg aac acc att tct ttc gac aac aac       960
Asn Phe Gly Asn Pro Asp Ile Arg Asn Thr Ile Ser Phe Asp Asn Asn
305                 310                 315                 320

acc agc att ggg aac gga gcg gac act ggg cga gcc ctt cac aag cgg      1008
Thr Ser Ile Gly Asn Gly Ala Asp Thr Gly Arg Ala Leu His Lys Arg
                325                 330                 335

aca ttt gcg gat tca ggg gcg acg ggt acg ccc aac cgg tgg aga cga      1056
Thr Phe Ala Asp Ser Gly Ala Thr Gly Thr Pro Asn Arg Trp Arg Arg
            340                 345                 350

ggg tcg gtg att tcc att tgc gtc gag agg aac aac aat tat ctg gtt      1104
Gly Ser Val Ile Ser Ile Cys Val Glu Arg Asn Asn Asn Tyr Leu Val
        355                 360                 365

cca tat gcg tcc tcc ccc gtt ccc atc cga gca tcg gct atc gtc gca      1152
Pro Tyr Ala Ser Ser Pro Val Pro Ile Arg Ala Ser Ala Ile Val Ala
    370                 375                 380

tcc gcc atg gta cgt gca atc aac ttc tgg aac gca ggt ctg aac aag      1200
Ser Ala Met Val Arg Ala Ile Asn Phe Trp Asn Ala Gly Leu Asn Lys
385                 390                 395                 400

cga ttc gtc tcg ttc gag ttt gtg gag aac tgc aac gac gcc gtg ttc      1248
Arg Phe Val Ser Phe Glu Phe Val Glu Asn Cys Asn Asp Ala Val Phe
                405                 410                 415

cat act ctt gct gtt gac cag atc aag tct gcc aaa gag cct act gtg      1296
His Thr Leu Ala Val Asp Gln Ile Lys Ser Ala Lys Glu Pro Thr Val
            420                 425                 430

ctc gcg act gcc ccc ttc cct cct cgg ggt gaa gag ggt gct agg aac      1344
Leu Ala Thr Ala Pro Phe Pro Pro Arg Gly Glu Glu Gly Ala Arg Asn
        435                 440                 445

cgc aac atc ttc gtg tgg aat acg gct ttc gag gcc aac ttt cag aac      1392
Arg Asn Ile Phe Val Trp Asn Thr Ala Phe Glu Ala Asn Phe Gln Asn
    450                 455                 460

gtc ctt acc ttt atc atg tca cat gag ctg ggg cac act ctt ggc ctg      1440
Val Leu Thr Phe Ile Met Ser His Glu Leu Gly His Thr Leu Gly Leu
465                 470                 475                 480

gcg cat gag gac tgc aaa tcc aga gac caa cct tgc gaa gtt atc act      1488
Ala His Glu Asp Cys Lys Ser Arg Asp Gln Pro Cys Glu Val Ile Thr
                485                 490                 495

gac aag gtg gct ggg tca gtc gtg gaa agc cgt atc tcc ggc agc acc      1536
Asp Lys Val Ala Gly Ser Val Val Glu Ser Arg Ile Ser Gly Ser Thr
            500                 505                 510

aca cag ctg ttc aat ggc ccc acc ccg ctt gac ata gca ggg gcg aac      1584
Thr Gln Leu Phe Asn Gly Pro Thr Pro Leu Asp Ile Ala Gly Ala Asn
        515                 520                 525

gag tac tac tca ctt gca gcg gga ccc aac acc ccg gag aac atc gta      1632
Glu Tyr Tyr Ser Leu Ala Ala Gly Pro Asn Thr Pro Glu Asn Ile Val
    530                 535                 540
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ctc tgg cct gcg acg agg ggt ccg ttt atc aac tac ccg ccg cta ccg     1680
Leu Trp Pro Ala Thr Arg Gly Pro Phe Ile Asn Tyr Pro Pro Leu Pro
545                 550                 555                 560

aaa tgc aag tgg ttc ctc ggt att tgc tat tac tag                     1716
Lys Cys Lys Trp Phe Leu Gly Ile Cys Tyr Tyr
                565                 570


<210> SEQ ID NO 60
<211> LENGTH: 571
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 60

Met His Ile Ala Tyr Ile Leu Gly Leu Val Pro Leu Ala Phe Ala Gly
1               5                   10                  15

Val Ile Lys His Asp Pro Pro Lys Phe Gln Pro Ile Gln Ser Thr Arg
            20                  25                  30

Ile Val Arg Leu His Pro Asn Gly Asp Lys Ser Lys Cys Val Asp Leu
        35                  40                  45

Leu Gly Asn Thr Arg Gln Asp Gly Gln Pro Val Gln Ile Cys Asp Cys
    50                  55                  60

Asp Gly Thr Pro Ala Gln Asp Trp Val Leu Asn Ala Gly Arg Gly Gln
65                  70                  75                  80

Thr Lys Val Gln Leu Ala Gly Thr Ser Phe Cys Leu Asp Ala Thr His
                85                  90                  95

Pro Tyr Ala Ala Asp Gly Thr Asn Met Lys Ile Trp Lys Cys Leu Asp
            100                 105                 110

Val Gln Gln Gln Asp Trp Tyr Trp Thr Ser Asp Asn Arg Ile Val Leu
        115                 120                 125

Arg Asp Gln Gly Lys Cys Leu Asp Trp Ala Thr Gly Asp Arg Ser Asp
    130                 135                 140

Phe Asn Gln Leu Gln Val Trp Arg Cys Ser Thr Asp Asn Asn Asn Gln
145                 150                 155                 160

Val Trp Thr Thr Gly Pro Asp Tyr Gly Gly Asn His Gly Gly Asp Ala
                165                 170                 175

Gly Gly Asn Pro Gly Gly Asn Gln Gly Asp Asp Ser Arg Gly Lys Thr
            180                 185                 190

Asn Thr Gly Gly Asn Pro Gly Gly Asn Gln Gly Gly Asp Ser Gly Gly
        195                 200                 205

Lys Thr Asn His Ile Ile Pro Asp Pro Pro Gly Pro Asp Pro Asn Ser
    210                 215                 220

Glu Pro Leu Asn Pro Ala Leu Glu Ala Ile Val Asn Val Thr Glu Ala
225                 230                 235                 240

Ala Gly Pro Trp Pro Pro Met Ile Asn Phe Asp Gly Asp Tyr Ser Asn
                245                 250                 255

Asp Asp Val Thr Val Ser Asp Gln Val Pro Phe Asp Tyr Cys Ile Gly
            260                 265                 270

Glu Gly Ser Gly Asn Pro Thr Asp Asp Glu Gly Gln Gln Gln Gly Gln
        275                 280                 285

Asn Phe Thr Ala Asn Val Ala Gly Ile Gly Arg Asp Phe Cys Leu Asp
    290                 295                 300

Asn Phe Gly Asn Pro Asp Ile Arg Asn Thr Ile Ser Phe Asp Asn Asn
305                 310                 315                 320

Thr Ser Ile Gly Asn Gly Ala Asp Thr Gly Arg Ala Leu His Lys Arg
                325                 330                 335
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Thr Phe Ala Asp Ser Gly Ala Thr Gly Thr Pro Asn Arg Trp Arg Arg
            340                 345                 350

Gly Ser Val Ile Ser Ile Cys Val Glu Arg Asn Asn Asn Tyr Leu Val
        355                 360                 365

Pro Tyr Ala Ser Ser Pro Val Pro Ile Arg Ala Ser Ala Ile Val Ala
    370                 375                 380

Ser Ala Met Val Arg Ala Ile Asn Phe Trp Asn Ala Gly Leu Asn Lys
385                 390                 395                 400

Arg Phe Val Ser Phe Glu Phe Val Glu Asn Cys Asn Asp Ala Val Phe
                405                 410                 415

His Thr Leu Ala Val Asp Gln Ile Lys Ser Ala Lys Glu Pro Thr Val
            420                 425                 430

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

Arg Asn Ile Phe Val Trp Asn Thr Ala Phe Glu Ala Asn Phe Gln Asn
    450                 455                 460

Val Leu Thr Phe Ile Met Ser His Glu Leu Gly His Thr Leu Gly Leu
465                 470                 475                 480

Ala His Glu Asp Cys Lys Ser Arg Asp Gln Pro Cys Glu Val Ile Thr
                485                 490                 495

Asp Lys Val Ala Gly Ser Val Val Glu Ser Arg Ile Ser Gly Ser Thr
            500                 505                 510

Thr Gln Leu Phe Asn Gly Pro Thr Pro Leu Asp Ile Ala Gly Ala Asn
        515                 520                 525

Glu Tyr Tyr Ser Leu Ala Ala Gly Pro Asn Thr Pro Glu Asn Ile Val
    530                 535                 540

Leu Trp Pro Ala Thr Arg Gly Pro Phe Ile Asn Tyr Pro Pro Leu Pro
545                 550                 555                 560

Lys Cys Lys Trp Phe Leu Gly Ile Cys Tyr Tyr
                565                 570


<210> SEQ ID NO 61
<211> LENGTH: 1500
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1500)

<400> SEQUENCE: 61

atg ccg agc ctg acc cag acc aaa gat ctg gcg agc ctg ctg agc gat           48
Met Pro Ser Leu Thr Gln Thr Lys Asp Leu Ala Ser Leu Leu Ser Asp
1               5                   10                  15

gcg agc cat ttt aaa cag aaa ggc tat att aac ggc gaa tgg gtg agc           96
Ala Ser His Phe Lys Gln Lys Gly Tyr Ile Asn Gly Glu Trp Val Ser
            20                  25                  30

gcg agc gat ggc gcg acc ttt ccg ctg tat aac ccg gcg acc ggc gcg          144
Ala Ser Asp Gly Ala Thr Phe Pro Leu Tyr Asn Pro Ala Thr Gly Ala
        35                  40                  45

aaa ctg gcg gat atg ccg cat atg ccg cgc agc cag gtg gcg gaa gcg          192
Lys Leu Ala Asp Met Pro His Met Pro Arg Ser Gln Val Ala Glu Ala
    50                  55                  60

att aac gcg gcg aaa gcg gcg ttt ccg gcg tgg gcg gcg ctg acc gcg          240
Ile Asn Ala Ala Lys Ala Ala Phe Pro Ala Trp Ala Ala Leu Thr Ala
65                  70                  75                  80

tat cag cgc cag aac tat ctg ctg aaa ctg ttt aaa gaa atg gaa gaa          288
Tyr Gln Arg Gln Asn Tyr Leu Leu Lys Leu Phe Lys Glu Met Glu Glu
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                85                  90                  95

cat agc gaa gat ctg gcg att att ctg tgc acc gaa aac ggc aaa ccg      336
His Ser Glu Asp Leu Ala Ile Ile Leu Cys Thr Glu Asn Gly Lys Pro
            100                 105                 110

ctg gcg gaa agc cgc gtg gaa att agc tat ggc gcg agc ttt ctg acc      384
Leu Ala Glu Ser Arg Val Glu Ile Ser Tyr Gly Ala Ser Phe Leu Thr
        115                 120                 125

tgg aac gcg gcg gaa gcg ctg cgc acc tat ggc cag acc att ccg agc      432
Trp Asn Ala Ala Glu Ala Leu Arg Thr Tyr Gly Gln Thr Ile Pro Ser
    130                 135                 140

ccg ttt ccg ggc acc cgc aac acc gtg att aaa cag ccg att ggc gtg      480
Pro Phe Pro Gly Thr Arg Asn Thr Val Ile Lys Gln Pro Ile Gly Val
145                 150                 155                 160

tgc ggc ctg att acc ccg tgg aac ttt ccg aac gcg atg att acc cgc      528
Cys Gly Leu Ile Thr Pro Trp Asn Phe Pro Asn Ala Met Ile Thr Arg
                165                 170                 175

aaa atg gcg ccg gcg ctg gcg gcg ggc tgc acc gtg gtg att aaa gcg      576
Lys Met Ala Pro Ala Leu Ala Ala Gly Cys Thr Val Val Ile Lys Ala
            180                 185                 190

ccg gcg gaa acc ccg ctg agc gcg ctg gcg atg tgc gtg ctg tgc gaa      624
Pro Ala Glu Thr Pro Leu Ser Ala Leu Ala Met Cys Val Leu Cys Glu
        195                 200                 205

cgc gtg ggc att ccg ccg ggc gtg gtg aac gtg gtg acc atg gat aaa      672
Arg Val Gly Ile Pro Pro Gly Val Val Asn Val Val Thr Met Asp Lys
    210                 215                 220

ggc cag cgc gaa atg gcg gcg ggc ctg gaa ctg tgc gaa aac gtg aaa      720
Gly Gln Arg Glu Met Ala Ala Gly Leu Glu Leu Cys Glu Asn Val Lys
225                 230                 235                 240

gtg agc aaa att agc ttt acc ggc agc acc ccg gtg ggc cgc ctg ctg      768
Val Ser Lys Ile Ser Phe Thr Gly Ser Thr Pro Val Gly Arg Leu Leu
                245                 250                 255

atg aaa cag agc agc ggc acc ctg aaa aaa ctg agc ttt gaa ctg ggc      816
Met Lys Gln Ser Ser Gly Thr Leu Lys Lys Leu Ser Phe Glu Leu Gly
            260                 265                 270

ggc aac gcg gcg ttt att att ttt gat gat gcg gat ctg gat ctg gcg      864
Gly Asn Ala Ala Phe Ile Ile Phe Asp Asp Ala Asp Leu Asp Leu Ala
        275                 280                 285

gtg aac ggc gtg att ctg agc aaa ttt cgc gcg gcg ggc cag acc tgc      912
Val Asn Gly Val Ile Leu Ser Lys Phe Arg Ala Ala Gly Gln Thr Cys
    290                 295                 300

att tgc gcg aac cgc att ttt gtg cat agc aaa att tat gat gat ttt      960
Ile Cys Ala Asn Arg Ile Phe Val His Ser Lys Ile Tyr Asp Asp Phe
305                 310                 315                 320

gcg cgc cgc ctg gtg gaa cgc gtg aaa gcg ttt aaa gtg ggc aac ggc     1008
Ala Arg Arg Leu Val Glu Arg Val Lys Ala Phe Lys Val Gly Asn Gly
                325                 330                 335

att gaa gaa ggc gtg acc att ggc ccg ctg gtg agc cag cgc ggc gtg     1056
Ile Glu Glu Gly Val Thr Ile Gly Pro Leu Val Ser Gln Arg Gly Val
            340                 345                 350

gaa aaa gtg gaa cgc cat gtg cag gat gcg gtg ggc ctg ggc gcg aaa     1104
Glu Lys Val Glu Arg His Val Gln Asp Ala Val Gly Leu Gly Ala Lys
        355                 360                 365

gtg ctg gtg ggc ggc aaa cgc att gat aaa ggc gaa ggc agc tgc ttt     1152
Val Leu Val Gly Gly Lys Arg Ile Asp Lys Gly Glu Gly Ser Cys Phe
    370                 375                 380

tat gaa ccg acc gtg ctg gtg gat gtg ccg cgc cag tgc gcg gtg agc     1200
Tyr Glu Pro Thr Val Leu Val Asp Val Pro Arg Gln Cys Ala Val Ser
385                 390                 395                 400

aac gaa gaa acc ttt ggc ccg ctg gcg ccg ctg ttt aaa ttt gat gat     1248
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Asn Glu Glu Thr Phe Gly Pro Leu Ala Pro Leu Phe Lys Phe Asp Asp
                405                 410                 415

gaa gat gat gtg gtg gaa cgc gcg aac agc agc gaa gtg ggc ctg gcg      1296
Glu Asp Asp Val Val Glu Arg Ala Asn Ser Ser Glu Val Gly Leu Ala
            420                 425                 430

gcg tat ttt ttt acc aaa gat ctg gcg cgc acc cat cgc gtg gcg gaa      1344
Ala Tyr Phe Phe Thr Lys Asp Leu Ala Arg Thr His Arg Val Ala Glu
        435                 440                 445

aaa ctg gaa gtg ggc atg gtg gcg gtg aac acc ggc gcg att gcg cag      1392
Lys Leu Glu Val Gly Met Val Ala Val Asn Thr Gly Ala Ile Ala Gln
    450                 455                 460

agc tgc gtg ccg ttt ggc ggc gtg aaa cag agc ggc ttt ggc cgc gaa      1440
Ser Cys Val Pro Phe Gly Gly Val Lys Gln Ser Gly Phe Gly Arg Glu
465                 470                 475                 480

ggc ggc ccg agc ggc att gat gaa ttt atg gtg gaa aaa ctg att acc      1488
Gly Gly Pro Ser Gly Ile Asp Glu Phe Met Val Glu Lys Leu Ile Thr
                485                 490                 495

att ggc ggc ctg                                                      1500
Ile Gly Gly Leu
            500


<210> SEQ ID NO 62
<211> LENGTH: 500
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 62

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

Ala Ser His Phe Lys Gln Lys Gly Tyr Ile Asn Gly Glu Trp Val Ser
            20                  25                  30

Ala Ser Asp Gly Ala Thr Phe Pro Leu Tyr Asn Pro Ala Thr Gly Ala
        35                  40                  45

Lys Leu Ala Asp Met Pro His Met Pro Arg Ser Gln Val Ala Glu Ala
    50                  55                  60

Ile Asn Ala Ala Lys Ala Ala Phe Pro Ala Trp Ala Ala Leu Thr Ala
65                  70                  75                  80

Tyr Gln Arg Gln Asn Tyr Leu Leu Lys Leu Phe Lys Glu Met Glu Glu
                85                  90                  95

His Ser Glu Asp Leu Ala Ile Ile Leu Cys Thr Glu Asn Gly Lys Pro
            100                 105                 110

Leu Ala Glu Ser Arg Val Glu Ile Ser Tyr Gly Ala Ser Phe Leu Thr
        115                 120                 125

Trp Asn Ala Ala Glu Ala Leu Arg Thr Tyr Gly Gln Thr Ile Pro Ser
    130                 135                 140

Pro Phe Pro Gly Thr Arg Asn Thr Val Ile Lys Gln Pro Ile Gly Val
145                 150                 155                 160

Cys Gly Leu Ile Thr Pro Trp Asn Phe Pro Asn Ala Met Ile Thr Arg
                165                 170                 175

Lys Met Ala Pro Ala Leu Ala Ala Gly Cys Thr Val Val Ile Lys Ala
            180                 185                 190

Pro Ala Glu Thr Pro Leu Ser Ala Leu Ala Met Cys Val Leu Cys Glu
        195                 200                 205

Arg Val Gly Ile Pro Pro Gly Val Val Asn Val Val Thr Met Asp Lys
    210                 215                 220

Gly Gln Arg Glu Met Ala Ala Gly Leu Glu Leu Cys Glu Asn Val Lys
225                 230                 235                 240
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Val Ser Lys Ile Ser Phe Thr Gly Ser Thr Pro Val Gly Arg Leu Leu
                245                 250                 255

Met Lys Gln Ser Ser Gly Thr Leu Lys Lys Leu Ser Phe Glu Leu Gly
            260                 265                 270

Gly Asn Ala Ala Phe Ile Ile Phe Asp Asp Ala Asp Leu Asp Leu Ala
        275                 280                 285

Val Asn Gly Val Ile Leu Ser Lys Phe Arg Ala Ala Gly Gln Thr Cys
    290                 295                 300

Ile Cys Ala Asn Arg Ile Phe Val His Ser Lys Ile Tyr Asp Asp Phe
305                 310                 315                 320

Ala Arg Arg Leu Val Glu Arg Val Lys Ala Phe Lys Val Gly Asn Gly
                325                 330                 335

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

Glu Lys Val Glu Arg His Val Gln Asp Ala Val Gly Leu Gly Ala Lys
        355                 360                 365

Val Leu Val Gly Gly Lys Arg Ile Asp Lys Gly Glu Gly Ser Cys Phe
    370                 375                 380

Tyr Glu Pro Thr Val Leu Val Asp Val Pro Arg Gln Cys Ala Val Ser
385                 390                 395                 400

Asn Glu Glu Thr Phe Gly Pro Leu Ala Pro Leu Phe Lys Phe Asp Asp
                405                 410                 415

Glu Asp Asp Val Val Glu Arg Ala Asn Ser Ser Glu Val Gly Leu Ala
            420                 425                 430

Ala Tyr Phe Phe Thr Lys Asp Leu Ala Arg Thr His Arg Val Ala Glu
        435                 440                 445

Lys Leu Glu Val Gly Met Val Ala Val Asn Thr Gly Ala Ile Ala Gln
    450                 455                 460

Ser Cys Val Pro Phe Gly Gly Val Lys Gln Ser Gly Phe Gly Arg Glu
465                 470                 475                 480

Gly Gly Pro Ser Gly Ile Asp Glu Phe Met Val Glu Lys Leu Ile Thr
                485                 490                 495

Ile Gly Gly Leu
            500


<210> SEQ ID NO 63
<211> LENGTH: 1200
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1200)

<400> SEQUENCE: 63

atg tgc agc agc cat gcg acc gcg gtg gaa agc gtg agc ccg gcg ccg         48
Met Cys Ser Ser His Ala Thr Ala Val Glu Ser Val Ser Pro Ala Pro
1               5                   10                  15

cgc aaa agc cag tat gaa gtg aaa tat gat ccg gat ctg gtg ctg aaa         96
Arg Lys Ser Gln Tyr Glu Val Lys Tyr Asp Pro Asp Leu Val Leu Lys
            20                  25                  30

agc gcg gaa ttt aaa gaa ctg aaa cag ggc gat aaa gaa ctg gaa gat        144
Ser Ala Glu Phe Lys Glu Leu Lys Gln Gly Asp Lys Glu Leu Glu Asp
        35                  40                  45

ccg aaa gcg aac ctg gcg tgc gcg tat gat gaa aaa cat aac gtg aaa        192
Pro Lys Ala Asn Leu Ala Cys Ala Tyr Asp Glu Lys His Asn Val Lys
    50                  55                  60
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atg att aac aaa ccg att ccg aaa gcg cgc cag gat gaa gtg gtg gtg       240
Met Ile Asn Lys Pro Ile Pro Lys Ala Arg Gln Asp Glu Val Val Val
65                  70                  75                  80

cat att aaa gcg acc ggc att tgc ggc agc gat gtg cat ttt tgg aaa       288
His Ile Lys Ala Thr Gly Ile Cys Gly Ser Asp Val His Phe Trp Lys
                85                  90                  95

cat ggc cag att ggc ccg acc atg att gtg acc gat acc tgc ggc gcg       336
His Gly Gln Ile Gly Pro Thr Met Ile Val Thr Asp Thr Cys Gly Ala
            100                 105                 110

ggc cat gaa agc gcg ggc gaa gtg gtg gaa gtg ggc ccg ggc gtg gaa       384
Gly His Glu Ser Ala Gly Glu Val Val Glu Val Gly Pro Gly Val Glu
        115                 120                 125

cag tgg aaa gtg ggc gat cgc gtg gcg att gaa tgc ggc gtg ccg tgc       432
Gln Trp Lys Val Gly Asp Arg Val Ala Ile Glu Cys Gly Val Pro Cys
    130                 135                 140

ggc cag gcg agc tgc ggc ccg tgc gtg acc ggc cgc tat aac gcg tgc       480
Gly Gln Ala Ser Cys Gly Pro Cys Val Thr Gly Arg Tyr Asn Ala Cys
145                 150                 155                 160

ccg cag gtg gtg ttt ttt agc acc ccg ccg tat cat ggc acc ctg acc       528
Pro Gln Val Val Phe Phe Ser Thr Pro Pro Tyr His Gly Thr Leu Thr
                165                 170                 175

cgc tat cat gcg cat ccg gcg agc tgg ctg cat cgc ctg ccg gat aac       576
Arg Tyr His Ala His Pro Ala Ser Trp Leu His Arg Leu Pro Asp Asn
            180                 185                 190

ctg agc tat gaa gaa ggc gcg ctg tgc gaa ccg ttt gcg gtg gcg ctg       624
Leu Ser Tyr Glu Glu Gly Ala Leu Cys Glu Pro Phe Ala Val Ala Leu
        195                 200                 205

gcg gcg ctg gaa cgc gcg ggc aac cgc ctg ggc gat ccg gtg ctg att       672
Ala Ala Leu Glu Arg Ala Gly Asn Arg Leu Gly Asp Pro Val Leu Ile
    210                 215                 220

tgc ggc gcg ggc ccg att ggc ctg gtg acc ctg ctg gcg agc cat gcg       720
Cys Gly Ala Gly Pro Ile Gly Leu Val Thr Leu Leu Ala Ser His Ala
225                 230                 235                 240

gcg ggc tgc acc ccg att gtg att acc gat ctg cag gcg agc cgc ctg       768
Ala Gly Cys Thr Pro Ile Val Ile Thr Asp Leu Gln Ala Ser Arg Leu
                245                 250                 255

gaa gtg gcg aaa aaa ctg att ccg acc gtg aaa acc gtg cag att gaa       816
Glu Val Ala Lys Lys Leu Ile Pro Thr Val Lys Thr Val Gln Ile Glu
            260                 265                 270

cgc agc tgg acc agc aaa gaa acc agc gaa gcg att aaa gaa gcg gcg       864
Arg Ser Trp Thr Ser Lys Glu Thr Ser Glu Ala Ile Lys Glu Ala Ala
        275                 280                 285

ggc acc ggc att cgc gtg gcg att gat gcg acc ggc ttt gaa agc agc       912
Gly Thr Gly Ile Arg Val Ala Ile Asp Ala Thr Gly Phe Glu Ser Ser
    290                 295                 300

att acc gcg gcg att tat agc gtg gtg ttt ggc ggc aaa gtg ttt gtg       960
Ile Thr Ala Ala Ile Tyr Ser Val Val Phe Gly Gly Lys Val Phe Val
305                 310                 315                 320

att ggc gcg ggc ccg agc gaa cag aaa tat ccg ttt ggc tat tgc agc      1008
Ile Gly Ala Gly Pro Ser Glu Gln Lys Tyr Pro Phe Gly Tyr Cys Ser
                325                 330                 335

gcg aac gaa att gat ctg cag ttt cag tat cgc tat gcg cat cag tat      1056
Ala Asn Glu Ile Asp Leu Gln Phe Gln Tyr Arg Tyr Ala His Gln Tyr
            340                 345                 350

ccg aaa gcg ctg cgc att gtg agc ggc ggc ctg att aac ctg aaa ccg      1104
Pro Lys Ala Leu Arg Ile Val Ser Gly Gly Leu Ile Asn Leu Lys Pro
        355                 360                 365

ctg ctg acc cat acc ttt ccg ctg aac aaa gcg gtg gaa gcg ttt cat      1152
Leu Leu Thr His Thr Phe Pro Leu Asn Lys Ala Val Glu Ala Phe His
    370                 375                 380
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gtg gcg gcg gat ccg acc aaa ggc gcg att aaa gtg cag att att gat     1200
Val Ala Ala Asp Pro Thr Lys Gly Ala Ile Lys Val Gln Ile Ile Asp
385                 390                 395                 400


<210> SEQ ID NO 64
<211> LENGTH: 400
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 64

Met Cys Ser Ser His Ala Thr Ala Val Glu Ser Val Ser Pro Ala Pro
1               5                   10                  15

Arg Lys Ser Gln Tyr Glu Val Lys Tyr Asp Pro Asp Leu Val Leu Lys
            20                  25                  30

Ser Ala Glu Phe Lys Glu Leu Lys Gln Gly Asp Lys Glu Leu Glu Asp
        35                  40                  45

Pro Lys Ala Asn Leu Ala Cys Ala Tyr Asp Glu Lys His Asn Val Lys
    50                  55                  60

Met Ile Asn Lys Pro Ile Pro Lys Ala Arg Gln Asp Glu Val Val Val
65                  70                  75                  80

His Ile Lys Ala Thr Gly Ile Cys Gly Ser Asp Val His Phe Trp Lys
                85                  90                  95

His Gly Gln Ile Gly Pro Thr Met Ile Val Thr Asp Thr Cys Gly Ala
            100                 105                 110

Gly His Glu Ser Ala Gly Glu Val Val Glu Val Gly Pro Gly Val Glu
        115                 120                 125

Gln Trp Lys Val Gly Asp Arg Val Ala Ile Glu Cys Gly Val Pro Cys
    130                 135                 140

Gly Gln Ala Ser Cys Gly Pro Cys Val Thr Gly Arg Tyr Asn Ala Cys
145                 150                 155                 160

Pro Gln Val Val Phe Phe Ser Thr Pro Pro Tyr His Gly Thr Leu Thr
                165                 170                 175

Arg Tyr His Ala His Pro Ala Ser Trp Leu His Arg Leu Pro Asp Asn
            180                 185                 190

Leu Ser Tyr Glu Glu Gly Ala Leu Cys Glu Pro Phe Ala Val Ala Leu
        195                 200                 205

Ala Ala Leu Glu Arg Ala Gly Asn Arg Leu Gly Asp Pro Val Leu Ile
    210                 215                 220

Cys Gly Ala Gly Pro Ile Gly Leu Val Thr Leu Leu Ala Ser His Ala
225                 230                 235                 240

Ala Gly Cys Thr Pro Ile Val Ile Thr Asp Leu Gln Ala Ser Arg Leu
                245                 250                 255

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

Arg Ser Trp Thr Ser Lys Glu Thr Ser Glu Ala Ile Lys Glu Ala Ala
        275                 280                 285

Gly Thr Gly Ile Arg Val Ala Ile Asp Ala Thr Gly Phe Glu Ser Ser
    290                 295                 300

Ile Thr Ala Ala Ile Tyr Ser Val Val Phe Gly Gly Lys Val Phe Val
305                 310                 315                 320

Ile Gly Ala Gly Pro Ser Glu Gln Lys Tyr Pro Phe Gly Tyr Cys Ser
                325                 330                 335

Ala Asn Glu Ile Asp Leu Gln Phe Gln Tyr Arg Tyr Ala His Gln Tyr
            340                 345                 350
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Pro Lys Ala Leu Arg Ile Val Ser Gly Gly Leu Ile Asn Leu Lys Pro
        355                 360                 365

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

Val Ala Ala Asp Pro Thr Lys Gly Ala Ile Lys Val Gln Ile Ile Asp
385                 390                 395                 400


<210> SEQ ID NO 65
<211> LENGTH: 1689
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1689)

<400> SEQUENCE: 65

atg gtg tgc gtg att agc gat ccg gat tgg tgg cgc cag gcg gtg gtg       48
Met Val Cys Val Ile Ser Asp Pro Asp Trp Trp Arg Gln Ala Val Val
1               5                   10                  15

tat cag att tat ccg cgc agc ttt gcg gat gcg aac ggc gat ggc att       96
Tyr Gln Ile Tyr Pro Arg Ser Phe Ala Asp Ala Asn Gly Asp Gly Ile
            20                  25                  30

ggc gat ctg aaa ggc att acc gcg cgc gtg ccg tat ctg aaa gcg ctg      144
Gly Asp Leu Lys Gly Ile Thr Ala Arg Val Pro Tyr Leu Lys Ala Leu
        35                  40                  45

ggc gtg gat gcg att tgg ctg agc ccg ttt tat ccg agc gcg ctg cgc      192
Gly Val Asp Ala Ile Trp Leu Ser Pro Phe Tyr Pro Ser Ala Leu Arg
    50                  55                  60

gat ggc ggc tat gat gtg gcg gat tat cgc gat gtg gat ccg aaa att      240
Asp Gly Gly Tyr Asp Val Ala Asp Tyr Arg Asp Val Asp Pro Lys Ile
65                  70                  75                  80

ggc acc ctg gaa gaa ttt gat gaa atg acc gcg gcg ttt cag aaa gtg      288
Gly Thr Leu Glu Glu Phe Asp Glu Met Thr Ala Ala Phe Gln Lys Val
                85                  90                  95

ggc att cgc gtg att gtg gat att gtg ccg aac cat agc agc gat gat      336
Gly Ile Arg Val Ile Val Asp Ile Val Pro Asn His Ser Ser Asp Asp
            100                 105                 110

cat gaa tgg ttt cag gcg gcg ctg aaa gcg ggc aaa ggc agc ccg gaa      384
His Glu Trp Phe Gln Ala Ala Leu Lys Ala Gly Lys Gly Ser Pro Glu
        115                 120                 125

cgc gaa cgc tat att ttt cgc gat ggc ctg ggc ccg aac aaa gat cag      432
Arg Glu Arg Tyr Ile Phe Arg Asp Gly Leu Gly Pro Asn Lys Asp Gln
    130                 135                 140

ccg ccg acc gat tgg att tgc agc ttt ggc ggc agc gcg tgg agc ccg      480
Pro Pro Thr Asp Trp Ile Cys Ser Phe Gly Gly Ser Ala Trp Ser Pro
145                 150                 155                 160

agc ggc atg aac gat ggc cag tgg tat ttt cat tgg ttt gat agc agc      528
Ser Gly Met Asn Asp Gly Gln Trp Tyr Phe His Trp Phe Asp Ser Ser
                165                 170                 175

cag ccg gat tgg aac tgg gaa aac ccg gat gtg aaa gcg gat ttt ctg      576
Gln Pro Asp Trp Asn Trp Glu Asn Pro Asp Val Lys Ala Asp Phe Leu
            180                 185                 190

aaa acc ctg aaa ttt tgg ggc gat cgc ggc gtg agc ggc ttt cgc att      624
Lys Thr Leu Lys Phe Trp Gly Asp Arg Gly Val Ser Gly Phe Arg Ile
        195                 200                 205

gat gtg gcg cat ggc ctg gcg aaa gat atg agc gaa ccg ctg ccg aac      672
Asp Val Ala His Gly Leu Ala Lys Asp Met Ser Glu Pro Leu Pro Asn
    210                 215                 220

tgg gaa cag ctg acc aaa ctg acc cat cag aaa ctg acc aac ggc aac      720
Trp Glu Gln Leu Thr Lys Leu Thr His Gln Lys Leu Thr Asn Gly Asn
225                 230                 235                 240
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agc gaa ctg gat cat ccg ctg ctg gat cgc aaa gaa gtg cat gat att      768
Ser Glu Leu Asp His Pro Leu Leu Asp Arg Lys Glu Val His Asp Ile
                245                 250                 255

tat cgc agc tgg cgc gaa gtg ttt aac cag ttt aac ccg ccg ctg atg      816
Tyr Arg Ser Trp Arg Glu Val Phe Asn Gln Phe Asn Pro Pro Leu Met
            260                 265                 270

gcg gtg gcg gaa gcg tgg gtg gcg ccg gat cag aaa ccg ctg tat gcg      864
Ala Val Ala Glu Ala Trp Val Ala Pro Asp Gln Lys Pro Leu Tyr Ala
        275                 280                 285

agc agc gaa ggc ctg ggc cag acc ttt agc ttt gat att ctg ctg tgc      912
Ser Ser Glu Gly Leu Gly Gln Thr Phe Ser Phe Asp Ile Leu Leu Cys
    290                 295                 300

aac ttt gat gcg gaa gaa tat cgc cag tgc att aaa agc agc ctg gcg      960
Asn Phe Asp Ala Glu Glu Tyr Arg Gln Cys Ile Lys Ser Ser Leu Ala
305                 310                 315                 320

ggc agc aaa aaa agc gat agc acc acc acc tgg gtg ctg agc aac cat     1008
Gly Ser Lys Lys Ser Asp Ser Thr Thr Thr Trp Val Leu Ser Asn His
                325                 330                 335

gat gtg atg cgc cat ccg acc cgc ttt ggc ctg ccg aac gtg ccg aac     1056
Asp Val Met Arg His Pro Thr Arg Phe Gly Leu Pro Asn Val Pro Asn
            340                 345                 350

gcg aac cat gcg atg acc acc gat acc tat aac aaa ttt ctg aaa acc     1104
Ala Asn His Ala Met Thr Thr Asp Thr Tyr Asn Lys Phe Leu Lys Thr
        355                 360                 365

aaa ctg acc gat ccg aaa gtg gat att gaa cag ggc ctg cgc cgc gcg     1152
Lys Leu Thr Asp Pro Lys Val Asp Ile Glu Gln Gly Leu Arg Arg Ala
    370                 375                 380

aaa gcg gcg acc ctg atg att ctg gcg ctg ccg ggc agc acc tat ctg     1200
Lys Ala Ala Thr Leu Met Ile Leu Ala Leu Pro Gly Ser Thr Tyr Leu
385                 390                 395                 400

tat cag ggc gaa gaa ctg ggc ctg cag gaa gtg gtg gaa att ccg gat     1248
Tyr Gln Gly Glu Glu Leu Gly Leu Gln Glu Val Val Glu Ile Pro Asp
                405                 410                 415

gaa gaa cgc cag gat ccg att ttt att cgc acc aaa ggc gaa gaa gtg     1296
Glu Glu Arg Gln Asp Pro Ile Phe Ile Arg Thr Lys Gly Glu Glu Val
            420                 425                 430

ggc cgc gat ggc tgc cgc gtg ccg att ccg tgg gtg gcg gat gaa aaa     1344
Gly Arg Asp Gly Cys Arg Val Pro Ile Pro Trp Val Ala Asp Glu Lys
        435                 440                 445

aac ttt ggc tat ggc ccg ggc aaa cgc gcg cat ctg ccg cag ccg gcg     1392
Asn Phe Gly Tyr Gly Pro Gly Lys Arg Ala His Leu Pro Gln Pro Ala
    450                 455                 460

tgg ttt aaa gat tat gcg gtg gat gtg gaa gaa aaa gat gcg aac agc     1440
Trp Phe Lys Asp Tyr Ala Val Asp Val Glu Glu Lys Asp Ala Asn Ser
465                 470                 475                 480

gtg ctg agc ctg tat cgc cgc gcg ctg ggc ctg cgc aaa ggc ctg cag     1488
Val Leu Ser Leu Tyr Arg Arg Ala Leu Gly Leu Arg Lys Gly Leu Gln
                485                 490                 495

agc gcg gaa gaa ctg gaa tgg gtg gaa aac ccg aac aaa gaa gtg ctg     1536
Ser Ala Glu Glu Leu Glu Trp Val Glu Asn Pro Asn Lys Glu Val Leu
            500                 505                 510

cat ttt cgc cgc ccg ggc ggc tgg gaa gtg gtg gtg aac att ggc aaa     1584
His Phe Arg Arg Pro Gly Gly Trp Glu Val Val Val Asn Ile Gly Lys
        515                 520                 525

gat agc gtg gat ctg ccg aaa ggc agc gtg ctg att agc agc agc aac     1632
Asp Ser Val Asp Leu Pro Lys Gly Ser Val Leu Ile Ser Ser Ser Asn
    530                 535                 540

aac gcg ctg aaa ggc ggc agc att ccg ggc gaa acc acc gtg tgg ctg     1680
Asn Ala Leu Lys Gly Gly Ser Ile Pro Gly Glu Thr Thr Val Trp Leu
```

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545                 550                 555                 560

aaa agc gcg                                                         1689
Lys Ser Ala


<210> SEQ ID NO 66
<211> LENGTH: 563
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 66

Met Val Cys Val Ile Ser Asp Pro Asp Trp Trp Arg Gln Ala Val Val
1               5                   10                  15

Tyr Gln Ile Tyr Pro Arg Ser Phe Ala Asp Ala Asn Gly Asp Gly Ile
            20                  25                  30

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

Gly Val Asp Ala Ile Trp Leu Ser Pro Phe Tyr Pro Ser Ala Leu Arg
    50                  55                  60

Asp Gly Gly Tyr Asp Val Ala Asp Tyr Arg Asp Val Asp Pro Lys Ile
65                  70                  75                  80

Gly Thr Leu Glu Glu Phe Asp Glu Met Thr Ala Ala Phe Gln Lys Val
                85                  90                  95

Gly Ile Arg Val Ile Val Asp Ile Val Pro Asn His Ser Ser Asp Asp
            100                 105                 110

His Glu Trp Phe Gln Ala Ala Leu Lys Ala Gly Lys Gly Ser Pro Glu
        115                 120                 125

Arg Glu Arg Tyr Ile Phe Arg Asp Gly Leu Gly Pro Asn Lys Asp Gln
    130                 135                 140

Pro Pro Thr Asp Trp Ile Cys Ser Phe Gly Gly Ser Ala Trp Ser Pro
145                 150                 155                 160

Ser Gly Met Asn Asp Gly Gln Trp Tyr Phe His Trp Phe Asp Ser Ser
                165                 170                 175

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

Lys Thr Leu Lys Phe Trp Gly Asp Arg Gly Val Ser Gly Phe Arg Ile
        195                 200                 205

Asp Val Ala His Gly Leu Ala Lys Asp Met Ser Glu Pro Leu Pro Asn
    210                 215                 220

Trp Glu Gln Leu Thr Lys Leu Thr His Gln Lys Leu Thr Asn Gly Asn
225                 230                 235                 240

Ser Glu Leu Asp His Pro Leu Leu Asp Arg Lys Glu Val His Asp Ile
                245                 250                 255

Tyr Arg Ser Trp Arg Glu Val Phe Asn Gln Phe Asn Pro Pro Leu Met
            260                 265                 270

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

Ser Ser Glu Gly Leu Gly Gln Thr Phe Ser Phe Asp Ile Leu Leu Cys
    290                 295                 300

Asn Phe Asp Ala Glu Glu Tyr Arg Gln Cys Ile Lys Ser Ser Leu Ala
305                 310                 315                 320

Gly Ser Lys Lys Ser Asp Ser Thr Thr Thr Trp Val Leu Ser Asn His
                325                 330                 335

Asp Val Met Arg His Pro Thr Arg Phe Gly Leu Pro Asn Val Pro Asn
            340                 345                 350
```

```
Ala Asn His Ala Met Thr Thr Asp Thr Tyr Asn Lys Phe Leu Lys Thr
        355                 360                 365

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

Lys Ala Ala Thr Leu Met Ile Leu Ala Leu Pro Gly Ser Thr Tyr Leu
385                 390                 395                 400

Tyr Gln Gly Glu Glu Leu Gly Leu Gln Glu Val Val Glu Ile Pro Asp
                405                 410                 415

Glu Glu Arg Gln Asp Pro Ile Phe Ile Arg Thr Lys Gly Glu Glu Val
            420                 425                 430

Gly Arg Asp Gly Cys Arg Val Pro Ile Pro Trp Val Ala Asp Glu Lys
        435                 440                 445

Asn Phe Gly Tyr Gly Pro Gly Lys Arg Ala His Leu Pro Gln Pro Ala
    450                 455                 460

Trp Phe Lys Asp Tyr Ala Val Asp Val Glu Glu Lys Asp Ala Asn Ser
465                 470                 475                 480

Val Leu Ser Leu Tyr Arg Arg Ala Leu Gly Leu Arg Lys Gly Leu Gln
                485                 490                 495

Ser Ala Glu Glu Leu Glu Trp Val Glu Asn Pro Asn Lys Glu Val Leu
            500                 505                 510

His Phe Arg Arg Pro Gly Gly Trp Glu Val Val Val Asn Ile Gly Lys
        515                 520                 525

Asp Ser Val Asp Leu Pro Lys Gly Ser Val Leu Ile Ser Ser Ser Asn
    530                 535                 540

Asn Ala Leu Lys Gly Gly Ser Ile Pro Gly Glu Thr Thr Val Trp Leu
545                 550                 555                 560

Lys Ser Ala


<210> SEQ ID NO 67
<211> LENGTH: 729
<212> TYPE: DNA
<213> ORGANISM: Cryptococcus neoformans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(729)

<400> SEQUENCE: 67

atg ccg agc gtg gtg ttt gat gtg gtg ggc acc tgc ttt agc tat gat       48
Met Pro Ser Val Val Phe Asp Val Val Gly Thr Cys Phe Ser Tyr Asp
1               5                   10                  15

aac ggc gcg gaa gcg ctg cag gcg cgc ctg ggc ccg aaa ctg gcg aaa       96
Asn Gly Ala Glu Ala Leu Gln Ala Arg Leu Gly Pro Lys Leu Ala Lys
            20                  25                  30

tat ggc att ccg agc aaa ctg ctg ttt tat agc tgg gtg tgc agc acc      144
Tyr Gly Ile Pro Ser Lys Leu Leu Phe Tyr Ser Trp Val Cys Ser Thr
        35                  40                  45

gaa cgc gat tat agc tat ctg agc cag att aaa cag tat aaa gcg ttt      192
Glu Arg Asp Tyr Ser Tyr Leu Ser Gln Ile Lys Gln Tyr Lys Ala Phe
    50                  55                  60

ttt gcg att ctg agc aac acc ctg acc cgc gtg ctg ttt cag gcg ggc      240
Phe Ala Ile Leu Ser Asn Thr Leu Thr Arg Val Leu Phe Gln Ala Gly
65                  70                  75                  80

gtg ccg gtg gaa gcg ctg gat gat ttt ttt acc gcg gat gat gtg gat      288
Val Pro Val Glu Ala Leu Asp Asp Phe Phe Thr Ala Asp Asp Val Asp
                85                  90                  95

tat att atg aac gaa tat aaa aaa ctg aaa gcg cgc ccg ggc ctg gcg      336
Tyr Ile Met Asn Glu Tyr Lys Lys Leu Lys Ala Arg Pro Gly Leu Ala
            100                 105                 110
```

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gaa atg atg cag acc ctg cgc gat ggc ggc ttt gaa gtg tgg tgc tgc      384
Glu Met Met Gln Thr Leu Arg Asp Gly Gly Phe Glu Val Trp Cys Cys
        115                 120                 125

agc gat gcg aac gtg gat cgc gtg aaa ggc tat ttt gat aac gcg ggc      432
Ser Asp Ala Asn Val Asp Arg Val Lys Gly Tyr Phe Asp Asn Ala Gly
    130                 135                 140

gtg gaa atg ccg ctg gat cat att ctg agc gcg gat atg gtg aaa gcg      480
Val Glu Met Pro Leu Asp His Ile Leu Ser Ala Asp Met Val Lys Ala
145                 150                 155                 160

ggc aaa ccg gaa gcg gcg gtg tat aaa ttt gcg cgc gaa aaa gcg ggc      528
Gly Lys Pro Glu Ala Ala Val Tyr Lys Phe Ala Arg Glu Lys Ala Gly
                165                 170                 175

agc gat cag ccg ggc gaa gtg agc gtg ttt gcg gcg agc cat gcg tgg      576
Ser Asp Gln Pro Gly Glu Val Ser Val Phe Ala Ala Ser His Ala Trp
            180                 185                 190

gat tgc gcg gcg gcg aaa gcg gcg ggc ttt ctg acc gcg tat acc acc      624
Asp Cys Ala Ala Ala Lys Ala Ala Gly Phe Leu Thr Ala Tyr Thr Thr
        195                 200                 205

acc tat gaa tat gat gaa tgc gaa gtg att ttt ggc aaa agc gat ctg      672
Thr Tyr Glu Tyr Asp Glu Cys Glu Val Ile Phe Gly Lys Ser Asp Leu
    210                 215                 220

gtg gcg ccg gat ctg gtg agc ctg ggc aaa ggc att gtg gaa aaa tgg      720
Val Ala Pro Asp Leu Val Ser Leu Gly Lys Gly Ile Val Glu Lys Trp
225                 230                 235                 240

ggc aaa aaa                                                          729
Gly Lys Lys


<210> SEQ ID NO 68
<211> LENGTH: 243
<212> TYPE: PRT
<213> ORGANISM: Cryptococcus neoformans

<400> SEQUENCE: 68

Met Pro Ser Val Val Phe Asp Val Val Gly Thr Cys Phe Ser Tyr Asp
1               5                   10                  15

Asn Gly Ala Glu Ala Leu Gln Ala Arg Leu Gly Pro Lys Leu Ala Lys
            20                  25                  30

Tyr Gly Ile Pro Ser Lys Leu Leu Phe Tyr Ser Trp Val Cys Ser Thr
        35                  40                  45

Glu Arg Asp Tyr Ser Tyr Leu Ser Gln Ile Lys Gln Tyr Lys Ala Phe
    50                  55                  60

Phe Ala Ile Leu Ser Asn Thr Leu Thr Arg Val Leu Phe Gln Ala Gly
65                  70                  75                  80

Val Pro Val Glu Ala Leu Asp Asp Phe Phe Thr Ala Asp Asp Val Asp
                85                  90                  95

Tyr Ile Met Asn Glu Tyr Lys Lys Leu Lys Ala Arg Pro Gly Leu Ala
            100                 105                 110

Glu Met Met Gln Thr Leu Arg Asp Gly Gly Phe Glu Val Trp Cys Cys
        115                 120                 125

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

Val Glu Met Pro Leu Asp His Ile Leu Ser Ala Asp Met Val Lys Ala
145                 150                 155                 160

Gly Lys Pro Glu Ala Ala Val Tyr Lys Phe Ala Arg Glu Lys Ala Gly
                165                 170                 175

Ser Asp Gln Pro Gly Glu Val Ser Val Phe Ala Ala Ser His Ala Trp
            180                 185                 190
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Asp Cys Ala Ala Ala Lys Ala Ala Gly Phe Leu Thr Ala Tyr Thr Thr
        195                 200                 205

Thr Tyr Glu Tyr Asp Glu Cys Glu Val Ile Phe Gly Lys Ser Asp Leu
    210                 215                 220

Val Ala Pro Asp Leu Val Ser Leu Gly Lys Gly Ile Val Glu Lys Trp
225                 230                 235                 240

Gly Lys Lys
```

What is claimed is:

1. A method of testing compounds for activity to inhibit germination of spores, the method comprising:

(a) providing bacterial, fungal, or plant spores transformed to contain and express a detectable marker, wherein the marker when expressed, is operationally linked to a spore-specific or yeast-specific protein, in a medium and under environmental conditions in which the spores will germinate, and measuring a first signal output generated by the marker prior to the spores initiating germination;

(b) contacting the spores of step (a) with a compound whose activity to inhibit germination of spores is to be measured;

(c) incubating the spores of step (b) under environmental conditions and for a time wherein spores not treated with the compound will germinate; and

(d) determining extent of germination of the spores by measuring a second signal output generated by the marker, wherein a difference between the first signal output and the second signal output is proportional to the extent of germination of the spores.

2. The method of claim **1**, wherein the spores of step (a) are of a genus selected from the group consisting of *Histoplasma, Blastomyces, Aspergillus, Coccidioides, Sporothrix, Penicillium*, and *Cryptococcus.*

3. The method of claim **1**, wherein the spores of step (a) are a species selected from the group consisting of *Histoplasma capsulatum, Blastomyces dermatitidis, Aspergillus fumigatus, Coccidioides immitis, Sporothrix schenkii, Penicillium marneffei*, and *Cryptococcus neoformans.*

4. The method of claim **1**, wherein the detectable marker, when expressed, is a fluorophore or a chemiluminescent marker.

5. A method of testing compounds for activity to inhibit germination of spores, the method comprising:

(a) providing bacterial, fungal, or plant spores transformed to contain and express a detectable marker, wherein the marker when expressed, is operationally linked to a gene selected from the group consisting of SEQ. ID. NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 30, 31, 33, and 35, in a medium and under environmental conditions in which the spores will germinate, and measuring a first signal output generated by the marker prior to the spores initiating germination, wherein the detectable marker, when expressed, is a fluorophore or a chemiluminescent marker;

(b) contacting the spores of step (a) with a compound whose activity to inhibit germination of spores is to be measured;

(c) incubating the spores of step (b) under environmental conditions and for a time wherein spores not treated with the compound will germinate; and

(d) determining extent of germination of the spores by measuring a second signal output generated by the marker, wherein a difference between the first signal output and the second signal output is proportional to the extent of germination of the spores.

6. The method of claim **4**, wherein the spores of step (a) are of a genus selected from the group consisting of *Histoplasma, Blastomyces, Aspergillus, Coccidioides, Sporothrix, Penicillium*, and *Cryptococcus.*

7. The method of claim **4**, wherin the spores of step (a) are a species selected from the group consisting of *Histoplasma capsulatum, Blastomyces dermatitidis, Aspergillus fumigatus, Coccidioides immitis, Sporothrix schenkii, Penicillium marneffei*, and *Cryptococcus neoformans.*

8. The method of claim **1**, wherein the detectable marker, when expressed, is a fluorophore or a chemiluminescent marker.

9. The method of claim **1**, wherein the detectable marker, when expressed, is luciferase.

10. The method of claim **1**, wherein the detectable marker, when expressed, is luciferase.

11. A method of testing compounds for activity to inhibit germination of spores, the method comprising:

(a) providing bacterial, fungal, or plant spores transformed to contain and express a detectable marker, wherein the marker when expressed, is operationally linked to a gene encoding a spore-specific protein selected from the group consisting of XP_567740.1 (SEQ. ID. NO: 2), XP_566791.1 (SEQ. ID. NO: 4), XP_570303.1 (SEQ. ID. NO: 6), XP_571089.1 (SEQ. ID. NO: 8), XP_571997.1 (SEQ. ID. NO: 10), XP_569295.1 (SEQ. ID. NO: 12), XP_569173.1 (SEQ. ID. NO: 14), XP_569068.1 (SEQ. ID. NO: 16), XP_569336.1 (SEQ. ID. NO: 18), XP_567136.1 (SEQ. ID. NO: 20), XP_568990.1 (SEQ. ID. NO: 22), XP_570610.1 (SEQ. ID. NO: 24), XP_571921.1 (SEQ. ID. NO: 26), XP_572925.1 (SEQ. ID. NO: 28), XP_570796.1 (SEQ. ID. NO: 30), XP_571548.1 (SEQ. ID. NO: 32), XP_570447.1 (SEQ. ID. NO: 34), and XP_571343.1 (SEQ. ID. NO: 36), in a medium and under environmental conditions in which the spores will germinate, and measuring a first signal output generated by the marker prior to the spores initiating germination;

(b) contacting the spores of step (a) with a compound whose activity to inhibit germination of spores is to be measured;

(c) incubating the spores of step (b) under environmental conditions and for a time wherein spores not treated with the compound will germinate; and

(d) determining extent of germination of the spores by measuring a second signal output generated by the marker, wherein a difference between the first signal output and the second signal output is proportional to the extent of germination of the spores.

12. A method of testing compounds for activity to inhibit germination of spores, the method comprising:

(a) providing bacterial, fungal, or plant spores transformed to contain and express a detectable marker, wherein the marker when expressed, is operationally linked to a gene selected from the group consisting of SEQ. ID. NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 30, 31, 33, and 35, in a medium and under environmental conditions in which the spores will germinate, and measuring a first signal output generated by the marker prior to the spores initiating germination;

(b) contacting the spores of step (a) with a compound whose activity to inhibit germination of spores is to be measured;

(c) incubating the spores of step (b) under environmental conditions and for a time wherein spores not treated with the compound will germinate; and

(d) determining extent of germination of the spores by measuring a second signal output generated by the marker, wherein a difference between the first signal output and the second signal output is proportional to the extent of germination of the spores.

13. The method of claim **12**, wherein the marker, when expressed, is operationally connected to a protein encoded by gene CNK01510 (SEQ. ID. NO: 1).

14. A method of testing compounds for activity to inhibit germination of spores, the method comprising:

(a) providing bacterial, fungal, or plant spores transformed to contain and express a detectable marker, wherein the marker is operationally linked to a spore-specific or yeast-specific protein, in a medium and under environmental conditions in which the spores will germinate, and measuring a first signal output generated by the marker prior to the spores initiating germination;

(b) contacting the spores of step (a) with a compound whose activity to inhibit germination of spores is to be measured;

(c) incubating the spores of step (b) under environmental conditions and for a time wherein spores not treated with the compound will germinate;

(d) determining extent of germination of the spores by measuring a second signal output generated by the marker, wherein a difference between the first signal output and the second signal output is proportional to the extent of germination of the spores, and

(e) plotting area and aspect ratio of the spores and any germinated cells after the incubation of step (c).

15. A method of testing compounds for activity to inhibit germination of spores, the method comprising:

(a) providing bacterial, fungal, or plant spores transformed to contain and express a detectable marker, wherein the marker when expressed, is operationally linked to a gene encoding a spore-specific protein selected from the group consisting of XP_567740.1 (SEQ. ID. NO: 2), XP_566791.1 (SEQ. ID. NO: 4), XP_570303.1 (SEQ. ID. NO: 6), XP_571089.1 (SEQ. ID. NO: 8), XP_571997.1 (SEQ. ID. NO: 10), XP_569295.1 (SEQ. ID. NO: 12), XP_569173.1 (SEQ. ID. NO: 14), XP_569068.1 (SEQ. ID. NO: 16), XP_569336.1 (SEQ. ID. NO: 18), XP_567136.1 (SEQ. ID. NO: 20), XP_568990.1 (SEQ. ID. NO: 22), XP_570610.1 (SEQ. ID. NO: 24), XP_571921.1 (SEQ. ID. NO: 26), XP_572925.1 (SEQ. ID. NO: 28), XP_570796.1 (SEQ. ID. NO: 30), XP_571548.1 (SEQ. ID. NO: 32), XP_570447.1 (SEQ. ID. NO: 34), and XP_571343.1 (SEQ. ID. NO: 36)), in a medium and under environmental conditions in which the spores will germinate, and measuring a first signal output generated by the marker prior to the spores initiating germination, wherein the detectable marker, when expressed, is a fluorophore or a chemiluminescent marker;

(b) contacting the spores of step (a) with a compound whose activity to inhibit germination of spores is to be measured;

(c) incubating the spores of step (b) under environmental conditions and for a time wherein spores not treated with the compound will germinate; and

(d) determining extent of germination of the spores by measuring a second signal output generated by the marker, wherein a difference between the first signal output and the second signal output is proportional to the extent of germination of the spores.

16. The method of claim **5**, wherein the marker, when expressed, is operationally connected to a protein encoded by gene CNK01510 (SEQ. ID. NO: 1).

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