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심사청구일자 없음

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(71) 출원인

부타맥스 어드밴스드 바이오퓨얼스 엘엘씨

미국 19880 델라웨어주 윌밍톤 파우더 밀 로드
200 익스페리멘탈 스테이션 비268/알226

(72) 발명자

안토니, 래리, 카메론

미국 19014 펜실베이니아주 아스톤 코리 레인 501

마지오-홀, 로리 앤

미국 19810 델라웨어주 윌밍톤 노스 록필드 드라
이브 3413

(뒷면에 계속)

(74) 대리인

양영준, 양영환, 김영

전체 청구항 수 : 총 24 항

(54) 효모에서 증가된 이중성 Fe-S 효소 활성

(57) 요약

효모 균주는 그의 활성을 위해 Fe-S 클러스터의 결함을 필요로 하는 이중성 단백질의 증가된 활성을 갖도록 조작되었다. 효모 균주는 내인성 Fe-S 단백질의 감소된 활성을 갖는다. 이중성 진균류 또는 식물 2Fe-2S 다이하이드록시-산 탈수효소 및 Fe-S 프로판다이올 탈수효소 반응화효소의 활성은 발린, 아이소루신, 루신, 판토텐산(비타민 B5), 아이소부탄올, 2-부타논 및 2-부탄올과 같은 이들 효소를 포함하는 생합성 경로를 이용해 제조되는 생성물의 증가된 생성을 위해 증가되었다.

(72) 발명자

로트만, 스티븐, 캐리

미국 19809 델라웨어주 월링톤 킨린 드라이브 1311

툼, 진-프랑코이스

미국 19803 델라웨어주 월링톤 하버힐 로드 627

특허청구의 범위

청구항 1

적어도 하나의 이중성 Fe-S 클러스터 단백질을 포함하는 재조합 효모 숙주 세포로서, 여기서, 효모 숙주는 적어도 하나의 내인성 Fe-S 클러스터 단백질의 감소된 발현을 갖는 재조합 효모 숙주 세포.

청구항 2

제 1 항에 있어서, 적어도 하나의 내인성 Fe-S 클러스터 단백질을 인코딩하는 유전자에 분열을 포함하는 재조합 효모 세포.

청구항 3

제 1 항에 있어서, 내인성 Fe-S 클러스터 단백질이 다이하이드록시-산 탈수효소, 아이소프로필말레이트 탈수효소, 설파이트 환원효소, 글루타메이트 탈수소효소, 비오틴 합성효소, 아코니테이즈, 호모아코니테이즈, 리포에이트 합성효소, 페레독신 숙성화, NADH 유비퀴논 산화환원효소, 석시네이트 탈수소효소, 유비퀴놀-시토크롬-c 환원효소, ABC 단백질 Rli1, NTPase Nbp35, 및 수소화효소-형 단백질로 이루어진 군으로부터 선택되는, 재조합 효모 숙주 세포.

청구항 4

제 1 항에 있어서, 효모가 사카로마이세스(Saccharomyces), 스킴조사카로마이세스(Schizosaccharomyces), 한센룰라(Hansenula), 칸디다, 클루이베로마이세스(Kluyveromyces), 야로위아(Yarrowia) 및 피치아(Pichia)로 이루어진 군으로부터 선택되는, 재조합 효모 숙주 세포.

청구항 5

제 1 항에 있어서, 내인성 Fe-S 단백질이 미토콘드리아에서 발현되는, 재조합 효모 숙주 세포.

청구항 6

제 1 항에 있어서, 내인성 Fe-S 클러스터 단백질이 하기로 이루어진 군으로부터 선택되는 활성을 갖는, 재조합 효모 숙주 세포: 다이하이드록시-산 탈수효소 및 아이소프로필말레이트 탈수효소 활성.

청구항 7

제 6 항에 있어서, 숙주 세포가 서열 번호:114에서 나타낸 바와 같은 아미노산 서열을 갖는 폴리펩타이드를 인코딩하는 유전자를 발현하는 사카로마이세스인, 재조합 효모 숙주 세포.

청구항 8

제 1 항에 있어서, 적어도 하나의 이중성 Fe-S 클러스터 단백질이 진균류 2Fe-2S 다이하이드록시-산 탈수효소 및 식물 2Fe-2S 다이하이드록시-산 탈수효소로 이루어진 군으로부터 선택되는, 재조합 효모 숙주 세포.

청구항 9

제 8 항에 있어서, 이중성 진균류 또는 식물 2Fe-2S 클러스터 다이하이드록시-산 탈수효소가 시토플라스마에서 발현되는, 재조합 효모 숙주 세포.

청구항 10

제 8 항에 있어서, 이중성 진균류 또는 식물 2Fe-2S 클러스터 다이하이드록시-산 탈수효소가 표 9의 프로파일 HMM을 $< 10^{-5}$ 의 E 값과 일치시키는 아미노산 서열을 갖는 폴리펩타이드이고, 여기서, 폴리펩타이드가 서열 번호:179에 상응하는 스트렙토코쿠스 뮤탄스(Streptococcus mutans) DHAD 효소의 아미노산 서열에서 위치 56, 129, 및 201에 상응하는 모든 3개의 보존된 시스테인을 추가로 포함하는, 재조합 효모 숙주 세포.

청구항 11

제 8 항에 있어서, 이중성 진균류 또는 식물 2Fe-2S 클러스터 다이하이드록시-산 탈수효소가 서열 번호:46, 48,

50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150 및 152로 이루어진 군으로부터 선택되는 아미노산 서열에 적어도 약 95% 서열 동일성을 갖는 아미노산 서열을 갖는 폴리펩타이드인, 재조합 효모 숙주 세포.

청구항 12

제 8 항에 있어서, 이중성 진균류 또는 식물 2Fe-2S 클러스터 다이하이드록시-산 탈수효소가 단백질 서열의 전장에 걸쳐 갭 페널티(GAP PENALTY)=10, 갭 길이 페널티(GAP LENGTH PENALTY)=0.1, 및 단백질 중량 매트릭스의 고넷(Gonnet) 250 시리즈의 디폴트 파라미터(default parameter)를 사용하는 클러스탈 W 정렬 방법을 이용해 서열 번호:114에 대해 적어도 약 90% 동일한 아미노산 서열을 갖는 폴리펩타이드인, 재조합 효모 숙주 세포.

청구항 13

제 10 항 내지 제 12 항 중 어느 한 항에 있어서, 세포가 아이소부탄올 생합성 경로를 포함하는, 재조합 숙주 세포.

청구항 14

제 13 항에 있어서, 세포가 아이소부탄올을 생성하는, 재조합 숙주 세포.

청구항 15

아이소부탄올이 생성되는 조건 하에 제 14 항의 재조합 효모 숙주 세포를 배양하는 것을 포함하는, 아이소부탄올의 생성 방법.

청구항 16

제 1 항에 있어서, 적어도 하나의 이중성 Fe-S 클러스터 단백질이 Fe-S 프로판다이올 탈수효소 반응화효소(reactivase) 활성을 갖는, 재조합 효모 숙주 세포.

청구항 17

제 16 항에 있어서, Fe-S 프로판다이올 탈수효소 반응화효소 활성을 갖는 적어도 하나의 이중성 Fe-S 클러스터 단백질이 단백질 서열의 전장에 걸쳐 갭 페널티=10, 갭 길이 페널티=0.1, 및 단백질 중량 매트릭스의 고넷 250 시리즈의 디폴트 파라미터를 사용하는 클러스탈 W 정렬 방법을 이용해 서열 번호:44에 대해 적어도 약 90% 동일한 아미노산 서열을 갖는 프로판다이올 탈수효소 반응화효소인, 재조합 숙주 세포.

청구항 18

제 16 항 또는 제 17 항에 있어서, 세포가 2-부탄올을 생성하는, 재조합 숙주 세포.

청구항 19

제 16 항 또는 제 17 항에 있어서, 세포가 2-부타논을 생성하는, 재조합 숙주 세포.

청구항 20

제 18 항에 있어서, 세포가 2-부탄올 생합성 경로를 포함하는, 재조합 숙주 세포.

청구항 21

제 19 항에 있어서, 세포가 2-부타논 생합성 경로를 포함하는, 재조합 숙주 세포.

청구항 22

하기 단계를 포함하는, 2,3-다이하이드록시아이소발레레이트의 α-케토아이소발레레이트로의 전환 방법:

a) (1) 2Fe-2S 다이하이드록시-산 탈수효소를 인코딩하는 적어도 하나의 이중성 유전자를 포함하는 재조합 효모 숙주 세포(여기서, 재조합 효모 숙주 세포는 적어도 하나의 내인성 Fe-S 클러스터 단백질의 감소된 활성을 가짐); 및 (2) 2,3-다이하이드록시아이소발레레이트의 공급원을 제공하는 단계; 및

b) 2,3-다이하이드록시아이소발레레이트가 숙주 세포에 의해 α -케토아이소발레레이트로 전환되는 조건 하에, (a)의 재조합 숙주 세포를 2,3-다이하이드록시아이소발레레이트의 상기 공급원과 함께 배양하는 단계.

청구항 23

2-부타논이 생성되는 조건 하에 제 21 항의 재조합 효모 숙주 세포를 배양하는 단계를 포함하는, 2-부타논의 생성 방법.

청구항 24

하기 단계를 포함하는, 2,3-부탄다이올의 2-부타논으로의 전환 방법:

a) (1) Fe-S 프로판다이올 탈수효소 반응화효소를 인코딩하는 적어도 하나의 이중성 유전자를 포함하는 재조합 효모 숙주 세포(여기서, 재조합 효모 숙주 세포는 적어도 하나의 내인성 Fe-S 클러스터 단백질의 감소된 활성을 가짐); 및 (2) 2,3-부탄다이올의 공급원을 제공하는 단계; 및

b) 2,3-부탄다이올이 숙주 세포에 의해 2-부타논으로 전환되는 조건 하에, (a)의 재조합 숙주 세포를 2,3-부탄다이올의 상기 공급원과 함께 배양하는 단계.

명세서

기술분야

[0001] 관련 출원과의 상호 참조

[0002] 본 출원은 2008년 9월 29일에 출원된 미국 가출원 제 61/100,801 호 및 2008년 9월 29일에 출원된 제 61/100,806 호에 관한 것이고, 이를 우선권으로 주장한다. 각각의 전체는 본원에 참조로서 삽입된다.

[0003] 본 발명은 산업 미생물학 분야 및 활성을 위해 철-황 클러스터가 필요한 단백질의 발현에 관한 것이다. 더욱 구체적으로는, 효모 세포에서의 이중성 Fe-S 단백질 활성의 발현은 특정 숙주 유전자 불활성화를 통해 향상된다.

배경기술

[0004] 시판의 제품의 발효 생성을 위한 효모의 조작(Engineering of yeast)은 활동적이고 성장하는 분야이다. 일부 생성물의 생합성을 위해 조작된 효소 경로는 활성을 위해 철-황(Fe-S) 클러스터의 결합을 필요로 하는 효소를 포함한다. 다이하이드록시-산 탈수효소(DHAD)는 한 예이다. DHAD는 발린, 아이소루신, 루신 및 판토텐산(비타민 B5)을 생성하는 자연 발생 생합성 경로의 일부이다. DHAD 활성의 증가된 발현은 분지쇄 아미노산 또는 판토텐산의 증진된 미생물 생성에 바람직하다. 또한, 2,3-다이하이드록시아이소발레레이트에서 α -케토아이소발레레이트로의 DHAD 촉매화된 전환은 동시계속출원인 미국 특허 공보 제 US 20070092957 A1 호에서 개시된 복합 아이소부탄올 생합성 경로에서 보편적인 단계이다. 아이소부탄올의 생성을 위한 재조합 미생물의 조작이 거기에 개시되어 있고, 이는 연료 첨가제로서 유용하고, 이의 이용가능성은 석유화학 연료에 대한 요구를 감소시킬 수 있다.

[0005] 다이올 탈수효소는 동시계속출원인 미국 특허 공보 제 US 2007-0292927A1 호에서 개시된 2-부타논 및 2-부탄올의 생성을 위한 생합성 경로에서 효소 활성을 제공한다. 그의 조효소 B-12 독립성으로 인해 이러한 경로에서 발현하기에 유용한 부탄다이올 탈수효소는 미국 특허 공보 제 US20090155870 호에서 개시된다. B12-독립적 부탄다이올 탈수효소의 활성에 필요한 Fe-S 클러스터 단백질인 다이올 탈수효소 반응화효소(reactivase)는 또한, 미국 특허 공보 제 US20090155870 호에서 개시된다. 메틸 에틸 케톤(MEK)이라고도 하는 2-부타논은 광범위하게 사용되는 용매, 추출용 용제(extractant) 및 산화 반응의 활성화제뿐만 아니라, 2-부탄올의 화학적 합성을 위한 기질이다. 2-부탄올은 연료 첨가제로서 유용하고, 이의 이용가능성은 석유화학 연료를 위한 요구를 감소시킬 수 있다.

[0006] 효소를 함유하는 Fe-S 클러스터를 포함한 경로에서 합성된 화합물의 향상된 생성을 위해, 흥미 있는 생성 숙주에서의 이러한 효소 활성을 높은 수준으로 발현시킬 수 있는 숙주 세포를 제공하는 것이 바람직하다. 많은 통상의 관련 있는 박테리아 및 효모가 Fe-S 클러스터 함유 단백질의 활성을 발현시킬 수 있는 한편, 이러한 활성은 도입된 생합성 경로를 증진시키는데 통상적으로 유용한 것보다 한참 미만의 수준에 있다. 결과적으로, Fe-S 클러스터 함유 단백질의 활성을 Fe-S 요건을 갖는 도입된 경로를 증진시키기에 충분히 높은 수준에서 발현시킬

수 있는 숙주 세포의 발견을 위한 필요성이 존재한다. 이중성 Fe-S 클러스터 함유 효소의 높은 기능성 발현을 수득하는 것은 Fe-S 클러스터 요건으로 인해 문제가 있으며, 이는 이용가능성 및 클러스터의 아포-단백질로의 적절한 로딩을 수반한다.

발명의 내용

- [0007] 적어도 하나의 이중성 Fe-S 클러스터 단백질을 포함하는 재조합 효모 숙주 세포가 본원에서 제공되며, 여기서, 효모 숙주는 적어도 하나의 내인성 Fe-S 클러스터 단백질의 발현을 감소시킨다. 재조합 효모 세포는 아이소부탄올, 2-부탄올 및 2-부타논을 포함하는 생성물의 생성을 위한 적합한 조건 하에 배양될 수 있다.
- [0008] 한 측면에서, 재조합 효모 세포는 적어도 하나의 내인성 Fe-S 클러스터 단백질을 인코딩하는 유전자에서 분열(disruption)을 포함한다.
- [0009] 또다른 측면에서, 내인성 Fe-S 클러스터 단백질은 다이하이드록시-산 탈수효소, 아이소프로필말레이트 탈수효소, 설과이트 환원효소, 글루타메이트 탈수소효소, 비오틴 합성효소, 아코니테이즈(acetate kinase), 호모아코니테이즈, 리포에이트(lipoate) 합성효소, 페레독신(ferredoxin) 숙성화(maturation), NADH 유비퀴논 산화환원 효소, 석시네이트 탈수소효소, 유비퀴놀-시토크롬-c 환원효소, ABC 단백질 Rli1, NTPase Nbp35, 및 수소화효소-형 단백질로 이루어진 군으로부터 선택된다.
- [0010] 또다른 측면에서, 효모는 사카로마이세스(Saccharomyces), 스킴조사카로마이세스(Schizosaccharomyces), 한센룰라(Hansenula), 칸디다, 클루이베로마이세스(Kluyveromyces), 야로위아(Yarrowia) 및 피치아(Pichia)로 이루어진 군으로부터 선택된다.
- [0011] 또다른 측면에서, 내인성 Fe-S 단백질은 미토콘드리아에서 발현되고, 또다른 실시 양태에서, 내인성 Fe-S 클러스터 단백질은 하기로 이루어진 군으로부터 선택되는 활성을 갖는다: 다이하이드록시-산 탈수효소 및 아이소프로필말레이트 탈수효소 활성.
- [0012] 또다른 측면에서, 숙주 세포는 서열 번호:114로 나타낸 바와 같은 아미노산 서열을 갖는 폴리펩타이드를 인코딩하는 유전자를 발현하는 사카로마이세스이다.
- [0013] 일부 실시 양태에서, 적어도 하나의 이중성 Fe-S 클러스터 단백질은 진균류 2Fe-2S 다이하이드록시-산 탈수효소 및 식물 2Fe-2S 다이하이드록시-산 탈수효소로 이루어진 군으로부터 선택된다. 한 실시 양태에서, 이중성 진균류 또는 식물 2Fe-2S 클러스터 다이하이드록시-산 탈수효소는 시토크롬에서 발현된다. 한 실시 양태에서, 이중성 진균류 또는 식물 2Fe-2S 클러스터 다이하이드록시-산 탈수효소는 표 9의 프로파일(Profile) HMM을 $< 10^{-5}$ 의 E 값과 함께 매칭시키는 아미노산 서열을 갖는 폴리펩타이드로서, 여기서, 폴리펩타이드는 추가로, 모든 3개의 보존된 시스테인을 포함하며, 이는 서열 번호:179에 상응하는 스트렙토코쿠스(Streptococcus) 뮤탄스(mutans) DHAD 효소의 아미노산 서열에서 위치 56, 129, 및 201에 상응한다. 한 실시 양태에서, 이중성 진균류 또는 식물 2Fe-2S 클러스터 다이하이드록시-산 탈수효소는 서열 번호:46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150 및 152로 이루어진 군으로부터 선택되는 아미노산 서열에 대해 적어도 약 95%의 서열 동일성을 갖는 아미노산 서열을 갖는 폴리펩타이드이다. 한 실시 양태에서, 이중성 진균류 또는 식물 2Fe-2S 클러스터 다이하이드록시-산 탈수효소는 단백질 서열의 전장에 걸쳐 갭 페널티(GAP PENALTY)=10, 갭 길이 페널티(GAP LENGTH PENALTY)=0.1, 및 단백질 중량 매트릭스의 고넷(Gonnet) 250 시리즈의 디폴트 파라미터(default parameter)를 사용하는 클러스탈 W 정렬 방법을 이용해 서열 번호:114에 대해 적어도 약 90% 동일한 아미노산 서열을 갖는 폴리펩타이드이다.
- [0014] 또다른 측면에서, 2,3-다이하이드록시아이소발레레이트에서 α -케토아이소발레레이트로의 전환 방법이 제공되며, 상기 방법은 하기 단계를 포함한다:
- [0015] a) (1) 2Fe-2S 다이하이드록시-산 탈수효소를 인코딩하는 적어도 하나의 이중성 유전자를 포함하는 재조합 효모 숙주 세포(여기서, 재조합 효모 숙주 세포는 적어도 하나의 내인성 Fe-S 클러스터 단백질의 감소된 활성을 가짐); 및 (2) 2,3-다이하이드록시아이소발레레이트의 공급원을 제공하는 단계; 및
- [0016] b) 2,3-다이하이드록시아이소발레레이트가 숙주 세포에 의해 α -케토아이소발레레이트로 전환되는 조건 하에 (a)의 재조합 숙주 세포를 상기 2,3-다이하이드록시아이소발레레이트의 공급원과 함께 배양하는 단계.
- [0017] 또다른 측면에서, 2,3-부탄다이올에서 2-부타논으로의 전환 방법이 제공되며, 상기 방법은 하기 단계를 포함한

다:

- [0018] a) (1) Fe-S 프로판다이올 탈수효소 반응화효소를 인코딩하는 적어도 하나의 이중성 유전자를 포함하는 재조합 효모 숙주 세포(여기서, 재조합 효모 숙주 세포는 적어도 하나의 내인성 Fe-S 클러스터 단백질의 감소된 활성을 가짐); 및 (2) 2,3-부탄다이올의 공급원을 제공하는 단계; 및
- [0019] b) 2,3-부탄다이올이 숙주 세포에 의해 2-부타논으로 전환되는 조건 하에 (a)의 재조합 숙주 세포를 2,3-부탄다이올의 상기 공급원과 함께 배양하는 단계.
- [0020] 또한, 아이소부탄올이 생성되는 조건 하에 본원에서 개시된 재조합 효모 숙주 세포를 배양하는 단계를 포함하는, 아이소부탄올의 생성 방법이 제공된다.
- [0021] 다른 실시 양태에서, 적어도 하나의 이중성 Fe-S 클러스터 단백질은 Fe-S 프로판다이올 탈수효소 반응화효소 활성을 갖는다. 일부 실시 양태에서, Fe-S 프로판다이올 탈수효소 반응화효소 활성을 갖는 적어도 하나의 이중성 Fe-S 클러스터 단백질은 단백질 서열의 전장에 걸쳐 갭 페널티=10, 갭 길이 페널티=0.1, 및 단백질 중량 매트릭스의 고넷 250 시리즈의 디폴트 파라미터를 사용하는 클러스탈 W 정렬 방법을 이용해 서열 번호:44에 나타난 바와 같은 아미노산 서열에 적어도 약 90% 동일한 아미노산 서열을 갖는 프로판다이올 탈수효소 반응화효소이다.
- [0022] 일부 실시 양태에서, 세포는 2-부탄올을 생성하고, 일부 실시 양태에서, 세포는 2-부타논을 생성한다. 일부 실시 양태에서, 세포는 2-부탄올 생합성 경로를 포함하고, 일부 실시 양태에서, 세포는 2-부타논 생합성 경로를 포함한다.

도면의 간단한 설명

- [0023] 도면의 간단한 설명 및 서열 설명

본 발명은 하기 상세한 설명, 도면 및 본원의 일부를 형성하는 첨부하는 서열 설명으로부터 더욱 완전히 이해될 수 있다.

<도 1>

도 1은 아이소부탄올 생성에 대한 생합성 경로를 보여준다.

<도 2>

도 2는 2-부타논 및 2-부탄올 생성에 대한 생합성 경로를 보여준다.

표 9는 실시예 1에서 기술된 바와 같이 제조된 검정되는 기능을 갖는 효소를 바탕으로 한 다이하이드록시-산 탈수효소에 대한 프로파일 HMM의 표이다. 표 9는 여기서 전자적으로 제출되고, 본원에 참조로서 삽입된다.

하기 서열은 37 C.F.R. 1.821-1.825 ("뉴클레오타이드 서열 및/또는 아미노산 서열 개시를 포함하는 특허 출원에 관한 요건 - 서열 규정")("Requirements for Patent Applications Containing Nucleotide Sequences and/or Amino Acid Sequence Disclosures - the Sequence Rules")에 준거하여, 세계 지적 재산 기구(WIPO) 표준 ST.25(1998)와 EPO 및 PCT의 서열 목록 요건(규정 5.2 및 49.5(a-bis), 및 관리 지시의 섹션 208 및 별첨 C)(Rules 5.2 and 49.5(a-bis), and Section 208 and Annex C of the Administrative Instructions)에 부합하는 것이다. 뉴클레오타이드 및 아미노산 서열 데이터에 사용된 기호 및 체제는 37 C.F.R. § 1.822에 제시된 규정을 준수한다.

<표 1>

불활성화 표적 Fe-S 단백질 인코딩 유전자

개체 및 유전자	서열 번호 핵산	서열 번호 펩타이드
사카로마이세스 세레비시애(cerevisiae) LEU1	1	2
스키조사카로마이세스 폼베(pombe) LEU1	3	4
칸디다 갈브라타(galbrata) CBS 138 LEU1	5	6
칸디다 알비칸스(albicans) SC 5314 LEU1	7	8
클루이베로마이세스 락티스(lactis) LEU1	9	10
야로위아 리폴리티카(lipolytica) LEU1	11	12
피치아 스티피티스(stipitis) LEU1	13	14
사카로마이세스 세레비시애 YJM789 ILV3	111	112
스키조사카로마이세스 폼베 ILV3	93	94
칸디다 갈브라타 CBS 138 ILV3	107	108
칸디다 알비칸스 SC5314 ILV3	101	102
클루이베로마이세스 락티스 ILV3	113	114
야로위아 리폴리티카 ILV3	105	106
피치아 스티피티스 CBS 6054 ILV3	103	104
사카로마이세스 세레비시애 ACO1	153	154
스키조사카로마이세스 폼베 (염색체 II) ACO1	155	156
스키조사카로마이세스 폼베 (염색체 I) ACO1	157	158
클루이베로마이세스 락티스 NRRL Y-1140 ACO1	159	160
칸디다 알비칸스 SC5314 ACO1	161	162
야로위아 리폴리티카 CLIB122 ACO1	163	164
피치아 스티피티스 CBS 6054 ACO1	165	166
칸디다 글라브라타 CBS138 (염색체 F) ACO1	167	168
칸디다 글라브라타 CBS138 (염색체 D) ACO1	169	170
칸디다 글라브라타 CBS138 (염색체 K) ACO1	171	172

<표 2>

표 1에서 나타난 것 이외에 진균류 및 식물 2Fe-2S DHAD

설명	서열 번호 핵산	서열 번호 펩타이드
클라마이도모나스 레인하르트티이(<i>Chlamydomonas reinhardtii</i>)	45	46
오스트레오코쿠스 루치마리누스(<i>Ostreococcus lucimarinus</i>) CCE9901	47	48
비티스 비니페라(<i>Vitis vinifera</i>) (명명되지 않은 단백질 생성물: CAO71581.1)	49	50
비티스 비니페라 (CAN67446.1)	51	52
아라비도시스 탈리아나	53	54
오리자 사티바(<i>Oryza sativa</i>)(인디카 쿨티바(<i>indica cultivar</i>)-균)	55	56
파이스코미트렐라 파텐스 아종 파텐스(<i>Physcomitrella patens</i> subsp. <i>patens</i>)	57	58
캐토미움 글로보숨(<i>Chaetomium globosum</i>) CBS 148.51	59	60
뉴로스포라 크라사(<i>Neurospora crassa</i>) OR74A	61	62
마그나포테 그리세아(<i>Magnaporthe grisea</i>) 70-15	63	64
기베렐라 제애(<i>Gibberella zeae</i>) PH-1	65	66
아스페르길루스 니거(<i>Aspergillus niger</i>)	67	68
네오사르토르야 피세리(<i>Neosartorya fischeri</i>) NRRL 181 (XP_001266525.1)	69	70
네오사르토르야 피세리 NRRL 181 (XP_001262996.1)	71	72
아스페르길루스 니거 (An03g04520)	73	74
아스페르길루스 니거 (An14g03280)	75	76
아스페르길루스 테레우스(<i>terreus</i>) NIH2624	77	78
아스페르길루스 클라바투스(<i>clavatus</i>) NRRL 1	79	80
아스페르길루스 니둘란스(<i>nidulans</i>) FGSC A4	81	82
아스페르길루스 오리제(<i>oryzae</i>)	83	84

아엘로마이세스 캡슐라투스(<i>Ajellomyces capsulatus</i>) NAM1	85	86
콕시디오이데스 이미티스(<i>Coccidioides immitis</i>) RS	87	88
보트라이오티니아 푸켈리아나(<i>Botryotinia fuckeliana</i>) B05.10	89	90
패오스페리아 노도룸(<i>Phaeosphaeria nodorum</i>) SN15	91	92
피치아 쉐리에르몽디이(<i>guilliermondii</i>) ATCC 6260	95	96
데바료마이세스 한세나이(<i>Debaryomyces hansenii</i>) CBS767	97	98
로데로마이세스 엘롱기스포르투스(<i>Lodderomyces elongisporus</i>) NRRL YB-4239	99	100
반테르발토자이마 폴리스포라(<i>Vanderwaltozyma polyspora</i>) DSM 70294	109	110
아쉬브야 고사이피이(<i>Ashbya gossypii</i>) ATCC 10895	115	116
락카리아 비콜로(<i>Laccaria bicolor</i>) S238N-H82	117	118
코프리놉시스 시네레아 오카야마(<i>Coprinopsis cinerea okayama</i>)7#130	119	120
크립토크쿠스 네오포르만스 변이체(<i>Cryptococcus neoformans</i> var.) 네오포르만스 JEC21	121	122
유스틸라고 마이디스(<i>Ustilago maydis</i>) 521	123	124
말라세지아 글로보사(<i>Malassezia globosa</i>) CBS 7966	125	126
아스페르길루스 클라바투스 NRRL 1	127	128
네오사르토르야 피세리(<i>Neosartorya fischeri</i>) NRRL 181 (추정상(Putative))	129	130
아스페르길루스 오리제	131	132
아스페르길루스 니거(<i>An18g04160</i>)	133	134
아스페르길루스 테레우스 NIH2624	135	136
콕시디오이데스 이미티스 RS(CIMG_04591)	137	138
파라콕시디오이데스 브라질리엔시스(<i>Paracoccidioides brasiliensis</i>)	139	140
패오스페리아 노도룸 SN15	141	142
기베렐라 제애 PH-1	143	144
뉴로스포라 크라사 OR74A	145	146
코프리놉시스 시네레아 오카야마 7#130	147	148
락카리아 비콜로 S238N-H82	149	150
유스틸라고 마이디스 521	151	152

<표 3>

발현 유전자

설명	서열 번호 핵산	서열 번호 펩타이드
로세부리아 이눌리니보란스(Roseburia inulinivorans)(RdhtA)	15	43
로세부리아 이눌리니보란스 (RdhtB)	16	44
바실루스 서브틸리스(Bacillus subtilis)(alsS)	27	28
비브리오 콜레라(KARI)	35	36
슈도모나스 애루기노사(Pseudomonas aeruginosa)PAO1(KARI)	37	38
슈도모나스 플루오레센스(fluorescens) PF5(KARI)	39	40
아크로모박테르 자일로속시단스(Achromobacter xylosoxidans)(sadB)	41	42
클로스트리듐 부티리쿰(Clostridium butyricum)으로부터의 B12- 독립적 글리세롤 탈수효소	190	191
클로스트리듐 부티리쿰으로부터의 B-12 독립적 부탄다이올 탈수효소 반응 효소	192	193

서열 번호:17은 합성 rdhtAB 서열이다.

서열 번호:18-21 및 30-33은 본원의 실시예에서 기술되고 사용된 PCR, 클로닝 또는 서열화 분석을 위한 프라이머이다.

서열 번호:22는 이중 종결자 서열이다.

서열 번호:23은 사카로마이세스 세레비시애 ADH 종결자이다.

서열 번호:24는 사카로마이세스 세레비시애 CYC1 종결자이다.

서열 번호:25는 사카로마이세스 세레비시애 FBA 프로모터이다.

서열 번호:26은 사카로마이세스 세레비시애 GPM 프로모터이다.

서열 번호:29는 pNY13 벡터이다.

서열 번호:34는 사카로마이세스 세레비시애 CUP1 프로모터이다.

서열 번호:173은 클루이베로마이세스 락티스로부터의 ILV3 DHAD에 대한 코돈 최적화된 코딩 영역이다.

<표 4>

프로파일 HMM에 대해 사용된 기능적으로 확인된 DHAD

개체	서열 번호 핵산	서열 번호 펩타이드
니트로소모나스 유로파에아(Nitrosomonas europaea) ATCC 19718	174	175
시네코시스티스 종 (Synechocystis sp.) PCC 6803	176	177
스트렙토코쿠스 뮤탄스(Streptococcus mutans) UA159	178	179
스트렙토코쿠스 테모필루스(thermophilus) LMG 18311	180	181
랄스토니아 메탈리두란스(Ralstonia metallidurans) CH34	182	183
랄스토니아 유포로파(eutropha) JMP134	184	185
락토코쿠스 락티스 아종 크레모리스 (Lactococcus lactis subsp. cremoris) SK11	186	187
프라보박테리움 존소니아(Flavobacterium johnsoniae) UW101	188	189

발명을 실시하기 위한 구체적인 내용

- [0024] 내인성 Fe-S 함유 단백질의 발현이 억제 또는 분열되는 경우, 효모 숙주 세포 내 도입된 Fe-S 함유 단백질이 높은 활성 수준을 갖는다는 발견이 본원에서 개시된다. 본 발명은 Fe-S 클러스터 단백질인 적어도 하나의 이중성 단백질의 발현을 제공하도록 조작되고, 적어도 하나의 내인성 Fe-S 클러스터 단백질의 감소된 발현에 대해 조작된 재조합 효모 세포에 관한 것이다. 이들 세포에서, 이중성 Fe-S 클러스터 단백질의 활성이 향상되고, 그리하여 효소 활성을 포함하는 생합성 경로에서 제조된 생성물의 향상된 생성이 존재한다. Fe-S 단백질을 포함하는 경로로부터의 시판의 유용한 생성물의 예는 발린, 아이소루신, 루신, 판토텐산, 아이소부탄올, 2-부탄올 및 2-부탄올을 포함한다.
- [0025] 명세서 및 청구범위를 설명하기 위해 하기의 약어 및 정의를 사용한다.
- [0026] 본원에서 사용되는 바와 같이, "포함하다", "포함하는", "포함되어 있다", "포함되어 있는", "갖는다", "갖는", "함유하다" 또는 "함유하는"이라는 용어 또는 이들의 임의의 다른 변형은 배타적이지 않은 포함을 커버하고자 한다. 예를 들어, 요소들의 목록을 포함하는 조성물, 혼합물, 공정, 방법, 용품, 또는 장치는 반드시 그러한 요소만으로 제한되지는 않고, 명확하게 열거되지 않거나 그러한 조성물, 혼합물, 공정, 방법, 용품, 또는 장치에 내재적인 다른 요소를 포함할 수도 있다. 더욱이, 명백히 반대로 기술되지 않는다면, "또는"은 포괄적인 '또는'을 말하며 배타적인 '또는'을 말하는 것은 아니다. 예를 들어, 조건 A 또는 B는 하기 중 어느 하나에 의해 만족된다: A는 참(또는 존재함)이고 B는 거짓(또는 존재하지 않음), A는 거짓(또는 존재하지 않음)이고 B는 참(또는 존재함), A 및 B 모두가 참(또는 존재함).
- [0027] 또한, 본 발명의 요소 또는 성분 앞의 부정 관사("a" 및 "an")는 요소 또는 성분의 경우 (즉, 존재)의 수에 관해서는 비제한적인 것으로 의도된다. 따라서, 부정 관사("a" 및 "an")는 하나 또는 적어도 하나를 포함하는 것으로 파악되어야 하며, 요소 또는 성분의 단수형은 그 수가 명백하게 단수임을 의미하는 것이 아니라면 복수형도 포함한다.
- [0028] 본원에서 사용되는 바와 같은 용어 "발명" 또는 "본 발명"은 비제한적인 용어이며, 특정 발명의 임의의 단일의 실시 양태를 언급하는 것으로 의도되지 않고, 상세한 설명 및 청구범위에 기술된 바와 같은 모든 가능한 실시 양태를 포함한다.

- [0029] 본원에서 사용된 바와 같이, 적용된 발명의 성분 또는 반응물의 분량을 개질하는 용어 "약"은, 예를 들어, 현실에서 농축물을 제조하거나 용액을 사용함에 있어서의 통상적 측정 및 액체 취급 과정; 이들 과정에서의 우발적인 오차; 조성물을 제조하거나 방법을 실행하기 위해 적용된 성분의 제조, 공급원 또는 순도의 차이 등을 통해 발생할 수 있는 수치 분량의 변이를 말한다. 용어 "약"은 또한 특정 초기 혼합물로부터 생산된 조성물에 대한 상이한 평형 조건으로 인해 달라지는 양을 포함한다. 용어 "약"에 의한 개질 여부를 불문하고, 청구범위는 분량의 균등물을 포함한다. 한 실시 양태에서, 용어 "약"은 10%의 보고된 수치 이내, 바람직하게는 5%의 보고된 수치 내를 의미한다.
- [0030] 용어 "Fe-S 클러스터 단백질"은 철-황 클러스터를 결합하고, 그의 활성을 위해 클러스터의 결합을 필요로 하는 단백질이다.
- [0031] 용어 "2Fe-2S DHAD"는 활성을 위해 결합된 $[2\text{Fe-2S}]^{2+}$ 클러스터를 필요로 하는 DHAD 효소를 말한다.
- [0032] 용어 "Fe-S 프로판다이올 탈수효소 반응화효소"는 활성을 위해 결합된 Fe-S 클러스터를 필요로 하는 프로판다이올 탈수효소 반응화효소를 말한다.
- [0033] 용어 "아이소부탄올 생합성 경로"는 피루베이트로부터 아이소부탄올을 생성하는 효소 경로를 말한다.
- [0034] 용어 "2-부탄올 생합성 경로"는 피루베이트로부터 2-부탄올을 생성하는 효소 경로를 말한다.
- [0035] 용어 "2-부타논 생합성 경로"는 피루베이트로부터 2-부타논을 생성하는 효소 경로를 말한다.
- [0036] 여기서, 축약된 DHAD이라고도 하는 용어 "다이하이드록시-산 탈수효소"는 2,3-다이하이드록시아이소발레레이트를 α -케토아이소발레레이트로 전환시키는 효소를 말할 것이다.
- [0037] 용어 "다이올 탈수효소" 또는 "프로판다이올 탈수효소"라고도 하는 "부탄다이올 탈수효소"는 2,3-부탄다이올의 2-부타논으로의 전환을 촉매시키는 효소 활성을 갖는 폴리펩타이드(또는 폴리펩타이드들)를 말한다. 보조인자 아데노실 코발라민(조효소 B12, 또는 비타민 B12로도 알려져 있음; 비타민 B12는 또한 조효소 B12가 아닌 다른 형태의 코발라민을 말할 수 있음)을 이용하지 않는 부탄다이올 탈수효소는 Fe-S 클러스터 단백질인 다이올 탈수효소 반응화효소와의 연관성을 필요로 하는 조효소 B12-독립적 다이올 탈수효소이다. B12-독립적 다이올 탈수효소의 예는 클로스트리듐 글리콜리쿰(*Clostridium glycolicum*)(문헌[Hartmanis et al. (1986) Arch. Biochem. Biophys. 245:144-152]), 클로스트리듐 부티리쿰(단백질 서열 번호:191; 코딩 영역 서열 번호:190; 문헌[O'Brien et al. (2004) Biochemistry 43:4635-4645]), 및 로세부리아 이놀리니보란스(코딩: 서열 번호 15; 단백질: 서열 번호:43; 동시계속출원인 미국 특허 공보 제 US20090155870 호에서 개시됨)으로부터의 것을 포함한다.
- [0038] 용어 "다이올 탈수효소 반응화효소" 또는 "부탄다이올 탈수효소 반응화효소"라고도 알려져 있는 "프로판다이올 탈수효소 반응화효소"는 다이올 탈수효소에 대한 반응화 인자를 말하며, 이 효소는 촉매 동안에 불활성화를 없앤다. 조효소 B12-독립적 다이올 탈수효소와 연관된 다이올 탈수효소 반응화효소는 Fe-S 클러스터 단백질일 수 있다. 예는 클로스트리듐 글리콜리쿰(문헌[Hartmanis et al. (1986) Arch. Biochem. Biophys. 245:144-152]), 클로스트리듐 부티리쿰(단백질 서열 번호:193; 코딩 영역 서열 번호:192; 문헌[O'Brien et al. (2004) Biochemistry 43:4635-4645]), 및 로세부리아 이놀리니보란스(코딩: 서열 번호 16; 단백질: 서열 번호:44; 공동 소유이고 동시계속출원인 미국 특허 공보 제 US20090155870 호에서 개시됨)로부터의 것을 포함한다.
- [0039] 용어 "감소된 발현"은 세포 숙주 내 단백질의 발현에 적용되는 경우에서처럼 단백질의 활성이 야생형 형태(예를 들어 안티센스 기법으로서)와 비교해 저하되거나 예를 들어 유전자 분열, 결실 또는 불활성화와 비교해 실질적으로 제거된 경우의 상황을 포함할 것이다.
- [0040] 용어 "탄소 기질" 또는 "발효성 탄소 기질"은 본 발명의 숙주 유기체에 의하여 대사될 수 있는 탄소 공급원 및 특히 단당류, 올리고당류, 다당류 및 일원자-탄소(one-carbon) 기질 또는 이들의 혼합물로 이루어진 군으로부터 선택된 탄소 공급원을 말한다.
- [0041] 용어 "유전자"는 임의로, 코딩 서열에 앞서는 조절 서열(5' 비코딩 서열) 및 뒤따르는 조절 서열(3' 비코딩 서열)을 포함하는, 특정 단백질로 발현될 수 있는 핵산 절편을 말한다. "천연 유전자(native gene)"는 그 자신의 조절 서열과 함께 자연에서 발견되는 유전자를 말한다. "키메라 유전자"는 자연에서 함께 발견되지 않는 조절 및 코딩 서열을 포함하는, 천연 유전자가 아닌 임의의 유전자를 말한다. 따라서, 키메라 유전자는 상이한 공급원으로부터 유래된 조절 서열과 코딩 서열, 또는 동일한 공급원으로부터 유래되었지만, 자연에서 발견되는 것과

상이한 방식으로 배열된 조절 서열과 코딩 서열을 포함할 수 있다. "내인성 유전자"는 유기체의 게놈에서 그의 자연적 위치에 있는 천연 유전자를 말한다. "외래 유전자" 또는 "이종성 유전자"는 정상적으로는 숙주 유기체 내에서 발견되지 않으나, 유전자 이전에 의해 숙주 유기체 내로 도입되는 유전자를 말한다. "이종성 유전자"는 천연 코딩 영역, 또는 그의 일부를 포함하며, 이는 상응하는 천연 유전자와 상이한 형태로 공급원 유기체 내로 재도입된다. 예를 들어, 이종성 유전자는 천연 숙주 내로 재도입되는 비-천연 조절 영역을 포함하는 키메라 유전자의 일부인 천연 코딩 영역을 포함할 수 있다. 또한, 외래 유전자는 비-천연 유기체 내로 삽입되는 천연 유전자, 또는 키메라 유전자를 포함할 수 있다. "형질전이유전자(transgene)"는 형질전환 과정에 의해 게놈으로 도입된 유전자이다.

[0042] 본원에 사용된 바와 같이, 용어 "코딩 영역"은 특정 아미노산 서열을 코딩하는 DNA 서열을 말한다. "적합한 조절 서열"은 코딩 서열의 업스트림(5' 비코딩 서열), 이의 내부 또는 이의 다운스트림(3' 비코딩 서열)에 위치하고, 전사, RNA 가공 또는 안정성 또는 연관된 코딩 서열의 번역에 영향을 미치는 뉴클레오타이드 서열을 말한다. 조절 서열은 프로모터, 번역 리더 서열(translation leader sequence), 인트론, 폴리아데닐화 인식 서열, RNA 가공 부위, 효과기(effector) 결합 부위 및 스템-루프 구조(stem-loop structure)를 포함할 수 있다.

[0043] 용어 "프로모터"는 코딩 서열이나 기능적 RNA의 발현을 조절할 수 있는 DNA 서열을 말한다. 일반적으로, 코딩 서열은 프로모터 서열에 대해 3'에 위치한다. 프로모터는, 천연 유전자로부터 그 전체가 유래될 수도 있고, 자연에서 발견되는 상이한 프로모터로부터 유래된 상이한 요소로 구성될 수도 있으며, 심지어 합성 DNA 분절을 포함할 수도 있다. 상이한 프로모터는 상이한 조직 또는 세포 유형에서, 또는 상이한 발생 단계에서, 또는 상이한 환경적 또는 생리학적 조건에 반응하여 유전자의 발현을 유도할 수 있음을 당업자는 이해할 것이다. 유전자가 대부분의 세포 유형에서 대부분의 시간에 발현되도록 하는 프로모터는 통상적으로 "구성적 프로모터"로 언급된다. 또한, 대부분의 경우에 조절 서열의 정확한 경계는 완벽하게 정의되지 않았으므로, 상이한 길이의 DNA 절편이 동일한 프로모터 활성을 가질 수 있는 것으로 인지된다.

[0044] 용어 "조작적으로 연결된"은 하나의 기능이 나머지에 의해 영향을 받도록 하는, 단일 핵산 절편 상에서의 핵산 서열의 회합을 말한다. 예를 들어, 프로모터가 코딩 서열의 발현에 영향을 미칠 수 있는 경우에, 프로모터는 그 코딩 서열에 조작적으로 연결된다(즉, 코딩 서열은 프로모터의 전사 조절 하에 있다). 코딩 서열은 센스(sense) 또는 안티센스(antisense) 배향으로 조절 서열에 조작적으로 연결될 수 있다.

[0045] 본원에서 사용되는 바와 같은 용어 "발현"은 전사 및 본 발명의 핵산 절편으로부터 유래된 센스 RNA(mRNA) 또는 안티센스 RNA의 안정한 축적을 말한다. 발현은 mRNA로부터 폴리펩타이드로의 번역을 말할 수도 있다.

[0046] 본원에서 사용되는 바와 같은 용어 "형질전환"은 유전적으로 안정한 유전성으로 귀결하는, 숙주 유기체로의 핵산 절편의 이전을 말한다. 형질전환된 핵산 절편을 함유하는 숙주 유기체는 "트랜스제닉(transgenic)" 또는 "재조합" 또는 "형질전환" 유기체로 언급된다.

[0047] 본원에서 사용된 바와 같이, 용어 "플라스미드" 및 "백터"는 세포의 중심 대사의 일부는 아니고, 보통 환경의 이중-가닥 DNA 분자 형태인 종종 유전자를 전달하는 염색체의 구성원을 말한다. 그러한 요소는 임의의 공급원으로부터 유래된, 단일 가닥 또는 이중 가닥 DNA 또는 RNA의 선형 또는 환형의, 자가 복제 서열, 게놈 도입 서열, 파지 또는 뉴클레오타이드 서열일 수 있으며, 여기에서 많은 뉴클레오타이드 서열은 프로모터 절편 및 적절한 3' 미번역 서열과 함께 선택된 유전자 생성물에 대한 DNA 서열을 세포에 도입시킬 수 있는 독특한 구축물 내로 연결되거나 재조합된다.

[0048] 본원에서 사용된 바와 같이, 용어 "코돈 축퇴성"은 인코딩된 폴리펩타이드의 아미노산 서열에 영향을 주지 않으면서 뉴클레오타이드 서열의 변이를 허용하는 유전적 코드 내에서의 성질을 말한다. 주어진 아미노산을 특정하기 위한 뉴클레오타이드 코돈의 사용에 있어서 특정 숙주 세포에서 나타나는 "코돈-바이어스(codon-bias)"가 당업자에게 주지되어 있다. 그러므로, 숙주 세포 내의 발현을 개선하기 위해 유전자를 합성할 경우, 그의 코돈 사용 빈도가 숙주 세포가 선호하는 코돈의 사용 빈도에 근접하도록 유전자를 고안하는 것이 바람직하다.

[0049] 용어 "코돈-최적화"는 그것이 다양한 숙주의 형질전환을 위한 핵산 분자의 코딩 영역 또는 유전자를 말함에 따라, DNA에 의해 인코딩된 폴리펩타이드를 변경시키지 않고, 숙주 유기체의 전형적인 코돈 사용을 반영하기 위한 유전자 또는 핵산 분자의 코딩 영역에서의 코돈 변경을 말한다.

[0050] 본원에서 사용되는 바와 같은 "단리된 핵산 절편" 또는 "단리된 핵산 분자"는 상호호환적으로 사용될 것이며, 임의로 합성의, 비-천연 또는 변경된 뉴클레오타이드 염기를 함유하는 단일 가닥 또는 이중 가닥의 RNA 또는 DNA의 중합체를 의미할 것이다. DNA의 중합체 형태인 단리된 핵산 절편은 cDNA, 게놈 DNA 또는 합성 DNA의 하

나 이상의 분절로 이루어질 수 있다.

[0051] 핵산 절편은, 단일 가닥 형태의 핵산 절편이 적절한 온도와 용액 이온 강도 조건 하에서 다른 핵산 절편에 어닐링할 수 있을 경우, cDNA, 게놈 DNA, 또는 RNA 분자와 같은 또다른 핵산 절편에 "혼성화가능"하다. 혼성화 및 세정 조건은 주지되어 있으며 문헌[Sambrook, J., Fritsch, E. F. and Maniatis, T. Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory: Cold Spring Harbor, NY (1989), 특히 이에 수록된 제11장 및 표 11.1]에 예시되어 있다(전체가 본원에 참조로서 삽입됨). 온도와 이온 강도의 조건이 혼성화의 "엄격도"를 결정한다. 엄격성 조건을 조정하여, 중간 정도로 유사한 절편(예를 들어 관계가 먼 유기체로부터의 상동 서열) 내지 고도로 유사한 절편(예를 들어 밀접하게 관련된 유기체로부터의 기능성 효소를 중복시키는 유전자)을 스크리닝할 수 있다. 혼성화후 세정은 엄격성 조건을 결정한다. 한 세트의 바람직한 조건에서는, 실온에서 15분 동안 6X SSC, 0.5% SDS로 시작하여 45℃에서 30분 동안 2X SSC, 0.5% SDS로 반복하고, 50℃에서 30분 동안 0.2X SSC, 0.5% SDS로 2회 반복하는 일련의 세정을 사용한다. 더욱 바람직한 세트의 엄격성 조건에서는 더 높은 온도를 사용하며, 0.2X SSC, 0.5% SDS 내에서의 최종 2회 30분 세정의 온도를 60℃까지 증가시킨다는 점을 제외하고는 세정이 상기와 동일하다. 다른 바람직한 세트의 높은 엄격성 조건에서는 65℃에서 0.1X SSC, 0.1% SDS 내에서의 2회 최종 세정을 사용한다. 추가의 세트에서 엄격성 조건은, 예를 들어 0.1X SSC, 0.1% SDS, 65℃에서의 혼성화 및 2X SSC, 0.1% SDS에 의한 세정 후에 0.1X SSC, 0.1% SDS에 의한 세정을 포함한다.

[0052] 혼성화의 엄격성에 따라 염기 사이의 불일치가 가능하지만, 혼성화를 위해서는 2개의 핵산이 상보적 서열을 함유해야 한다. 핵산을 혼성화시키기 위한 적절한 엄격성은, 당업계에서 잘 알려진 변수인 핵산의 길이 및 상보성의 정도에 의존한다. 2개 뉴클레오타이드 서열 사이의 유사성 또는 상동성의 정도가 클수록, 이들 서열을 가진 핵산의 혼성체의 T_m 수치가 커진다. 핵산 혼성화의 상대적 안정성(더 높은 T_m에 상응함)은 하기의 순서로 감소한다: RNA:RNA, DNA:RNA, DNA:DNA. 길이가 100개 뉴클레오타이드를 초과하는 혼성체에 대하여 T_m을 계산하는 수학적식이 유도되었다(문헌[Sambrook et al., supra, 9.50-9.51] 참조). 더 짧은 핵산, 즉, 올리고뉴클레오타이드의 혼성화에 있어서는 불일치의 위치가 더욱 중요해지며 올리고뉴클레오타이드의 길이가 그의 특이성을 결정한다(문헌[Sambrook et al., supra, 11.7-11.8] 참조). 한 실시 양태에서는 혼성가능한 핵산의 길이가 적어도 약 10개 뉴클레오타이드이다. 바람직하게는 혼성가능한 핵산의 최소 길이가 적어도 약 15개 뉴클레오타이드이고; 더욱 바람직하게는 적어도 약 20개 뉴클레오타이드이며; 가장 바람직하게는 길이가 적어도 약 30개 뉴클레오타이드이다. 또한, 프로브의 길이와 같은 인자에 따라 필요한 경우에 온도 및 세정 용액 염 농도를 조정할 수 있음을 당업자는 인식할 것이다.

[0053] 아미노산 또는 뉴클레오타이드 서열의 "실질적 부분"은 당업자에 의한 서열의 수동적 평가, 또는 BLAST (문헌[Altschul, S. F., et al., J. Mol. Biol., 215:403-410 (1993)])와 같은 알고리즘을 사용하는 컴퓨터-자동화 서열 비교 및 규명화에 의해 폴리펩타이드 또는 유전자를 추정상으로 규명하기에 충분한 폴리펩타이드의 아미노산 서열 또는 유전자의 뉴클레오타이드 서열을 포함하는 부분이다. 일반적으로, 폴리펩타이드 또는 핵산 서열을 공지의 단백질 또는 유전자와 상동적인 것으로 추정상 동정하기 위해서는 10개 이상 연속되는 아미노산 또는 30개 이상의 뉴클레오타이드의 서열이 필요하다. 더욱이, 뉴클레오타이드 서열에 있어서는, 서열-의존적인 유전자 규명(예를 들어, 서던 혼성화(Southern hybridization)) 및 단리(예를 들어, 박테리아 콜로니 또는 박테리오파아지 플라크의 체자리 혼성화(in situ hybridization)) 방법에 20-30개의 연속된 뉴클레오타이드를 포함하는 유전자 특이적 올리고뉴클레오타이드 프로브가 사용될 수 있다. 또한, 12-15개 염기의 짧은 올리고뉴클레오타이드를 PCR에서 증폭 프라이머로 사용하여, 프라이머를 포함하는 특정 핵산 절편을 수득할 수 있다. 따라서, 뉴클레오타이드 서열의 "실질적 부분"은 서열을 포함하는 핵산 절편을 특이적으로 규명하고/거나 단리하기에 충분한 서열을 포함한다. 본 명세서는 특정 단백질을 인코딩하는 완전한 아미노산 및 뉴클레오타이드 서열을 교시한다. 본원에서 보고된 서열의 유익성을 가지고, 당업자는 개시된 서열의 전체 또는 상당 부분을 당업계에 공지된 목적으로 사용할 수 있게 되었다. 따라서 본 발명은, 첨부하는 서열 목록에 보고된 완전 서열과 더불어 상기 정의된 서열들의 상당한 부분을 포함한다.

[0054] 용어 "상보적"은 서로 혼성화할 수 있는 뉴클레오타이드 염기 간의 관계를 기술하는데 사용된다. 예를 들어, DNA에 있어서 아데노신은 티민에 상보적이고 사이토신은 구아닌에 상보적이다.

[0055] 당업계에 공지된 바와 같이, 용어 "동일성 백분율"은 2개 이상의 폴리펩타이드 서열 또는 2개 이상의 폴리뉴클레오타이드 서열 사이의 관계로서, 서열들을 비교함으로써 결정된다. 당업계에서 "동일성"은 또한 폴리펩타이드 또는 폴리뉴클레오타이드 서열 사이의 서열 관련성의 정도를 의미하며, 경우에 따라 이러한 서열의 스트링

(string) 사이의 일치에 의해 결정된다. "동일성" 및 "유사성"은, 하기의 문헌에 기술된 것들을 포함하나 이에 한정되지 않는 공지 방법을 통해 용이하게 계산할 수 있다: 1.) 계산 분자생물학(Computational Molecular Biology)(Lesk, A. M., Ed.) 옥스포드 대학교: 뉴욕(1988); 2.) 생물전산학(Biocomputing): 정보학 및 게놈 프로젝트(Informatics and Genome Projects)(Smith, D. W., Ed.) 아카데미: 뉴욕(1993); 3.) 서열 데이터의 전산 분석, 제1부(Computer Analysis of Sequence Data, Part I)(Griffin, A. M., and Griffin, H. G., Eds.) 휴머니아(Humania): 뉴저지(1994); 4.) 분자생물학에서의 서열 분석(Sequence Analysis in Molecular Biology)(von Heinje, G., Ed.) 아카데미(1987); 및 5.) 서열 분석 프라이머(Sequence Analysis Primer)(Gribskov, M. and Devereux, J., Eds.) 스톡턴(Stockton): NY (1991).

[0056] 동일성을 결정하는 바람직한 방법은 시험 서열 사이에 최상의 일치를 부여하도록 고안된다. 동일성 및 유사성을 결정하는 방법은 공중에게 이용가능한 컴퓨터 프로그램에 명시되어 있다. 레이저진(LASERGENE) 생물정보학 계산 모음(bioinformatics computing suite)(위스콘신주 메디슨 소재의 디엔에이스타 인코포레이티드(DNASTAR Inc.))의 맥얼라인(등록상표)(MegAlign™) 프로그램을 사용하여 서열 정렬 및 동일성 백분율 계산을 수행할 수 있다. 몇가지 종류의 알고리즘, 예를 들어 클러스탈 V로 분류되는 정렬 방법(문헌[Higgins and Sharp, CABIOS. 5:151-153 (1989); Higgins, D.G. et al., Comput. Appl. Biosci., 8:189-191 (1992)]에 의해 기술됨)에 상응하고 레이저진 생물정보학 계산 모음의 맥얼라인(등록상표) 프로그램(디엔에이스타 인코포레이티드)에서 찾을 수 있는 "클러스탈 V 정렬 방법"을 포함하는 "클러스탈 정렬 방법"을 사용하여 서열의 다중 정렬을 수행한다. 다중 정렬에 있어서 디폴트 값은 갭 페널티=10 및 갭 길이 페널티=10에 상응한다. 클러스탈 방법을 사용하는 단백질 서열의 동일성 백분율 계산 및 짝 정렬(pairwise alignments)에 있어서 디폴트 파라미터는 크투플(KTUPLE)=1, 갭 페널티=3, 윈도우(WINDOW)=5 및 다아이고날 세이브드(DIAGONALS SAVED)=5이다. 핵산에 있어서 이들 파라미터는 크투플=2, 갭 페널티=5, 윈도우=4 및 다아이고날 세이브드=4이다. 클러스탈 V 프로그램을 사용하여 서열들을 정렬한 후에, 동일한 프로그램 내의 "서열 거리" 표를 보면 "동일성 백분율"을 얻을 수 있다. 부가적으로 "클러스탈 W 정렬 방법"이 이용가능하며, 이는 클러스탈 W로 분류된 정렬 방법(Higgins and Sharp, CABIOS. 5:151-153 (1989); Higgins, D.G. et al., Comput. Appl. Biosci. 8:189-191(1992))에 상응하고 레이저진 생물정보학 계산 모음(디엔에이스타 인코포레이티드)의 맥얼라인(등록상표) v6.1 프로그램에서 찾을 수 있다. 다중 정렬을 위한 디폴트 파라미터(갭 페널티=10, 갭 길이 페널티=0.2, 딜레이 다이버전 시퀀스(Delay Divergen Seqs)(%)=30, DNA 이전(DNA Transition) 중량=0.5, 단백질 중량 매트릭스=고넷 시리즈, DNA 중량 매트릭스=IUB). 클러스탈 W 프로그램을 사용하여 서열들을 정렬한 후에, 동일한 프로그램 내의 "서열 거리" 표를 보면 "동일성 백분율"을 얻을 수 있다.

[0057] 동일하거나 유사한 기능 또는 활성을 가진 폴리펩타이드를 다른 종으로부터 규명함에 있어서 여러 수준의 서열 동일성이 유용하다는 것이 당업자에게 주지되어 있다. 동일성 백분율의 유용한 예는: 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 또는 95%를 포함하나 이에 제한되지 않거나, 55%내지 100%의 임의의 정수 백분율이 본 발명을 기술하는데 유용할 수 있으며, 예컨대 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% 또는 99%이다. 적합한 핵산 절편은 상기 상동성을 가질뿐만 아니라, 전형적으로는 적어도 50개의 아미노산, 바람직하게는 적어도 100개의 아미노산, 더욱 바람직하게는 적어도 150개의 아미노산, 더욱 더 바람직하게는 적어도 200개의 아미노산, 및 가장 바람직하게는 적어도 250개의 아미노산을 갖는 폴리펩타이드를 인코딩한다.

[0058] 용어 "서열 분석 소프트웨어"는 뉴클레오타이드 또는 아미노산 서열을 분석하는데 유용한 임의의 컴퓨터 알고리즘 또는 소프트웨어 프로그램을 말한다. "서열 분석 소프트웨어"는 시판되거나 독립적으로 개발할 수 있다. 통상적인 서열 분석 소프트웨어는 하기의 것들을 포함하나 이에 한정되지 않는다: 1.) GCG 프로그램 모음(위스콘신 패키지 버전 9.0, 위스콘신주 메디슨 소재의 제네틱스 컴퓨터 그룹(GCG: Genetics Computer Group)); 2.) BLASTP, BLASTN, BLASTX (문헌[Altschul et al., J. Mol. Biol., 215:403-410 (1990)]); 3.) 디엔에이스타(위스콘신주 메디슨 소재의 디엔에이스타 인코포레이티드); 4.) 시퀀처(Sequencher)(미시간주 엔아버 소재의 젠 코드 코포레이션(Gene Codes Corporation)); 및 5.) 스미스-워터만 알고리즘(문헌[W. R. Pearson, Comput. Methods Genome Res., [Proc. Int. Symp.] (1994), Meeting Date 1992, 111-20. Editor(s): Suhai, Sandor. Plenum: New York, NY])을 포함하는 FASTA 프로그램. 본 출원의 맥락에서, 서열 분석 소프트웨어가 분석을 위해 사용된 경우에는, 그 분석 결과가 달리 명시되지 않는 한, 참조한 프로그램의 "디폴트 값"에 기준할 것이라는 사실을 이해할 것이다. 본 명세서에서 사용되는 바와 같은 "디폴트 값"은 소프트웨어를 처음으로 개시할 경우에 이러한 소프트웨어에 본래 부여된 임의의 수치 또는 파라미터 세트를 의미할 것이다.

- [0059] 여기서 사용된 표준 재조합 DNA 및 분자 클로닝 기술은 당업계에 주지된 것으로서 문헌Sambrook, J., Fritsch, E. F. and Maniatis, T., Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1989) (이후 "Maniatis"로 지칭); 및 [Silhavy, T. J., Bannan, M.L. and Enquist, L. W., Experiments with Gene Fusions, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1984)]; 및 문헌[Ausubel, F. M. et al., Current Protocols in Molecular Biology, published by Greene Publishing Assoc. and Wiley-Interscience (1987)]에 기술되어 있다. 본원에서 사용되는 추가의 방법은 문헌[Methods in Enzymology, Volume 194, Guide to Yeast Genetics and Molecular and Cell Biology](Part A, 2004, Christine Guthrie and Gerald R. Fink (Eds.), Elsevier Academic Press, San Diego, CA)에 있다.
- [0060] 효모에서의 향상된 Fe-S 클러스터 단백질 활성의 발견
- [0061] 그의 활성을 위해 요구되는 결합된 철-황 클러스터(Fe-S)를 함유하는 단백질은 이중성 발현 시스템에서 사용되는 경우 낮은 활성을 가질 수 있다. Fe-S 클러스터의 형성 및 이의 아포-단백질로의 이전은 시스템인 탈황효소, 스캐폴드 단백질 및 샤페론을 포함하는 적어도 여러 단백질을 수반하는 다단계 방법이다. 따라서, 이중성 Fe-S 단백질은 내인성 숙주 시스템에 의해 효과적으로 구성될 수 없다. 출원인은 효모 숙주 세포에서 이중성 단백질로서 발현되는 Fe-S 단백질의 활성을 증가시키는 방법을 발견하였다. 출원인은 효모 숙주 세포에서 내인성 Fe-S 단백질의 생성을 감소시킴으로써, 발현되는 이중성 Fe-S 클러스터 단백질의 활성의 향상이 달성될 수 있음을 발견하였다. 이중성 진균류 또는 식물 2Fe-2S 다이하이드록시-산 탈수효소(DHAD) 또는 Fe-S 프로판다이올 탈수효소 반응화효소(RdhtB)의 효모에서의 발현은 아이소프로필말레이트 탈수효소를 인코딩하는 내인성 유전자 (LEU1) 또는 다이하이드록시-산 탈수효소를 인코딩하는 내인성 유전자(ILV3)가 효모 숙주 세포에서 불활성화된 경우 향상되었다.
- [0062] 내인성 Fe-S 단백질을 인코딩하는 유전자의 불활성화가 있는 효모 숙주 세포에서, 발현되는 이중성 Fe-S 단백질의 활성은 Fe-S 단백질 인코딩 유전자의 불활성화가 없는 효모 숙주 세포에서의 활성의 적어도 약 1.4배로 증가될 수 있다. 예를 들어, 클루이베로마이세스 락티스 DHAD는 결실이 없는 숙주와 비교해 LEU1 결실 숙주에서 1.4배의 활성을 가졌고; 로세부리아 이놀리니보란스 RdhtB는 활성화된 RdhtA 단백질 활성에 의해 측정되는 바와 같이 LEU 결실 숙주에서 1.7배의 비교 활성을 가졌고(하기에서 기술됨); 시토줄에서 발현되는 사카로마이세스 세레비시에 DHAD는 미토콘드리아 ILV3 결실 숙주에서 1.5배의 비교 활성을 가졌고; 시토줄에서 발현되는 클루이베로마이세스 락티스 DHAD는 미토콘드리아 ILV3 결실 숙주에서 7.4배의 비교 활성을 가졌다.
- [0063] 내인성 Fe-S 단백질의 발현이 감소된 효모 숙주 세포
- [0064] 감소된 내인성 Fe-S 단백질 발현은 유전자 조작을 받기가 쉬운 임의의 효모 세포에서 조작될 수 있다. 예는 사카로마이세스, 스킨조사카로마이세스, 한센룰라, 칸디다, 클루이베로마이세스, 야로위아 및 피치아의 효모를 포함한다. 적합한 균주는 사카로마이세스 세레비시에, 스킨조사카로마이세스 폼베, 클루이베로마이세스 락티스, 클루이베로마이세스 서모톨레란스(thermotolerans), 칸디다 글라브라타, 칸디다 알비칸스, 피치아 스티피티스 및 야로위아 리폴리티카를 포함하나 이에 제한되지 않는다. 사카로마이세스 세레비시에가 특히 적합하다.
- [0065] 이들 효모 중 임의의 효모에서, 임의의 내인성 Fe-S 단백질은 감소된 발현을 위한 표적일 수 있다. 감소된 발현을 위한 표적일 수 있는 효모에서 Fe-S 단백질은 예를 들어, 하기 단백질(인코딩 유전자와 함께): 아코니테이즈(ACO1), 호모아코니테이즈(LYS4), DHAD (ILV3), 리포에이트 합성효소(LIP5), 비오틴 합성효소(BIO2), 페레독신 숙성화(YAH1), NADH 유비퀴논 산화환원효소(NDI1), 석시네이트 탈수소효소(SDH2), 유비퀴놀-시토크롬-c 환원효소(RIP1), 아이소프로필말레이트 이성질체화효소(LEU1), 설파이트 환원효소(ECM17), 글루타메이트 탈수소효소(GLT1), ABC 단백질 Rli1(RLI1), NTPase Nbp35(NBP35), 및 수소화효소-형 단백질(NARI1)을 포함한다. 개별 Fe-S 단백질의 발현이 감소된 효모 세포는 특정 영양분이 있는 성장 배지의 보충과 같이 성장을 위한 특별한 조건을 필요로 할 수 있으며, 이는 당업자에게 잘 알려져 있다. 예를 들어, LEU1이 분열된 균주에는 루신이 보충되고, DHAD가 분열된 균주에는 루신, 아이소루신, 및 발린이 보충되고, LYS4가 분열된 균주에는 라이신이 보충된다. 분열이 있는 일부 균주에는 성장용 보충제가 필요 없다. 감소된 발현을 표적으로 할 수 있는 특히 적합한 Fe-S 단백질은 아이소프로필말레이트 이성질체화효소(LEU1), 다이하이드록시산 탈수효소(ILV3), 설파이트 환원효소(ECM17), 글루타메이트 탈수소효소(GLT1), 및 비오틴 합성효소(BIO2)를 포함한다. 감소된 발현은 적어도 하나의 내인성 Fe-S 단백질에 대해 조작되고, 2개 이상의 내인성 Fe-S 단백질은 감소될 수 있다.
- [0066] LEU1은 아이소프로필말레이트 탈수효소를 포함하고, 이 효소는 분지쇄 아미노산 생합성, 구체적으로는 루신의 합성에 수반되는 EC 4.2.1.33에 속한다. 활성을 위해 4Fe-4S 클러스터를 필요로 하는 효소인 아이소프로필말레

이트 탈수효소를 인코딩하는 임의의 유전자는 본 개시문헌의 효모 숙주 세포에서 불활성화될 수 있다. 효모 LEU1 불활성화 표적 유전자 및 그의 인코딩된 단백질의 예는 사카로마이세스 세레비시애(코딩 서열 번호:1; 단백질 서열 번호:2), 스킨조사카로마이세스 폼베(코딩 서열 번호:3; 단백질 서열 번호:4), 칸디다 갈브라타 균주 CBS 138(코딩 서열 번호:5; 단백질 서열 번호:6), 칸디다 알비칸스 SC5314(코딩 서열 번호:7; 단백질 서열 번호:8), 클루이베로마이세스 락티스(코딩 서열 번호:9; 단백질 서열 번호:10), 야로위아 리폴리티카(코딩 서열 번호:11; 단백질 서열 번호:12) 및 피치아 스티피티스(코딩 서열 번호:13; 단백질 서열 번호:14)로부터의 것이다.

[0067] 유사하게는 본원에서 기술된 효모 숙주 중 임의의 숙주에서, 내인성 ILV3 유전자는 불활성화되어, 내인성 Fe-S 단백질 발현을 감소시킬 수 있다. ILV3은 분지쇄 아미노산 생합성에 수반되는 미토콘드리아 DHAD를 인코딩한다. 미토콘드리아 DHAD는 핵 유전자에 의해 인코딩되고, 미토콘드리아 표적화 신호 서열을 가져서, 미토콘드리아로 이동되고 거기에 위치한다. 임의의 ILV3 유전자는 본 개시문헌의 효모 숙주 세포에서 불활성화될 수 있다. 효모 ILV3 불활성화 표적 유전자 및 그의 인코딩된 단백질의 예는 사카로마이세스 세레비시애 YJM78(코딩 서열 번호:111; 단백질 서열 번호:112), 스킨조사카로마이세스 폼베(코딩 서열 번호:93; 단백질 서열 번호:94), 칸디다 갈브라타 균주 CBS 138(코딩 서열 번호:107; 단백질 서열 번호:108), 칸디다 알비칸스 SC5314(코딩 서열 번호:101; 단백질 서열 번호:102), 클루이베로마이세스 락티스(코딩 서열 번호:113; 단백질 서열 번호:114), 야로위아 리폴리티카(코딩 서열 번호:105; 단백질 서열 번호:106) 및 피치아 스티피티스 CBS 6054(코딩 서열 번호:103; 단백질 서열 번호:104)로부터의 것이다.

[0068] 아이소프로필말레이트 탈수효소를 인코딩하는 유전자 및 DHAD 효소 유전자가 잘 알려져 있기 때문에, 그리고 게놈 서열화의 만연때문에, 이들 효소의 추가의 적합한 종(species)은 생물정보학 접근법을 사용해 서열 유사성을 바탕으로 당업자에 의해 쉽게 규명될 수 있다. 전형적으로는, 본원에 제공된 것과 같이 공지된 아이소프로필말레이트 탈수효소 아미노산 서열을 사용한 공개 이용가능한 데이터베이스의 BLAST(상기 기술됨) 탐색이 사용되어, 본 발명의 균주에서 불활성화를 위한 표적일 수 있는 이들 효소 및 그의 인코딩 서열을 규명한다. 예를 들어, 서열 번호:2, 4, 6, 8, 10, 12 및 14의 아이소프로필말레이트 탈수효소 단백질 및 서열 번호:94, 102, 104, 106, 108, 112, 및 114의 DHAD 단백질 중 임의에 대해 적어도 약 70-75%, 75%-80%, 80-85%, 85%-90%, 90%-95% 또는 98% 서열 동일성의 아미노산 서열 동일성을 갖는 내인성 효모 아이소프로필말레이트 탈수효소 및 DHAD 단백질은 본 발명의 균주에서 감소된 발현을 가질 수 있다. 동일성은 갭 페널티=10, 갭 길이 페널티=0.1, 및 단백질 중량 매트릭스의 곱셈 250 시리즈의 디폴트 파라미터를 사용한 클러스탈 W 정렬 방법을 바탕으로 한다.

[0069] 추가로, 본원에서 제공되는 LEU1 코딩 영역 및 ILV3의 서열이 사용되어, 자연적으로 다른 호모로그를 규명할 수 있다. 예를 들어, 본원에서 기술된 코딩 영역의 각각이 사용되어, 상동성 단백질을 인코딩하는 유전자를 분리할 수 있다. 서열-의존성 프로토콜을 사용하는 상동 유전자의 분리는 당업계에 주지되어 있다. 서열-의존성 프로토콜의 예는 하기의 것들을 포함하나 이에 한정되지 않는다: 1.) 핵산 혼성화 방법; 2.) DNA 및 RNA 증폭 방법, 예를 들어 핵산 증폭 기술의 다양한 용도[예를 들어, 중합효소 연쇄반응(PCR: polymerase chain reaction), 미국 특허 제4,683,202호(Mullis et al.); 연결효소 연쇄반응(LCR: ligase chain reaction)(Tabor, S. et al., Proc. Acad. Sci. USA 82:1074 (1985)); 또는 가닥 대체 증폭(SDA: strand displacement amplification)(Walker, et al., Proc. Natl. Acad. Sci. U.S.A., 89:392 (1992)); 및 3.) 상보성에 의한 스크리닝 및 라이브러리 구축 방법.

[0070] 예를 들어, 아이소프로필말레이트 탈수효소에 유사한 단백질 또는 폴리펩타이드를 인코딩하는 유전자 및 본원에서 제공되는 DHAD 인코딩 유전자는 DNA 혼성화 프로브로서 본 발명의 핵산 절편의 전부 또는 일부를 사용함으로써 직접 분리되어, 당업자에게 잘 알려진 방법론을 사용해 임의의 목적하는 유기체로부터의 라이브러리를 스크리닝할 수 있다. 개시된 핵산 서열에 기초한 특이적 올리고뉴클레오타이드 프로브는 당업계에 공지된 방법(Maniatis, supra)에 의해 고안되고 합성될 수 있다. 또한, 전체 서열을 직접 사용하여, 당업자에게 공지된 방법(예를 들어 무작위 프라이머 DNA 표지화(random primers DNA labeling), 새깅 번역(nick translation) 또는 종단 표지화(end-labeling) 기법)에 의해 DNA 프로브를 합성하거나, 이용가능한 시험관내 전사 시스템을 사용하여 RNA 프로브를 합성할 수 있다. 또한, 특이적 프라이머를 고안하고 사용하여 본 서열의 일부(또는 전체 길이)를 증폭할 수 있다. 생성 증폭 생성물은 증폭 반응 동안에 직접 표지될 수 있거나 또는 증폭 반응 후에 표지될 수 있고, 프로브로서 사용되어, 적절한 엄격성의 조건 하에서의 혼성화에 의해 전장 DNA 절편을 분리할 수 있다.

[0071] 통상적으로, PCR 유형의 증폭 기술에서는 프라이머들이 상이한 서열을 가지며 서로에 대해 상보적이지 않다. 목적하는 시험 조건에 따라, 표적 핵산의 효율적이면서도 충실한 복제를 제공하도록 프라이머의 서열을 고안해

야 한다. PCR 프라이머 디자인의 방법은 보편적이고 당업계에 잘 알려져 있다(문헌[Thein and Wallace, "The use of oligonucleotides as specific hybridization probes in the Diagnosis of Genetic Disorders", in Human Genetic Diseases: A Practical Approach, K. E. Davis Ed., (1986) pp 33-50, IRL: Herndon, VA]; 및 [Rychlik, W., In Methods in Molecular Biology, White, B. A. Ed., (1993) Vol. 15, pp 31-39, PCR Protocols: Current Methods and Applications. Humana: Totowa, NJ]).

[0072] 일반적으로, 기술된 서열의 2 개 짧은 분절을 중합효소 연쇄반응 프로토콜에 사용하여 DNA 또는 RNA로부터 상동 유전자를 암호화하는 더 긴 핵산 절편을 증폭할 수 있다. 중합효소 연쇄반응을 클로닝된 핵산 절편의 라이브러리 상에서 수행할 수도 있으며, 여기에서 한 프라이머의 서열은 기술된 핵산 절편으로부터 유래되고, 다른 프라이머의 서열은 미생물 유전자를 암호화하는 mRNA 전구체의 3' 말단의 폴리아데닐산 구역의 존재를 이용한다.

[0073] 대안적으로, 제2 프라이머 서열은 클로닝 벡터로부터 유래된 서열에 기초할 수 있다. 예를 들어, 당업자는 전사체 내의 단일 지점 및 3' 또는 5' 말단 사이의 영역의 카피를 증폭하는 PCR을 이용함으로써 RACE 프로토콜(문헌[Frohman et al., PNAS USA 85:8998 (1988)])에 따라 cDNA를 생성시킬 수 있다. 본 서열로부터 3' 및 5' 방향으로 배향된 프라이머를 고안할 수 있다. 상업적으로 이용가능한 3' RACE 또는 5' RACE 시스템(예를 들어, 메틸랜드주 게이트스버그 소재의 BRL)을 사용하여 특이적 3' 또는 5' cDNA 절편을 분리할 수 있다(문헌[Ohara et al., PNAS USA 86:5673 (1989); Loh et al., Science 243:217 (1989)]).

[0074] 대안적으로는, 제공되는 아이소프로필말레이트 탈수효소 및 DHAD 인코딩 서열은 호모로그의 규명을 위한 혼성화 시약으로서 적용될 수 있다. 핵산 혼성화 시험의 기본 구성요소는 프로브, 관심의 대상인 유전자 또는 유전자 절편을 함유하는 것으로 추정되는 시료, 및 특이적 혼성화 방법을 포함한다. 통상적으로 프로브는, 검출하고자 하는 핵산 서열에 상보적인 단일-가닥 핵산 서열이다. 프로브는 검출될 핵산 서열에 대하여 "혼성화가능"하다. 프로브의 길이는 5개 염기 내지 수만개 염기 범위에서 변동될 수 있으며, 실행하고자 하는 구체적 시험에 의존한다. 통상적으로 약 15개 염기 내지 약 30개 염기의 프로브 길이가 적합하다. 검출하고자 하는 핵산 서열에는 프로브 분자의 일부만이 상보적일 필요가 있다. 또한, 프로브 및 표적 서열 사이의 상보성이 완벽할 필요는 없다. 불완전하게 상보적인 분자 사이에도 혼성화가 일어나며, 이 경우에 혼성화 영역 내의 어떤 분획의 염기들은 적절한 상보적 염기와 대합하지 않는다.

[0075] 혼성화 방법은 잘 정립되어 있다. 통상적으로, 핵산 혼성화가 가능한 조건하에 프로브 및 시료를 혼합해야 한다. 이는 적절한 농도 및 온도 조건하에 무기 또는 유기염의 존재하에 프로브 및 시료를 접촉시킴을 포함한다. 프로브 및 시료 핵산 사이에 임의의 가능한 혼성화가 일어날 수 있도록 충분히 긴 시간 동안 프로브 및 시료 핵산을 접촉시켜야 한다. 혼합물 내의 프로브 또는 표적의 농도는 혼성화가 일어나기 위해 필요한 시간을 결정한다. 프로브 또는 표적의 농도가 높을수록, 필요한 혼성화 인큐베이션 시간은 짧아진다. 임의로, 무질서 유발제(chaotropic agent)를 첨가할 수 있다. 무질서 유발제는 뉴클레아제 활성을 저해함으로써 핵산을 안정화시킨다. 또한, 무질서 유발제는 짧은 올리고뉴클레오타이드 프로브의 민감하고 엄격한 혼성화를 실온에서 가능하게 한다(문헌[Van Ness and Chen, Nucl. Acids Res. 19:5143-5151 (1991)]). 적합한 무질서 유발제는 특히, 구아니딘 클로라이드, 구아니딘 티오시아네이트, 소듐 티오시아네이트, 리튬 테트라클로로아세테이트, 소듐 퍼클로레이트, 루비듐 테트라클로로아세테이트, 포타슘 요오다이드 및 세슘 트라이플루오로아세테이트를 포함한다. 통상적으로, 무질서 유발제는 약 3M의 최종 농도로 존재한다. 필요한 경우, 혼성화 혼합물에 포름아미드를 통상 30-50%(v/v)로 첨가할 수 있다.

[0076] 다양한 혼성화 용액을 적용할 수 있다. 통상적으로, 이들은 약 20 내지 60부피%, 바람직하게는 30%의 극성 유기용매를 함유한다. 일반적인 혼성화 용액은 약 30-50% v/v 포름아미드, 약 0.15 내지 1M 소듐 클로라이드, 약 0.05 내지 0.1M 완충제(예를 들어, 소듐 시트레이트, 트리스-HCl, PIPES 또는 HEPES(약 6-9의 pH 범위)), 약 0.05 내지 0.2% 세제(detergent)(예를 들어, 소듐 도데실설페이트), 또는 0.5-20mM 범위의 EDTA, FICOLL(파마시아 인코포레이티드(Pharmacia Inc.))(약 300-500kDa), 폴리비닐피롤리돈(약 250-500kDa) 및 혈청 알부민을 적용한다. 통상적인 혼성화 용액에는, 약 0.1 내지 5mg/ml의 표지되지 않은 담체 핵산, 절편화된 핵 DNA(예를 들어, 송아지 흉선 또는 연어 정자 DNA, 또는 효모 RNA), 및 임의로 약 0.5 내지 2% wt/vol 글리신도 포함된다. 다양한 극성 수용성 또는 팽윤성 약제(예를 들어, 폴리에틸렌 글리콜), 음이온성 중합체(예를 들어, 폴리아크릴레이트 또는 폴리메틸아크릴레이트) 및 음이온성 당류 중합체(saccharidic polymer)(예를 들어, 덱스트란 설페이트)를 포함하는 부피 배제 약제(volume exclusion agent)와 같은 다른 첨가제도 포함될 수 있다.

[0077] 핵산 혼성화는 다양한 검정법 체제에 적용시킬 수 있다. 가장 적합한 것 중의 하나는 샌드위치 검정법 체제이다. 샌드위치 검정법은 비변성(non-denaturing) 조건하에서의 혼성화에 특히 적응가능하다. 샌드위치-유형 검

정법의 주요 구성요소는 고체 지지체이다. 고체 지지체에는, 서열의 일부에 대해 상보적이고 표지되지 않은 핵산 프로브가 흡착되거나 공유적으로 결합되어 고정화된다.

[0078] 본 발명의 효모 세포에서 감소된 활성을 표적으로 할 수 있는 다른 Fe-S 단백질 중 임의의 단백질에 대한 핵산 인코딩 서열 및 단백질은 당업자에게 잘 알려진 생물정보학 및 다른 방법을 사용해 규명될 수 있다. 예를 들어, 아코니테이즈 서열은 생물정보학 데이터베이스에서 검색하는 키워드에 의해 규명된다. 이 방법에 의해 규명되는 여러 서열은 사카로마이세스 세레비시애(코딩 서열 번호:153; 단백질 서열 번호:154), 염색체 II 상의 스킨조사카로마이세스 폼베(코딩 서열 번호:155; 단백질 서열 번호:156), 염색체 I 상의 스킨조사카로마이세스 폼베(코딩 서열 번호:157; 단백질 서열 번호:158), 클루이베로마이세스 락티스(코딩 서열 번호:15; 단백질 서열 번호:160), 칸디다 알비칸스 SC5314(코딩 서열 번호:161; 단백질 서열 번호:162), 야로위아 리폴리티카(코딩 서열 번호:163; 단백질 서열 번호:164), 피치아 스티피티스 CBS 6054(코딩 서열 번호:165; 단백질 서열 번호:166), 칸디다 갈브라타 CBS 138 염색체 F(코딩 서열 번호:167; 단백질 서열 번호:168), 칸디다 갈브라타 CBS 138 염색체 D(코딩 서열 번호:169; 단백질 서열 번호:170), 및 칸디다 갈브라타 CBS 138 염색체 K(코딩 서열 번호:171; 단백질 서열 번호:172)로부터의 것들이다.

[0079] Fe-S 단백질을 인코딩하는 유전자, 예를 들어 LEU1, ILV3, 또는 ACO1은 유전적 개질을 이용해 임의의 효모 세포에서 분열될 수 있다. 표적 유전자의 유전적 개질을 위한 다수의 방법이 당업자에게 공지되어 있으며, 본 발명의 효모 균주를 창출하기 위해 사용될 수 있다. 표적 단백질의 발현을 감소 또는 제거하는데 사용될 수 있는 개질은 전체 유전자 또는 유전자의 일부의 결실, DNA 절편을 유전자(프로모터 또는 코딩 영역에서) 내로 삽입하여 단백질이 발현되지 않거나 더 낮은 수준에서 발현되도록 하는 것, 정지 코돈을 첨가하는 코딩 영역 내로의 돌연변이 또는 골격 이동을 도입하여 기능성 단백질이 발현되지 않게 하고, 아미노산을 변경하기 위해 하나 이상의 돌연변이를 코딩 영역 내로 도입하여 비-기능성 또는 덜 효소적으로 활성인 단백질이 발현되게 하는 것을 포함하나 이에 제한되지 않는 분열이다. 또한, 유전자의 발현은 안티센스 RNA 또는 간섭 RNA의 발현에 의해 차단될 수 있고, 구축물이 도입되어 공동저해가 초래될 수 있다. 또한, 전사체의 합성 또는 안정성은 돌연변이에 의해 저감될 수 있다. 마찬가지로, mRNA로부터 단백질이 번역되는 효율을 돌연변이에 의해 조정할 수 있다. 이들 방법 모두는 LEU1 또는 ILV3과 같이 공지된 또는 규명된 코딩 서열을 사용하여 당업자에 의해 쉽게 실행될 수 있다.

[0080] LEU1, ILV3, 또는 ACO1 코딩 서열을 둘러싼 DNA 서열은 또한 일부 개질 과정에서 유용하고, GOPID 13838을 규명하는 것과 함께, NCBI(National Center for Biotechnology Information)에 의해 조직되는 게놈 프로젝트 중 게놈 프로젝트 ID9518에 의해 조직되는 완전한 게놈 서열 내 사카로마이세스 세레비시애와 같은 효모에 대해 이용 가능하다. 효모 게놈 서열의 추가의 예는 야로위아 리폴리티카, GOPIC 13837, 및 칸디다 알비칸스의 것을 포함하며, 이는 GPID 10771, 10701 및 16373에 포함된다. 추가의 게놈은 완전히 서열화되었고 주석이 달렸으며, 하기 효모 균주 칸디다 갈브라타 CBS 138, 클루이베로마이세스 락티스 NRRL Y-1140, 피치아 스티피티스 CBS 6054, 및 스킨조사카로마이세스 폼베 972h-에 대해 공공적으로 이용가능하다.

[0081] 특히, LEU1 또는 ILV3과 같이 표적 코딩 서열을 둘러싼 DNA 서열은 상동성 재조합을 이용하는 개질 방법에 대해 유용하다. 예를 들어, 이 방법에서 측면(flanking) 서열은 선택성 마커 유전자를 결합하도록 위치되어, 상동성 재조합을 매개함으로써, 마커 유전자가 표적 유전자를 대신한다. 또한, 부분 표적 유전자 서열 및 선택성 마커 유전자를 결합하는 측면 서열은 상동성 재조합을 매개하는데 사용될 수 있고, 그리하여, 마커 유전자는 표적 유전자의 일부를 대신한다. 또한, 선택성 마커는 부위-특이적 재조합 부위에 의해 결합될 수 있어서, 상응하는 부위-특이적 재조합효소의 발현 후에, 내성 유전자는 표적 유전자를 반응화시키지 않으면서 표적 유전자로부터 절단된다. 부위-특이적 재조합은 표적 유전자 인코딩된 단백질의 발현을 분열시키는 재조합 부위 뒤에 남겨진다. 상동성 재조합 벡터는 선택성 마커의 절단 후에 표적 유전자 내에 결실을 남겨두도록 구축될 수 있으며, 이는 당업자에게 잘 알려져 있다.

[0082] 유사분열 재조합을 사용하여 결실이 생기게 할 수 있다(문헌[Wach et al. (1994) Yeast 10:1793-1808]). 이 방법은, 표적 DNA 서열과 경계를 이루며 20bp만큼 짧을 수 있는 선택가능한 마커를 게놈 영역 사이에 함유하는 DNA 절편의 제조를 수반한다. 마커 유전자의 말단에 혼성화되고 효모 게놈에 재조합할 수 있는 게놈 영역을 포함하는 올리고뉴클레오타이드를 프라이머로 사용하여, 선택가능한 마커 유전자의 PCR 증폭에 의해 이 DNA 절편을 제조할 수 있다. 선형의 DNA 절편은 효모 내로 효율적으로 형질전환되고 게놈 내에 재조합됨으로써, 표적 DNA 서열의 결실을 포함하는 유전자 대체를 유발한다(문헌[Methods in Enzymology, v194, pp 281-301 (1991)]).

- [0083] 더욱이, 프로모터 대체 방법은 Mnaimneh 등((2004) 세포 118(1):31-44) 및 본원의 실시예 12에서 기술된 바와 같이 발현을 조정하기 위한 또다른 수단을 허용하는 내인성 전사 조절 요소를 교환하는데 사용될 수 있다.
- [0084] 또한, 임의의 효모 세포 내 표적 유전자는 무작위 돌연변이를 사용해 분열될 수 있고, 이는 이어서 감소된 표적 유전자 엔사이드(encided) 활성을 갖는 균주를 규명하기 위해 스크리닝된다. 이러한 유형의 방법을 사용해, 예를 들어 표적 Fe-S 단백질의 발현에 영향을 주는 계놈의 LEU1, ILV3, 또는 임의의 다른 영역의 DNA 서열은 알려질 필요 없다.
- [0085] 유전적 돌연변이를 제작하는 방법은 보편적이고, 당업계에 잘 알려져 있고, 돌연변이체를 제작하는 실행에 적용될 수 있다. 보편적으로 사용되는 무작위 유전적 개질 방법(문헌[Methods in Yeast Genetics, 2005, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY]에서 리뷰됨)은 자연적 돌연변이, 돌연변이 유발 유전자에 의해 야기되는 돌연변이, 화학적 돌연변이, UV 또는 X-선을 사용한 조사, 또는 트랜스포존(transposon) 돌연변이를 포함한다.
- [0086] 효모의 화학적 돌연변이는 보편적으로 하기 DNA 돌연변이원 중 하나를 사용해 효모 세포를 처리하는 것을 수반한다: 에틸 메탄설폰에이트(EMS), 아질산, 다이에틸 설페이트, 또는 N-메틸-N'-니트로-N-니트로소-구아니딘(MNNG). 이러한 돌연변이 방법은 스펜서(Spencer) 등에서 리뷰되었다(문헌[Mutagenesis in Yeast, 1996, Yeast Protocols: Methods in Cell and Molecular Biology. Humana Press, Totowa, NJ]). EMS를 사용한 화학적 돌연변이는 문헌[Methods in Yeast Genetics, 2005, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY.]에서 기술된 바와 같이 수행될 수 있다. 자외선(UV) 광 또는 X-선을 사용한 조사 또한, 효모 세포에서 무작위 돌연변이를 생성하는데 사용될 수 있다. UV 조사에 의한 돌연변이의 일차 효과는 DNA 복제의 정확도(fidelity)에 분열을 일으키는 피리미딘 이량체의 형성이다. 효모의 UV-돌연변이에 대한 프로토콜은 스펜서 등에서 발견될 수 있다(문헌[Mutagenesis in Yeast, 1996, Yeast Protocols: Methods in Cell and Molecular Biology. Humana Press, Totowa, NJ]). 돌연변이 유발 유전자 표현형의 도입은 또한, 효모에서 무작위 염색체 돌연변이를 발생시키는데 사용될 수 있다. 보편적인 돌연변이 유발 유전자 표현형은 하나 이상의 하기 유전자의 분열을 통해 수득될 수 있다: PMS1, MAG1, RAD18 또는 RAD51. -돌연변이 유발 유전자 표현형의 복구는 야생형 대립 유전자의 삽입에 의해 쉽게 수득될 수 있다. 이들 또는 다른 알려진 무작위 돌연변이 방법 중 임의의 방법으로부터 생성되는 개질된 세포의 수합은 감소된 Fe-S 단백질 활성에 대해 스크리닝될 수 있다.
- [0087] 이중성 Fe-S 단백질
- [0088] 임의의 진균류 또는 식물 2Fe-2S 클러스터 다이하이드록시-산 탈수효소(DHAD) 및 임의의 Fe-S 프로판다이올 탈수효소 반응효소는 감소된 내인성 Fe-S 클러스터 단백질 발현에 대해 본원에서 개시된 바와 같이 조작된 효모 숙주 세포에서 이중성 단백질로서 발현될 수 있고, 증가된 활성이 수득될 수 있다. 이중성 단백질은 상응하는 내인성 단백질의 발현과 상이한 방식으로 발현되는 것을 포함한다. 예를 들어 효모에서, 내인성 DHAD는 핵에서 ILV3에 의해 인코딩되고, 발현된 DHAD 단백질은 미토콘드리아 표적화 신호 서열을 가져서, 단백질이 미토콘드리아 내로 위치하게 된다. Fe-S 클러스터는 분지쇄 아미노산 생합성에서 그의 활성을 위해 미토콘드리아 내 DHAD 단백질에 첨가된다. 시토플라스트 내에 위치하는 생합성 경로에의 참여를 위해 시토플라스트에서 DHAD 활성을 발현시키는 것이 바람직하다. 효모에서의 DHAD의 시토플라스트 발현은 이중성 발현인데, 왜냐하면 천연 단백질이 미토콘드리아에 위치하기 때문이다. 예를 들어, 사카로마이세스 세레비시에 내 S. 세레비시에 DHAD의 이중성 발현은 미토콘드리아 표적화 신호가 제거된 S. 세레비시에 DHAD 코딩 영역을 발현시킴으로써 수득되어서, 단백질은 시토플라스트에 머무른다. 본 발명의 개시문헌에서 사용될 수 있는 2Fe-2S DHAD는 진균류 및 식물로부터의 것을 포함한다. 대표적인 진균류 또는 식물 2Fe-2S DHAD는 표 1 및 2에 열거된다. 95% 이상의 아미노산 서열 동일성을 갖는 진균류 또는 식물 2Fe-2S DHAD는 간략화를 위해 이러한 목록을 제공하는 분석으로부터 제거되었다. 그러나, 이들 서열 중 임의의 서열에 대해 95% 이상의 아미노산 동일성을 갖는 임의의 서열은 본 발명에서 유용하다. 2Fe-2S DHAD를 수득하는데 사용되는 분석은 본원에서 참조로서 삽입된 공동소유되고 동시계속출원중인 미국 특허 출원 제 61/100792 호에서 기술되어 있다. 분석은 하기와 같다: 여기서, 프로파일 히든 마르코프 모델(Hidden Markov Model, HMM)은 8개의 기능적으로 확인된 DHAD의 아미노산 서열을 바탕으로 제조하였다. 이들 DHAD는 니트로소모나스 유로페아(DNA 서열 번호:174; 단백질 서열 번호:175), 시네코시스티스 중 PCC6803(DNA SEQ ID:176; 단백질 서열 번호:177), 스트렙토코쿠스 뮤탄스(DNA 서열 번호:178; 단백질 서열 번호:179), 스트렙토코쿠스 테오피루스(DNA 서열 번호:180; 단백질 서열 번호:181), 랄스토니아 메탈리두란스(DNA 서열 번호:182; 단백질 서열 번호:183), 랄스토니아 유트로파(DNA 서열 번호:184; 단백질 서열 번호:185), 및 락토코쿠스 락티스(DNA 서열 번호:186; 단백질 서열 번호:187)로부터이다. 또한, 프라보박테리움 온소니에(DNA 서열 번호:188; 단백질 서열 번호:189)로부터의 DHAD는 이. 콜라이(E. coli)에서 발현되고 프로파일을 제조하는데 사용된

경우, 다이하이드록시-산 탈수효소 활성을 갖는 것으로 발견되었다. 프로파일 HMM은 HMMER 소프트웨어 패키지를 사용해 제조되었다(프로파일 HMM의 배경 이론은 문헌[R. Durbin, S. Eddy, A. Krogh, and G. Mitchison, Biological sequence analysis: probabilistic models of proteins and nucleic acids, Cambridge University Press, 1998; Krogh et al., 1994; J. Mol. Biol. 235:1501-1531])에서 기술되고, 이는 HMMER에서 이용가능한 사용자 가이드에 따른다(문헌[Janelia Farm Research Campus, Ashburn, VA]). HMMER 소프트웨어 프로그램의 출력은 표 9에서 주어진 입력 서열을 특징으로 하는 프로파일 히든 마르코프 모델(HMM)이다.

[0089] 프로파일 HMM을 $< 10^{-5}$ 의 E 값에 일치시키는 임의의 단백질은 DHAD 관련 단백질이고, 이는 4Fe-4S DHAD, 2Fe-2S DHAD, 아라보네이트 탈수효소, 및 포스포글루코네이트 탈수효소를 포함한다. 다음, 프로파일 HMM을 매칭하는 서열은 스트렙토코쿠스 뮤탄스 DHAD 내 위치 56, 129 및 201에 상응하는 3개의 보존된 시스테인의 존재에 대해 분석된다. 모든 3개의 보존된 시스테인의 존재는 $[2Fe-2S]^{2+}$ 클러스터를 갖는 단백질의 특징이다. 3개의 보존된 시스테인을 갖는 단백질은 아라보네이트 탈수효소 및 2Fe-2S DHAD를 포함한다. 2Fe-2S DHAD는 스트렙토코쿠스 뮤탄스 DHAD 아미노산 서열 내 하기 위치에 상응하는 위치에서 2Fe-2S DHAD 또는 아라보네이트 탈수효소 내에 존재하는 것으로 발견된 시그내처(signature) 보존된 아미노산에 대해 분석함으로써 아라보네이트 탈수효소와 구분될 수 있다. 이들 시그내처 아미노산은 하기 위치(90%초과의 발생률)에서 각각 2Fe-2S DHAD 또는 아라보네이트 탈수효소 내에 존재한다: 88 아스파라긴산 대(vs) 글루탐산; 113 비보존된 산 대 글루탐산; 142 아르기닌 또는 아스파라긴 대 비보존; 165: 비보존 대 글리신; 208 아스파라긴 대 비보존; 454 루신 대 비보존; 477 페닐알라닌 또는 타이로신 대 비보존; 및 487 글리신 대 비보존.

[0090] 서열 번호:46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150 및 152와 같이 진균류 또는 식물 기점을 갖는 이러한 방법에 의해 규명되는 단백질은 이들 서열 중 임의의 서열에 대해 적어도 약 95%, 96%, 97%, 98%, 또는 99%의 아미노산 동일성을 갖는 임의의 단백질뿐만 아니라 본 발명에서 사용될 수 있다. 단백질 서열의 전장에 걸쳐 갭 페널티=10, 갭 길이 페널티=0.1, 및 단백질 중량 매트릭스의 고넷 250 시리즈의 디폴트 파라미터를 사용하는 클러스탈 W 정렬 방법을 이용해 서열 번호:114에 대해 적어도 약 90%의 아미노산 서열 동일성을 갖는 DHAD 및 클루이베로마이세스 락티스로부터의 DHAD(서열 번호:114)가 특히 적합하다.

[0091] 또한, 본 발명에서 사용될 수 있는 진균류 또는 식물 2Fe-2S DHAD는 DHAD 관련 단백질의 계통수의 진균류 또는 식물 2Fe-2S DHAD 분지 내 그의 위치에 의해 규명될 수 있다. 또한, 사용될 수 있는 2Fe-2S DHAD는 그의 서열이 본원에 제공되는 진균류 또는 식물 2Fe-2S DHAD 중 임의의 것과의 서열 비교를 이용해 규명될 수 있으며, 여기서, 서열 동일성은 적어도 약 80%-85%, 85%-90%, 90%-95% 또는 95%-99%일 수 있다.

[0092] 추가로, 본원에서 제공되는 진균류 또는 식물 2Fe-2S DHAD의 서열은 자연상에서 다른 호모로그를 규명하는데 사용될 수 있다. 예를 들어, 서열 번호:45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149 및 151로서 본원에서 주어지는 DHAD 인코딩 핵산 절편의 각각은 LEU1 코딩 영역에 대해 상기에서 기술된 바와 같이 상동성 단백질을 인코딩하는 유전자를 단리하는데 사용될 수 있다.

[0093] 로세부리아 이눌리니보란스의 조효소 B12-독립적 프로판다이올 탈수효소 반응효소는 활성을 위해 Fe-S 클러스터를 필요로 하는 단백질이다. 이 단백질, RdhtB는 본원에 참조로서 삽입된 동시계속출원인 미국 특허 공보 제 US20090155870 호에 개시된다. RdhtB는 로세부리아 이눌리니보란스의 조효소 B12-독립적 프로판다이올 탈수효소를 반응화시키고, 이는, RdhtA라고 명명되며 또한 공동 소유되고 동시계속출원중인 미국 특허 공보 제 US20090155870 호에서 개시된다. RdhtB의 활성은 RdhtB가 RdhtA 활성화에 필요하기 때문에 RdhtA의 활성을 검정함으로써 평가될 수 있다. RdhtB의, 그리고 따라서 RdhtA의 활성은 본원에서 개시된 감소된 내인성 Fe-S 단백질 발현이 있는 효모 숙주에서 발현시킴으로써 향상된다. 활성을 위해 Fe-S 클러스터를 필요로 하는 임의의 조효소 B12-독립적 프로판다이올 탈수효소 반응효소의 이중성 발현은 감소된 내인성 Fe-S 단백질 발현을 갖는 효모 균주에서 향상될 수 있다. 조효소 B12-독립적 프로판다이올 탈수효소 반응효소는 조효소 B12의 존재 또는 부재 하에, 연관된 프로판다이올 탈수효소 효소의 프로판다이올 탈수효소 활성을 평가함으로써 당업자에 의해 쉽게 규명될 수 있다. 예는 클로스트리듐 부티리쿰(코딩 영역 서열 번호:192; 단백질 서열 번호:193)의 다이올 탈수효소 반응효소이다.

[0094] 사용될 수 있는 다른 조효소 B12-독립적 프로판다이올 탈수효소 반응효소는 당업자에 의해 RdhtB 서열 변

호:44의 서열과 비교해 서열의 생물정보학 분석을 통해 규명될 수 있다. 조효소 B12-독립적 프로판다이올 탈수효소 반응화효소 활성 및 적어도 약 80%-85%, 85%-90%, 90%-95% 또는 95%-99%의 서열 번호:44에 대한 서열 동일성을 갖는 단백질이 사용될 수 있다. 단백질 서열의 전장에 걸쳐 갭 페널티=10, 갭 길이 페널티=0.1, 및 단백질 중량 매트릭스의 고넷 250 시리즈의 디폴트 파라미터를 이용하는 클러스탈 W 정렬 방법을 사용해 서열 번호:44에서 나타난 아미노산 서열에 대해 적어도 약 90% 동일한 것들이 특히 적합하다.

[0095] 또한, 사용될 수 있는 다른 조효소 B12-독립적 프로판다이올 탈수효소 반응화효소 호모로그는 LEU1 코딩 영역에 대해 상기에서 기술된 바와 같은 방법에 의해 RdhtB 코딩 영역(서열 번호:16)을 사용해 규명될 수 있다.

[0096] 이중성 Fe-S 단백질의 발현

[0097] 발현은 Fe-S 단백질을 인코딩하는 서열을 형질전환시킴으로써 달성된다. 발현되는 코딩 영역은 당업자에 의해 잘 알려진 바와 같이, 표적 숙주 세포에 대해 최적화된 코돈일 수 있다. 효모에서의 유전자 발현 방법은 당업계에 알려져 있다(예를 들어 문헌[Methods in Enzymology, Volume 194, Guide to Yeast Genetics and Molecular and Cell Biology (Part A, 2004, Christine Guthrie and Gerald R. Fink (Eds.), Elsevier Academic Press, San Diego, CA]를 참조). 효모에서의 유전자의 발현은 전형적으로는 흥미있는 코딩 영역에 조작적으로 연결된 프로모터, 및 전사 종결자를 필요로 한다. 많은 효모 프로모터가 효모에서 유전자에 대한 발현 카세트를 구축하는데 사용될 수 있으며, 이는 하기 유전자로부터 유도된 프로모터를 포함하나 이에 제한되지 않는다: CYC1, HIS3, GAL1, GAL10, ADH1, PGK, PHO5, GAPDH, ADC1, TRP1, URA3, LEU2, ENO, TPI, CUP1, FBA, GPD, GPM, 및 AOX1. 적합한 전사 종결자는 FBAt, GPDt, GPMt, ERG10t, GAL1t, CYC1, 및 ADH1을 포함하나 이에 제한되지 않는다.

[0098] 적합한 프로모터, 전사 종결자, 및 코딩 영역은 이. 콜라이-효모 서틀 벡터 내로 클로닝되고, 효모 세포 내로 형질전환될 수 있다. 이들 벡터는 이. 콜라이 및 효모 균주 모두에서 균주 증식을 허용한다. 전형적으로는 사용되는 벡터는 목적하는 숙주 내에서의 자율 복제 또는 염색체 함입을 허용하는 서열 및 선택성 마커를 함유한다. 효모에서 통상적으로 사용되는 플라스미드는 서틀 벡터 pRS423, pRS424, pRS425 및 pRS426(메틀랜드주 락빌 소재의 아메리칸 타입 컬처 콜렉션(American Type Culture Collection))으로서, 이들은 이. 콜라이 복제 기점(예를 들어, pMB1), 효모 2 μ 복제 기점, 및 영양 선택(nutritional selection)을 위한 마커를 포함한다. 이들 4 가지 벡터를 위한 선택 마커는 His3(벡터 pRS423), Trp1(벡터 pRS424), Leu2(벡터 pRS425) 및 Ura3(벡터 pRS426)이다. 기술된 Fe-S 단백질 코딩 영역을 인코딩하는 키메라 유전자가 있는 발현 벡터의 구축은 이. 콜라이에서의 표준 분자 클로닝 기법에 의해 또는 효모에서의 갭 수선 재조합 방법에 의해 수행될 수 있다.

[0099] 갭 수선 클로닝 접근법은 효모에서의 고효율 상동성 재조합을 이용한다. 전형적으로는, 효모 벡터 DNA는 분해되어(예를 들어, 그의 다수의 클로닝 부위에서), 그의 서열 내에 "갭"을 만든다. 서로, 및 벡터 DNA의 5' 및 3' 말단과 서열상 중복되는 ≥ 21 bp 서열을 5' 및 3' 말단 모두에 함유하는, 관심의 대상인 다수의 삽입 DNA가 생성된다. 예를 들어, "유전자 X"에 대한 효모 발현 벡터를 구축하기 위해, 효모 프로모터 및 효모 종결자가 발현 카세트에 대해 선택된다. 프로모터 및 종결자는 효모 게놈 DNA로부터 증폭되고, 유전자 X는 그의 공급원 유기체로부터 PCR 증폭되거나 유전자 X 서열을 포함하는 클로닝 벡터로부터 수득된다. 선형화된 벡터의 5' 말단 및 프로모터 서열의 사이, 프로모터 및 유전자 X의 사이, 유전자 X 및 종결자 서열의 사이, 및 종결자 및 선형화된 벡터의 3' 말단 사이에는 적어도 21bp의 중복 서열이 있다. 다음, "갭핑된(gapped)" 벡터 및 삽입 DNA는 효모 균주 내로 공동형질전환되고, 플라스미드 상의 영양성 선택 마커의 상보성을 허용하는 적절한 화합물 혼합물을 함유하는 배지 상에 플레이팅된다. 선택된 세포로부터 제조된 플라스미드 DNA를 사용하는 PCR 맵핑에 의해 정확한 삽입 조합의 존재를 확인할 수 있다. 그 다음에는, 효모로부터 단리된 플라스미드 DNA(통상적으로 농도가 낮음)를 이. 콜라이 균주, 예를 들어, TOP10에 형질전환시킨 후, 미니 프랩(mini prep) 및 제한효소 맵핑(restriction mapping)으로 플라스미드 구축물을 추가로 확인할 수 있다. 마지막으로, 서열 분석에 의해 구축물을 확인할 수 있다.

[0100] 갭 수선 기법과 같이, 효모 게놈 내로의 함입은 또한 효모에서 상동성 재조합 시스템의 이점을 취한다. 전형적으로는, 코딩 영역 + 조절 요소(프로모터 및 종결자) 및 영양요구성 마커를 함유하는 카세트는 삽입이 요구되는 게놈 구역의 5' 및 3' 영역에 상동성인 서열의 40-70개 염기쌍을 함유하고 카세트에 혼성화되는 프라이머를 사용해 높은-정확도 DNA 증합효소를 사용해 PCR-증폭된다. 다음, PCR 생성물은 효모 내로 형질전환되고, 함입된 영양요구성 마커에 대한 선택을 허용하는 적절한 화합물 혼합물을 함유하는 배지 상에 플레이팅된다. 예를 들어, "유전자 X"를 염색체 위치 내로 함입하기 위해, "Y", 프로모터-코딩 영역X-종결자 구축물은 플라스미드 DNA 구축물로부터 PCR 증폭되고, SOE PCR에 의해 또는 보편적인 제한 분해물 및 클로닝에 의해 독립영양 마커(예컨

대 URA3)에 합류된다. 프로모터-코딩 영역X-종결자-URA3 영역을 함유하는 전체 카세트는 효모 염색체 상의 위치 "Y"의 5' 및 3' 영역에 상동성인 40-70bp를 함유하는 프라이머 서열을 사용해 PCR 증폭된다. PCR 생성물은 효모 내로 형질전환되고, 우라실이 결여된 성장 배지 상에서 선택된다. 형질전환체는 콜로니 PCR에 의해 또는 염색체 DNA의 직접적인 서열화에 의해 확인될 수 있다.

- [0101] 본 발명의 효모 세포에서 발현되는 임의의 코딩 영역은 당업자에게 잘 알려진 바와 같이 조작되는 특정 숙주 효모 세포에서의 발현을 위해 최적화된 코돈일 수 있다. 예를 들어, S. 세레비시에 내 K. 락티스 및 P. 스티피티스 ILV3 코딩 영역의 발현을 위해, 각각은 본원 실시예 1에서 S. 세레비시에 발현에 대해 코돈 최적화되었다.
- [0102] 이종성 Fe-S 단백질 활성이 향상된 생성물 생합성
- [0103] 그의 생합성 경로에 기여하는 Fe-S 단백질을 갖는 임의의 생성물의 생성은 내인성 Fe-S 단백질 발현이 감소된 효모 숙주에서 이종성 발현된 Fe-S 단백질의 본원에서 개시된 향상된 활성으로부터 이점을 취할 수 있다. 예를 들어, DHAD는 아이소부탄올의 생합성 경로에서의 단계를 제공하고, RdhB는 2-부타논 또는 2-부탄올을 생성하기 위한 생합성 경로에 기여한다.
- [0104] 아이소부탄올의 합성을 위해 DHAD에 의해 수행되는 단계를 포함하는 생합성 경로는 본원에서 참조로서 삽입된, 공동소유이고 동시계속출원인 미국 특허 출원 제 20070092957 A1 호에서 개시된다. 개시된 아이소부탄올 생합성 경로의 다이어그램은 도 1에서 제공된다. 본원에서 개시된 균주에서의 아이소부탄올의 생성은 증가된 DHAD 활성으로부터 이점을 얻는다. 미국 특허 공보 제 US20070092957 A1 호에서 기술된 바와 같이, 실시예 아이소부탄올 생합성 경로에서의 단계는 하기의 전환을 포함한다:
- [0105] 예를 들어 아세토락테이트 합성효소에 의해 촉매화된 - 피루베이트에서 아세토락테이트로의 전환(도 1 경로 단계 a);
- [0106] 예를 들어 아세토하이드록시산 아이소머리덕테이즈(isomeroreductase)에 의해 촉매화된 - 아세토락테이트에서 2,3-다이하이드록시아이소발레레이트로의 전환(도 1 경로 단계 b);
- [0107] 예를 들어 DHAD라고도 하는 아세토하이드록시산 탈수효소에 의해 촉매화된 - 2,3-다이하이드록시아이소발레레이트에서 α -케토아이소발레레이트로의 전환(도 1 경로 단계 c);
- [0108] 예를 들어 분지쇄 α -케토산 탈탄소효소에 의해 촉매화된 - α -케토아이소발레레이트에서 아이소부티르알데하이드로의 전환(도 1 경로 단계 d); 및
- [0109] 예를 들어 분지쇄 알코올 탈수소효소에 의해 촉매화된 - 아이소부티르알데하이드에서 아이소부탄올로의 전환(도 1 경로 단계 e).
- [0110] 대안적인 경로의 단계 f, g, h, I, j, 및 k에 대해, 기질에서 생성물로의 전환, 및 이러한 반응에 수반되는 효소는 US 20070092957 A1에 기술된다.
- [0111] 아이소부탄올 경로에 대한 효소의 발현에 사용될 수 있는 유전자는 US 20070092957 A1에 기술되고, 사용될 수 있는 추가의 유전자는 생물정보학을 통해 또는 상기 기술된 바와 같이 실험적으로 당업자에 의해 규명될 수 있다. 특히 높은 활성을 갖는 케톨-산 리덕토아이소머레이즈(KARI) 효소의 모든 3개의 경로에서의 바람직한 사용은 공동소유되고 동시계속출원인 미국 특허 공보 제 US20080261230 호에서 개시된다. 거기에서 개시된 높은 활성의 KARI의 예는 비브리오 콜레라(DNA: 서열 번호:35; 단백질 서열 번호:36), 슈도모나스 에루기노사 PA01(DNA: 서열 번호:37; 단백질 서열 번호:38), 및 슈도모나스 플루오레센스 PF5(DNA: 서열 번호:39; 단백질 서열 번호:40)로부터의 것들이다.
- [0112] 개시된 생합성 경로를 이용하는 아이소부탄올 생성을 위한 사카로마이세스 세레비시에에 의해 예시되는 키메라 유전자의 구축 및 효모의 유전적 조작은 US 20070092957 A1에서 추가로 기술된다.
- [0113] 2-부타논 및 2-부탄올의 합성을 위한 프로판다이올 탈수효소를 포함한 생합성 경로는 본원에서 참조로서 삽입된, 공동소유이고 동시계속출원인 미국 특허 공보 제 US20070292927A1 호에서 개시된다. 개시된 2-부타논 및 2-부탄올 생합성 경로의 다이어그램은 도 2에서 제공된다. 2-부타논은 2-부타논에서 2-부탄올로의 마지막 도식된 전환 단계가 생략된 경우 만들어지는 생성물이다. 본원에서 개시된 균주에서의 2-부타논 또는 2-부탄올의 생성은 증가된 조효소 B12-독립적 프로판다이올 탈수효소 반응효소 활성으로부터 이점을 얻는다. 미국 특허 공보 제 US20070292927A1 호에서 기술된 바와 같이, 개시된 생합성 경로에서의 단계는 하기의 전환을 포함한다:

- [0114] 예를 들어 아세토락테이트 합성효소에 의해 촉매화되는 피루베이트에서 아세토락테이트로의 전환(도 2 단계 a);
- [0115] 예를 들어 아세토락테이트 탈탄소효소에 의해 촉매화되는 아세토락테이트에서 아세토인으로의 전환(도 2 단계 b);
- [0116] 예를 들어 부탄다이올 탈수소효소에 의해 촉매화되는 아세토인에서 2,3-부탄다이올로의 전환(도 2 단계 i);
- [0117] 예를 들어 다이올 탈수소효소 글리세롤 탈수소효소, 또는 프로판다이올 탈수소효소에 의해 촉매화되는 2,3-부탄다이올에서 2-부타논으로의 전환(도 2 단계 j); 및
- [0118] 예를 들어 부탄올 탈수소효소에 의해 촉매화되는 2-부타논에서 2-부탄올로의 전환(도 2 단계 f).
- [0119] 이들 효소의 발현에 사용될 수 있는 유전자는 미국 특허 공보 제 US20070292927A1 호에 기술된다. 로세부리아 이놀리니보란스로부터의 부탄다이올 탈수소효소, RdhtA(단백질 서열 번호:43, 코딩 영역 서열 번호:15)의 효모에 서의 이러한 경로에서의 사용은 공동소유되고 동시계속출원인 미국 특허 공보 제 US20090155870 호에서 개시된다. 이 효소는 로세부리아 이놀리니보란스로부터의 부탄다이올 탈수소효소 반응효소, RdhtB(단백질 서열 번호:44, 코딩 영역 서열 번호:16)와의 공액에서 사용된다. 이러한 부탄다이올 탈수소효소는 그것이 조효소 B₁₂를 필요로 하지 않기 때문에 많은 숙주에서 요구된다.
- [0120] US 20070292927A1 개시된 생합성 경로를 사용한 2-부탄올 생성을 위한 효모의 유전적 조작 및 키메라 유전자의 구축은 미국 특허 공보 제 US20090155870 호에서 추가로 기술된다.
- [0121] 발효 배지
- [0122] 본원에서 개시된 효모는 생합성 경로의 일부로서 Fe-S 단백질질을 갖는 생성물의 생성을 위한 발효 배지에서 성장될 수 있다. 발효 배지는 적합한 탄소 기질을 함유해야 한다. 적합한 기질은 단당류, 예를 들어 포도당 및 과당, 올리고당류, 예를 들어 락토스 또는 수크로스, 다당류, 예를 들어 전분 또는 셀룰로오스 또는 그 혼합물 및 재생가능한 원료로부터의 미정제 혼합물, 예를 들어 유청 투과액, 옥수수 침지수, 사탕무 당밀 및 보리 맥아를 포함할 수 있으나 이에 한정되지 않는다. 또한, 탄소 기질은 1-탄소 기질, 예를 들어, 이산화탄소, 또는 중요 생화학적 중간체로의 대사적 전환이 입증된 메탄올일 수도 있다. 메틸로트로픽 유기체(methylotrophic organism)는 또한, 1 탄소 및 2 탄소 기질에 부가하여 다수의 다른 탄소 함유 화합물, 예를 들어 메틸아민, 글루코사민 및 다양한 아미노산을 대사 활성화에 이용하는 것으로 공지되어 있다. 예를 들어, 메틸로트로픽 효모는 메틸아민으로부터의 탄소를 이용하여 트레할로스 또는 글리세롤을 형성하는 것으로 공지되어 있다(문헌[Bellion et al., Microb. Growth C1 Compd., [Int. Symp.], 7th (1993), 415-32. Editor(s): Murrell, J. Collin; Kelly, Don P. Publisher: Intercept, Andover, UK]). 마찬가지로, 다양한 종의 칸디다는 알라닌 또는 올레산을 대사작용한다(문헌[Sulter et al., Arch. Microbiol. 153:485-489 (1990)]). 그러므로, 본 발명에 이용되는 탄소 공급원은 광범위한 탄소 함유 기질을 포함할 수 있으며 유기체의 선택에 의해서만 한정되는 것으로 생각된다.
- [0123] 상기 언급한 탄소 기질 및 그 혼합물 모두가 본 발명에 적합한 것으로 생각되지만, 바람직한 탄소 기질은 포도당, 과당 및 수크로스이다.
- [0124] 적절한 탄소 공급원외에도, 발효 배지는 적합한 무기질, 염, 보조인자, 완충제 및 다른 성분을 함유해야 하고, 이는 당업계에 알려져 있으며, 목적하는 생성물의 생성에 필요한 효소 경로의 촉진 및 배양물의 성장에 적합하다.
- [0125] 배양 조건
- [0126] 통상적으로 세포는 약 20℃ 내지 약 37℃ 범위의 온도에서 적절한 배지 내에 성장시킨다. 본 발명에서 적합한 성장 배지는, 효모 질소 베이스, 암모늄 설페이트, 및 탄소/에너지 공급원으로서의 텍스트로스를 포함하는 브로스(broth) 또는 대부분의 사카로마이세스 세레비시에 균주의 성장을 위한 최적 비율로 펩톤, 효모 추출물 및 텍스트로스를 블렌딩한 YPD 배지와 같이 상업적으로 제조된 통상적인 배지이다. 그밖에 정의되거나 합성된 성장 배지도 사용할 수 있으며, 특정 미생물의 성장에 적절한 배지는 미생물학 또는 발효과학 분야의 당업자에게 공지되어 있다.
- [0127] 발효에 적합한 pH 범위는 pH 3.0 내지 pH 7.5이며, 여기서 초기 조건으로서 바람직한 범위는 pH 4.5.0 내지 pH 6.5이다.

- [0128] 발효는 유산소 또는 무산소 조건하에서 수행될 수 있으며, 여기서 유산소 또는 미량산소(microaerobic) 조건이 바람직하다.
- [0129] 당업계에 공지된 다수의 방법, 예를 들어, 고속액체 크로마토그래피(HPLC) 또는 기체 크로마토그래피(GC)를 사용하여 발효 배지 내에 생성된 부탄올의 양을 결정할 수 있다.
- [0130] 산업적 배치(Batch) 및 연속 발효
- [0131] 본 방법은 배치 발효 방법을 적용한다. 고전적인 배치 발효는 배지의 조성이 발효 시작시에 정해지며, 발효 중에 인공적으로 변경되지 않는 폐쇄 시스템이다. 따라서, 발효의 시작시에 배지에 원하는 유기체(들)가 접종되며, 상기 시스템에 어떠한 것도 첨가하지 않고서 발효가 발생하게 한다. 그러나, 전형적으로 "배치" 발효는 탄소 공급원의 첨가와 관련하여 배치식이며, pH 및 산소 농도와 같은 인자를 조절하려는 시도가 흔히 이루어진다. 배치 시스템에서, 이 시스템의 대사산물 및 바이오매스 조성물은 발효가 중단되는 시점까지 끊임없이 변화한다. 배치 배양 내에서 세포는 정적 유도기(static lag phase)를 통하여 고 성장 대수기(log phase)로, 그리고 마지막으로 성장 속도가 감소되거나 정지되는 정체기(stationary phase)로 완화된다. 미처리될 경우, 정체기의 세포는 결국 죽을 것이다. 대수기의 세포는 일반적으로 최종 생산물 또는 중간체의 대량 생산에 책임이 있다.
- [0132] 표준 배치 시스템의 한 변종은 유가식(Fed-Batch) 시스템이다. 또한, 유가식 발효 공정이 본 발명에서 적합하며, 이는 발효가 진행됨에 따라 기질이 증분식으로 첨가된다는 것을 제외하고는 전형적인 배치 시스템을 포함한다. 유가식 시스템은 이화 대사산물 억제에 세포의 대사 작용을 저해하는 경향이 있을 때 그리고 배지 중에 한정된 양의 기질이 있는 것이 바람직한 경우 유용하다. 유가식 시스템 중 실제 기질 농도의 측정은 어려우며, 따라서 pH, 용존 산소 및 CO₂와 같은 폐 가스의 분압과 같은 측정가능한 인자의 변화를 기반으로 하여 계산된다. 배치식 및 유가식 발효는 통상적이며, 당업계에 잘 알려져 있고, 그 예를 본 명세서에 참고로 포함된 문헌[Thomas D. Brock, Biotechnology: A Textbook of Industrial Microbiology, Second Edition (1989) Sinauer Associates, Inc., Sunderland, MA..] 또는 문헌[Deshpande, Mukund V., Appl. Biochem. Biotechnol., 36:227, (1992)]에서 찾을 수 있다.
- [0133] 본 발명이 배치 방식으로 수행되더라도, 방법은 연속 발효 방법에 적용될 것임이 고려된다. 연속식 발효는 규정된 발효 배지가 계속하여 생물 반응기에 첨가되고, 동일한 양의 조절 배지가 가공을 위하여 동시에 제거되는 개방 시스템이다. 연속 발효는 일반적으로, 세포가 주로 로그상 성장에 존재하는 경우 일정한 고밀도에서 배양물을 유지시킨다.
- [0134] 연속식 발효는 세포 성장 또는 최종 생산물 농도에 영향을 주는 하나의 인자 또는 임의의 개수의 인자의 조절을 허용한다. 예를 들어, 한 가지 방법은 제한 영양소, 예를 들어 탄소 공급원 또는 질소의 수준을 고정된 비율로 유지하고 모든 다른 파라미터는 조정되게 할 것이다. 다른 시스템에서, 성장에 영향을 미치는 많은 인자는, 배지 탁도에 의해 측정되는 세포 농도가 일정하게 유지되는 한편, 지속적으로 변경될 수 있다. 연속식 시스템은 정상 상태 성장 조건을 유지하도록 노력하며, 따라서 배출되는 배지로 인한 세포 손실은 발효에서 세포 성장 속도에 대하여 균형이 맞추어져야 한다. 연속식 발효 공정에 있어서 영양소 및 성장 인자를 조정하는 방법뿐만 아니라, 생산물 형성 속도를 최대화하는 기술도 산업 미생물학 분야에서 잘 알려져 있으며, 다양한 방법이 브록(Brock)의 상기 문헌에 상술되어 있다.
- [0135] 본 발명은 배치, 유가식 또는 연속 방법을 사용해 실행될 수 있고, 알려진 발효 방식은 적합하다. 부가적으로, 세포는 전세포 촉매로서 기질 상에 고정되어 1-부탄올 생성을 위한 발효 조건에 처해질 수 있다고 생각된다.
- [0136] 발효 배지로부터 부탄올을 분리하는 방법
- [0137] 생물적생성된 부탄올은 당업계에 알려진 방법을 사용해 발효 배지로부터 분리될 수 있다. 예를 들어, 원심분리, 여과, 경사분리(decantation) 등에 의해 발효 배지로부터 고체를 제거할 수 있다. 그 다음에, 증류, 액-액 추출 또는 막-기체의 분리와 같은 방법을 사용하여, 상기와 같이 고체를 제거하기 위해 처리한 발효 배지로부터 부탄올을 분리할 수 있다. 부탄올과 물은 비등점이 낮은 공비 혼합물(azeotropic mixture)을 형성하므로, 증류를 이용하면 혼합물을 그의 공비 조성까지만 분리할 수 있다. 다른 분리 방법과 조합하여 증류를 사용하여 공비점 부근의 분리를 달성할 수 있다. 부탄올의 분리 및 정제를 위하여 증류와 조합하여 사용할 수 있는 방법은 경사분리, 액-액 추출, 흡착 및 막-기체의 기술을 포함하나 이에 한정되지 않는다. 또한, 동반물질(entrainer)을 사용하는 공비 증류를 이용하여 부탄올을 분리할 수 있다(예를 들어, 문헌[Doherty and Malone, Conceptual Design of Distillation Systems, McGraw Hill, New York, 2001]).

- [0138] 부탄올-물 혼합물은 불균질 공비 혼합물을 형성하므로, 경사분리와 조합하여 증류를 이용함으로써 부탄올을 분리 정제할 수 있다. 이 방법에서는 부탄올을 함유하는 발효 브로스를 공비 조성 부근까지 증류한다. 그 다음에, 공비 혼합물을 응축시키고 경사분리에 의해 발효 배지로부터 부탄올을 분리한다. 경사분리된 수성상은 제1 증류 컬럼에 환류되어 돌아갈 수 있다. 부탄올이 풍부한 경사분리 유기상을 제2 증류 컬럼에서 증류에 의해 추가로 정제할 수 있다.
- [0139] 증류와 조합한 액-액 추출을 사용하여 발효 배지로부터 부탄올을 분리할 수도 있다. 이 방법에서는 적합한 용매로 액-액 추출하여 발효 브로스로부터 부탄올을 추출한다. 그 후에 부탄올-함유 유기상을 증류하여 용매로부터 부탄올을 분리한다.
- [0140] 흡착과 조합한 증류를 사용하여 발효 배지로부터 부탄올을 분리할 수도 있다. 이 방법에서는, 부탄올을 함유하는 발효 브로스를 공비 조성 부근까지 증류한 후에 분자체와 같은 흡착제를 사용하여 잔류하는 물을 제거한다(문헌[Aden et al. Lignocellulosic Biomass to Ethanol Process Design and Economics Utilizing Co-Current Dilute Acid Prehydrolysis and Enzymatic Hydrolysis for Corn Stover, Report NREL/TP-510-32438, National Renewable Energy Laboratory, June 2002]).
- [0141] 또한, 투과증발(pervaporation)과 조합한 증류를 사용하여 발효 배지로부터 부탄올을 분리 정제할 수도 있다. 이 방법에서는, 부탄올을 함유하는 발효 브로스를 공비 조성 부근까지 증류한 후에 친수성 막을 통한 투과증발에 의해 잔류하는 물을 제거한다(문헌[Guo et al., J. Membr. Sci. 245, 199-210 (2004)]).
- [0142] 실시예
- [0143] 본 발명은 추가로 하기 실시예에서 정의된다. 이들 실시예는 본 발명의 바람직한 실시 형태를 나타내는 한편, 단지 예시로 주어짐을 이해해야 한다. 당업자라면, 상기 논의 및 이러한 실시예로부터 본 발명의 본질적인 특징을 확인할 수 있으며, 본 발명의 사상 및 범주를 벗어나지 않고서도 본 발명을 다양하게 변경하고 수정하여 본 발명을 다양한 용도 및 조건에 적합하게 할 수 있다.
- [0144] 일반적인 방법
- [0145] 본 실시예에서 사용된 표준 재조합 DNA 및 분자 클로닝 기법은 당업계에 주지된 것으로서 문헌[Sambrook, J., Fritsch, E. F. and Maniatis, T. Molecular Cloning: A Laboratory Manual; Cold Spring Harbor Laboratory Press: Cold Spring Harbor, NY (1989) (Maniatis)]; 및 [T. J. Silhavy, M. L. Bannan, and L. Enquist, Experiments with Gene Fusions, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. 1984)]; 및 [Ausubel, F. M. et al., Current Protocols in Molecular Biology, pub. by Greene Publishing Assoc. and Wiley-Interscience (1987), and by Methods in Yeast Genetics, 2005, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY]에 의해 기술된다.
- [0146] 박테리아 배양물의 유지 및 성장을 위해 적합한 재료 및 방법은 당업계에 주지되어 있다. 하기 실시예에서 사용하기에 적합한 기술들은 문헌[Manual of Methods for General Bacteriology, Philipp Gerhardt, R. G. E. Murray, Ralph N. Costilow, Eugene W. Nester, Willis A. Wood, Noel R. Krieg and G. Briggs Phillips, eds, American Society for Microbiology, Washington, DC. (1994)]; 또는 [Thomas D. Brock, Biotechnology: A Textbook of Industrial Microbiology, Second Edition, Sinauer Associates, Inc., Sunderland, MA (1989)]에 정리된 바와 같이 찾을 수 있다. 미생물 세포의 성장 및 유지에 사용되는 모든 시약, 제한 효소 및 물질은 알드리치 케미칼스(밀워키, 위스콘신주 소재), BD 다이아그노스틱스 시스템(스파크, 메릴랜드주 소재), 라이프 테크놀로지스(록빌, 메릴랜드주 소재), 또는 시그마 케미칼 컴퍼니(세인트루이스, 미주리주 소재)로부터 입수하였다. 다르게 표시하지 않는 한, 미생물 균주는 버지니아주 메너서스 소재의 아메리칸 타입 컬처 콜렉션(ATCC)으로부터 입수하였다. 모든 올리고뉴클레오타이드 프라이머는 시그마-제노시스(Sigma-Genosys)(우드랜드, 텍사스주 소재) 또는 인테그레이티드 DNA 테크놀로지스(Integrated DNA Technologies)(코랄스빌, 아이오와주 소재)에 의해 합성하였다.
- [0147] 합성 완전한 배지는 문헌[Amberg, Burke and Strathern, 2005, Methods in Yeast Genetics, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY]에 기술된다.
- [0148] HPLC
- [0149] 발효 부산물 조성물의 분석은 당업계에 잘 알려져 있다. 예를 들어, 하나의 고성능 액체 크로마토그래피(HPLC) 방법은 쇼텍스 SH-1011 칼럼(Shodex SH-1011 column)을 쇼텍스 SH-G 가드 칼럼(Shodex SH-G guard column)(둘

다 와터스 코퍼레이션, 밀포드, 마이애미주 소재(Waters Corporation, Milford, MA)에서 이용가능함)과 함께, 굴절률(RI) 검출과 함께 이용한다. 0.01M H₂SO₄를 이동상으로서 사용하여 50℃의 컬럼 온도 및 0.5ml/분의 유속으로 크로마토그래피 분리를 수행한다. 아이소부탄올 체류 시간은 47.6분이다.

[0150] 약어의 의미는 다음과 같다: "s"는 초(들)를 의미하고, "min"은 분(들)을 의미하고, "h"는 시간(들)을 의미하고, "psi"는 제곱 인치 당 파운드(pounds per square inch)를 의미하고, "nm"은 나노미터를 의미하고, "d"는 일(day)(들)을 의미하고, "μl"은 마이크로리터(들)를 의미하고, "ml"은 밀리리터(들)를 의미하고, "L"은 리터(들)를 의미하고, "mm"은 밀리미터(들)를 의미하고, "nm"은 나노미터(들)를 의미하고, "mM"은 밀리몰을 의미하고, "M"은 몰을 의미하고, "mmol"은 밀리몰수(들)를 의미하고, "μmol"은 마이크로몰수(들)를 의미하고, "g"는 그램(들)을 의미하고, "μg"는 마이크로그램(들)을 의미하고, "ng"는 나노그램(들)을 의미하고, "PCR"은 중합효소 연쇄 반응을 의미하고, "OD"는 광학 밀도를 의미하고, "OD₆₀₀"은 600nm의 파장에서 측정되는 광학 밀도를 의미하고, "kDa"는 킬로달톤을 의미하고, "g"는 중력 상수(gravitation constant)를 의미하고, "bp"는 염기쌍(들)을 의미하고, "kbp"는 킬로염기쌍(들)을 의미하고, "% w/v"는 중량/부피%를 의미하고, "% v/v"는 부피/부피%를 의미하고, "wt %"는 중량%를 의미하고, "HPLC"는 고성능 액체 크로마토그래피를 의미하고, "GC"는 기체 크로마토그래피를 의미한다. 용어 "몰 선택도"는 소비된 당 기질의 몰 당 생성된 생성물의 몰수이며, 퍼센트로서 기술된다.

[0151] 실시예 1

[0152] S. 세레비시아의 LEU1 결실 균주에서 K. 락티스로부터의 DHAD의 발현

[0153] 효모 LEU1 유전자는 그의 기능을 위해 Fe-S 클러스터를 필요로 하는 효소인 아이소프로필말레이트 탈수효소를 인코딩한다. 클루이베로마이세스 락티스 DHAD 코딩 영역으로부터 발현되는 DHAD 활성화에 대한 LEU1 결실의 영향은 본 실시예에서 검사하였다. 효모에서의 유전자 발현을 위해, pRS423으로부터 유도된 서틀 벡터 pNY13(서열 번호:29)을 사용하였다. 이러한 서틀 벡터는 이. 콜라이에서의 유지를 위한 F1 복제 기점(1423 내지 1879) 및 효모에서의 복제를 위한 2개의 미크론 기점(micron origin)(뉴클레오타이드 7537 내지 8881)을 함유하였다. 벡터는 FBA 프로모터(뉴클레오타이드 2111 내지 3110) 및 FBA 종결자(뉴클레오타이드 4316 내지 5315)를 갖는다. 또한, 이는 효모에서의 선택을 위한 HIS3 마커(뉴클레오타이드 504 내지 1163) 및 이. 콜라이에서의 선택을 위한 앰피실린 내성 마커(뉴클레오타이드 6547 내지 7404)를 갖는다. pNY9는 HIS3 마커를 대체해 URA3 마커가 있는 동일한 벡터이다.

[0154] 클루이베로마이세스 락티스로부터의 DHAD에 대한 ILV3 코딩 영역은 DNA 2.0(멘로 파크, 캘리포니아주 소재(Menlo Park, CA))에 의해 S. 세레비시아에서의 발현에 대한 코돈-최적화를 이용해 합성하였다. 클로닝된 합성 서열을 PCR 증폭시켰다. 증폭 동안에, N-말단에 있는 DHAD에 대한 미토콘드리아 신호 펩타이드의 일부는 전방향 프라이머로서 ilv3(K)(0)-F(delet)를 역방향 프라이머로서 ilv3(K)(o)-R과 함께 사용하여 결실시켰고, 이는 세포질 발현을 위한 코딩 영역(서열 번호:173)을 초래하였다. 또한, SphI 부위는 전방향 프라이머에 삽입하였고, 한편 NotI 부위는 역방향 프라이머에 삽입하였다. PCR 생성물을 서틀 벡터 pNY9 및 pNY13 내로 클로닝하여, ILV3 코딩 영역은 FBA 프로모터의 조절 하에 있었다. PCR 생성물 및 각각의 벡터(pNY9, pNY13) 둘 다는 SphI 및 NotI을 사용해 분해하였다. 분해 후, 성분을 연결하고, 연결 혼합물을 TOP10 컴피턴트(competent) 세포(인비트로젠(Invitrogen)) 내로 형질전환시켰다. 형질전환체는 100μg/ml의 앰피실린이 보충된 LB 한천 플레이트에서 선택하였다. 양성 클론을 상기 기술된 전방향 및 역방향 프라이머를 사용하는 PCR에 의해 스크리닝하였다. 결과의 플라스미드를 각각 플라스미드 pNY13 및 pNY9로부터 유도된 pRS423::FBAP-ILV3(KL) 및 pRS426::FBAP-ILV3(KL)이라고 지정하였다.

[0155] S. 세레비시아에서 K. 락티스로부터의 DHAD의 발현을 연구하기 위해, 빈 벡터 pRS426과 함께 발현 벡터 pRS423::FBAP-ILV3(KL)을 균주 BY4743 및 BY4743 leu1::kanMX4(ATCC 4034377)에 형질전환시켰다. 컴피턴트 세포 제조 및 형질전환은 자이모 리서치(Zymo Research)의 프로즌 효모 형질전환 키트(Frozen Yeast Transformation kit)를 바탕으로 하였다. 형질전환체는 히스티딘 및 우라실(테크노바(Teknova))이 결여된 효모 합성 배지가 있는 한천 플레이트 상에서 선택하였다. 효소 검정법을 위해, 발현 구축물 및 빈 벡터 pRS426을 이동시키는 균주를 먼저 히스티딘 및 우라실이 결여된 5ml 합성 완전한 효모 배지에서 밤새 배양하였다. 5ml 밤새 배양물을 250ml 플라스크 내의 100ml의 배지 내로 이전시켰다. 배양물이 600nm에서 1 내지 2의 광학 밀도에 도달하였을 때, 배양물을 수확하였다. 표본을 10ml의 20mM 트리스(Tris)(pH 7.5)로 세정한 다음, 1ml의 동일한 트리스 완충제에서 재현탁시켰다. 표본을 0.1mm 실리카(라이싱 매트릭스 B, MP 바이오메디칼스(Lysing Matrix B, MP biomedical))가 함유된 2.0ml 튜브 내로 이전시켰다. 다음, 세포를 비드-비터(bead-

beater)(BI0101) 내에서 부수었다. 4℃, 13,000 rpm에서 30분 동안 마이크로퓨즈 내에서 원심분리하여 상층액을 수득하였다. 전형적으로는, 0.06 내지 0.1mg의 미정제 추출 단백질을 DHAD 검정법에서 사용하였다. 미정제 추출물 내 단백질을 코마시 염색(Coomassie stain)을 사용하는 브래드포드 검정법(Bradford assay)에 의해 측정하였다.

[0156] 다이하이드록시-산 탈수효소 효소 검정법

[0157] 시험관내 DHAD 효소 검정법은 플린트 등(Flint et al.)에 의해 기술된 검정법에 대한 변이이다(문헌[J. Biol. Chem. (1993) 268:14732-14742]). 검정법은 1.6ml 총 부피에서 수행하였고 하기로 이루어졌다: 800 μ l 2X 완충제(100mM 트리스 pH 8.0, 20mM MgCl₂), 160 μ l 10X 기질(15.6mg/ml 다이하이드록시아이소발레레이트), 미정제 추출물(전형적으로는 50-200 μ g 단백질), 및 물. 반응물은 37℃에서 인큐베이션하였다. 0, 30, 60, 및 90분의 시간 간격에서, 350 μ l의 반응 분취물을 제거하였고, 1N HCl 내 350 μ l의 0.05% 다이니트로페닐하이드라진으로 25℃에서 30분 동안 인큐베이션하였다. 반응을 중지시키기 위해, 350 μ l의 4N 수산화나트륨을 반응 혼합물에 첨가하였고, 반응물을 15,000 × g에서 2분 동안 원심분리하였다. 상층액을 플라스틱 일회용 큐벳에 이전시켰고, 540nm에서의 흡광도를 분광 광도계에서 측정하였다. 생성된 α -케토아이소발레레이트(KIV)의 양은, α -케토아이소발레레이트의 표준 곡선으로부터 수득되는 선형 회귀 방정식 내로 흡광도를 대입시킴으로써 측정하였다. 각 시점에서 생성되는 KIV의 양을 플로팅하여, 생성물을 측정하였다. 다음, 선형 회귀의 경사를 사용하여, 하기 식을 사용한 비활성을 계산하였다:

[0158] 비활성 계산 = (KIV 생성의 경사/1000) / 1.6 ml 반응물 당 단백질 mg = mmol/분 * mg

[0159] K. 락티스로부터의 탈수효소는 효모 균주 BY4743(Δ leu1)에서 발현된 경우, 0.2 내지 0.35 μ mol min⁻¹ mg⁻¹ 범위의 비활성을 가졌다. 반대로, 이 효소는 부모 효모 균주 BY4743에서 발현된 경우, 단지 0.14 μ mol min⁻¹ mg⁻¹ 범위의 비활성을 가졌다. 빈 벡터 pRS423 또는 pRS426을 함유하는 균주 BY4743(Δ leu1) 및 야생형 BY4743은 0.03 내지 0.1 μ mol min⁻¹ mg⁻¹ 범위의 활성 배경을 가졌다.

[0160] 실시예 2

[0161] S. 세레비시아의 LEU1 결실 균주에서 다이올 탈수효소의 발현

[0162] 조효소 B12-독립적 프로판다이올 탈수효소는 공동소유되고 동시계속출원인 미국 특허 공보 제 US20090155870 호에서 개시된다. 박테리움 로세부리아 이놀리니보란스에서 이 조효소 B12-독립적 (S-아데노실메티오닌(SAM)-독립적) 프로판다이올 탈수효소를 인코딩하는 서열(서열 번호:15) 및 그의 추정상 관련 반응화효소를 인코딩하는 서열(서열 번호:16)[Scott et al.(2006) J. Bacteriol.188:4340-9](이후, 각각 rdhtA 및 rdhtB라고 함)을 표준 방법에 의해 하나의 DNA 절편(서열 번호:17)으로서 합성하고, 이. 콜라이 벡터 내로 클로닝하였다(DNA2.0, 인코포레이티드(멘로 파크, 캘리포니아주 소재)에 의해). 이 클론을 PCR 주형으로서 사용하여, 개별 RdhtA 및 RdhtB 코딩 영역 절편을 제조하였다. 다이올 탈수효소에 대한 RdhtA 코딩 영역을 프라이머 N695 및 N696(서열 번호:18 및 19)을 사용한 PCR에 의해 증폭시켰다. 다이올 탈수효소 활성화효소에 대한 RdhtB 코딩 영역은 프라이머 N697 및 N698(서열 번호:20 및 21)을 사용한 PCR에 의해 증폭시켰다. 2개의 DNA 절편을 SOE PCR을 사용하여 반대 배향에서 서로 인접한 ADH 종결자(서열 번호:23) 및 CYC1 종결자(서열 번호:24)를 갖는 이중 종결자 DNA 절편(서열 번호:22)과 조합하였다(문헌[Horton et al. (1989) Gene 77:61-68]). 이중 종결자 절편을 pRS426::FBA-ILV5+GPM-kivD의 PacI 분해 후에 0.6kb 절편으로서 단리하였다(공동소유되고 동시계속출원인 미국 특허 공보 제 20070092957 A1 호의 실시예 17에서 기술됨). 결과의 4kb DNA 절편은 이중 종결자 서열에 인접한 각각의 코딩 영역의 3' 말단이 있는, 이중 종결자의 어느 면 상의 반대 배향에서 RdhtA 및 RdhtB 코딩 영역을 가졌다. 다음, 이 DNA 절편을 겔 수선 방법론(문헌[Ma et al. (1987) Genetics 58:201-216])에 의해 BbvCI를 사용한 분해에 의해 제조된 S. 세레비시아에 서틀 벡터 pRS426::FBA-ILV5+GPM-kivD 내로 클로닝하여, 그의 3' 말단 사이에서 ILV5 및 kivD 코딩 영역 및 이중 종결자 서열을 제거하였다. 결과의 플라스미드, pRS426::RdhtAB(하기)는 S. 세레비시아 FBA 프로모터(서열 번호:25)의 조절 하에 있는 RdhtA 유전자 및 S. 세레비시아 GPM 프로모터(서열 번호:26)의 조절 하에 있는 RdhtB 유전자를 함유하였다.

[0163] 플라스미드 pRS426 및 pRS426::RdhtAB를 표준 기법에 의해 S. 세레비시아 균주 BY4743(ATCC 201390) 및 BY4743 leu1::kanMX4(ATCC 4034377) 내로 도입하였다(문헌[Methods in Yeast Genetics, 2005, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, pp. 201-202]). 세포를 우라실로 결여된 합성 완전한 배지 상에 플레이팅하여, 형질전환체를 선택하였다. 형질전환체를 하기와 같이 생체내 검정법을 사용해 다이올

탈수효소 활성에 대해 시험하였다. 고체 배지 상에서 배양된 패칭된(patched) 세포를 사용하여, 액체 배지(20 ml)를 페트리 플레이트 내에 접종하였다. 사용된 배지는 5g/L 1,2-프로판다이올 9Aldrich Cat. No. 398039)의 첨가가 있고 그리고 없는 우라실이 결여된 합성 완전한 배지였다. 페트리 플레이트를 아나로팩(Anaeropack)TM 시스템 자(jar)(미즈비시 가스 케미칼 컴퍼니(Mitsubishi Gas Chemical Co.) Cat. No.50-70)에 이전시켰다. 팩-아나로 사켓(Pack-Anaero sachets)(미즈비시 가스 케미칼 컴퍼니 Cat. No. 10-01)을 사용해 혐기성 환경(<0.1% 산소)을 발생시켰다. 48시간 후에, 배양 상층액을 일반적인 방법에서 기술된 바와 같이 표본화하고, 여과하고, HPLC에 의해 분석하였다. 채류 시간이 38.8분인 프로판올을, 1,2-프로판다이올이 배지 내에 제공된 경우, pRS426::RdhtAB를 갖는 균주의 배양 상층액에서 관찰하였다. 표 5에 주어진 결과는, 더 많은 프로판올이 LEU1 결실이 없는 균주에서보다 LEU1 결실도 갖는 균주의 상층액에서 생성되었음을 보여준다. 통계 분석 결과, P 점수는 0.0005 미만이었다.

<표 5>

LEU1 녹아웃이 있는 효모 및 없는 효모에서 프로판다이올 탈수효소/반응화효소 발현을 이용한 프로판올 생성

균주	1,2-프로판다이올 첨가	프로판올 피크 구역
BY4743 Δ leu1::kanMX4/pRS426::RdhtAB	5 g/l	19472 ±1403 (n=6)
BY4743 Δ leu1::kanMX4/pRS426::RdhtAB	0 g/l	2478 (n=1)
BY4743 /pRS426::RdhtAB	5 g/l	11830 ±1963 (n=6)
BY4743 /pRS426::RdhtAB	0 g/l	2369 (n=1)
BY4743 Δ leu1::kanMX4/pRS426	5 g/l	2633 (n=1)
BY4743 /pRS426	5 g/l	2841 (n=1)

실시예 3:

미토콘드리아 ILV3의 분열을 통한 S. 세레비시애에서 시토졸 다이하이드록시-산 탈수효소(DHAD) 활성의 향상

백터/숙주 구축

S. 세레비시애 ILV3은 분지쇄 아미노산 생합성에 수반되는 미토콘드리아 다이하이드록시-산 탈수효소를 인코딩한다. S. 세레비시애에서 시험관내 효소 검정법을 위한 내인성 ILV3 발현으로부터 배경을 감소시키기 위해, ilv3::URA3 분열 카세트를 서열 번호:30 및 31로서 주어지는 프라이머 "ILV3::URA3 F" 및 "ILV3::URA3 R"이 있는 pRS426(ATCC No. 77107)으로부터의 URA3 마커의 PCR 증폭에 의해 구축하였다. 이들 프라이머는 상동성 재조합을 위한 ILV3 염색체 유전자 좌의 상류 및 하류 서열에 동일한 70bp 5' 및 3' 연장을 함유하는 1.4kb URA3 PCR 생성물을 생성하였다. PCR 생성물은 표준 유전적 기법을 사용해(문헌[Methods in Yeast Genetics, 2005, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, pp. 201-202]) BY4741 세포(ATCC 201388) 내로 형질전환시키고, 결과의 형질전환체를 우라실이 결여되고 30℃에서 2% 글루코스가 보충된 합성 완전한 배지 상에서 유지시켰다. 형질전환체는 서열 번호:32 및 33으로서 주어지는 프라이머 "ILV3 F 체크" 및 "URA3 REV 체크"를 사용하는 PCR에 의해 스크리닝하여, 내인성 ILV3 유전자 좌의 분열 및 올바른 위치에서의 합입을 확인하였다. 올바른 형질전환체는 유전형: BY4741 ilv3::URA3을 가졌다.

플라스미드 pRS423::FBAp-ILV3(KL) 및 pRS426::FBAp-ILV3(KL)의 구축을 실시예 1에서 기술하였다. pRS423::CUP1-alsS-FBA-ILV3의 구축은 본원에서 참조에 의해 삽입되는, 공동소유되고 동시계속출원인 미국 특허 공보 US20070092957 A1, 실시예 17에서 기술되었다. pRS423::CUP1-alsS-FBA-ILV3은 pRS423::CUP1p-alsS-FBAp-ILV3과 동일한 플라스미드이다. 이러한 구축물은 S. 세레비시애 CUP1 프로모터(서열 번호:34), 바실루스 서브틸리스로부터의 alsS 코딩 영역(서열 번호:27), 및 CYC1 종결자(서열 번호:24)를 함유하는 키메라 유전자; 및 또한, S. 세레비시애 FBA 프로모터(서열 번호:25), 미토콘드리아 표적화 신호 코딩 서열이 결여된 S. 세레비시애로부터의 ILV3 코딩 영역(서열 번호:111), 및 ADH1 종결자(서열 번호:23)를 함유하는 키메라 유전자를 함

유한다.

[0171] 표본 제조

[0172] 플라스미드 벡터 pRS423::CUP1p-alsS-FBAP-ILV3 및 pRS423::FBAP-ILV3(KL)을 표준 유전적 기법을 사용해 균주 BY4741 ilv3::URA3 내로 형질전환시키고(문헌[Methods in Yeast Genetics, 2005, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY]), 히스티딘이 결여된 합성 완전한 배지 상에서 유지시켰다. 플라스미드 벡터 pRS423::CUP1p-alsS-FBAP-ILV3 및 pRS426::FBAP-ILV3(KL)을 또한, 균주 BY4741 내로 형질전환시켰다. 혐기성 배양물을 히스티딘은 결여되고 2% 글루코스가 보충된 200ml 합성 완전한 배지를 함유하는 1000ml 플라스크 내에서, 이노바4000(Innova4000) 인큐베이터(뉴 브런스윅 사이언티픽, 에디슨, 뉴저지주(New Brunswick Scientific, Edison, NJ)) 내, 30℃ 및 225rpm에서 배양하였다. 배양물을 1.0-2.0의 OD600 측정에서 수확하고, 6000 × g에서 10분 동안 원심분리하여 펠렛화시켰다. 세포 펠렛을 10mM 트리스-HCl, pH 8.0으로 세정하고, 활성에 대해 검정할 때까지, 펠렛을 -80℃에서 보관하였다. 1ml의 0.5mm 비드 및 1.5ml의 효모 세포 현탁액을 사용하는 표준 비드 비팅 방법에 의해 세포 유리 추출물을 제조하였다. 추출물 내 단백질 농도는 코마시 염색을 이용하는 브래드포트 검정법에 의해 측정하였다. DHAD 효소 검정법 및 비활성 계산을 실시예 1에서 기술된 바와 같이 수행하였다. 표 6에서 주어지는 결과는 ILV3 결실이 없는 세포에서보다 ILV3 결실 세포에서 더 높은 DHAD 활성이 있었음을 보여준다.

[0173] <표 6>

ILV3 결실이 있는 효모 및 없는 효모에서의 DHAD 활성

균주	비활성 ($\mu\text{mol/min}\cdot\text{mg}$)	평균 비활성 ($\mu\text{mol/min}\cdot\text{mg}$)
BY4741	0.018	0.013
	0.014	
	0.008	
BY4741 pRS423::CUP1p-alsS-FBAP-ILV3	0.018	0.019
	0.020	
BY4741 pRS426::FBAP-ILV3(KL)	0.040	0.038
	0.036	
BY4741 ilv3::URA3	0.00006	0.00041
	0.00075	
BY4741 ilv3::URA3 pRS423::CUP1p-alsS-FBAP-ILV3	0.030	0.029
	0.028	
BY4741 ilv3::URA3 pRS423::FBAP-ILV3(KL)	0.317	0.281
	0.244	

[0174]

[0175] HPLC에 의한 알파-케토아이스발레레이트 형성의 확인

[0176] 시험관내 DHAD 효소 검정법으로부터의 알파-케토아이스발레레이트의 형성은 HPLC 및 세미카르바이자이드 유도체화(semicarbazide derivatization)를 사용해 달성하였다. DHAD 효소 검정법은 1.6ml의 총 부피에서 수행하였고, 이는 하기로 이루어졌다: 800 μl 2X 완충제(100mM 트리스 pH 8.0, 20mM MgCl_2), 160 μl 10X 기질(15.6mg/ml 다이하이드록시아이스발레레이트), 미정제 추출물(전형적으로는 50-200 μg 단백질), 및 물. 반응물을 37℃에서 인큐베이션시켰다. 0분 및 90분째의 시간 간격에서, 350 μl 의 반응 분취물을 제거하고, 얼음으로 이전시키고, 4℃, 13,000 × g에서 2분 동안 원심분리하여, 침전된 단백질을 제거하였다. 상층액을 얼음-냉각된 마이크로콘(Microcon) YM-10(시그마(Sigma)) 회전 칼럼으로 이전시키고, 4℃, 13,000 × g에서 20분 동안 원심분리하여, 효소 및 용해성 단백질을 제거하였다. 플로우스로(flowthrough)를 100 μl 유도체화 시약(1% 세미카르바이자이드 염산염 및 1.5% 나트륨 아세테이트 삼수화물)과 혼합하고, 실온에서 15분 동안 인큐베이션하였다. 반응물을 코스타 회전 필터(CoStar spin filter)(CoStar, 0.22 μm 필터)를 통해 13,000 × g, 4℃에서 5분 동안 회전시켜, 임의의 침전물을 제거하였다. 플로우스로를 분석을 위한 HPLC 바이알에 이전시켰다.

[0177] 유도체화된 알파-케토아이스발레레이트의 분석을 슈퍼가드(Superguard) LC-18-DB 가드 칼럼(수펠코(Supelco); 25cm × 4.6mm, 5 μm)이 있는 수펠코 LC-18 칼럼 상에서 역상 크로마토그래피를 사용해 수행하였다. 주사 부피는 10 μl 이었다. 이동상은 메탄올(A) 및 50mM NaOAc pH 7.2이었다. 이용되는 구배 프로그램은 표 7에서 주어지고, 250nm에서 검출하였다.

9(N)	-514	-1116	1207	-315	447	-1650	-304	-778	-224	825	-277	1457	-1738	-123	-618	-627	-454	-603	-1186	763	14
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
10(N)	-815	-1190	-1360	-922	-904	-1967	-797	-442	-670	381	1700	3009	-2099	-654	-934	-1051	-791	-445	-1490	-979	15
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
11(K)	-1530	-2498	-1722	-855	-3141	-2248	-428	-2627	2828	-2404	-1656	-927	662	-2	2047	-1421	-1337	-2324	-2357	-2081	16
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
12(Y)	-872	-1887	-861	-290	-1369	-1801	1662	-1797	325	-1793	-1031	893	-1876	56	2219	-812	-780	-1514	-1555	2287	17
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
13(S)	-830	-1586	-1471	-1099	-2717	-1642	-1010	-2479	-266	-2518	-1746	-1065	-2069	-676	1822	2748	-1000	-1950	-2597	-2189	18
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
14(Q)	-851	-2131	-775	-153	-2554	-1735	-211	-2205	1908	-2094	-1244	-386	-1802	2254	974	1001	-747	-1819	-2181	-1667	19
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
15(T)	-405	-1258	-618	-100	-1490	-1466	1158	-1121	1	-1299	-514	578	-1607	65	-433	960	1849	343	-1677	-1143	20
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
16(I)	-1772	-1325	-4307	-3877	-1405	-3993	-3383	2935	-3705	820	-217	-3632	-3761	-3400	-3682	-3260	-1742	2033	-2838	-2525	21
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
17(T)	-1018	-1329	-2004	-1771	-409	-1993	-1000	-1256	-1512	-1464	-966	-1543	-2367	-1428	-1638	-1257	3050	-1090	-1012	2448	22
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18(Q)	-1509	-3056	1970	44	-3310	-1668	-896	-3242	-877	-3158	-2439	-322	-2123	3562	-1493	-1259	-1550	-2779	-3260	-2446	23
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-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
19(D)	-1006	-2199	2178	-88	-3159	1997	-936	-2974	-948	-2977	-2174	-382	-1960	-589	-1571	1295	-1157	-2369	-3178	-2430	24
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
20(M)	445	-796	-1082	-521	-841	-1643	-412	-403	-370	-692	2213	-646	536	1166	-698	-630	660	831	-1204	-767	25
-	-149	-500	233	43	-381	399	106	-626	210	-466	-720	275	394	45	96	359	117	-369	-294	-249	
-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												

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22(R)	-1753	-2648	-2072	-1047	-3365	-2405	-452	-2782	1989	-2495	-1773	-1062	-2379	2402	2643	-1629	-1506	-2504	-2397	-2190	27
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-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
23(S)	-330	-1010	-1820	-1628	-2778	-1229	-1652	-2481	-1592	-2691	-1841	-1273	2130	-1426	-1834	2449	1034	-1716	-2961	-2504	28
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-	-16	-7108	-8150	-894	-1115	-701	-1378	*	*												
26(R)	-1847	-2640	-2014	-1161	-3282	-2428	-579	-2818	687	-2553	-1869	-1165	-2462	2447	3181	-1746	-1630	-2555	-2447	-2228	31
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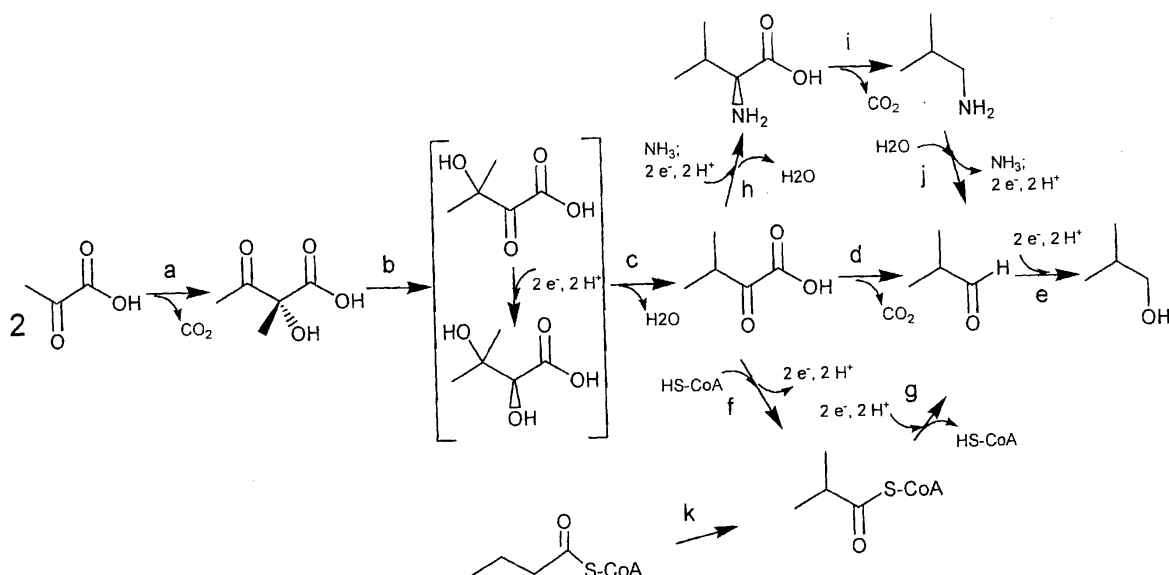
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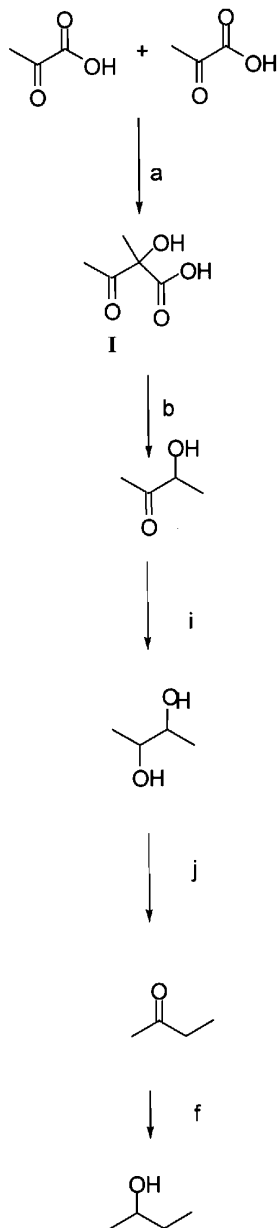
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서열 목록

SEQUENCE LISTING

<110> Butamax(TM) Advanced Biofuels, LLC

Anthony, Larry

Maggio-Hall, Lori

Rothman, Steve

Tomb, Jean-Francois

<120> INCREASED HETEROLOGOUS Fe-S ENZYME ACTIVITY IN YEAST

<130> CL 4213

<150> US 61/100,801

<151> 2008-09-29

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<151> 2008-09-29

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 Glu Gly Leu Glu Asn Ala Gly Arg Lys Val Arg Arg Val Asp Cys Thr

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 Leu Ala Thr Val Asp His Asn Ile Pro Thr Glu Ser Arg Lys Asn Phe
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 85 90 95

 Lys Thr Leu Glu Asn Asn Val Lys Gln Phe Gly Val Pro Tyr Phe Gly
 100 105 110
 Met Ser Asp Ala Arg Gln Gly Ile Val His Thr Ile Gly Pro Glu Glu
 115 120 125
 Gly Phe Thr Leu Pro Gly Thr Thr Val Val Cys Gly Asp Ser His Thr
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 Ser Thr His Gly Ala Phe Gly Ser Leu Ala Phe Gly Ile Gly Thr Ser
 145 150 155 160

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 165 170 175
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 180 185 190
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 Gly Thr Gly Cys Val Ile Glu Phe Ala Gly Glu Ala Ile Glu Ala Leu
 210 215 220

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 Ala Arg Ala Gly Met Ile Lys Pro Asp Glu Thr Thr Phe Gln Tyr Thr
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 Ala Tyr Trp Lys Thr Leu Lys Thr Asp Glu Gly Ala Lys Phe Asp His
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 340 345 350

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 370 375 380
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 Tyr Lys Asp Gln Asp Gln Ser Ser Pro Lys Val Glu Val Thr Ser Glu
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 Ile Pro Val Lys Ser Asp Asp Thr Pro Ala Lys Pro Ser Ser Ser Gly
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 595 600 605

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 645 650 655
 Asn Asn Ser Phe Lys Asn Gly Leu Leu Pro Ile Arg Leu Asp Gln Gln
 660 665 670

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 675 680 685
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 690 695 700
 Leu Val Asp His Phe Glu Ile Glu Pro Phe Arg Lys His Cys Leu Val
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 Asn Gly Leu Asp Asp Ile Gly Ile Thr Leu Gln Lys Glu Glu Tyr Ile
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 Ser Arg Tyr Glu Ala Leu Arg Arg Glu Lys Tyr Ser Phe Leu Glu Gly
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Cys Leu Glu Ala Asp Gly Val Leu Leu Gly Ala Val Gly Gly Pro Glu			
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Trp Thr Asn Pro Asn Cys Arg Pro Glu Gln Gly Leu Leu Lys Leu Arg			
85	90	95	
Lys Ser Met Gly Val Trp Ala Asn Leu Arg Pro Cys Asn Phe Ala Ser			
100	105	110	
Lys Ser Leu Val Lys Tyr Ser Pro Leu Lys Pro Glu Ile Val Glu Gly			
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Asn Val Leu Ala Thr Ser Arg Leu Trp Arg Lys Thr Val Ala Lys Ile			
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Phe Lys Glu Glu Tyr Pro His Leu Thr Leu Lys Asn Gln Leu Ile Asp			
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245	250	255	
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260	265	270	
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<212> DNA

<213> Candida galbrata

<400> 5

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gaggttactt ctccacaggc ctttgaaggt ttgactaatg cgaacagacc agtaagaagg 180
 gtggattgta ctttggccac agttgaccac aacatcccaa ccgagtcag aaagagtttc 240
 aagaacttgg actctttcat tacacaaacc gactcccgt tacaagtga gactttggaa 300
 cagaactga agcaatttgg cgtaccatac ttgggtctaa ccgagaagag acaaggtatc 360
 gtccatacta ttggtctga gcaaggtttc accttacctg gtaccactgt ggtgtgtggt 420
 gactcccaca cttctactca cgggtgcattc ggtgcattgg cattcggtat cgggtacctc 480
 gaagtcgaac acgtcttggc tacccaaact atcattcaaa gtaaatccaa gaatatgaga 540

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 attgggtgta tcggtactgc tgggtggtact ggttccgtca ttgaatttgc tggatgaagct 660
 atagagaact tatctatgga agctcgtatg tctatgtgta atatgtccat tgaggccggt 720
 gcaagagctg gtatgatcaa accagacaat gtcactttcg aatatttcaa aggaagacca 780
 ttggccccaa ctggtgccga atgggacaag gctgttgctt actggaagac ttgcatctct 840
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attacctggg gtactttctcc acaagatgcg ctaccaatca gtgcatcagt tccagatcca 960

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acttccaaca gaaactttga aggtcgtcaa ggtgccttat ctctacaca tttaatgtct 1380

ccagccatgg ctgctgctac agctgttgca ggtcactttg tagacatcag agaatttaaa 1440

tataataacg ctgacgatgc taaagttact atatcttctg atgaagacga agaacttgaa 1500

gaagctgcgt atgagcacac tgaaccacaa cagcccggcg atgccccaac tgatgttgag 1560

aatgatcagt tgaaggacat cccagtcgaa tccgaaacaa aaagattaaa gacggacgat 1620

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aagagaaccg gtttagatc aggtctatct tacgaatgga gatttgtcaa ggatgacagt 1800

ggaaaagata aagaaacaga ttttgtgtg aatgtcaacc catggaggaa agctgaggtc 1860

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aacagtttca agaattggtt gttaccaatt agaattgatc aagataccat cgtaaacaag 2040

ctagttcctg ttgcaaagcg tggtaagaat ctggttatta actiaccaga tcaaaccatc 2100

tctgattcgg atggcaatgt tttggttgaa cattttgaag ttgaagcatt cagaaagcat 2160

tgtctagtaa atggtctaga tgacattggc atcacattgc agaaagaaca atacatcgac 2220

caatacgaaa agattagaag agaaaagtac tcattttatg aaggtaggtc taagttgcta 2280

catttccag ccaagcagtt ccaaaaaaag agaactccat taacgactta tgacactgtt 2340

catcaagatt ggtaa 2355

<210> 6

<211> 784

<212> PRT

<213> Candida galbrata

<400> 6

Met Val Thr Thr Glu Thr Lys Gly Pro Arg Thr Leu Tyr Asp Lys Val

1	5	10	15
Phe Asp Ala His Val Val His Lys Asp Glu Asn Gly Ser Tyr Leu Leu			
	20	25	30
Tyr Ile Asp Arg His Leu Val His Glu Val Thr Ser Pro Gln Ala Phe			
	35	40	45
Glu Gly Leu Thr Asn Ala Asn Arg Pro Val Arg Arg Val Asp Cys Thr			
	50	55	60
Leu Ala Thr Val Asp His Asn Ile Pro Thr Glu Ser Arg Lys Ser Phe			
65	70	75	80
Lys Asn Leu Asp Ser Phe Ile Thr Gln Thr Asp Ser Arg Leu Gln Val			
	85	90	95
Lys Thr Leu Glu Gln Asn Val Lys Gln Phe Gly Val Pro Tyr Phe Gly			
	100	105	110
Leu Thr Glu Lys Arg Gln Gly Ile Val His Thr Ile Gly Pro Glu Gln			
	115	120	125
Gly Phe Thr Leu Pro Gly Thr Thr Val Val Cys Gly Asp Ser His Thr			
	130	135	140
Ser Thr His Gly Ala Phe Gly Ala Leu Ala Phe Gly Ile Gly Thr Ser			
145	150	155	160
Glu Val Glu His Val Leu Ala Thr Gln Thr Ile Ile Gln Ser Lys Ser			
	165	170	175
Lys Asn Met Arg Ile Arg Val Asp Gly Lys Leu Ser Pro Gly Ile Thr			
	180	185	190
Ser Lys Asp Leu Ile Leu His Ile Ile Gly Val Ile Gly Thr Ala Gly			
	195	200	205
Gly Thr Gly Ser Val Ile Glu Phe Ala Gly Glu Ala Ile Glu Asn Leu			
	210	215	220
Ser Met Glu Ala Arg Met Ser Met Cys Asn Met Ser Ile Glu Ala Gly			
225	230	235	240
Ala Arg Ala Gly Met Ile Lys Pro Asp Asn Val Thr Phe Glu Tyr Phe			
	245	250	255

Lys Gly Arg Pro Leu Ala Pro Thr Gly Ala Glu Trp Asp Lys Ala Val
 260 265 270
 Ala Tyr Trp Lys Thr Leu His Ser Asp Glu Gly Ala Lys Phe Asp His
 275 280 285

 Glu Ile Val Ile Lys Gly Ser Glu Ile Ile Pro Thr Ile Thr Trp Gly
 290 295 300
 Thr Ser Pro Gln Asp Ala Leu Pro Ile Ser Ala Ser Val Pro Asp Pro
 305 310 315 320
 Ala Asn Val Asp Asp Pro Ile Lys Lys Ser Gly Met Glu Arg Ala Leu
 325 330 335
 Glu Tyr Met Gly Leu Lys Pro Asn Thr Pro Leu Lys Ser Ile Tyr Val
 340 345 350

 Asp Lys Val Phe Ile Gly Ser Cys Thr Asn Gly Arg Ile Glu Asp Leu
 355 360 365
 Arg Asn Ala Ala Lys Val Leu Asn Gly His Lys Ile Ala Pro Asn Ile
 370 375 380
 Lys Arg Ala Met Val Val Pro Gly Ser Gly Leu Val Lys Val Gln Ala
 385 390 395 400
 Glu Glu Glu Gly Leu Asp Lys Val Phe Ile Ala Ala Gly Phe Glu Trp
 405 410 415

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

 Tyr Asn Asn Ala Asp Asp Ala Lys Val Thr Ile Ser Ser Asp Glu Asp
 485 490 495
 Glu Glu Leu Glu Glu Ala Ala Tyr Glu His Thr Glu Pro Gln Gln Pro

500 505 510
 Gly Asp Ala Pro Thr Asp Val Glu Asn Asp Gln Leu Lys Asp Ile Pro
 515 520 525
 Val Glu Ser Glu Thr Lys Arg Leu Lys Thr Asp Asp Thr Lys Pro Val
 530 535 540

 Ala Gly Gly Met Asp Pro Phe Val Val Leu Asn Gly Leu Ala Ala Pro
 545 550 555 560
 Leu Glu Lys Ala Asn Val Asp Thr Asp Ala Ile Ile Pro Lys Gln Phe
 565 570 575
 Leu Lys Thr Ile Lys Arg Thr Gly Leu Arg Ser Gly Leu Phe Tyr Glu
 580 585 590
 Trp Arg Phe Val Lys Asp Asp Ser Gly Lys Asp Lys Glu Thr Asp Phe
 595 600 605

 Val Leu Asn Val Asn Pro Trp Arg Lys Ala Glu Val Leu Val Val Thr
 610 615 620
 Gly Asp Asn Phe Gly Cys Gly Ser Ser Arg Glu His Ala Pro Trp Ala
 625 630 635 640
 Leu Lys Asp Phe Gly Ile Lys Ser Ile Ile Ala Pro Ser Phe Gly Asp
 645 650 655
 Ile Phe Tyr Asn Asn Ser Phe Lys Asn Gly Leu Leu Pro Ile Arg Ile
 660 665 670

 Asp Gln Asp Thr Ile Val Asn Lys Leu Val Pro Val Ala Lys Ala Gly
 675 680 685
 Lys Asn Leu Val Ile Asn Leu Pro Asp Gln Thr Ile Ser Asp Ser Asp
 690 695 700
 Gly Asn Val Leu Val Glu His Phe Glu Val Glu Ala Phe Arg Lys His
 705 710 715 720
 Cys Leu Val Asn Gly Leu Asp Asp Ile Gly Ile Thr Leu Gln Lys Glu
 725 730 735

 Gln Tyr Ile Asp Gln Tyr Glu Lys Ile Arg Arg Glu Lys Tyr Ser Phe
 740 745 750

Tyr Glu Gly Gly Ser Lys Leu Leu His Phe Pro Ala Lys Gln Phe Pro

755 760 765

Lys Lys Arg Thr Pro Leu Thr Thr Tyr Asp Thr Val His Gln Asp Trp

770 775 780

<210> 7

<211> 2331

<212> DNA

<213> Candida albicans

<400> 7

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tctggttcat atttattata cattgataga catttagtcc atgaggttac ttccccacaa 120

gcatttgaag ggtaaagaa tgctggtcgt tcagtcagaa gaaccgattg tacattagcc 180

acagttgatc ataatatccc aactatttca agagcaaatt tcaagaatgt cgattcattc 240

atagagcaag atgattctag attgcaagtt aagactttag aacaaaacgt caaggatitt 300

gatgttactt attttggtat gacagacgac agacaaggta ttgtccatgt tgttggtcca 360

gaacaaggtt tcactttacc aggtaccact gttgtttgtg gtgactcca tacttctact 420

catgggtgctt ttggttcatt ggcttttgggt attggtactt ctgaagtgga acatgtttta 480

gctacgcaaa ctattattca agccaaatcg aaaaacatga gaattactat tgatggatgat 540

ttgtctgaag gtatcacttc gaaagatttg gttttgcatg tcattgggtg tattggtact 600

gctgggtgga ctggttgtgt tattgaattt gctggtaaag ccattgagaa ttgtcaatg 660

gaagcaagaa tgtcgaatag taatatggcc attgaagccg gtgccagagc tggatgatc 720

aaaccagatg atactacatt caattacatc aaaggtagac cattggctcc aaagggacaa 780

gaatgggaaa aggccatgaa atattggaaa actttacata ctgatgaagg agctaagttt 840

gattacgata ttaaaattgc tgcttccgat attgttccaa ctatcattg gggttaactca 900

ccacaagatg cgttaccaat aactgctagt gtcccagacc cagcaactgt gaccgatcca 960

attaagaaat cgggtatgga aagagcattg aaatatcaag gtttaactcc aaacacacct 1020

ttcaaagaaa tcaaaattga taaagcattc attggttcat gtaccaactc tcgtattgaa 1080

gatttaagag cagctgctaa agttgccaaa ggtcacaaaa aagccgacaa tgtgaaattg 1140

gtcttgggtg tgccgggttc tggtttaatt aaaaagcaag ctgaaaaaga aggtttggat 1200

aagatttttg aagccgctgg attttcatgg agagaagccg gatgttcaat gtgtcttgggt 1260

atgaaccag atattttgga tcctgaagaa agatgtgctt ctacttccaa cagaaatttc 1320

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 ccaaaagatg aaccagaatt taaaagggcc agaaccgaga tcgacaactc tgctgctggt 1620
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 acaggagaca attttggttg tggatcaagt cgtgagcatg ctccttgggc tttgaaagat 1920
 tttggtatca aaagtataat tgcccatca tttggtgata tcttttataa taattctttt 1980
 aaaaatttcc ttttgccaat cagaataccg caagaaatca ttgaatctaa attggttccc 2040
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 gaaaccgacg aagtccttgat tgaacatttc gatgtggaag agtttagaaa acattgtttg 2160

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 gaagctaaaa gaagaatcaa gttttctttc ttggaaggag gttctaaatt aatcaaacct 2280
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<210> 8

<211> 776

<212> PRT

<213> candida albicans

<400> 8

Met Ala Pro Lys Thr Leu Tyr Asp Lys Val Phe Glu Asp His Ile Val

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His Lys Asp Asp Ser Gly Ser Tyr Leu Leu Tyr Ile Asp Arg His Leu

20 25 30

Val His Glu Val Thr Ser Pro Gln Ala Phe Glu Gly Leu Lys Asn Ala

35 40 45

Gly Arg Ser Val Arg Arg Thr Asp Cys Thr Leu Ala Thr Val Asp His

50 55 60

Asn Ile Pro Thr Ile Ser Arg Ala Asn Phe Lys Asn Val Asp Ser Phe

65 70 75 80

Ile Glu Gln Asp Asp Ser Arg Leu Gln Val Lys Thr Leu Glu Gln Asn
85 90 95

Val Lys Asp Phe Asp Val Thr Tyr Phe Gly Met Thr Asp Asp Arg Gln
100 105 110

Gly Ile Val His Val Val Gly Pro Glu Gln Gly Phe Thr Leu Pro Gly
115 120 125

Thr Thr Val Val Cys Gly Asp Ser His Thr Ser Thr His Gly Ala Phe
130 135 140

Gly Ser Leu Ala Phe Gly Ile Gly Thr Ser Glu Val Glu His Val Leu
145 150 155 160

Ala Thr Gln Thr Ile Ile Gln Ala Lys Ser Lys Asn Met Arg Ile Thr
165 170 175

Ile Asp Gly Asp Leu Ser Glu Gly Ile Thr Ser Lys Asp Leu Val Leu
180 185 190

His Val Ile Gly Val Ile Gly Thr Ala Gly Gly Thr Gly Cys Val Ile
195 200 205

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

Ser Ile Cys Asn Met Ala Ile Glu Ala Gly Ala Arg Ala Gly Met Ile
225 230 235 240

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

Pro Lys Gly Gln Glu Trp Glu Lys Ala Met Lys Tyr Trp Lys Thr Leu
260 265 270

His Thr Asp Glu Gly Ala Lys Phe Asp Tyr Asp Ile Lys Ile Ala Ala
275 280 285

Ser Asp Ile Val Pro Thr Ile Thr Trp Gly Asn Ser Pro Gln Asp Ala
290 295 300

Leu Pro Ile Thr Ala Ser Val Pro Asp Pro Ala Thr Val Thr Asp Pro
305 310 315 320

Ile Lys Lys Ser Gly Met Glu Arg Ala Leu Lys Tyr Gln Gly Leu Thr

325 330 335
 Pro Asn Thr Pro Phe Lys Glu Ile Lys Ile Asp Lys Ala Phe Ile Gly
 340 345 350

 Ser Cys Thr Asn Ser Arg Ile Glu Asp Leu Arg Ala Ala Ala Lys Val
 355 360 365
 Ala Lys Gly His Lys Lys Ala Asp Asn Val Lys Leu Val Leu Val Val
 370 375 380
 Pro Gly Ser Gly Leu Ile Lys Lys Gln Ala Glu Lys Glu Gly Leu Asp
 385 390 395 400
 Lys Ile Phe Glu Ala Ala Gly Phe Ser Trp Arg Glu Ala Gly Cys Ser
 405 410 415

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

 Pro Gln Ile Gln Ile Ala His Glu Ile Glu Asp Lys Glu Leu Gln Glu
 485 490 495
 Ala Val Tyr Glu His Glu Lys Glu Tyr Ile Glu Asp Thr Pro Glu Thr
 500 505 510
 Gln Ala Glu Arg Leu Glu Asp Ile Pro Lys Asp Glu Pro Glu Phe Lys
 515 520 525
 Arg Ala Arg Thr Glu Ile Asp Asn Ser Ala Ala Gly Thr Pro Ser Ile
 530 535 540

 Asp Asn Ser Phe Lys Val Leu Thr Gly Ile Thr Ala Pro Leu Tyr Lys
 545 550 555 560
 Ala Asn Val Asp Thr Asp Ala Ile Ile Pro Lys Gln Phe Leu Lys Thr
 565 570 575

Ile Lys Arg Thr Gly Leu Lys Asp Gly Leu Phe Tyr Glu Leu Arg Phe
580 585 590

Val Lys Gly Glu Asn Gly Lys Asp Val Glu Thr Asp Phe Val Leu Asn
595 600 605

Thr Glu Pro Tyr Arg Lys Ala Glu Ile Leu Leu Val Thr Gly Asp Asn
610 615 620

Phe Gly Cys Gly Ser Ser Arg Glu His Ala Pro Trp Ala Leu Lys Asp
625 630 635 640

Phe Gly Ile Lys Ser Ile Ile Ala Pro Ser Phe Gly Asp Ile Phe Tyr
645 650 655

Asn Asn Ser Phe Lys Asn Phe Leu Leu Pro Ile Arg Ile Pro Gln Glu
660 665 670

Ile Ile Glu Ser Lys Leu Val Pro Val Val Thr Ser Gly His Arg Leu
675 680 685

Thr Ile Asp Leu Pro Asn Gln Gln Ile Arg Asp Gly Glu Thr Asp Glu
690 695 700

Val Leu Ile Glu His Phe Asp Val Glu Glu Phe Arg Lys His Cys Leu
705 710 715 720

Val Asn Gly Leu Asp Asp Ile Gly Leu Thr Leu Gln Lys Glu Glu Tyr
725 730 735

Ile Lys Glu Tyr Glu Ala Lys Arg Arg Ile Lys Phe Ser Phe Leu Glu
740 745 750

Gly Gly Ser Lys Leu Ile Lys Pro Ile Lys Gly Thr Lys Lys Ser Ile
755 760 765

Tyr Gly Asn Arg Ala Gln Glu Trp
770 775

<210> 9

<211> 2358

<212> DNA

<213> Kluyveromyces lactis

<400> 9

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caggaccata ttgtccataa ggatgaatct ggatcatatt tgttgtatat tgatagacat 120

ttggttcatg aagttaacttc tccacaagct tttgaaggtt taaagaatgc tggtagaaaa 180

gttagaagag ttgattgtac cttggctaca gtggatcaca acatccctac tgaatccaga 240

aagaattttg tcgatactgc atctttcatt aagcaagccg attcccgttt gcaagttcaa 300

actttggaac aaaacgttaa ggattttgga gtcacathtt ttggtatgac tgatgctaga 360

caaggatatc tgcatattat tggtcagaa caaggtttca cattgccagg caccactgtg 420

gtgtgtgggt attcccatac ttctactcac ggtgcgtttg gtgcacttgc atttggtatt 480

ggtacctctg aagttgagca cgtcttggct acccaaacca ttattcaggc caagtcgaag 540

aacatgagaa ttiacgttga tggtcatttg tccccatcag tgactttctaa ggatttgatc 600

ttacacatca tcggtgtcat tggttactgc ggtgggtactg gttgtgttat cgaattcgca 660

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ggtagacctt tggtctcaaa gggcgctgaa tggaacaagg ctgtcgcta ctggaagact 840

ttacacaccg atgaagggtc tcagtttgat tacgatatca ctattaaatc aactgatgtc 900

atcccaacaa tcacttgggg tactttctca caagatgcat tgccaatcac tgcctctgtt 960

ccagatccgg caaccatctc tgatcctgct gtaaaggcta ctgtggaaag agctttgaaa 1020

tacatgggct tgactccaaa cgttccattg aaagaacttt ctatcgataa ggtctttatc 1080

ggttcttgta ccaatgctag aattgaggat ttgagagctg ctgctgccgt cgttaaggga 1140

cataagaaag ctgataatgt taaattggct atggttgttc caggttctgg tttggtgaag 1200

aaacaagctg aatctgaagg cttagacaag atttttgagg aagctggttt cgaatggaga 1260

gaagctgggt gtctatgtg tctaggtatg aaccagata ttttgaccc tgaagaacgt 1320

tgtgcttcta cttccaacag aaactttgaa ggccgtcaag gtgctctatc tagaactcat 1380

ttaatgtctc cagcaatggc tgctgctgct ggtattgctg gtcatttcgt tgacattaga 1440

gatcatgaat acagaaacag cgatgttcca aaggtttcca ttgagcaaga agctgaagac 1500

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gtggatgaac aagtcgatga tcaacaattg gatatccac cttctgatca tgtaacaaag 1620

gaaacccctc tcaagatgc tccaacatct gctccaaaag gtatggatcc tttctaaaa 1680

ttggacggta ttgctgctcc agttgacaag gcgaacgttg aactgatgc catcattcca 1740

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aggttcacca aaggtcctga cggttaaggat gtagaaactg attgggtctt gaacgttgaa 1860
 ccttgagaaa atgctgaaat cttggtcatt acttggtgata actttggttg tggttcttcc 1920
 agagaacacg caccatgggc cttgaaggat ttcggtatca agtgtatgat tgccccatct 1980
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cagaaagaag agtacattgc taagtatgaa gccatgagaa gagacaggtt ctctttctta 2280
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 agggctcaag agtggtaa 2358

<210> 10

<211> 785

<212> PRT

<213> Kluyveromyces lactis

<400> 10

Met Thr Ala Pro Ala Ala Thr Glu Ser Asn Gly Pro Gln Thr Leu Tyr

1 5 10 15

Asp Lys Val Phe Gln Asp His Ile Val His Lys Asp Glu Ser Gly Ser

20 25 30

Tyr Leu Leu Tyr Ile Asp Arg His Leu Val His Glu Val Thr Ser Pro

35 40 45

Gln Ala Phe Glu Gly Leu Lys Asn Ala Gly Arg Lys Val Arg Arg Val

50 55 60

Asp Cys Thr Leu Ala Thr Val Asp His Asn Ile Pro Thr Glu Ser Arg

65 70 75 80

Lys Asn Phe Val Asp Thr Ala Ser Phe Ile Lys Gln Ala Asp Ser Arg

85 90 95

Leu Gln Val Gln Thr Leu Glu Gln Asn Val Lys Asp Phe Gly Val Thr

100 105 110

Phe Phe Gly Met Thr Asp Ala Arg Gln Gly Ile Val His Ile Ile Gly

115 120 125

Pro Glu Gln Gly Phe Thr Leu Pro Gly Thr Thr Val Val Cys Gly Asp

130	135	140	
Ser His Thr Ser Thr His Gly Ala Phe Gly Ala Leu Ala Phe Gly Ile			
145	150	155	160
Gly Thr Ser Glu Val Glu His Val Leu Ala Thr Gln Thr Ile Ile Gln			
	165	170	175
Ala Lys Ser Lys Asn Met Arg Ile Tyr Val Asp Gly Pro Leu Ser Pro			
	180	185	190
Ser Val Thr Ser Lys Asp Leu Ile Leu His Ile Ile Gly Val Ile Gly			
	195	200	205
Thr Ala Gly Gly Thr Gly Cys Val Ile Glu Phe Ala Gly Gln Ala Ile			
210	215	220	
Glu Glu Leu Ser Met Glu Ala Arg Met Ser Met Cys Asn Met Ala Ile			
225	230	235	240
Glu Gly Gly Ala Arg Ala Gly Leu Ile Gln Pro Asp Gln Thr Thr Phe			
	245	250	255
Asp Tyr Ile Lys Gly Arg Pro Leu Ala Pro Lys Gly Ala Glu Trp Asn			
	260	265	270
Lys Ala Val Ala Tyr Trp Lys Thr Leu His Thr Asp Glu Gly Ala Gln			
275	280	285	
Phe Asp Tyr Asp Ile Thr Ile Lys Ser Thr Asp Val Ile Pro Thr Ile			
290	295	300	
Thr Trp Gly Thr Ser Pro Gln Asp Ala Leu Pro Ile Thr Ala Ser Val			
305	310	315	320
Pro Asp Pro Ala Thr Ile Ser Asp Pro Ala Val Lys Ala Thr Val Glu			
	325	330	335
Arg Ala Leu Lys Tyr Met Gly Leu Thr Pro Asn Val Pro Leu Lys Glu			
340	345	350	
Leu Ser Ile Asp Lys Val Phe Ile Gly Ser Cys Thr Asn Ala Arg Ile			
355	360	365	
Glu Asp Leu Arg Ala Ala Ala Val Val Lys Gly His Lys Lys Ala			
370	375	380	

Asp Asn Val Lys Leu Ala Met Val Val Pro Gly Ser Gly Leu Val Lys
 385 390 395 400
 Lys Gln Ala Glu Ser Glu Gly Leu Asp Lys Ile Phe Glu Glu Ala Gly
 405 410 415

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

 Asp His Glu Tyr Arg Asn Ser Asp Val Pro Lys Val Ser Ile Glu Gln
 485 490 495
 Glu Ala Glu Asp Lys Ile Leu Gln Asn Ala Val Tyr Glu His Glu Lys
 500 505 510
 Glu Pro Ile Glu Glu Gly Glu Ser Val Asp Glu Gln Val Asp Asp Gln
 515 520 525
 Gln Leu Asp Ile Pro Pro Ser Asp His Val Thr Lys Glu Thr Pro Leu
 530 535 540

 Lys Asp Ala Pro Thr Ser Ala Pro Lys Gly Met Asp Pro Phe Leu Lys
 545 550 555 560
 Leu Asp Gly Ile Ala Ala Pro Val Asp Lys Ala Asn Val Asp Thr Asp
 565 570 575
 Ala Ile Ile Pro Lys Gln Phe Leu Lys Thr Ile Lys Arg Thr Gly Leu
 580 585 590
 Lys Ser Gly Leu Phe Tyr Glu Trp Arg Phe Thr Lys Gly Pro Asp Gly
 595 600 605

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 Arg Glu His Ala Pro Trp Ala Leu Lys Asp Phe Gly Ile Lys Cys Met
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 Ile Ala Pro Ser Phe Gly Asp Ile Phe Tyr Asn Asn Ser Phe Lys Asn
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Gly Leu Leu Pro Ile Arg Leu Pro Glu Asp Leu Ile Val Glu Lys Leu
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 Ser Pro Leu Ala Glu Ala Gly Ala Lys Leu Ile Val Asp Leu Pro Ser
 690 695 700
 Gln Lys Ile Met Asp Ala Glu Gly Asn Val Leu Val Asp His Phe Asp
 705 710 715 720
 Val Glu Pro Phe Arg Lys His Cys Leu Val Asn Gly Leu Asp Asp Ile
 725 730 735

Gly Ile Thr Met Gln Lys Glu Glu Tyr Ile Ala Lys Tyr Glu Ala Met
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Gln Val Arg Arg Lys Asp Cys Thr Leu Ala Thr Val Asp His Asn Ile

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Pro Thr Thr Thr Arg Lys Asp Phe Lys Ser Ile Gly Thr Phe Ile Lys

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Asp Phe Gly Val Arg Tyr Phe Gly Met Asp Asp Lys Arg Gln Gly Ile

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Val His Val Val Gly Pro Glu Gln Gly Phe Thr Leu Pro Gly Thr Thr

115 120 125

Val Val Cys Gly Asp Ser His Thr Ser Thr His Gly Ala Phe Gly Ala

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Leu Ala Phe Gly Ile Gly Thr Ser Glu Val Glu His Val Leu Ala Thr

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Gly Lys Leu Gln Pro Gly Ile Thr Ser Lys Asp Leu Ile Leu His Ile
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Asp Ser Asp Ala Glu Phe Asp Ile Asp Val Asn Ile Lys Gly Glu Asp
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Ser Gly Leu Val Lys Arg Lys Ala Glu Ala Glu Gly Leu Asp Lys Val
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 Lys Pro Asp Gln Thr Thr Phe Asp Tyr Ile Ser Gly Arg Pro Leu Ala
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<220><223> primer

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35 40 45

Gly Asp Phe Gly Ile Gly Thr Phe Asn Lys Leu Asp Gly Glu Leu Ile

50 55 60

Gly Phe Asp Gly Glu Phe Tyr Arg Leu Arg Ser Asp Gly Thr Ala Thr

65 70 75 80

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Phe Glu Lys Glu Ile Asn Ser Met Leu Pro Ser Arg Asn Leu Phe Tyr
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Leu Thr Pro Ala Tyr Ala Asn Gly Ile Ala Val Ser Gly Tyr His Leu
180 185 190

His Phe Ile Asp Glu Gly Arg Asn Ser Gly Gly His Val Phe Asp Tyr
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 <213> artificial sequence
 <220><223> primer
 <400> 30

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agcgggtgtt ggcggg 76

<210> 31

<211> 68

<212> DNA

<213> artificial sequence

<220><223> primer

<400> 31

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tttcacac 68

<210> 32

<211> 22

<212> DNA

<213> artificial sequence

<220><223> primer

<400> 32

gttcttattc cctcttgtat cc 22

<210> 33

<211> 20

<212> DNA

<213> artificial sequence

<220><223> primer

<400> 33

cttggcagca acaggactag 20

<210> 34

<211> 448

<212> DNA

<213> Saccharomyces cerevisiae

<400> 34

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tacttcacca cccittatit caggetgata tcttagcctt gttactagtt agaaaaagac 180

atitttgctg tcagtcactg tcaagagatt cttttgctgg catttcttct agaagcaaaa 240

agagcgatgc gtcttttccg ctgaaccgtt ccagcaaaaa agactaccaa cgcaatatgg 300

attgtcagaa tcatataaaa gagaagcaaa taactccttg tcttgtatca attgcattat 360

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aaactgtaca atcaatcaat caatcatc 448

<210> 35

<211> 1485

<212> DNA

<213> *Vibrio cholerae*

<400> 35

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cgttttatgg cgcgagaaga gtttgaacc gaagctgatt acctaaaagg taagaaagtg 120

gtgatcgtag gttgtggggc tcaaggccta aaccaaggcc tcaatatgcg tgattcaggt 180

ttggatgttt cttacgtctt gcgtcaggct gcgattgatg aacagcgtca gtcatttaag 240

aatgccaaga ataatggctt caacgtgggt agttatgaac aactcatccc aaccgcagat 300

ttggtgatta acttgacgcc agacaagcag cacaccagtg tggatcaatgc ggtgatgcct 360

ctgatgaagc aaggtgctgc cttgggttac tcacacggtt ttaatatcgt tgaagagggc 420

atgcagatcc gtaaagacat cacggttgtg atggtggcac caaaatgtcc gggtagcgaa 480

gttcgtgaag agtataagcg cggtttcggc gttcctactc ttatcgcggt acacctgaa 540

aacgatccac aaggtgaagg ttgggaaatt gctaaagcgt gggctgcggc aacgggtggc 600

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<210> 36

<211> 494

<212> PRT

<213> Vibrio cholerae

<400> 36

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Leu Gly Arg Cys Arg Phe Met Ala Arg Glu Glu Phe Ala Thr Glu Ala

20 25 30

Asp Tyr Leu Lys Gly Lys Lys Val Val Ile Val Gly Cys Gly Ala Gln

35 40 45

Gly Leu Asn Gln Gly Leu Asn Met Arg Asp Ser Gly Leu Asp Val Ser

50 55 60

Tyr Ala Leu Arg Gln Ala Ala Ile Asp Glu Gln Arg Gln Ser Phe Lys

65 70 75 80

Asn Ala Lys Asn Asn Gly Phe Asn Val Gly Ser Tyr Glu Gln Leu Ile

85 90 95

Pro Thr Ala Asp Leu Val Ile Asn Leu Thr Pro Asp Lys Gln His Thr

100 105 110

Ser Val Val Asn Ala Val Met Pro Leu Met Lys Gln Gly Ala Ala Leu

115 120 125

Gly Tyr Ser His Gly Phe Asn Ile Val Glu Glu Gly Met Gln Ile Arg

130 135 140

Lys Asp Ile Thr Val Val Met Val Ala Pro Lys Cys Pro Gly Thr Glu

145 150 155 160

Val Arg Glu Glu Tyr Lys Arg Gly Phe Gly Val Pro Thr Leu Ile Ala

165 170 175

Val His Pro Glu Asn Asp Pro Gln Gly Glu Gly Trp Glu Ile Ala Lys

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

Arg Glu Lys Phe Met Pro Lys Val Gly Thr Asp Val Ile Gly Lys Gly
 435 440 445
 Leu Gly Val Val Ser Asn Gln Val Asp Asn Ala Thr Leu Ile Glu Val
 450 455 460
 Asn Ser Ile Ile Arg Asn His Pro Val Glu Tyr Ile Gly Glu Glu Leu
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 Arg Gly Tyr Met Lys Asp Met Lys Arg Ile Ala Val Gly Asp
 485 490

<210> 37

<211> 1014

<212> DNA

<213> Pseudomonas aeruginosa

<400> 37

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<210> 38

<211> 338

<212> PRT

<213> Pseudomonas aeruginosa

<400> 38

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Lys Lys Val Ala Ile Ile Gly Tyr Gly Ser Gln Gly His Ala His Ala
20 25 30

Cys Asn Leu Lys Asp Ser Gly Val Asp Val Thr Val Gly Leu Arg Ser
35 40 45

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

Asp Val Lys Thr Ala Val Ala Ala Ala Asp Val Val Met Ile Leu Thr
65 70 75 80

Pro Asp Glu Phe Gln Gly Arg Leu Tyr Lys Glu Glu Ile Glu Pro Asn
85 90 95

Leu Lys Lys Gly Ala Thr Leu Ala Phe Ala His Gly Phe Ser Ile His
100 105 110

Tyr Asn Gln Val Val Pro Arg Ala Asp Leu Asp Val Ile Met Ile Ala
115 120 125

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

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

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

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

Gly Glu Gln Ala Val Leu Cys Gly Gly Cys Val Glu Leu Val Lys Ala
195 200 205

Gly Phe Glu Thr Leu Val Glu Ala Gly Tyr Ala Pro Glu Met Ala Tyr
210 215 220

Phe Glu Cys Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Tyr Glu
 225 230 235 240
 Gly Gly Ile Ala Asn Met Asn Tyr Ser Ile Ser Asn Asn Ala Glu Tyr
 245 250 255
 Gly Glu Tyr Val Thr Gly Pro Glu Val Ile Asn Ala Glu Ser Arg Ala
 260 265 270

Ala Met Arg Asn Ala Leu Lys Arg Ile Gln Asp Gly Glu Tyr Ala Lys
 275 280 285
 Met Phe Ile Thr Glu Gly Ala Ala Asn Tyr Pro Ser Met Thr Ala Tyr
 290 295 300
 Arg Arg Asn Asn Ala Ala His Pro Ile Glu Gln Ile Gly Glu Lys Leu
 305 310 315 320
 Arg Ala Met Met Pro Trp Ile Ala Ala Asn Lys Ile Val Asp Lys Ser
 325 330 335

Lys Asn

<210> 39

<211> 1014

<212> DNA

<213> Pseudomonas fluorescens

<400> 39

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gacgtgactg ttggcctcgc taaaggctcg gctaccgttg ccaaggctga agcccacggc	180
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<210> 40

<211> 338

<212> PRT

<213> Pseudomonas fluorescens

<400> 40

Met Lys Val Phe Tyr Asp Lys Asp Cys Asp Leu Ser Ile Ile Gln Gly

1 5 10 15

Lys Lys Val Ala Ile Ile Gly Tyr Gly Ser Gln Gly His Ala Gln Ala

20 25 30

Cys Asn Leu Lys Asp Ser Gly Val Asp Val Thr Val Gly Leu Arg Lys

35 40 45

Gly Ser Ala Thr Val Ala Lys Ala Glu Ala His Gly Leu Lys Val Thr

50 55 60

Asp Val Ala Ala Ala Val Ala Gly Ala Asp Leu Val Met Ile Leu Thr

65 70 75 80

Pro Asp Glu Phe Gln Ser Gln Leu Tyr Lys Asn Glu Ile Glu Pro Asn

85 90 95

Ile Lys Lys Gly Ala Thr Leu Ala Phe Ser His Gly Phe Ala Ile His

100 105 110

Tyr Asn Gln Val Val Pro Arg Ala Asp Leu Asp Val Ile Met Ile Ala

115 120 125

Pro Lys Ala Pro Gly His Thr Val Arg Ser Glu Phe Val Lys Gly Gly

130 135 140

Gly Ile Pro Asp Leu Ile Ala Ile Tyr Gln Asp Ala Ser Gly Asn Ala

145 150 155 160

Lys Asn Val Ala Leu Ser Tyr Ala Ala Gly Val Gly Gly Gly Arg Thr

165 170 175

Gly Ile Ile Glu Thr Thr Phe Lys Asp Glu Thr Glu Thr Asp Leu Phe

180 185 190

Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Val Glu Leu Val Lys Ala

195 200 205

Gly Phe Glu Thr Leu Val Glu Ala Gly Tyr Ala Pro Glu Met Ala Tyr

210 215 220

Phe Glu Cys Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Tyr Glu

225 230 235 240

Gly Gly Ile Ala Asn Met Asn Tyr Ser Ile Ser Asn Asn Ala Glu Tyr

245 250 255

Gly Glu Tyr Val Thr Gly Pro Glu Val Ile Asn Ala Glu Ser Arg Gln

260 265 270

Ala Met Arg Asn Ala Leu Lys Arg Ile Gln Asp Gly Glu Tyr Ala Lys

275 280 285

Met Phe Ile Ser Glu Gly Ala Thr Gly Tyr Pro Ser Met Thr Ala Lys

290 295 300

Arg Arg Asn Asn Ala Ala His Gly Ile Glu Ile Ile Gly Glu Gln Leu

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325 330 335

Lys Asn

<210> 41

<211> 1047

<212> DNA

<213> Achromobacter xylosoxidans

<400> 41

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gatctcggca tctacaaagg caagaatcca gaggtcgccg acgggcgcac cctgggccat 180

gaaggggtag gcgtcatcga ggaagtgggc gagagtgtca cgcagttcaa gaaaggcgac 240
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<210> 42

<211> 348

<212> PRT

<213> Achromobacter xylosoxidans

<400> 42

Met Lys Ala Leu Val Tyr His Gly Asp His Lys Ile Ser Leu Glu Asp

1	5	10	15
Lys	Pro	Lys	Pro
Thr	Leu	Gln	Lys
Pro	Thr	Asp	Val
Val	Val	Arg	Val
20	25	30	
Leu	Lys	Thr	Thr
Ile	Cys	Gly	Thr
Asp	Leu	Gly	Ile
Tyr	Lys	Gly	Lys
35	40	45	
Asn	Pro	Glu	Val
Ala	Asp	Gly	Arg
Ile	Leu	Gly	His
Glu	Gly	Val	Gly
50	55	60	
Val	Ile	Glu	Glu
Val	Gly	Glu	Ser
Val	Thr	Gln	Phe
Lys	Lys	Gly	Asp

65	70	75	80
Lys	Val	Leu	Ile
Ser	Cys	Val	Thr
Ser	Cys	Gly	Ser
Cys	Asp	Tyr	Cys

85 90 95
 Lys Lys Gln Leu Tyr Ser His Cys Arg Asp Gly Gly Trp Ile Leu Gly
 100 105 110
 Tyr Met Ile Asp Gly Val Gln Ala Glu Tyr Val Arg Ile Pro His Ala
 115 120 125
 Asp Asn Ser Leu Tyr Lys Ile Pro Gln Thr Ile Asp Asp Glu Ile Ala

 130 135 140
 Val Leu Leu Ser Asp Ile Leu Pro Thr Gly His Glu Ile Gly Val Gln
 145 150 155 160
 Tyr Gly Asn Val Gln Pro Gly Asp Ala Val Ala Ile Val Gly Ala Gly
 165 170 175
 Pro Val Gly Met Ser Val Leu Leu Thr Ala Gln Phe Tyr Ser Pro Ser
 180 185 190
 Thr Ile Ile Val Ile Asp Met Asp Glu Asn Arg Leu Gln Leu Ala Lys

 195 200 205
 Glu Leu Gly Ala Thr His Thr Ile Asn Ser Gly Thr Glu Asn Val Val
 210 215 220
 Glu Ala Val His Arg Ile Ala Ala Glu Gly Val Asp Val Ala Ile Glu
 225 230 235 240
 Ala Val Gly Ile Pro Ala Thr Trp Asp Ile Cys Gln Glu Ile Val Lys
 245 250 255
 Pro Gly Ala His Ile Ala Asn Val Gly Val His Gly Val Lys Val Asp

 260 265 270
 Phe Glu Ile Gln Lys Leu Trp Ile Lys Asn Leu Thr Ile Thr Thr Gly
 275 280 285
 Leu Val Asn Thr Asn Thr Thr Pro Met Leu Met Lys Val Ala Ser Thr
 290 295 300
 Asp Lys Leu Pro Leu Lys Lys Met Ile Thr His Arg Phe Glu Leu Ala
 305 310 315 320
 Glu Ile Glu His Ala Tyr Gln Val Phe Leu Asn Gly Ala Lys Glu Lys

 325 330 335

Ala Met Lys Ile Ile Leu Ser Asn Ala Gly Ala Ala

340

345

<210> 43

<211> 843

<212> PRT

<213> Roseburia inulinivorans

<400> 43

Met Gly Asn Tyr Asp Ser Thr Pro Ile Ala Lys Ser Asp Arg Ile Lys

1 5 10 15

Arg Leu Val Asp His Leu Tyr Ala Lys Met Pro Glu Ile Glu Ala Ala

20 25 30

Arg Ala Glu Leu Ile Thr Glu Ser Phe Lys Ala Thr Glu Gly Gln Pro

35 40 45

Val Val Met Arg Lys Ala Arg Ala Phe Glu His Ile Leu Lys Asn Leu

50 55 60

Pro Ile Ile Ile Arg Pro Glu Glu Leu Ile Val Gly Ser Thr Thr Ile

65 70 75 80

Ala Pro Arg Gly Cys Gln Thr Tyr Pro Glu Phe Ser Tyr Glu Trp Leu

85 90 95

Glu Ala Glu Phe Glu Thr Val Glu Thr Arg Ser Ala Asp Pro Phe Tyr

100 105 110

Ile Ser Glu Glu Thr Lys Lys Arg Leu Leu Ala Ala Asp Ala Tyr Trp

115 120 125

Lys Gly Lys Thr Thr Ser Glu Leu Ala Thr Ser Tyr Met Ala Pro Glu

130 135 140

Thr Leu Arg Ala Met Lys His Asn Phe Phe Thr Pro Gly Asn Tyr Phe

145 150 155 160

Tyr Asn Gly Val Gly His Val Thr Val Gln Tyr Glu Thr Val Leu Ala

165 170 175

Ile Gly Leu Asn Gly Val Lys Glu Lys Val Arg Lys Glu Met Glu Asn

180 185 190

Cys His Phe Gly Asp Ala Asp Tyr Ser Thr Lys Met Cys Phe Leu Glu

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

Gly Trp His Asp Ala Ala Phe Phe Asn Met Cys Arg Pro Leu Glu Met
450 455 460

Val Phe Ser Asn Gly Tyr Asp Asn Gly Glu Ile Ala Ser Ile Gln Thr
465 470 475 480

Gly Asn Val Glu Ser Phe Gln Ser Phe Asp Glu Phe Met Glu Ala Tyr
485 490 495

Arg Lys Gln Met Leu Tyr Asn Ile Glu Leu Met Val Asn Ala Asp Asn
500 505 510

Ala Ile Asp Tyr Ala His Ala Lys Leu Ala Pro Leu Pro Phe Glu Ser
515 520 525

Cys Leu Val Asp Asp Cys Ile Lys Arg Gly Met Ser Ala Gln Glu Gly
530 535 540

Gly Ala Ile Tyr Asn Phe Thr Gly Pro Gln Gly Phe Gly Ile Ala Asn
545 550 555 560

Val Ala Asp Ser Leu Tyr Thr Ile Lys Lys Leu Val Phe Glu Glu Lys
565 570 575

Arg Ile Thr Met Gly Glu Leu Lys Lys Ala Leu Glu Met Asn Tyr Gly
580 585 590

Lys Gly Leu Asp Ala Thr Thr Ala Gly Asp Ile Ala Met Gln Val Ala
595 600 605

Lys Gly Leu Lys Asp Ala Gly Gln Glu Val Gly Pro Asp Val Ile Ala
610 615 620

Asn Thr Ile Arg Gln Val Leu Glu Met Glu Leu Pro Glu Asp Val Arg
625 630 635 640

Lys Arg Tyr Glu Glu Ile His Glu Met Ile Leu Glu Leu Pro Lys Tyr
645 650 655

Gly Asn Asp Ile Asp Glu Val Asp Glu Leu Ala Arg Glu Ala Ala Tyr
660 665 670

Phe Tyr Thr Arg Pro Leu Glu Thr Phe Lys Asn Pro Arg Gly Gly Met
675 680 685

Tyr Gln Ala Gly Leu Tyr Pro Val Ser Ala Asn Val Pro Leu Gly Ala

690 695 700
 Gln Thr Gly Ala Thr Pro Asp Gly Arg Leu Ala His Thr Pro Val Ala
 705 710 715 720
 Asp Gly Val Gly Pro Thr Ser Gly Phe Asp Ile Ser Gly Pro Thr Ala
 725 730 735

 Ser Cys Asn Ser Val Ala Lys Leu Asp His Ala Ile Ala Ser Asn Gly
 740 745 750
 Thr Leu Phe Asn Met Lys Met His Pro Thr Ala Met Ala Gly Glu Lys
 755 760 765
 Gly Leu Glu Ser Phe Ile Ser Leu Ile Arg Gly Tyr Phe Asp Gln Gln
 770 775 780
 Gly Met His Met Gln Phe Asn Val Val Asp Arg Ala Thr Leu Leu Asp
 785 790 795 800

 Ala Gln Ala His Pro Glu Lys Tyr Ser Gly Leu Ile Val Arg Val Ala
 805 810 815
 Gly Tyr Ser Ala Leu Phe Thr Thr Leu Ser Lys Ser Leu Gln Asp Asp
 820 825 830
 Ile Ile Lys Arg Thr Glu Gln Ala Asp Asn Arg
 835 840

 <210> 44
 <211> 264
 <212> PRT
 <213> Roseburia inulinivorans
 <400> 44

 Met Lys Glu Tyr Leu Asn Thr Ser Gly Arg Ile Phe Asp Ile Gln Arg
 1 5 10 15

 Tyr Ser Ile His Asp Gly Pro Gly Val Arg Thr Ile Val Phe Leu Lys
 20 25 30
 Gly Cys Ala Leu Arg Cys Arg Trp Cys Cys Asn Pro Glu Ser Gln Ser
 35 40 45
 Phe Glu Val Glu Thr Met Thr Ile Asn Gly Lys Pro Lys Val Met Gly
 50 55 60

Lys Asp Val Thr Val Ala Glu Val Met Lys Thr Val Glu Arg Asp Met
65 70 75 80

Pro Tyr Tyr Leu Gln Ser Gly Gly Gly Ile Thr Leu Ser Gly Gly Glu
85 90 95

Cys Thr Leu Gln Pro Glu Phe Ser Leu Gly Leu Leu Arg Ala Ala Lys
100 105 110

Asp Leu Gly Ile Ser Thr Ala Ile Glu Ser Met Ala Tyr Ala Lys Tyr
115 120 125

Glu Val Ile Glu Thr Leu Leu Pro Tyr Leu Asp Thr Tyr Leu Met Asp
130 135 140

Ile Lys His Met Asn Pro Glu Lys His Lys Glu Tyr Thr Gly His Asp
145 150 155 160

Asn Leu Arg Met Leu Glu Asn Ala Leu Arg Val Ala His Ser Gly Gln
165 170 175

Thr Glu Leu Ile Ile Arg Val Pro Val Ile Pro Gly Phe Asn Ala Thr
180 185 190

Glu Gln Glu Leu Leu Asp Ile Ala Lys Phe Ala Asp Thr Leu Pro Gly
195 200 205

Val Arg Gln Ile His Ile Leu Pro Tyr His Asn Phe Gly Gln Gly Lys
210 215 220

Tyr Glu Gly Leu Asn Arg Asp Tyr Pro Met Gly Asp Thr Glu Lys Pro
225 230 235 240

Ser Asn Glu Gln Met Lys Ala Phe Gln Glu Met Ile Gln Lys Asn Thr
245 250 255

Ser Leu His Cys Gln Ile Gly Gly
260

<210> 45

<211> 1815

<212> DNA

<213> Chlamydomonas reinhardtii

<400> 45

atgtcgtcga ctgcgacat gcccgccag cgtcggcca tgaaggccgc tggcgcccag	60
agccgccgtg ccgtgaaggt gatgccgtg tccgtccgg agaagccgtc gtcgtccgc	120
ccggccgtcc cggcaggcct gaacaagtgc agcagccga tcacgaacc caagtaccag	180
ggcgctctc aggcattgt gttcgtacc ggtctcggg aggaggacat gatcaagccg	240
caggtgggca tctcctcgt gtggtacgag ggcaaccctt gcaacatgca cctgatggac	300
ctggcgccgg aggtgaagaa gggcgtggag gccatgggca tggcggcctt ccgcttcaac	360
accattggtg tcagcgacgg catttccatg ggaccgacg gcatgagctt cagcctgcag	420
agccgcgacc tgattgccga ctccattgag acggtcatga gcgcgcagtg gtacgacgcc	480
aacatctcgc tgcccggtg cgacaagaac atccccggca cgtgatggc catggccgc	540
ctgaaccgcc cctcgtcat gatctacggc ggcaactatca agcccgcca cagccgatg	600
gacggctccg tcttgacat cgtgtccgc ttccagagct acggcgcta ctggccggc	660
ctgatcaacg agggccagcg tgtggacatt gtgcgcaaca gctgccctgg cgtggcgcg	720
tgcggcgga tgtacactgc caacaccatg gcctcgcca ttgaggctct gggcatgacc	780
ctgccctaca gctcgtccat ccccgctgag gaccgctga agaaggacga gtgccgatg	840
gccggccgct acatgctgga gctgtcaag tccgacctga agcctctgga catcatgacc	900
tacaaggcct ttgagaacgc catggtgctg gtcatggcca ccggcggtc caccaacgcc	960
gtgtgcact tcatgccat ggcgcgccc tgcggcgtgc cctgaccct ggacacttc	1020
cagcgctgt ctgaccgac gcccttcac tgcgacctca agcctcggg ccgtacgtc	1080
atggaggaca tccacaaggt gggcgccacc cccgccgtgc tgaagtacct ggactccaag	1140
ggctacatca accgcgactg catgaccgtc actggcaaga ccatggcgcc caacctggcg	1200
gaggtgccgg agctgcgtgc gggccaggac gtggtgctgc ccgtggagaa gcccatcaag	1260
cagactggcc acatccagat cctgtacggc aacctggccc cggagggcag cgtggccaag	1320
atcactggca aggaggcct gctgttcgag ggcgaggcgc tgggtttga caacaggag	1380
gacatgatca ccatggtggg cgccgagccc aacaagtcc gcgcaaggt ggtggtgatc	1440
cgctacgagg gcccgaagg cgccccggc atccccgaga tgcacgcc cacctccgc	1500
atcatggcg ccggcctggg caaggagtgc gcgtcatca ccgacggacg cttcagcgcc	1560
ggcagccacg gcttcgtgat cgccacgtc acggcgagg cgcaggtcgg cgccccatc	1620
gccctggtca agaacggcga caagattgtg attgatgtgg agaagcgcgt gatggacatg	1680
aagatctccg accaggagct ggccgcgcgc aaggctgcct ggaaggcgcc cccgctgaag	1740
gccaccagcg gcacctgta caagtacac aagaacgtgt cgtcgcgctc cactggctgc	1800
gtcaccgact cgtaa	1815

<210> 46

<211> 604

<212> PRT

<213> Chlamydomonas reinhardtii

<400> 46

Met Ser Ser Thr Ala Thr Met Pro Gly Gln Arg Ser Ala Met Lys Ala

1 5 10 15

Ala Gly Ala Gln Ser Arg Arg Ala Val Lys Val Met Ala Val Ser Ala

20 25 30

Pro Glu Lys Pro Ser Ser Ser Ala Pro Ala Val Pro Ala Gly Leu Asn

35 40 45

Lys Phe Ser Ser Arg Ile Thr Gln Pro Lys Tyr Gln Gly Ala Ser Gln

50 55 60

Ala Met Leu Phe Ala Thr Gly Leu Arg Glu Glu Asp Met Ile Lys Pro

65 70 75 80

Gln Val Gly Ile Ser Ser Val Trp Tyr Glu Gly Asn Pro Cys Asn Met

85 90 95

His Leu Met Asp Leu Ala Ala Glu Val Lys Lys Gly Val Glu Ala Met

100 105 110

Gly Met Val Gly Phe Arg Phe Asn Thr Ile Gly Val Ser Asp Gly Ile

115 120 125

Ser Met Gly Thr Asp Gly Met Ser Phe Ser Leu Gln Ser Arg Asp Leu

130 135 140

Ile Ala Asp Ser Ile Glu Thr Val Met Ser Ala Gln Trp Tyr Asp Ala

145 150 155 160

Asn Ile Ser Leu Pro Gly Cys Asp Lys Asn Met Pro Gly Thr Leu Met

165 170 175

Ala Met Ala Arg Leu Asn Arg Pro Ser Leu Met Ile Tyr Gly Gly Thr

180 185 190

Ile Lys Pro Gly His Ser Arg Met Asp Gly Ser Val Leu Asp Ile Val

195 200 205

Ser Ala Phe Gln Ser Tyr Gly Ala Tyr Ser Ala Gly Leu Ile Asn Glu

210 215 220

Ala Gln Arg Val Asp Ile Val Arg Asn Ser Cys Pro Gly Ala Gly Ala

225 230 235 240

Cys Gly Gly Met Tyr Thr Ala Asn Thr Met Ala Ser Ala Ile Glu Ala

245 250 255

Leu Gly Met Thr Leu Pro Tyr Ser Ser Ser Ile Pro Ala Glu Asp Pro

260 265 270

Leu Lys Lys Asp Glu Cys Arg Met Ala Gly Arg Tyr Met Leu Glu Leu

275 280 285

Leu Lys Ser Asp Leu Lys Pro Leu Asp Ile Met Thr Tyr Lys Ala Phe

290 295 300

Glu Asn Ala Met Val Leu Val Met Ala Thr Gly Gly Ser Thr Asn Ala

305 310 315 320

Val Leu His Phe Ile Ala Met Ala Arg Ala Cys Gly Val Pro Leu Thr

325 330 335

Leu Asp Asp Phe Gln Arg Val Ser Asp Arg Thr Pro Phe Ile Cys Asp

340 345 350

Leu Lys Pro Ser Gly Arg Tyr Val Met Glu Asp Ile His Lys Val Gly

355 360 365

Gly Thr Pro Ala Val Leu Lys Tyr Leu Asp Ser Lys Gly Tyr Ile Asn

370 375 380

Arg Asp Cys Met Thr Val Thr Gly Lys Thr Met Gly Gly Asn Leu Ala

385 390 395 400

Glu Val Pro Glu Leu Arg Ala Gly Gln Asp Val Val Leu Pro Val Glu

405 410 415

Lys Pro Ile Lys Gln Thr Gly His Ile Gln Ile Leu Tyr Gly Asn Leu

420 425 430

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

435 440 445

Phe Glu Gly Glu Ala Leu Val Phe Asp Asn Glu Glu Asp Met Ile Thr

450 455 460
Met Val Gly Ala Glu Pro Asn Lys Phe Arg Gly Lys Val Val Val Ile

465 470 475 480
Arg Tyr Glu Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met Leu Thr

 485 490 495
Pro Thr Ser Ala Ile Met Gly Ala Gly Leu Gly Lys Glu Cys Ala Leu

 500 505 510
Ile Thr Asp Gly Arg Phe Ser Gly Gly Ser His Gly Phe Val Ile Gly

 515 520 525
His Val Thr Pro Glu Ala Gln Val Gly Gly Pro Ile Ala Leu Val Lys

 530 535 540
Asn Gly Asp Lys Ile Val Ile Asp Val Glu Lys Arg Val Met Asp Met

545 550 555 560
Lys Ile Ser Asp Gln Glu Leu Ala Ala Arg Lys Ala Ala Trp Lys Ala

 565 570 575
Pro Pro Leu Lys Ala Thr Ser Gly Thr Leu Tyr Lys Tyr Ile Lys Asn

 580 585 590
Val Ser Ser Ala Ser Thr Gly Cys Val Thr Asp Ser

 595 600

<210> 47

<211> 1704

<212> DNA

<213> *Ostreococcus lucimarinus*

<400> 47

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agccaaggag cgtcgcaggc gatgctgtac gccacgggcc tgacggaggc cgatatgaac 120

aaaccgcaga tcggcgtgtc ctcggtgtgg tggcaggga acccttgtaa caaacacttg 180

ctggacctgg cgggtaaagt ggcggaaggc gtcaaggcgg cggatatggt gagctttcag 240

tttaacaccg tgggggtgtc ggacgggatt tccatgggta cgccgggcat gtccttctcg 300

ttgcaatcgc gggatttgat cgcgatagc atcgagaccg tgatgggtgg acagtggtag 360

gacggaaata ttctctctcc ggggtgcgat aagaacatgc cgggtacgat catggccatg 420

ggtcgattga accgcccgtc gctgatgatt tacggcggta ccattcgccc tggccactcc 480
gccgtggatg gtggcacact cgatatcgta tccgcgttcc aatcgtagg acagttcgtt 540
accggcgcta tcacggagga acagcgcaaa gacatcgtgc gtaactcttg cccgggctct 600
ggcgcgtgcg gcggcatgta caccgccaac accatggcca gctgcatcga ggctctcggc 660
atgactcttc cgtattcttc ctccattccc gcggaagatc ctctcaagat ggatgaatgt 720

ttcatggctg gcgtgcgat gaagcatttg ctcgaaatcg acctgaagcc gcgtgacatc 780
atgactcgcg cggcgttcga aaacgccatg gtcaccgtca tcgctctcgg cggttccacc 840
aacgcggttc ttacttgat cgcgatggcg cactctgtcg gcatcaaatt gactctggac 900
gacttccaag ccgtctccaa caagacgccg ttcatcgtg acttaaagcc gtccggtgaag 960
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ctcgccatct gcccgattt gacgccgggg caagatgtta ttctcccgtg gagcacgccc 1140

atcaagaaga ctggtcactt gcaatgcttg tacggcaaca tcgcccaggg aggctccgtg 1200
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gaagaggaaa tgctcgagcg cttggcggca gactccgagt ctttcaaggg tagcgtcatc 1320
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tcggccatca tgggtgccgg tctcggaac gactgcgcgc tcatcacgga tggtcgattc 1440
tccggtggct cgcacggttt cgtcatcggt caggttacgc cggaagcgca agttggtggt 1500
aacatcggtt tgatcaagga cggtgatatc atcgaaattg atgccgaagt tcgcaccatc 1560

aacgcgccgg atgtcacgca cgccgagtgg gaaaagcgtc gagcggcgtg gaaggcgccg 1620
cctttggaag cgacgtcggg tacgtcttac aagtactgca agctcgtcgc cagcgttcg 1680
gaaggtgca tcacggactt gtga 1704

<210> 48

<211> 567

<212> PRT

<213> *Ostreococcus lucimarinus*

<400> 48

Met Pro Asp Gly Asp Ala Ser Asp Leu Asn Lys Trp Ser Arg Lys Ile

1 5 10 15

Thr Gln Pro Lys Ser Gln Gly Ala Ser Gln Ala Met Leu Tyr Ala Thr

Gly Leu Thr Glu Ala Asp Met Asn Lys Pro Gln Ile Gly Val Ser Ser
 35 40 45
 Val Trp Trp Gln Gly Asn Pro Cys Asn Lys His Leu Leu Asp Leu Ala
 50 55 60
 Gly Lys Val Ala Glu Gly Val Lys Ala Ala Asp Met Val Ser Phe Gln
 65 70 75 80
 Phe Asn Thr Val Gly Val Ser Asp Gly Ile Ser Met Gly Thr Pro Gly
 85 90 95
 Met Ser Phe Ser Leu Gln Ser Arg Asp Leu Ile Ala Asp Ser Ile Glu
 100 105 110
 Thr Val Met Gly Gly Gln Trp Tyr Asp Gly Asn Ile Ser Leu Pro Gly
 115 120 125
 Cys Asp Lys Asn Met Pro Gly Thr Ile Met Ala Met Gly Arg Leu Asn
 130 135 140
 Arg Pro Ser Leu Met Ile Tyr Gly Gly Thr Ile Arg Pro Gly His Ser
 145 150 155 160
 Ala Val Asp Gly Gly Thr Leu Asp Ile Val Ser Ala Phe Gln Ser Tyr
 165 170 175
 Gly Gln Phe Val Thr Gly Ala Ile Thr Glu Glu Gln Arg Lys Asp Ile
 180 185 190
 Val Arg Asn Ser Cys Pro Gly Ser Gly Ala Cys Gly Gly Met Tyr Thr
 195 200 205
 Ala Asn Thr Met Ala Ser Cys Ile Glu Ala Leu Gly Met Thr Leu Pro
 210 215 220
 Tyr Ser Ser Ser Ile Pro Ala Glu Asp Pro Leu Lys Met Asp Glu Cys
 225 230 235 240
 Phe Met Ala Gly Ala Ala Met Lys His Leu Leu Glu Ile Asp Leu Lys
 245 250 255
 Pro Arg Asp Ile Met Thr Arg Ala Ala Phe Glu Asn Ala Met Val Thr
 260 265 270
 Val Ile Ala Leu Gly Gly Ser Thr Asn Ala Val Leu His Leu Ile Ala

275 280 285
 Met Ala His Ser Val Gly Ile Lys Leu Thr Leu Asp Asp Phe Gln Ala
 290 295 300
 Val Ser Asn Lys Thr Pro Phe Ile Ala Asp Leu Lys Pro Ser Gly Lys
 305 310 315 320
 Tyr Val Met Glu Asp Val His Lys Val Gly Gly Thr Pro Ala Val Leu
 325 330 335
 Lys Tyr Leu Met Ser Glu Gly Met Ile Asp Gly Ser Cys Met Thr Val

 340 345 350
 Thr Gly Lys Thr Leu Ala Glu Asn Leu Ala Ile Cys Pro Asp Leu Thr
 355 360 365
 Pro Gly Gln Asp Val Ile Leu Pro Val Ser Thr Pro Ile Lys Lys Thr
 370 375 380
 Gly His Leu Gln Cys Leu Tyr Gly Asn Ile Ala Gln Gly Gly Ser Val
 385 390 395 400
 Ala Lys Ile Thr Gly Lys Glu Gly Leu Tyr Phe Lys Gly Phe Ala Lys

 405 410 415
 Cys Tyr Asp Ser Glu Glu Glu Met Leu Glu Ala Leu Ala Ala Asp Ser
 420 425 430
 Glu Ser Phe Lys Gly Ser Val Ile Val Ile Arg Tyr Glu Gly Pro Lys
 435 440 445
 Gly Gly Pro Gly Met Pro Glu Met Leu Thr Pro Thr Ser Ala Ile Met
 450 455 460
 Gly Ala Gly Leu Gly Asn Asp Cys Ala Leu Ile Thr Asp Gly Arg Phe

 465 470 475 480
 Ser Gly Gly Ser His Gly Phe Val Ile Gly His Val Thr Pro Glu Ala
 485 490 495
 Gln Val Gly Gly Asn Ile Gly Leu Ile Lys Asp Gly Asp Ile Ile Glu
 500 505 510
 Ile Asp Ala Glu Val Arg Thr Ile Asn Ala Pro Asp Val Thr Asp Ala
 515 520 525

Glu Trp Glu Lys Arg Arg Ala Ala Trp Lys Ala Pro Pro Leu Glu Ala

530 535 540
 Thr Ser Gly Thr Leu Tyr Lys Tyr Cys Lys Leu Val Ala Ser Ala Ser
 545 550 555 560
 Glu Gly Cys Ile Thr Asp Leu
 565

<210> 49

<211> 1695

<212> DNA

<213> Vitis vinifera

<400> 49

atgcaagcag ctctgataac cccttctcct cgcgccattc ccaccggttc catcactgcc	60
acgagaacca caattccccc tcatgtgcgc ctctgtgtctg tccgagcatc gaccgaggta	120
gcccaatcgc cgccaccgcg agtgaaagag acggcccaca agtcaacaa gtacagctct	180
catgtcaccg agcccaagtc ccaggcggcg tcacaagcca tcctctatgg cgtgggtctc	240
tccgatgagg acatgcacaa gcctcaaadc ggtatatcat cggtttggtg cgagggaac	300
acctgcaaca tgcatttggt gaagctttca gaggtgtga aggagggggt gagagatgcc	360
ggcatggttg ggttcaggtt caacactgtt ggtgtcagcg atgccatctc aatgggcacg	420
agaggcatgt gctatagctt gcagtctagg gatttgattg ctgatagtat tgagacggtc	480
atgtctgctc agtggatga tggcaacatt tctattcccg gttgtgacaa aaatatgcca	540
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atcaagcctg gtcattttca aggccatact tacgacataa tatctgcctt tcaggtttat	660
ggagagttcg tcagtgggtc cataactgat gaacagagga tgaatgttgt ccgaaattca	720
tgccaggag caggagcttg tgggtggaatg tatacagcca atacgatggc ttctgtctatt	780
gaagttatgg gaatgtctct tcccttcagc tcttcaacac cggtgaaga cccattgaag	840
ttgcatgagt gccatttggc tggaaaatat ctcttggtt tgataaaaat ggacttaaaa	900
ccacagata ttatcactat gaagtcacta cggaatgcta tggttgttgt catggcattg	960
ggtggatcta ccaatgtgtg attacattta attgccattg caaggtctgt tggctctcag	1020
ttaactcttg atgattttca gaaagtaagt gatgaggttc cattccttgc tgatcttaag	1080
cccattggca aatacgtcat ggaggacata cacaagattg gaggaacacc ggcaatcatt	1140
cgcttccttt tggaaaatgg gtttttagat ggggattgta taacagttac tgggaagaca	1200

ttggctgaaa atgcagaact ttttccttct ttgccagag atcagcaaat aataagaccg 1260
 ttggcaaacc ccataaagaa gactggacac ctccaaactt tataatgaaa tcttgacca 1320
 gagggttctg ttgcaaaaat tactggaaaa gaagggtat atttctctgg tcctgcactt 1380
 gtccttgaag gtgaggaagc tatgattgca gctatagcag agaatcctat gagctttaag 1440

gggaaagtag ttattattag aggagagga cccaaggggg ggccaggaat gcctgaaatg 1500
 ttgactccaa caagcgcaat aatgggagca ggtcttgga aggatgttg tttgttgact 1560
 gatggtaggt tttcaggagg ttcacatgga tatgttgttg gccacatatg tcctgaagca 1620
 catgtacatt ttcctttcct tcattccagt ttattttttt attttttga tcagaaacga 1680
 agaagattat attaa 1695

<210> 50

<211> 564

<212> PRT

<213> Vitis vinifera

<400> 50

Met Gln Ala Ala Leu Ile Thr Pro Ser Pro Arg Ala Ile Pro Thr Gly

1 5 10 15
 Ser Ile Thr Ala Thr Arg Thr Thr Ile Pro Pro His Val Arg Leu Val
 20 25 30
 Ser Val Arg Ala Ser Thr Glu Val Ala Gln Ser Pro Pro Pro Ala Val
 35 40 45
 Lys Glu Thr Ala His Lys Leu Asn Lys Tyr Ser Ser His Val Thr Glu
 50 55 60
 Pro Lys Ser Gln Gly Gly Ser Gln Ala Ile Leu Tyr Gly Val Gly Leu

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

130 135 140
 Tyr Ser Leu Gln Ser Arg Asp Leu Ile Ala Asp Ser Ile Glu Thr Val
 145 150 155 160
 Met Ser Ala Gln Trp Tyr Asp Gly Asn Ile Ser Ile Pro Gly Cys Asp
 165 170 175
 Lys Asn Met Pro Gly Thr Ile Met Ala Met Gly Arg Leu Asn Arg Pro
 180 185 190
 Ser Ile Met Val Tyr Gly Gly Ala Ile Lys Pro Gly His Phe Gln Gly

 195 200 205
 His Thr Tyr Asp Ile Ile Ser Ala Phe Gln Val Tyr Gly Glu Phe Val
 210 215 220
 Ser Gly Ser Ile Thr Asp Glu Gln Arg Met Asn Val Val Arg Asn Ser
 225 230 235 240
 Cys Pro Gly Ala Gly Ala Cys Gly Gly Met Tyr Thr Ala Asn Thr Met
 245 250 255
 Ala Ser Ala Ile Glu Val Met Gly Met Ser Leu Pro Phe Ser Ser Ser

 260 265 270
 Thr Pro Ala Glu Asp Pro Leu Lys Leu His Glu Cys His Leu Ala Gly
 275 280 285
 Lys Tyr Leu Leu Asp Leu Ile Lys Met Asp Leu Lys Pro Arg Asp Ile
 290 295 300
 Ile Thr Met Lys Ser Leu Arg Asn Ala Met Val Val Val Met Ala Leu
 305 310 315 320
 Gly Gly Ser Thr Asn Ala Val Leu His Leu Ile Ala Ile Ala Arg Ser

 325 330 335
 Val Gly Leu Gln Leu Thr Leu Asp Asp Phe Gln Lys Val Ser Asp Glu
 340 345 350
 Val Pro Phe Leu Ala Asp Leu Lys Pro Ser Gly Lys Tyr Val Met Glu
 355 360 365
 Asp Ile His Lys Ile Gly Gly Thr Pro Ala Ile Ile Arg Phe Leu Leu
 370 375 380

Glu Asn Gly Phe Leu Asp Gly Asp Cys Ile Thr Val Thr Gly Lys Thr

385 390 395 400

Leu Ala Glu Asn Ala Glu Leu Phe Pro Ser Leu Pro Arg Asp Gln Gln

405 410 415

Ile Ile Arg Pro Leu Ala Asn Pro Ile Lys Lys Thr Gly His Leu Gln

420 425 430

Thr Leu Tyr Gly Asn Leu Ala Pro Glu Gly Ser Val Ala Lys Ile Thr

435 440 445

Gly Lys Glu Gly Leu Tyr Phe Ser Gly Pro Ala Leu Val Phe Glu Gly

450 455 460

Glu Glu Ala Met Ile Ala Ala Ile Ala Glu Asn Pro Met Ser Phe Lys

465 470 475 480

Gly Lys Val Val Ile Ile Arg Gly Glu Gly Pro Lys Gly Gly Pro Gly

485 490 495

Met Pro Glu Met Leu Thr Pro Thr Ser Ala Ile Met Gly Ala Gly Leu

500 505 510

Gly Lys Asp Val Ala Leu Leu Thr Asp Gly Arg Phe Ser Gly Gly Ser

515 520 525

His Gly Tyr Val Val Gly His Ile Cys Pro Glu Ala His Val His Phe

530 535 540

Leu Phe Leu His Pro Val Leu Phe Phe Tyr Phe Phe Asp Gln Lys Arg

545 550 555 560

Arg Arg Leu Tyr

<210> 51

<211> 1839

<212> DNA

<213> Vitis vinifera

<400> 51

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<210> 52

<211> 612

<212> PRT

<213> *Vitis vinifera*

<400> 52

Met Gln Val Ala Leu Ile Thr Pro Ser Pro Arg Ala Ile Pro Thr Gly

1 5 10 15

Ser Ile Thr Ala Thr Arg Thr Thr Ile Pro Pro His Val Arg Leu Val

20 25 30

Ser Val Arg Ala Ser Thr Glu Val Ala Gln Ser Pro Pro Pro Ala Val

35 40 45

Lys Glu Thr Ala His Lys Leu Asn Lys Tyr Ser Ser His Val Thr Glu

50 55 60

Pro Lys Ser Gln Gly Gly Ser Gln Ala Ile Leu Tyr Gly Val Gly Leu

65 70 75 80

Ser Asp Glu Asp Met His Lys Pro Gln Ile Gly Ile Ser Ser Val Trp

85 90 95

Tyr Glu Gly Asn Thr Cys Asn Met His Leu Leu Lys Leu Ser Glu Ala

100 105 110

Val Lys Glu Gly Val Arg Asp Ala Gly Met Val Gly Phe Arg Phe Asn

115 120 125

Thr Val Gly Val Ser Asp Ala Ile Ser Met Gly Thr Arg Gly Met Cys

130 135 140

Tyr Ser Leu Gln Ser Arg Asp Leu Ile Ala Asp Ser Ile Glu Thr Val

145 150 155 160

Met Ser Ala Gln Trp Tyr Asp Gly Asn Ile Ser Ile Pro Gly Cys Asp

165 170 175

Lys Asn Met Pro Gly Thr Ile Met Ala Met Gly Arg Leu Asn Arg Pro

180 185 190

Ser Ile Met Val Tyr Gly Gly Ala Ile Lys Arg Gln Ile Asp Asn Tyr

195 200 205

Asn Trp Asp Pro Asn His Thr Ile Leu Cys Ser Val Ala His His Phe

210 215 220

Ile Leu Arg Tyr Glu Met Leu Tyr Glu Val Ile Phe Glu Lys Trp His

225 230 235 240

Asp Pro Gly His Phe Gln Gly His Thr Tyr Asp Ile Ile Ser Ala Phe

245 250 255

Gln Leu Trp Ser Glu Gly Gly Val Cys Val Val Ser Leu Val Pro Trp

260 265 270

Phe Met Glu Ser Ser Ser Ser Gly Ser Ile Thr Asp Glu Gln Arg Met

275 280 285

Asn Val Val Arg Asn Ser Cys Pro Gly Ala Gly Ala Cys Gly Gly Met

290 295 300

Tyr Thr Ala Asn Thr Met Ala Ser Ala Ile Glu Val Met Gly Met Ser

305 310 315 320

Leu Pro Phe Ser Ser Ser Thr Pro Ala Glu Asp Pro Leu Lys Leu His

325 330 335

Glu Cys His Leu Ala Gly Lys Tyr Leu Leu Asp Leu Ile Lys Met Asp

340 345 350

Leu Lys Pro Arg Asp Ile Ile Thr Met Lys Ser Leu Arg Asn Ala Met

355 360 365

Val Val Val Met Ala Leu Gly Gly Ser Thr Asn Ala Val Leu His Leu

370 375 380

Ile Ala Ile Ala Arg Ile Ala His Asp Lys Ile Leu Gly Arg Ser Val

385 390 395 400

Gly Leu Gln Leu Thr Leu Asp Asp Phe Gln Lys Val Ser Asp Glu Val

405 410 415

Pro Phe Leu Ala Asp Leu Lys Pro Ser Gly Lys Tyr Val Met Glu Asp

420 425 430

Ile His Lys Ile Gly Gly Thr Pro Ala Ile Ile Arg Phe Leu Leu Glu

435 440 445

Asn Gly Phe Leu Asp Gly Asp Cys Ile Thr Gly Pro Ala Leu Val Phe

450 455 460

Glu Gly Glu Glu Ala Met Ile Ala Ala Ile Ala Glu Asn Pro Met Ser

465 470 475 480
Phe Lys Gly Lys Val Val Ile Ile Arg Gly Glu Gly Pro Lys Gly Gly

 485 490 495
Pro Gly Met Pro Glu Met Leu Thr Pro Thr Ser Ala Ile Met Gly Ala

 500 505 510
Gly Leu Gly Lys Asp Val Ala Leu Leu Thr Asp Gly Arg Phe Ser Gly

 515 520 525
Gly Ser His Gly Tyr Val Val Gly His Ile Cys Pro Glu Ala His Glu

 530 535 540
Gly Gly Pro Ile Gly Leu Ile Glu Asn Gly Asp Ile Ile Thr Ile Asp

545 550 555 560
Val Gln Lys Arg Arg Met Asp Val Gln Leu Thr Asp Glu Glu Met Asn

 565 570 575
Glu Arg Arg Lys Lys Trp Ser Pro Pro Pro Tyr Lys Ala Asn Gln Gly

 580 585 590
Val Leu Tyr Lys Tyr Ile Lys Asn Val Lys Ser Ala Ser Asp Gly Cys

 595 600 605
Val Thr Asp Glu

610

<210> 53

<211> 1827

<212> DNA

<213> Arabidopsis thaliana

<400> 53

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aacatgcatt tgctgaaatt gtctgaggct gtgaaagaag gagttgaaaa tgcaggaatg 360

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<210> 54

<211> 608

<212> PRT

<213> Arabidopsis thaliana

<400> 54

Met Gln Ala Thr Ile Phe Ser Pro Arg Ala Thr Leu Phe Pro Cys Lys

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Pro Leu Leu Pro Ser His Asn Val Asn Ser Arg Arg Pro Ser Ile Ile
20 25 30

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

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

Ser Gln Gly Gly Ser Gln Ala Ile Leu His Gly Val Gly Leu Ser Asp
65 70 75 80

Asp Asp Leu Leu Lys Pro Gln Ile Gly Ile Ser Ser Val Trp Tyr Glu
85 90 95

Gly Asn Thr Cys Asn Met His Leu Leu Lys Leu Ser Glu Ala Val Lys
100 105 110

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

Gly Val Ser Asp Ala Ile Ser Met Gly Thr Arg Gly Met Cys Phe Ser
130 135 140

Leu Gln Ser Arg Asp Leu Ile Ala Asp Ser Ile Glu Thr Val Met Ser
145 150 155 160

Ala Gln Trp Tyr Asp Gly Asn Ile Ser Ile Pro Gly Cys Asp Lys Asn
165 170 175

Met Pro Gly Thr Ile Met Ala Met Gly Arg Leu Asn Arg Pro Gly Ile
180 185 190

Met Val Tyr Gly Gly Thr Ile Lys Pro Gly His Phe Gln Asp Lys Thr
195 200 205

Tyr Asp Ile Val Ser Ala Phe Gln Ser Tyr Gly Glu Phe Val Ser Gly
210 215 220

Ser Ile Ser Asp Glu Gln Arg Lys Thr Val Leu His His Ser Cys Pro
225 230 235 240

Gly Ala Gly Ala Cys Gly Gly Met Tyr Thr Ala Asn Thr Met Ala Ser
245 250 255

Ala Ile Glu Ala Met Gly Met Ser Leu Pro Tyr Ser Ser Ser Ile Pro

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

Glu Cys Ala Leu Leu Thr Asp Gly Arg Phe Ser Gly Gly Ser His Gly
515 520 525

Phe Val Val Gly His Ile Cys Pro Glu Ala Gln Glu Gly Gly Pro Ile
530 535 540

Gly Leu Ile Lys Asn Gly Asp Ile Ile Thr Ile Asp Ile Gly Lys Lys
545 550 555 560

Arg Ile Asp Thr Gln Val Ser Pro Glu Glu Met Asn Asp Arg Arg Lys
565 570 575

Lys Trp Thr Ala Pro Ala Tyr Lys Val Asn Arg Gly Val Leu Tyr Lys
580 585 590

Tyr Ile Lys Asn Val Gln Ser Ala Ser Asp Gly Cys Val Thr Asp Glu
595 600 605

<210> 55

<211> 1785

<212> DNA

<213> Oryza sativa

<400> 55

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aagtacagcg cgcgcatac ggagcccaag tcgcaggggg cgctgcaggc ggtgctctac 180
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gccctgctga ccgatggcag attttctgga ggatcacatg gatttgttgt aggccacatt 1560
tgtcctgaag cacaggaggg aggtccaatt ggtcttgttc aaaacggtga caaaattacc 1620
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aagctcgtgt ccctgcac aagaggatgc gtcaccgatg agtag 1785

<210> 56

<211> 594

<212> PRT

<213> Oryza sativa

<400> 56

Met Gln Ser Leu Ala Leu Thr Ser Pro Ser Leu Pro Ala Pro Ala Thr

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Arg	Arg	Arg	Arg
Leu	Glu	Arg	Ile
Arg	Ala	Thr	Ala
20	25	30	
Val	Ser	Asp	Glu
Pro	Lys	Leu	Asn
Lys	Tyr	Ser	Ala
Arg	Ile	Thr	Glu
35	40	45	
Pro	Lys	Ser	Gln
Gly	Ala	Ser	Gln
Ala	Val	Leu	Tyr
Gly	Val	Gly	Leu
50	55	60	
Thr	Asp	Ala	Asp
Leu	Arg	Lys	Pro
Gln	Val	Gly	Val
Ser	Ser	Val	Trp

65 70 75 80

Tyr Glu Gly Asn Thr Cys Asn Met His Leu Leu Arg Leu Ala Glu Ala
 85 90 95
 Val Arg Asp Gly Val Arg Glu Ala Gly Met Val Ala Phe Arg Phe Asn
 100 105 110
 Thr Val Gly Val Ser Asp Ala Ile Ser Met Gly Thr Arg Gly Met Cys
 115 120 125
 Tyr Ser Leu Gln Ser Arg Asp Leu Ile Ala Asp Ser Ile Glu Thr Val
 130 135 140
 Met Gly Ala Gln His Tyr Asp Ala Asn Ile Ser Ile Pro Gly Cys Asp
 145 150 155 160
 Lys Asn Met Pro Gly Thr Ile Met Ala Met Gly Arg Leu Asn Arg Pro
 165 170 175
 Ser Ile Met Ile Tyr Gly Gly Thr Ile Lys Pro Gly His Phe Gln Gly
 180 185 190
 Asn Ser Tyr Asp Ile Val Ser Ala Phe Gln Cys Tyr Gly Glu Phe Val
 195 200 205
 Thr Gly Ser Ile Ser Asp Glu Gln Arg Lys Asn Val Leu Arg Asn Ser
 210 215 220
 Cys Pro Gly Ala Gly Ala Cys Gly Gly Met Tyr Thr Ala Asn Thr Met
 225 230 235 240
 Ala Ser Ala Ile Glu Thr Met Gly Met Ser Leu Pro Tyr Ser Ser Ser
 245 250 255
 Thr Pro Ala Glu Asp Pro Leu Lys Leu Glu Glu Cys Arg Leu Ala Gly
 260 265 270
 Lys Tyr Leu Leu Glu Leu Leu Lys Met Asp Leu Lys Pro Glu Asp Ile
 275 280 285
 Ile Thr Glu Lys Ser Leu Arg Asn Ala Met Val Ile Val Met Ala Leu
 290 295 300
 Gly Gly Ser Thr Asn Ala Val Leu His Leu Ile Ala Ile Ala Arg Ser
 305 310 315 320
 Val Gly Leu Gln Leu Thr Leu Asp Asp Phe Gln Lys Val Ser Asp Gln

325 330 335
 Val Pro Phe Leu Ala Asp Leu Lys Pro Ser Gly Lys Tyr Val Met Glu
 340 345 350
 Asp Leu His Lys Ile Gly Gly Thr Pro Ala Val Ile His Tyr Leu Leu
 355 360 365
 Glu Gln Gly Leu Leu Asp Gly Asp Cys Met Thr Val Thr Gly Lys Thr
 370 375 380
 Leu Ala Glu Asn Ala Lys Ile Phe Pro Pro Leu Ser Glu Gly Gln Gln

 385 390 395 400
 Ile Ile Arg Pro Leu Asp Asn Pro Ile Lys Ser Thr Gly His Ile Gln
 405 410 415
 Ile Leu Tyr Gly Asn Leu Ala Pro Glu Gly Ser Val Ala Lys Ile Thr
 420 425 430
 Gly Lys Glu Gly Met Phe Phe Ser Gly Pro Ala Leu Val Phe Glu Gly
 435 440 445
 Glu Glu Ser Met Ile Thr Ala Ile Ser Glu Asn Pro Ala Asn Phe Lys

 450 455 460
 Gly Lys Val Val Val Ile Arg Gly Glu Gly Pro Lys Gly Gly Pro Gly
 465 470 475 480
 Met Pro Glu Met Leu Thr Pro Thr Ser Ala Ile Met Gly Ala Gly Leu
 485 490 495
 Gly Lys Glu Cys Ala Leu Leu Thr Asp Gly Arg Phe Ser Gly Gly Ser
 500 505 510
 His Gly Phe Val Val Gly His Ile Cys Pro Glu Ala Gln Glu Gly Gly

 515 520 525
 Pro Ile Gly Leu Val Gln Asn Gly Asp Lys Ile Thr Ile Asp Val Val
 530 535 540
 Lys Arg Val Ile Asp Val Glu Leu Thr Glu Ala Glu Leu Glu Glu Arg
 545 550 555 560
 Arg Arg Lys Trp Thr Pro Pro Pro His Lys Ala Ala Arg Gly Ala Leu
 565 570 575

Trp Lys Tyr Thr Lys Leu Val Ser Pro Ala Ser Arg Gly Cys Val Thr

580

585

590

Asp Glu

<210> 57

<211> 1767

<212> DNA

<213> Physcomitrella patens

<400> 57

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<210> 58

<211> 588

<212> PRT

<213> Physcomitrella patens

<400> 58

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Pro Gln Ser Val Glu Ala Pro Ala Gly Ser Ala Thr Asp Ser Ala Lys
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Leu Asn Lys Tyr Ser Ser Arg Val Thr Gln Pro Lys Ala Gln Gly Ala
 35 40 45

Ser Gln Ala Ile Leu Tyr Gly Val Gly Leu Ser Glu Glu Asp Met Asn
 50 55 60

Lys Pro Gln Val Gly Ile Ser Ser Val Trp Tyr Glu Gly Asn Thr Cys
 65 70 75 80

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

Glu Ala Gly Met Val Gly Phe Arg Phe Asn Thr Val Gly Val Ser Asp
 100 105 110

Ala Val Ser Met Gly Thr Glu Gly Met Cys Tyr Ser Leu Gln Ser Arg
 115 120 125

Asp Leu Ile Ala Asp Ser Val Glu Thr Val Met Gly Gly Gln Trp Tyr
 130 135 140

Asp Ala Asn Ile Ser Ile Pro Gly Cys Asp Lys Asn Met Pro Gly Val
 145 150 155 160
 Val Met Ala Met Gly Arg Leu Asn Arg Pro Ser Ile Met Ile Tyr Gly
 165 170 175
 Gly Thr Ile Lys Pro Gly His Phe Asn Gly Gln Thr Leu Asp Ile Val
 180 185 190
 Ser Ala Phe Gln Ser Tyr Gly Glu Tyr Val Ser Gly Ser Ile Ser Glu
 195 200 205

 Asp Glu Arg Met Asp Val Val Arg Asn Ser Cys Pro Gly Phe Gly Ala
 210 215 220
 Cys Gly Gly Met Tyr Thr Ala Asn Thr Met Ala Ser Ala Ile Glu Ala
 225 230 235 240
 Leu Gly Met Ser Leu Pro Tyr Ser Ser Ser Ile Pro Ala Glu Asp Pro
 245 250 255
 Leu Lys Ile Glu Glu Cys Lys Leu Ala Gly Lys Tyr Ile Leu Glu Leu
 260 265 270

 Leu Lys Arg Asp Leu Lys Pro Arg Asp Ile Ile Thr Arg Lys Ser Leu
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 Asn Asn Ala Met Val Val Val Met Ala Leu Gly Gly Ser Thr Asn Ala
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 Val Leu His Leu Ile Ala Ile Ala Arg Ser Val Gly Val Glu Leu Thr
 305 310 315 320
 Leu Asp Asp Phe Gln Asp Val Ser Asp Lys Thr Pro Phe Ile Ala Asp
 325 330 335

 Leu Lys Pro Ser Gly Lys Tyr Val Met Glu Asp Leu His Lys Ile Gly
 340 345 350
 Gly Val Pro Ala Val Leu Lys Tyr Leu Leu Glu Lys Gly Leu Ile Asp
 355 360 365
 Gly Ser Cys Met Thr Val Thr Gly Lys Thr Ile Ala Glu Asn Leu Ala
 370 375 380
 Glu Cys Pro Pro Leu Ser Glu Gly Gln Lys Ile Ile Met Pro Leu Glu

385 390 395 400

Asn Pro Ile Lys Lys Thr Gly His Leu Gln Ile Leu Trp Gly Asn Leu

405 410 415

Ala Pro Glu Gly Ser Val Ala Lys Ile Thr Gly Lys Glu Gly Leu Tyr

420 425 430

Phe Ser Gly Pro Ala Arg Val Phe Glu Gly Glu Glu Ala Met Leu Asp

435 440 445

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

450 455 460

Arg Gly Glu Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met Leu Thr

465 470 475 480

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

485 490 495

Leu Thr Asp Gly Arg Phe Ser Gly Gly Ser His Gly Phe Val Val Gly

500 505 510

His Ile Cys Pro Glu Ala Gln Val Gly Gly Pro Ile Gly Leu Val Arg

515 520 525

Asp Gly Asp Val Ile Thr Ile Asp Val Glu Lys Arg Lys Ile Asn Val

530 535 540

Asp Leu Thr Ala Gln Glu Leu Ala Asp Arg Lys Leu Leu Trp Arg Ala

545 550 555 560

Pro Pro Tyr Lys Ala Ser Arg Gly Thr Leu Tyr Lys Tyr Ile Lys Asn

565 570 575

Val Lys Ser Ala Ser Glu Gly Cys Val Thr Asp Glu

580 585

<210> 59

<211

> 1800

<212> DNA

<213> Chaetomium globosum

<400> 59

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<210> 60

<211> 599

<212> PRT

<213> Chaetomium globosum

<400> 60

Met Leu Ser Pro Ser Leu Leu Arg Thr Gly Ala Pro Arg Ala Leu Ala

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Met Ser Arg Val Leu Pro Phe Arg Asn Gln Tyr Arg Leu Leu Ser Thr

20 25 30

Thr Pro Arg Arg Tyr Ala Asp Glu Lys Leu Asn Arg Ile Ser Ser Lys

35 40 45

Ile Thr Gln Pro Lys Ser Gln Gly Ala Ser Gln Ala Met Leu Tyr Gly

50 55 60

Thr Gly Leu Thr Glu Ala Asp Met Ser Lys Ala Gln Val Gly Ile Ser

65 70 75 80

Ser Val Trp Tyr Glu Gly Asn Pro Cys Asn Met His Leu Met Glu Leu

85 90 95

Ser Gly His Val Arg Asn Ser Ile Glu Lys Ala Gly Leu Val Pro Met

100 105 110

Arg Phe Asn Thr Ile Gly Val Ser Asp Gly Ile Ser Met Gly Thr Thr

115 120 125

Gly Met Arg Tyr Ser Leu Gln Ser Arg Glu Ile Ile Ala Asp Ser Ile

130 135 140

Glu Thr Val Met Gln Gly Gln Trp Tyr Asp Ala Asn Val Ser Leu Pro

145 150 155 160

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

165 170 175

Asn Arg Pro Ser Ile Met Val Tyr Gly Gly Thr Ile Lys Pro Gly Cys

180 185 190

Thr Met Lys Gly Glu Pro Ile Asp Ile Val Ser Ala Phe Gln Ala Tyr

195 200 205

Gly Gln Tyr Ile Ser Gly Glu Ile Asp Glu Lys Gln Arg Phe Asp Ile

210 215 220

Ile Arg Asn Ala Cys Pro Gly Gly Gly Ala Cys Gly Gly Met Tyr Thr
 225 230 235 240
 Ala Asn Thr Met Ala Ser Ala Ile Glu Thr Leu Gly Met Thr Leu Pro
 245 250 255
 Gly Ser Ser Ser Phe Pro Ala Glu Asp Ala Arg Lys Lys Ala Glu Cys
 260 265 270
 Glu Ser Val Gly Glu Ala Ile Lys Asn Leu Leu Arg Glu Asn Ile Arg
 275 280 285

 Pro Ser Asp Ile Leu Thr Arg Gln Ala Phe Glu Asn Ala Met Val Val
 290 295 300
 Val Gly Val Leu Gly Gly Ser Thr Asn Ala Val Leu His Leu Ile Ala
 305 310 315 320
 Ile Ala Asp Ser Val Gly Ile Lys Leu Thr Ile Asp Asp Phe Gln Ala
 325 330 335
 Val Ser Asp Arg Ile Pro Leu Leu Ala Asp Leu Lys Pro Ser Gly Lys
 340 345 350

 Tyr Val Met Glu Asp Leu Phe Lys Ile Gly Gly Thr Pro Ala Leu Leu
 355 360 365
 Lys Phe Leu Leu Lys Glu Gly Leu Leu Asp Gly Ser Gly Ile Thr Val
 370 375 380
 Thr Gly Lys Thr Met Lys Glu Asn Val Ala Asp Leu Pro Gly Phe Pro
 385 390 395 400
 Ala Asp Gln Pro Ile Ile Arg Pro Leu Asn Asn Pro Leu Lys Pro Thr
 405 410 415

 Gly His Ile Gln Ile Leu Arg Gly Ser Leu Ala Pro Gly Gly Ser Val
 420 425 430
 Gly Lys Ile Thr Gly Lys Glu Gly Leu Arg Phe Glu Gly Thr Ala Lys
 435 440 445
 Val Tyr Asp Tyr Glu Asp Ala Phe Ile Glu Ala Leu Glu Arg Gly Glu
 450 455 460
 Ile Lys Lys Gly Glu Lys Thr Val Val Val Ile Arg Tyr Glu Gly Pro

465					470						475					480
Lys	Gly	Gly	Pro	Gly	Met	Pro	Glu	Met	Leu	Lys	Pro	Ser	Ser	Ala	Ile	
				485					490					495		
Met	Gly	Ala	Gly	Leu	Gly	Gln	Asp	Val	Ala	Leu	Ile	Thr	Asp	Gly	Arg	
			500					505					510			
Phe	Ser	Gly	Gly	Ser	His	Gly	Phe	Leu	Ile	Gly	His	Ile	Val	Pro	Glu	
		515					520					525				
Ala	Met	Glu	Gly	Gly	Pro	Ile	Gly	Leu	Val	Arg	Asp	Gly	Asp	Lys	Ile	
530						535					540					

Val Ile Asp Ala Asp Lys Arg Val Leu Asp Leu Glu Val Pro Ala Asp
545 550 555 560
Glu Met Ala Arg Arg Lys Ala Glu Trp Lys Ala Pro Glu Pro Arg Ala
565 570 575
Lys Arg Gly Thr Leu Lys Lys Tyr Ala Ser Leu Val Ser Asp Ala Ser
580 585 590
Gln Gly Cys Val Thr Asp Lys

595

<210> 61

<211> 1791

<212> DNA

<213> Neurospora crassa

<400> 61

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aagcgccgca aggagtggaa ggctcctgag cccaaggcta agcgtggtac tctcaggaag 1740
tacgcccagc tcgtcaagga tgctagctct ggctgcgtca ctgacgtta a 1791

<210> 62

<211> 596

<212> PRT

<213> Neurospora crassa

<400> 62

Met Leu Ala Pro Ser Leu Leu Arg Ala Gln Ala Pro Arg Ala Leu Ala

1 5 10 15

Ser Ala Arg Leu Ser Leu Arg Ser Leu Ser Thr Thr Pro Arg Arg Tyr

20 25 30

Asn Ala Gln Glu Lys Gln Leu Asn Lys Val Ser Ala Asn Ile Thr Gln

35 40 45
 Pro Lys Ser Gln Gly Ala Ser Gln Ala Met Leu Tyr Ala Thr Gly Leu
 50 55 60
 Asn Glu Asp Asp Met Asn Lys Ala Gln Val Gly Ile Ser Ser Val Trp
 65 70 75 80
 Tyr Glu Gly Asn Pro Cys Asn Met His Leu Leu Asp Leu Ser Gly Leu
 85 90 95
 Val Lys Glu Ser Val Ala Lys Ala Gly Leu Val Pro Met Arg Phe Asn

 100 105 110
 Thr Ile Gly Val Ser Asp Gly Ile Ser Met Gly Thr Thr Gly Met Arg
 115 120 125
 Tyr Ser Leu Gln Ser Arg Glu Ile Ile Ala Asp Ser Ile Glu Thr Val
 130 135 140
 Met Asn Gly Gln Trp Tyr Asp Ala Asn Ile Ser Leu Pro Gly Cys Asp
 145 150 155 160
 Lys Asn Met Pro Gly Val Leu Ile Ala Met Gly Arg Val Asn Arg Pro

 165 170 175
 Ser Ile Met Val Tyr Gly Gly Thr Ile Lys Pro Gly Cys Asn Met Lys
 180 185 190
 Gly Glu Asn Ile Asp Ile Val Ser Ala Phe Gln Ala Tyr Gly Gln Tyr
 195 200 205
 Ile Ser Gly Glu Ile Asp Glu Lys Gln Arg Phe Asp Ile Ile Arg Asn
 210 215 220
 Ala Cys Pro Gly Gly Gly Ala Cys Gly Gly Met Tyr Thr Ala Asn Thr

 225 230 235 240
 Met Ala Thr Ala Ile Glu Thr Leu Gly Met Thr Leu Pro Gly Ser Ser
 245 250 255
 Ser Tyr Pro Ala Glu Ser Pro Glu Lys Lys Asn Glu Cys Leu Ser Val
 260 265 270
 Gly Glu Ala Ile Lys Asn Leu Leu Arg Glu Asp Ile Arg Pro Thr Asp
 275 280 285

Ile Leu Thr Arg Gln Ala Phe Glu Asn Ala Met Ile Val Val Asn Ile

290 295 300

Leu Gly Gly Ser Thr Asn Ala Val Leu His Leu Ile Ala Ile Ala Asp

305 310 315 320

Ser Val Gly Ile Lys Leu Thr Ile Asp Asp Phe Gln Ala Val Ser Asp

325 330 335

Arg Thr Pro Phe Leu Ala Asp Leu Lys Pro Ser Gly Lys Trp Val Met

340 345 350

Glu Asp Leu Ser Lys Ile Gly Gly Thr Pro Ala Leu Leu Lys Phe Leu

355 360 365

Leu Lys Glu Gly Ile Leu Asp Gly Ser Gly Ile Thr Ser Thr Gly Lys

370 375 380

Thr Met Lys Glu Asn Val Glu Lys Phe Pro Asp Phe Pro Thr Asp Gln

385 390 395 400

Ala Ile Ile Arg Pro Leu Ser Asn Pro Ile Lys Glu Thr Gly His Ile

405 410 415

Gln Ile Leu Arg Gly Ser Leu Ala Pro Gly Gly Ser Val Gly Lys Ile

420 425 430

Thr Gly Lys Glu Gly Leu Arg Phe Glu Gly Lys Ala Arg Cys Phe Asp

435 440 445

Tyr Glu Asp Gly Phe Ile Glu Ala Leu Glu Arg Gly Glu Ile Lys Lys

450 455 460

Gly Glu Lys Thr Val Val Val Ile Arg Tyr Glu Gly Pro Lys Gly Gly

465 470 475 480

Pro Gly Met Pro Glu Met Leu Lys Pro Ser Ser Ala Ile Met Gly Tyr

485 490 495

Gly Leu Gly Lys Asp Val Ala Leu Ile Thr Asp Gly Arg Phe Ser Gly

500 505 510

Gly Ser His Gly Phe Leu Ile Gly His Ile Val Pro Glu Ala Met Glu

515 520 525

Gly Gly Pro Ile Gly Leu Val Arg Asp Gly Asp Thr Ile Val Ile Asp

530 535 540
Ala Glu Lys Lys Val Leu Asp Leu Glu Val Pro Glu Glu Glu Leu Ala

545 550 555 560
Lys Arg Arg Lys Glu Trp Lys Ala Pro Glu Pro Lys Ala Lys Arg Gly

565 570 575
Thr Leu Arg Lys Tyr Ala Gln Leu Val Lys Asp Ala Ser Ser Gly Cys

580 585 590
Val Thr Asp Ala

595
<210> 63
<211> 1788
<212> DNA
<213> Magnaporthe grisea
<400> 63

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gttagcgacg cgagcagtgg ttgcgtgacg gacaaggtcg cgcgataa 1788

<210> 64

<211> 595

<212> PRT

<213> Magnaporthe grisea

<400> 64

Met Met Ser Ser Asn Leu Leu Arg Ala Arg Val Pro Lys Ala Leu Ala

1 5 10 15

Ala Thr Arg Ser His Ala Ala Leu Phe Ser Thr Thr Ser Arg Arg Ala

20 25 30

Glu Gln Leu Asn Lys Thr Ser Ala Lys Ile Thr Gln Pro Lys Ser Gln

35 40 45

Gly Ala Ser Gln Ala Met Leu Tyr Ala Thr Gly Leu Thr Glu Glu Asp

50 55 60

Met Asn Lys Pro Gln Val Gly Ile Ser Ser Val Trp Tyr Glu Gly Asn

65 70 75 80

Pro Cys Asn Met His Ile Leu Lys Leu Ser Glu Arg Ile Arg Asp Ser

85 90 95

Val Lys Ala Ala Asn Leu Val Pro Met Arg Phe Asn Thr Ile Gly Val

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

Lys Ile Gly Gly Thr Pro Ser Leu Leu Arg Phe Leu Ala Lys Glu Gly
355 360 365

Leu Ile Asp Ala Ser Gly Ile Thr Val Thr Gly Lys Thr Met Lys Glu
370 375 380

Asn Leu Asp Lys Tyr Pro Asp Phe Pro Ala Asp Gln Pro Ile Ile Arg
385 390 395 400

Pro Leu Ser Asn Pro Leu Lys Ser Thr Gly His Ile Gln Ile Leu Arg
405 410 415

Gly Ser Leu Ala Pro Gly Gly Ser Val Gly Lys Ile Thr Gly Lys Glu
420 425 430

Gly Leu Gln Phe Thr Gly Lys Ala Arg Cys Tyr Asp Cys Glu Asp Asp
435 440 445

Phe Ile Glu Ser Leu Glu Arg Gly Glu Ile Lys Lys Gly Glu Lys Thr
450 455 460

Val Val Ile Ile Arg Tyr Glu Gly Pro Lys Gly Gly Pro Gly Met Pro
465 470 475 480

Glu Met Leu Lys Pro Ser Ser Ala Ile Met Gly Ala Gly Leu Gly Lys
485 490 495

Asp Val Ala Leu Ile Thr Asp Gly Arg Phe Ser Gly Gly Ser His Gly
500 505 510

Phe Leu Ile Gly His Val Val Pro Glu Ala Met Glu Gly Gly Pro Ile
515 520 525

Ala Leu Val Arg Asp Gly Asp Thr Ile Thr Ile Asp Ala Glu Lys Arg
530 535 540

Val Ile Asp Thr Asp Val Ser Asp Lys Thr Met Ala Glu Arg Arg Ala
545 550 555 560

Glu Trp Lys Ala Pro Pro Ile Arg Glu Thr Arg Gly Thr Leu Ala Lys
565 570 575

Tyr Ala Ala Leu Val Ser Asp Ala Ser Ser Gly Cys Val Thr Asp Lys
580 585 590

Val Ala Arg

595

<210> 65

<211> 1797

<212> DNA

<213> *Gibberella zeae*

<400> 65

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<210> 66

<211> 598

<212> PRT

<213> Gibberella zeae

<400> 66

Met Leu Ser Arg Ser Leu Leu Arg Ser Arg Ala Val Gly Ala Phe Pro

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Leu Ser Ala Arg Asn His Gly Arg Phe Leu Ser Thr Thr Ser Ile Arg

20 25 30

Ser Asp Asp Lys Leu Asn Lys Ile Ser Ser Asn Ile Thr Gln Pro Lys

35 40 45

Ala Gln Gly Ala Ser Gln Ala Met Leu Tyr Ala Thr Gly Leu Ser Glu

50 55 60

Ala Asp Met Asn Lys Ala Gln Val Gly Ile Ser Ser Val Trp Tyr Glu

65 70 75 80

Gly Asn Pro Cys Asn Met His Leu Met Asp Leu Ser Ala His Val Lys

85 90 95

Glu Ser Val Ala Lys Ala Gly Leu Ile Pro Tyr Arg Phe Asn Thr Ile

100 105 110

Gly Val Ser Asp Gly Ile Ser Met Gly Thr Thr Gly Met Arg Tyr Ser

115 120 125

Leu Gln Ser Arg Glu Ile Ile Ala Asp Ser Val Glu Thr Val Met Asn

130 135 140

Gly Gln Trp Tyr Asp Ala Asn Val Ser Leu Pro Gly Cys Asp Lys Asn

145 150 155 160

Met Pro Gly Val Ala Ile Ala Met Gly Arg Val Asn Arg Pro Ser Ile

165 170 175

Met Val Tyr Gly Gly Thr Ile Lys Pro Gly Cys Thr Lys Gln Gly Glu

180 185 190

Ser Ile Asp Ile Val Ser Ala Phe Gln Ala Tyr Gly Gln Tyr Ile Thr

195 200 205

Gly Glu Ile Thr Glu Glu Gln Arg Phe Asp Ile Ile Arg Asn Ala Cys

210 215 220

Pro Gly Gly Gly Ala Cys Gly Gly Met Tyr Thr Ala Asn Thr Met Ala

225 230 235 240

Thr Ala Ile Glu Thr Leu Gly Leu Thr Leu Pro Gly Ser Ser Ser Ser

245 250 255

Pro Ala Glu Asp Pro Ser Lys Ile Ala Glu Cys Glu Ala Val Gly Pro

260 265 270

Ala Ile Arg Asn Ile Leu Lys Glu Asp Ile Arg Pro Arg Asp Ile Met

275 280 285

Thr Arg Gln Ala Phe Glu Asn Ala Met Ile Val Thr Thr Ile Leu Gly

290 295 300

Gly Ser Thr Asn Ala Val Leu His Leu Ile Ala Ile Ala Asp Ser Val

305 310 315 320

Gly Ile Lys Leu Asp Ile Glu Asp Phe Gln Lys Val Ser Asp Arg Thr

325 330 335

Pro Phe Leu Ala Asp Leu Lys Pro Ser Gly Lys Trp Val Met Ala Asp

340 345 350

Met His Lys Ile Gly Gly Thr Pro Ala Leu Leu Lys Phe Leu Leu Lys

355 360 365

Glu Gly Ile Ile Asp Gly Ser Gly Ile Thr Val Thr Gly Lys Thr Met

370 375 380

Lys Gln Asn Val Glu Glu Leu Pro Gly Phe Pro Glu Asp Gln Thr Ile

385 390 395 400

Ile Arg Pro Leu Ser Asn Pro Ile Lys Pro Thr Gly His Ile Gln Ile

405 410 415

Leu Arg Gly Ser Leu Ala Pro Gly Gly Cys Val Gly Lys Ile Thr Gly

420 425 430
Lys Glu Gly Leu Arg Phe Glu Gly Lys Ala Arg Val Tyr Asp Ser Glu

435 440 445
Pro Ala Phe Ile Ser Ser Leu Glu Ala Gly Glu Ile Lys Lys Gly Glu

450 455 460
Lys Thr Val Val Ile Ile Arg Tyr Asp Gly Pro Lys Gly Gly Pro Gly

465 470 475 480
Met Pro Glu Met Leu Lys Pro Ser Ser Ala Ile Met Gly Ala Gly Leu

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

500 505 510
His Gly Phe Ile Ile Gly His Ile Val Pro Glu Ala Met Glu Gly Gly

515 520 525
Pro Ile Ala Leu Val Glu Asp Gly Asp Thr Ile Val Ile Asp Ala Glu

530 535 540
Ser Arg Ala Ile Asp Leu Val Val Pro Glu Ala Glu Val Asp Arg Arg

545 550 555 560
Arg Lys Ala Trp Lys Ala Pro Ala Pro Arg Tyr Thr Lys Gly Thr Leu

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Ser Lys Tyr Ala Arg Leu Val Thr Asn Ala Ser Glu Gly Cys Val Thr

580 585 590
Asp Ser Gly Leu Lys Asn

595

<210> 67

<211> 1797

<212> DNA

<213> Aspergillus niger

<400> 67

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cgaatttcct cgaaaatcac acaacccaaa tcccagggtg cttcgcaagc aatgctctac 180

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<210> 68
 <211> 598
 <212> PRT
 <213> Aspergillus niger

<400> 68

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Tyr Arg Ser Asp Glu Pro Leu Asn Arg Ile Ser Ser Lys Ile Thr Gln

35 40 45

Pro Lys Ser Gln Gly Ala Ser Gln Ala Met Leu Tyr Ala Thr Gly Leu

50 55 60

Thr Glu Glu Asp Met Ser Lys Pro Gln Val Gly Ile Ser Ser Val Trp

65 70 75 80

Phe Glu Gly Asn Pro Cys Asn Met His Leu His Asp Leu Ser Ala Ile

85 90 95

Val Arg Asp Ser Val Leu Arg Ala Gly Leu Val Pro Met Arg Phe Asn

100 105 110

Ser Val Gly Val Ser Asp Gly Ile Ser Met Gly Thr Lys Gly Met Arg

115 120 125

Tyr Ser Leu Gln Ser Arg Glu Leu Ile Ala Asp Gly Ile Glu Thr Val

130 135 140

Met Asn Ala Gln Trp Tyr Asp Ala Asn Val Ser Leu Pro Gly Cys Asp

145 150 155 160

Lys Asn Met Pro Gly Val Leu Ile Ala Met Gly Arg Thr Asn Arg Pro

165 170 175

Ser Ile Met Val Tyr Gly Gly Ser Ile Lys Pro Gly Cys Ser Ala Lys

180 185 190

Gly Gln Lys Leu Asp Leu Val Ser Ala Phe Gln Ser Tyr Gly Gln Phe

195 200 205

Ile Thr Gly Gln Ile Asp Glu Lys Glu Arg Phe Asp Ile Ile Arg Asn

210 215 220

Ala Cys Pro Gly Arg Gly Ala Cys Gly Gly Met Tyr Thr Ala Asn Thr

225 230 235 240

Leu Ala Thr Ala Ile Glu Thr Met Gly Met Thr Ile Pro Gly Ser Ser

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325				330				335							
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370				375				380							
Thr	Met	Lys	Glu	Asn	Val	Ala	Ser	Trp	Pro	Asp	Phe	Pro	Ala	Asp	Gln
385				390				395				400			
Asp	Ile	Ile	Arg	Pro	Leu	Asn	Asn	Pro	Ile	Lys	Pro	Ser	Gly	His	Leu
405				410				415							
Gln	Ile	Leu	Arg	Gly	Ser	Leu	Ala	Pro	Gly	Gly	Ser	Val	Gly	Lys	Ile
420				425				430							
Thr	Gly	Lys	Glu	Gly	Leu	Arg	Phe	Glu	Gly	Ile	Ala	Lys	Cys	Tyr	Asp
435				440				445							
Tyr	Glu	Asp	Ala	Phe	Ile	Glu	Ser	Leu	Glu	Arg	Gly	Glu	Ile	Lys	Lys
450				455				460							
Gly	Glu	Lys	Thr	Val	Val	Ile	Ile	Arg	Tyr	Glu	Gly	Pro	Lys	Gly	Gly
465				470				475				480			
Pro	Gly	Met	Pro	Glu	Met	Leu	Lys	Pro	Ser	Ala	Ala	Ile	Met	Gly	Ala
485				490				495							

Gly Leu Gly Gln Asp Val Ala Leu Leu Thr Asp Gly Arg Phe Ser Gly
500 505 510

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

Gly Gly Pro Ile Ala Leu Ala Arg Asp Gly Asp Arg Ile Val Ile Asp
530 535 540

Ala Glu Glu Arg Val Val Asp Leu Asp Ile Ser Thr Glu Glu Leu Glu
545 550 555 560

Lys Arg Arg Lys Glu Trp Asn Ala Pro Pro Leu Arg Tyr Gln Lys Gly
565 570 575

Thr Leu Lys Lys Tyr Cys Thr Leu Val Ser Asp Ala Ser His Gly Cys
580 585 590

Val Thr Asp Gly Pro Ile
595

<210> 69

<211> 1875

<212> DNA

<213> Neosartorya fischeri

<400> 69

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<210> 70

<211> 624

<212> PRT

<213> Neosartorya fischeri

<400> 70

Met Phe Ala Ser Ser Ile Arg Ser Arg Ala Leu Gly Leu Ser Pro Arg

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Ala Arg Phe Glu Asn Thr Tyr Glu Arg Thr Phe Pro Arg Ile Ala Ser

20 25 30

Leu Ser Leu Leu Lys Asn Arg Gln Ile Leu Ile Thr Ile Val Thr Ser

35 40 45

Arg Leu Pro Ser Ser Thr Thr Glu Arg Arg Tyr Lys Ser Asp Glu Thr

50 55 60

Leu Asn Arg Ile Ser Ser Lys Ile Thr Gln Pro Lys Ser Gln Gly Ala

65 70 75 80

Ser Gln Ala Met Leu Tyr Ala Thr Gly Leu Thr Glu Glu Asp Met Ser

85 90 95

Lys Pro Gln Val Gly Ile Ser Ser Val Trp Phe Glu Gly Asn Pro Cys

100 105 110

Asn Met His Leu His Asp Leu Ser Ala Ile Val Arg Asp Ser Val Leu

115 120 125

Arg Ala Gly Leu Val Pro Met Arg Phe Asn Ser Val Gly Val Ser Asp

130 135 140

Gly Ile Ser Met Gly Thr Lys Gly Met Arg Tyr Ser Leu Gln Ser Arg

145 150 155 160

Glu Leu Ile Ala Asp Gly Ile Glu Thr Val Met Asn Ala Gln Trp Tyr

165 170 175

Asp Ala Asn Val Ser Leu Pro Gly Cys Asp Lys Asn Met Pro Gly Val

180 185 190

Leu Met Ala Met Gly Arg Thr Asn Arg Pro Ser Ile Met Val Tyr Gly

195 200 205

Gly Ser Ile Lys Pro Gly Cys Ser Ala Lys Gly Gln Lys Leu Asp Leu

210 215 220

Val Ser Ala Phe Gln Ser Tyr Gly Gln Phe Ile Thr Gly Gln Ile Asp

225 230 235 240

Glu Lys Glu Arg Phe Asp Ile Ile Arg Asn Ala Cys Pro Gly Arg Gly

245 250 255

Ala Cys Gly Gly Met Tyr Thr Ala Asn Thr Leu Ala Thr Ala Ile Glu

260 265 270

Thr Met Gly Met Thr Val Pro Gly Ser Ser Ser Cys Pro Ala Asp Asp

275 280 285

Pro Lys Lys Leu Val Glu Cys Glu Asn Ile Gly Glu Val Val Lys Thr

290 295 300
 Met Leu Arg Glu Asp Ile Lys Pro Arg Asp Val Leu Thr Arg Gln Ala

 305 310 315 320
 Phe Glu Asn Ala Met Ile Val Val Asn Val Leu Gly Gly Ser Thr Asn
 325 330 335
 Ala Val Leu His Leu Ile Ala Ile Ala Asp Ser Val Gly Ile Lys Leu
 340 345 350
 Thr Ile Asp Asp Phe Gln Thr Val Ser Asp Lys Thr Pro Phe Leu Ala
 355 360 365
 Asp Leu Lys Pro Ser Gly Lys Tyr Leu Met Asn Asp Leu Tyr Asn Ile

 370 375 380
 Gly Gly Thr Pro Ala Leu Leu Lys Tyr Leu Leu Lys Glu Gly Leu Ile
 385 390 395 400
 Asp Gly Ser Gly Ile Thr Val Thr Gly Lys Thr Met Lys Glu Asn Val
 405 410 415
 Ala Ser Trp Pro Asp Phe Pro Ala Asn Gln Asp Ile Ile Arg Pro Leu
 420 425 430
 Ser Asn Pro Ile Lys Pro Ser Gly His Leu Gln Ile Leu Arg Gly Ser

 435 440 445
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 450 455 460
 Arg Phe Glu Gly Thr Ala Lys Cys Tyr Asp Tyr Glu Asp Ala Phe Ile
 465 470 475 480
 Glu Ser Leu Glu Arg Gly Glu Ile Lys Lys Gly Asp Lys Thr Val Val
 485 490 495
 Ile Ile Arg Tyr Glu Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met

 500 505 510
 Leu Lys Pro Ser Ala Ala Ile Met Gly Ala Gly Leu Gly Gln Asp Val
 515 520 525
 Ala Leu Leu Thr Asp Gly Arg Phe Ser Gly Gly Ser His Gly Phe Leu
 530 535 540

Ile Gly His Ile Val Pro Glu Ala Met Glu Gly Gly Pro Ile Ala Leu
 545 550 555 560
 Ala Arg Asp Gly Asp Arg Ile Val Ile Asp Ala Glu Glu Arg Val Val

565 570 575
 Asp Leu Asp Ile Pro Ile Glu Glu Leu Glu Lys Arg Arg Lys Glu Trp
 580 585 590

Lys Ala Pro Pro Leu Arg Tyr Gln Lys Gly Thr Leu Lys Lys Tyr Cys
 595 600 605

Thr Leu Val Ser Asp Ala Ser His Gly Cys Val Thr Asp Gly Pro Ile
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<210> 71

<211> 1626

<212> DNA

<213> Neosartorya fischeri

<400> 71

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ctttga 1626

<210> 72

<211> 541

<212> PRT

<213> Neosartorya fischeri

<400> 72

Met Leu Tyr Ala Thr Gly Leu Glu Glu Ala Asp Met Asn Lys Ala Gln

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Val Gly Ile Ser Ser Val Trp Phe Glu Gly Asn Pro Cys Asn Met His

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Leu Met Asp Leu Ser Leu Val Val Arg Asp Ser Val Ala Arg Ala Gly

35 40 45

Leu Val Pro Met Arg Phe Asn Ser Ile Gly Val Ser Asp Gly Ile Ser

50 55 60

Met Gly Thr Ser Gly Met Arg Tyr Ser Leu Gln Ser Arg Glu Ile Ile

65 70 75 80

Ala Asp Gly Ile Glu Thr Val Met Asn Gly Gln Trp Tyr Asp Ala Asn

85 90 95

Ile Ser Leu Pro Gly Cys Asp Lys Asn Met Pro Gly Val Val Met Ala

100 105 110

Met Gly Arg Val Asn Arg Pro Ser Ile Val Ile Tyr Gly Gly Ser Ile

115 120 125

Lys Pro Gly Cys Ser Ala Gly Gly Gln Thr Leu Asp Leu Val Ser Ala

130 135 140

Phe Gln Ser Tyr Gly Gln Tyr Ile Thr Gly Gln Ile Asp Glu Ala Gln

145 150 155 160

Arg Phe Asp Ile Ile Arg His Ala Cys Pro Gly Ser Gly Ala Cys Gly

165 170 175

Gly Met Tyr Thr Ala Asn Thr Met Ala Thr Ala Ile Glu Val Leu Gly

180 185 190

Leu Thr Val Pro Gly Ser Ser Ser Cys Pro Ala Glu Asp Pro Arg Lys

195 200 205

Lys Ala Glu Cys Glu Glu Ile Gly Glu Thr Val Lys Asn Leu Leu Lys

210 215 220

Glu Asp Ile Arg Pro Ser Asp Ile Leu Thr Arg Gln Ala Phe Glu Asn

225 230 235 240

Ala Met Ile Val Val Asn Ile Leu Gly Gly Ser Thr Asn Ala Val Met

245 250 255

His Leu Ile Ala Ile Ala Gln Ser Val Gly Ile Lys Leu Thr Ile Asp

260 265 270

Asp Phe Gln Ala Val Ser Asp Lys Thr Pro Phe Leu Ala Asp Leu Lys

275 280 285

Pro Ser Gly Lys Tyr Val Met His Asp Leu Tyr Lys Ile Gly Gly Thr

290 295 300

Pro Ala Leu Leu Arg Phe Leu Leu Lys Glu Gly Leu Ile Asp Gly Ser

305 310 315 320

Gly Ile Thr Val Thr Gly Lys Thr Met Lys Glu Asn Val Ala Ser Trp

325 330 335

Pro Asp Phe Pro Glu Asp Gln Pro Ile Ile Arg Pro Leu Ser Asp Pro

340 345 350

Ile Lys Pro Thr Gly His Leu Gln Ile Leu Arg Gly Ser Leu Ala Pro

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

370 375 380
Gly Ser Ala Lys Cys Tyr Asp Tyr Glu Asp Ala Phe Val Asp Ala Leu
385 390 395 400
Glu Lys Gly Glu Ile Lys Lys Gly Glu Lys Thr Val Val Ile Ile Arg
405 410 415
Tyr Glu Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met Leu Lys Pro
420 425 430
Ser Ala Ala Ile Met Gly Ala Gly Leu Gly Gln Asp Val Ala Leu Leu

435 440 445
Thr Asp Gly Arg Phe Ser Gly Gly Ser His Gly Phe Leu Ile Gly His
450 455 460
Ile Val Pro Glu Ala Met Asp Gly Gly Pro Ile Ala Leu Val Lys Asp
465 470 475 480
Gly Asp Arg Val Ile Ile Asp Ala Glu Lys Arg Val Val Asp Leu Asp
485 490 495
Ile Ser Gly Glu Glu Met Gln Arg Arg Lys Lys Ala Trp Lys Ala Pro

500 505 510
Glu Pro Arg Ala Lys Lys Gly Thr Leu Lys Lys Tyr Ala Ala Leu Val
515 520 525
Ser Asp Ala Ser His Gly Cys Val Thr Asp Gly Pro Leu
530 535 540

<210> 73

<211> 1845

<212> DNA

<213> Aspergillus niger

<400> 73

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<210> 74

<211> 613

<212> PRT

<213> Aspergillus niger

<400> 74

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Thr Thr Pro Phe Arg Ala Ala Arg Thr Leu Ala Phe Gly Gly Arg Ile

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Leu Ser Pro Lys Lys Ser Ser Ser Arg Leu Leu Ser Ser Thr Ala His

35 40 45

Ser Tyr Ala Asp Glu Thr Leu Asn Lys Val Ser Ser Lys Ile Thr Gln

50 55 60

Pro Lys Ser Gln Gly Ala Ser Gln Ala Met Leu Tyr Ala Thr Gly Leu

65 70 75 80

Thr Glu Lys Asp Met Ser Lys Ala Gln Val Gly Ile Ser Ser Val Trp

85 90 95

Phe Glu Gly Asn Pro Cys Asn Met His Leu Met Asp Leu Ser Ser Leu

100 105 110

Val Arg Glu Ser Val Ala Lys Ala Gly Leu Val Pro Met Arg Phe Asn

115 120 125

Ser Ile Gly Ala Ser Asp Gly Ile Ser Met Gly Thr Ser Gly Met Arg

130 135 140

Phe Ser Leu Gln Ser Arg Glu Ile Ile Ala Asp Gly Ile Glu Thr Val

145 150 155 160

Met Asn Ala Gln Trp Tyr Asp Ala Asn Ile Ser Leu Pro Gly Cys Asp

165 170 175

Lys Asn Met Pro Gly Val Leu Met Ala Met Gly Arg Val Asn Arg Pro

180 185 190

Ser Ile Met Val Tyr Gly Gly Ser Ile Lys Pro Gly Cys Ser Ala Gly

195 200 205

Gly Lys Pro Leu Asp Leu Val Ser Ala Phe Gln Ser Tyr Gly Gln Tyr

210 215 220

Leu Thr Gly Glu Ile Asp Glu Lys Glu Arg Phe Asp Ile Ile Arg His

225 230 235 240
 Ala Cys Pro Gly Ala Gly Ala Cys Gly Gly Met Tyr Thr Ala Asn Thr
 245 250 255
 Leu Ala Thr Ala Ile Glu Thr Leu Gly Met Thr Val Pro Gly Ser Ser
 260 265 270
 Ser Thr Pro Ala Glu Asp Pro Arg Lys Leu Ala Glu Cys Glu Asp Ile
 275 280 285
 Gly Gln Thr Val Lys Asn Leu Leu Lys Glu Asp Ile Arg Pro Lys Asp
 290 295 300

 Ile Met Thr Arg Gln Ala Phe Glu Asn Ala Met Ile Val Val Asn Ile
 305 310 315 320
 Leu Gly Gly Ser Thr Asn Ala Val Leu His Leu Ile Ala Ile Ala Asn
 325 330 335
 Ser Val Gly Ile Lys Leu Thr Ile Asp Asp Phe Gln Ala Val Ser Asp
 340 345 350
 Lys Thr Pro Phe Leu Ala Asp Leu Lys Pro Ser Gly Lys Tyr Val Met
 355 360 365

 His Asp Leu Tyr Lys Val Gly Gly Thr Pro Ala Leu Leu Lys Phe Leu
 370 375 380
 Leu Arg Glu Gly Leu Ile Asp Gly Ser Gly Val Thr Val Thr Gly Lys
 385 390 395 400
 Thr Met Lys Glu Asn Val Ala Ser Trp Pro Glu Phe Ser Pro Glu Gln
 405 410 415
 Pro Ile Ile Arg Pro Leu Ser Asn Pro Ile Lys Pro Thr Gly His Leu
 420 425 430

 Gln Ile Leu Arg Gly Ser Leu Ala Pro Gly Gly Ser Val Gly Lys Ile
 435 440 445
 Thr Gly Lys Glu Gly Leu Arg Phe Glu Gly Leu Ala Lys Cys Tyr Asp
 450 455 460
 Phe Glu Asp Ala Phe Ile Glu Ala Leu Glu Arg Gly Glu Ile Lys Lys
 465 470 475 480

Gly Glu Lys Thr Val Val Ile Ile Arg Tyr Glu Gly Pro Lys Gly Gly
485 490 495

Pro Gly Met Pro Glu Met Leu Lys Pro Ser Ser Ala Ile Met Gly Ala
500 505 510

Gly Leu Gly Gln Asp Val Ala Leu Leu Thr Asp Gly Arg Phe Ser Gly
515 520 525

Gly Ser His Gly Phe Leu Ile Gly His Val Val Pro Glu Ala Met Glu
530 535 540

Gly Gly Pro Ile Ala Leu Val Lys Asp Gly Asp Arg Ile Val Ile Asp
545 550 555 560

Ala Glu Gln Arg Val Val Asp Leu Leu Ile Thr Pro Glu Glu Met Ala
565 570 575

Lys Arg Arg Val Ser Trp Thr Ala Pro Ala Pro Arg Ala Lys Lys Gly
580 585 590

Thr Leu Ser Lys Tyr Ala Lys Leu Val Ser Asp Ala Ser His Gly Cys
595 600 605

Val Thr Asp Gly Pro
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<210> 75

<211> 1848

<212> DNA

<213> Aspergillus niger

<400

> 75

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accgtcaagg atgccagcca cggctgtatc accgactctc tcgaataa 1848

<210> 76

<211> 615

<212> PRT

<213> Aspergillus niger

<400> 76

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Ile Ala Lys Arg Ser Leu Leu Asn Ser Arg Pro Leu Ser Thr Thr Leu

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35	40	45
Val Ser Arg His Ile Thr Gln Pro Ile Ser Gln Gly Ala Ser Gln Ala		
50	55	60
Met Leu Tyr Ala Ala Gly Leu Thr Glu Ala Asp Met Asn Lys Ala Gln		
65	70	75
Val Gly Ile Ser Ser Val Trp Tyr Asn Gly Asn Pro Cys Asn Met His		
85	90	95
Leu Leu Asp Leu Asn Asn Arg Val Arg Glu Gly Val Gln Lys Ala Gly		
100	105	110
Leu Val Gly Phe Gln Phe Asn Thr Val Gly Val Ser Asp Ala Ile Ser		
115	120	125
Met Gly Thr Lys Gly Met Arg Phe Ser Leu Gln Ser Arg Asp Leu Ile		
130	135	140
Ala Asp Ser Ile Glu Thr Val Met Gly Gly Gln Trp Tyr Asp Ala Asn		
145	150	155
Ile Ser Ile Pro Gly Cys Asp Lys Asn Met Pro Gly Val Leu Met Ala		
165	170	175
Met Gly Arg Val Asn Arg Pro Ser Leu Met Val Tyr Gly Gly Thr Ile		
180	185	190
Lys Pro Gly Cys Ala Ser Met Gln Gly Asn Ala Asp Ile Asp Ile Val		
195	200	205
Ser Ala Phe Gln Ala Tyr Gly Gln Phe Ile Ser Lys Glu Ile Thr Glu		
210	215	220
Pro Gln Arg Phe Asp Ile Ile Arg Asn Ala Cys Pro Gly Gly Gly Ala		
225	230	235
Cys Gly Gly Met Tyr Thr Ala Asn Thr Met Ala Thr Ala Ile Glu Val		
245	250	255
Met Gly Met Thr Leu Pro Gly Ser Ser Ser Asn Pro Ala Glu Ser Asp		
260	265	270

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

Leu Lys Glu Asp Ile Arg Pro Ser Asp Ile Leu Thr Arg Gln Ala Phe
290 295 300

Glu Asn Ala Met Val Leu Val Asn Ile Thr Gly Gly Ser Thr Asn Ala
305 310 315 320

Val Leu His Leu Ile Ala Ile Ala Asp Ser Val Gly Ile Lys Leu Asp
325 330 335

Ile Glu Asp Phe Gln Ser Val Ser Asp Arg Ile Pro Phe Leu Ala Asp
340 345 350

Leu Lys Pro Ser Gly Lys Tyr Val Met Ala Asp Leu His Lys Ile Gly
355 360 365

Gly Thr Pro Ser Leu Leu Lys Phe Leu Leu Lys Glu Gly Leu Ile Asp
370 375 380

Gly Ser Gly Met Thr Val Thr Gly Gln Thr Leu Ala Lys Asn Leu Glu
385 390 395 400

Asn Val Pro Asp Phe Pro Glu Asp Gln Lys Ile Ile Arg Pro Leu Ser
405 410 415

Asn Pro Ile Lys Glu Thr Gly His Ile Gln Ile Leu Arg Gly Ser Leu
420 425 430

Ala Pro Gly Gly Ser Val Gly Lys Ile Thr Gly Lys Glu Gly Thr Val
435 440 445

Phe Thr Gly Lys Ala Arg Val Phe Asp Asp Glu Asp Asp Phe Ile Ala
450 455 460

Ala Leu Glu Arg Asn Glu Ile Lys Lys Glu Glu Lys Thr Val Val Val
465 470 475 480

Ile Arg Tyr Thr Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met Leu
485 490 495

Lys Pro Ser Ser Ala Leu Met Gly Ala Gly Leu Gly Gln Ser Cys Ala
500 505 510

Leu Ile Thr Asp Gly Arg Phe Ser Gly Gly Ser His Gly Phe Leu Ile

515	520	525	
Gly His Ile Val Pro Glu Ala Ala Val Gly Gly Pro Ile Gly Leu Val			
530	535	540	
Lys Asp Gly Asp Val Ile Thr Ile Asp Ala Glu Lys Arg Val Leu Asp			
545	550	555	560
Leu Asp Val Glu Glu Thr Glu Leu Ala Gln Arg Arg Lys Gln Trp Glu			
565	570	575	
Ala Asp Arg Ala Ala Gly Lys Leu Pro Pro Thr Gly Leu Thr Leu Arg			
580	585	590	
Gly Thr Leu Gly Lys Tyr Ala Arg Thr Val Lys Asp Ala Ser His Gly			
595	600	605	
Cys Ile Thr Asp Ser Leu Glu			
610	615		
<210> 77			
<211> 1833			
<212> DNA			
<213> Aspergillus terreus			
<400> 77			
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<210> 78

<211> 610

<212> PRT

<213> *Aspergillus terreus*

<400> 78

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Ala	Val	Arg	Pro
Leu	Ser	Thr	Thr
Leu	Pro	Lys	His
20	25	30	
Lys	Ala	Asp	Glu
Lys	Glu	Pro	Val
Leu	Asn	Lys	Val
Ser	Arg	His	Val
35	40	45	
Thr	Gln	Pro	Ile
Ser	Gln	Gly	Ala
Ser	Gln	Ala	Met
Leu	Tyr	Ala	Thr
50	55	60	

Gly Leu Thr Glu Ala Asp Met Asn Lys Ala Gln Val Gly Ile Ser Ser

65 70 75 80

Val Trp Tyr Asn Gly Asn Pro Cys Asn Met His Leu Leu Asp Leu Asn

85 90 95

Asn Arg Val Arg Glu Gly Val Gln Lys Ala Gly Leu Val Gly Phe Gln

100 105 110

Phe Asn Thr Val Gly Val Ser Asp Ala Ile Ser Met Gly Thr Ser Gly

115 120 125

Met Arg Phe Ser Leu Gln Ser Arg Asp Leu Ile Ala Asp Ser Ile Glu

130 135 140

Thr Val Met Gly Gly Gln Trp Tyr Asp Ala Asn Ile Ser Ile Pro Gly

145 150 155 160

Cys Asp Lys Asn Met Pro Gly Val Leu Met Ala Met Gly Arg Val Asn

165 170 175

Arg Pro Ser Leu Met Val Tyr Gly Gly Ser Ile Lys Pro Gly Cys Ala

180 185 190

Ser Met Gln Asn Asn Ala Asp Ile Asp Ile Val Ser Ala Phe Gln Ala

195 200 205

Tyr Gly Gln Phe Ile Ser Gly Glu Ile Thr Glu Pro Gln Arg Phe Asp

210 215 220

Ile Ile Arg Asn Ala Cys Pro Gly Gly Gly Ala Cys Gly Gly Met Tyr

225 230 235 240

Thr Ala Asn Thr Met Ala Thr Ala Ile Glu Val Met Gly Met Thr Leu

245 250 255

Pro Gly Ser Ser Ser Asn Pro Ala Glu Ser Ala Ala Lys Asn Ile Glu

260 265 270

Cys Leu Ala Ala Gly Glu Ala Ile Lys Lys Leu Leu Val Glu Asp Ile

275 280 285

Arg Pro Ser Asp Ile Leu Thr Arg Gln Ala Phe Glu Asn Ala Met Ile

290 295 300

Val Val Asn Ile Thr Gly Gly Ser Thr Asn Ala Val Leu His Leu Ile

305 310 315 320
 Ala Ile Ala Asp Ser Val Gly Ile Lys Leu Asp Ile Glu Asp Phe Gln

 325 330 335
 Lys Val Ser Asp Arg Val Pro Phe Leu Ala Asp Leu Lys Pro Ser Gly
 340 345 350
 Lys Tyr Val Met Ala Asp Leu His Lys Ile Gly Gly Thr Pro Ser Leu
 355 360 365
 Leu Lys Phe Leu Leu Lys Glu Gly Leu Ile Asp Gly Ser Gly Met Thr
 370 375 380
 Val Thr Gly Gln Thr Leu Ala Lys Asn Leu Glu Asn Val Pro Asp Phe

 385 390 395 400
 Pro Glu Asp Gln Lys Ile Ile Arg Pro Leu Ser Asn Pro Ile Lys Glu
 405 410 415
 Thr Gly His Ile Gln Ile Leu Arg Gly Ser Leu Ala Pro Gly Gly Ser
 420 425 430
 Val Gly Lys Ile Thr Gly Lys Glu Gly Thr Val Phe Thr Gly Lys Ala
 435 440 445
 Arg Val Phe Asp His Glu Asp Asp Phe Ile Ala Ala Leu Glu Arg Lys

 450 455 460
 Glu Ile Lys Lys Glu Glu Lys Thr Val Val Val Ile Arg Tyr Thr Gly
 465 470 475 480
 Pro Lys Gly Gly Pro Gly Met Pro Glu Met Leu Lys Pro Ser Ser Ala
 485 490 495
 Leu Met Gly Ala Gly Leu Gly Gly Ser Cys Ala Leu Ile Thr Asp Gly
 500 505 510
 Arg Phe Ser Gly Gly Ser His Gly Phe Leu Ile Gly His Ile Val Pro

 515 520 525
 Glu Ala Ala Val Gly Gly Pro Ile Gly Leu Val Lys Asp Gly Asp Val
 530 535 540
 Ile Thr Ile Asp Ala Val Lys Arg Val Leu Asp Leu Asp Val Asp Glu
 545 550 555 560

Thr Thr Leu Ala Glu Arg Arg Lys Gln Trp Glu Ala Asp Lys Glu Ala
 565 570 575
 Gly Arg Leu Pro Pro Thr Gly Leu Thr Leu Arg Gly Thr Leu Gly Lys

580 585 590
 Tyr Ala Arg Asn Val Lys Asp Ala Ser His Gly Cys Ile Thr Asp Ala
 595 600 605

Leu Asp
 610

<210> 79

<211> 1824

<212> DNA

<213> Aspergillus clavatus

<400> 79

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 attgtggtca acatcaccgg tggctccacc aacgccgtac ttacttgat cgccattgcc 960
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tgcattactg attatataga ataa 1824

<210> 80

<211> 607

<212> PRT

<213> *Aspergillus clavatus*

<400> 80

Met Leu Leu Ser Gln Thr Arg Gly Arg Val Pro Ser Val Leu Arg Ser

1 5 10 15

Phe Ser Arg Arg Ser Leu Ser Thr Thr Ile Pro Arg Tyr Thr Ala Asp

20 25 30

Lys Asp Asp Ser Ala Leu Asn Lys Val Ser Arg Asn Val Thr Gln Pro

35 40 45

Ile Ser Gln Gly Ala Ser Gln Ala Met Leu Tyr Ala Thr Gly Leu Thr

50 55 60

Glu Ala Asp Met Asn Lys Ala Gln Val Gly Ile Ser Ser Val Trp Tyr

65 70 75 80

Asn Gly Asn Pro Cys Asn Met His Leu Leu Asp Leu Ser Asn Arg Val

85 90 95

Arg Glu Gly Val Gln Lys Ala Gly Leu Val Gly Phe Gln Phe Asn Thr

100 105 110

Val Gly Val Ser Asp Ala Ile Ser Met Gly Thr Lys Gly Met Arg Phe

115 120 125

Ser Leu Gln Ser Arg Asp Leu Ile Ala Asp Ser Ile Glu Thr Val Met

130 135 140

Gly Gly Gln Trp Tyr Asp Ala Asn Ile Ser Ile Pro Gly Cys Asp Lys

145 150 155 160

Asn Met Pro Gly Val Leu Met Ala Met Gly Arg Val Asn Arg Pro Ser

165 170 175

Leu Met Val Tyr Gly Gly Thr Ile Lys Pro Gly Cys Ala Lys Thr Gln

180 185 190

Asn Asn Ala Asp Ile Asp Ile Val Ser Ala Phe Gln Ala Tyr Gly Gln

195 200 205

Phe Leu Thr Gly Glu Ile Thr Glu Pro Gln Arg Phe Asp Ile Ile Arg

210 215 220

Asn Ala Cys Pro Gly Gly Gly Ala Cys Gly Gly Met Tyr Thr Ala Asn

225 230 235 240

Thr Met Ala Thr Ala Ile Glu Val Met Gly Met Thr Leu Pro Gly Ser

245 250 255

Ser Ser Asn Pro Ala Glu Ser Lys Ala Lys Asp Leu Glu Cys Leu Ala

260 265 270

Ala Gly Glu Ala Ile Lys Arg Leu Leu Lys Glu Asp Ile Arg Pro Ser

275 280 285

Asp Ile Leu Thr Arg Gln Ala Phe Glu Asn Ala Met Ile Val Val Asn

290 295 300

Ile Thr Gly Gly Ser Thr Asn Ala Val Leu His Leu Ile Ala Ile Ala

305 310 315 320

Asp Ser Val Gly Ile Lys Leu Asp Ile Glu Glu Phe Gln Lys Val Ser

325 330 335

Asp Arg Thr Pro Phe Leu Ala Asp Leu Lys Pro Ser Gly Lys Tyr Val

340 345 350

Met Ala Asp Leu Tyr Asp Ile Gly Gly Thr Pro Ala Leu Leu Lys Phe

355 360 365
 Leu Leu Lys Glu Gly Val Ile Asp Gly Ser Gly Met Thr Val Thr Gly

 370 375 380
 Glu Thr Leu Ala Lys Asn Leu Glu Lys Val Pro Gly Phe Pro Glu Asp
 385 390 395 400
 Gln Lys Ile Ile Arg Pro Phe Ser Asn Pro Ile Lys Lys Thr Gly His
 405 410 415
 Ile Gln Ile Leu Arg Gly Ser Leu Ala Pro Gly Gly Ser Val Gly Lys
 420 425 430
 Ile Thr Gly Lys Glu Gly Thr Arg Phe Val Gly Lys Ala Arg Val Phe

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

 500 505 510
 Gly Gly Ser His Gly Phe Leu Ile Gly His Ile Val Pro Glu Ala Ala
 515 520 525
 Val Gly Gly Pro Ile Gly Leu Val Gln Asp Gly Asp Ile Ile Thr Ile
 530 535 540
 Asp Ala Glu Lys Arg Ile Leu Asp Leu Asp Val Pro Glu Pro Glu Leu
 545 550 555 560
 Ala Gln Arg Arg Lys Asp Trp Glu Ala Ala Lys Ala Ala Gly Lys Leu

 565 570 575
 Pro Gln Thr Gly Leu Thr Met Arg Gly Thr Leu Gly Lys Tyr Ala Arg
 580 585 590
 Thr Val Lys Asp Ala Ser His Gly Cys Ile Thr Asp Tyr Ile Glu
 595 600 605

<210> 81

<211> 1842

<212> DNA

<213> *Aspergillus nidulans*

<400> 81

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gagcccgtec tcaacaaggt ctcccgccat atcacacagc cgggtgccca ggggtgcttcc	180
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cgtgtccgag aggggtgtga aaaggctggc ctatcgggt accagttcaa caccattggt	360
gtcagtgatg gaatcagtat gggtagcagt ggtatgcgtt actcgcttca gagccgtgac	420
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gctgacatcg atatcgtctc tgccttccaa gcctacggcc agttcatcag cggtagatc	660
aacgagcccc agcgccttga tatcatccgc cagcctgcc ccggtggcgg cgcttgcggt	720
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gccttcgaga acgcatggt cgttgtcaac atcaccggcg gctccacaa tgctgtcctt	960
cacctcatcg ccattgccga ctccgtcggc atcaagetca caattgacga cttccaagcc	1020
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tcgcacggct tccttattgg acacatcgic ccagaggctg ccgtcgggtg gccgattggt 1620
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 aagttgcccc agaccgggtt gaacttgcgc gggacgcttg gaaagtatgc ccggaatgtc 1800

aaggatgcta gttccgggtg tattacggac gctttcgatt aa 1842

<210> 82

<211> 613

<212> PRT

<213> Aspergillus nidulans

<400> 82

Met Leu Leu Ser Gln Thr Arg Gly Arg Leu Pro Ser Ala Leu Arg Ser

1 5 10 15

Leu Ala Asn Arg Ala Ala Ile Arg Pro Ile Ser Thr Thr Leu Pro Arg

20 25 30

Gln Lys Ala Ser Pro Lys Asp Asp Glu Pro Val Leu Asn Lys Val Ser

35 40 45

Arg His Ile Thr Gln Pro Val Ser Gln Gly Ala Ser Gln Ala Met Leu

50 55 60

Tyr Ala Thr Gly Leu Thr Glu Ala Asp Met Asn Lys Ala Gln Val Gly

65 70 75 80

Ile Ser Ser Val Trp Tyr Asn Gly Asn Pro Cys Asn Met His Leu Leu

85 90 95

Asp Leu Asn Asn Arg Val Arg Glu Gly Val Gln Lys Ala Gly Leu Ile

100 105 110

Gly Tyr Gln Phe Asn Thr Ile Gly Val Ser Asp Gly Ile Ser Met Gly

115 120 125

Thr Ser Gly Met Arg Tyr Ser Leu Gln Ser Arg Asp Leu Ile Ala Asp

130 135 140

Ser Ile Glu Thr Val Met Gly Gly Gln Trp Tyr Asp Ala Asn Ile Ser

145 150 155 160

Ile Pro Gly Cys Asp Lys Asn Met Pro Gly Val Leu Met Ala Met Gly

165 170 175
 Arg Val Asn Arg Pro Ser Leu Met Val Tyr Gly Gly Thr Ile Lys Pro
 180 185 190
 Gly Cys Ala Ser Met Gln Gly Asn Ala Asp Ile Asp Ile Val Ser Ala
 195 200 205
 Phe Gln Ala Tyr Gly Gln Phe Ile Ser Gly Glu Ile Asn Glu Pro Gln
 210 215 220
 Arg Phe Asp Ile Ile Arg His Ala Cys Pro Gly Gly Gly Ala Cys Gly
 225 230 235 240

 Gly Met Tyr Thr Ala Asn Thr Met Ala Thr Ala Ile Glu Val Met Gly
 245 250 255
 Met Thr Leu Thr Gly Ser Ser Ser Asn Pro Ala Glu Ser Gln Ala Lys
 260 265 270
 Tyr Asp Glu Cys Leu Arg Ala Gly Glu Ala Ile Lys Arg Leu Leu Val
 275 280 285
 Glu Asp Ile Arg Pro Ser Asp Ile Met Thr Arg Gln Ala Phe Glu Asn
 290 295 300

 Ala Met Val Val Val Asn Ile Thr Gly Gly Ser Thr Asn Ala Val Leu
 305 310 315 320
 His Leu Ile Ala Ile Ala Asp Ser Val Gly Ile Lys Leu Thr Ile Asp
 325 330 335
 Asp Phe Gln Ala Val Ser Asp Arg Thr Pro Phe Leu Ala Asp Leu Lys
 340 345 350
 Pro Ser Gly Lys Tyr Val Met Ala Asp Leu His Asn Ile Gly Gly Thr
 355 360 365

 Pro Ser Leu Leu Lys Phe Leu Leu Lys Glu Gly Val Ile Asp Gly Ser
 370 375 380
 Gly Ile Thr Val Thr Gly Glu Thr Leu Ala Lys Asn Leu Glu Lys Val
 385 390 395 400
 Pro Asp Phe Pro Glu Asp Gln Lys Ile Ile Arg Pro Phe Ser Asn Pro
 405 410 415

Ile Lys Glu Thr Gly His Ile Gln Ile Leu Arg Gly Ser Leu Ala Pro
420 425 430

Gly Gly Cys Val Gly Lys Ile Thr Gly Lys Glu Gly Thr Val Phe Thr
435 440 445

Gly Lys Ala Arg Val Phe Asn His Glu Asp Asp Phe Ile Ala Ala Leu
450 455 460

Glu Arg Lys Glu Ile Thr Lys Asp Glu Gln Thr Val Val Val Ile Arg
465 470 475 480

Tyr Thr Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met Leu Lys Pro
485 490 495

Ser Ser Ala Leu Met Gly Ala Gly Leu Gly Gln Thr Cys Ala Leu Ile
500 505 510

Thr Asp Gly Arg Phe Ser Gly Gly Ser His Gly Phe Leu Ile Gly His
515 520 525

Ile Val Pro Glu Ala Ala Val Gly Gly Pro Ile Gly Leu Val His Asp
530 535 540

Gly Asp Val Ile Thr Ile Asp Ala Glu Lys Arg Val Leu Asp Leu Asp
545 550 555 560

Val Asp Glu Ala Glu Leu Ala Lys Arg Arg Lys Gln Trp Glu Ala Asp
565 570 575

Lys Ala Ala Gly Lys Leu Pro Gln Thr Gly Leu Asn Leu Arg Gly Thr
580 585 590

Leu Gly Lys Tyr Ala Arg Asn Val Lys Asp Ala Ser Ser Gly Cys Ile
595 600 605

Thr Asp Ala Phe Asp
610

<210> 83

<211> 1848

<212> DNA

<213> *Aspergillus oryzae*

<400

> 83

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gaagacgaca acgtcttgaa caaggtctcc cgccatgtca cacagcccat ctgcagggt	180
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aaccaccgcg tcaagcaagg tgtggaacag gcaggcttga tcggcatgca gttcaacacc	360
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cttgagggtg accaggagac tctcgccgag agacgcaagc agtgggaagc cgataaggag	1740
gccggcaagc tgcctccac cggctctgact atgagaggaa ccctcgga gttacgtagg	1800
accgtcaagg atgccagcca cggctgtatc accgatgtc ttgattaa	1848

<210> 84

<211> 615

<212> PRT

<213> *Aspergillus oryzae*

<400> 84

Met Leu Leu Ser Gln Thr Arg Gly Arg Met Pro Ser Ala Leu Arg Ser

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Leu Ser Arg Arg Ser Ala Val Asn Val Arg Pro Leu Ser Thr Thr Leu

20 25 30

Pro Lys Gln Lys Ala Ser Ser Ser Glu Asp Asp Asn Ala Leu Asn Lys

35 40 45

Val Ser Arg His Val Thr Gln Pro Ile Ser Gln Gly Ala Ser Gln Ala

50 55 60

Met Leu Tyr Ala Thr Gly Leu Thr Glu Glu Asp Met Asn Lys Ala Gln

65 70 75 80

Val Gly Ile Ser Ser Val Trp Tyr Ser Gly Asn Pro Cys Asn Met His

85 90 95

Leu Leu Asp Leu Asn His Arg Val Lys Gln Gly Val Glu Gln Ala Gly

100 105 110

Leu Ile Gly Met Gln Phe Asn Thr Val Gly Val Ser Asp Ala Ile Ser

115 120 125

Met Gly Thr Lys Gly Met Arg Tyr Ser Leu Gln Ser Arg Asp Leu Ile

130 135 140

Ala Asp Ser Ile Glu Thr Val Met Gly Gly Gln Trp Tyr Asp Ala Asn

145 150 155 160

Ile Ser Ile Pro Gly Cys Asp Lys Asn Met Pro Gly Val Leu Met Ala

165 170 175

Met Gly Arg Val Asn Arg Pro Ser Ile Met Leu Tyr Gly Gly Thr Ile

180 185 190

Lys Pro Gly Cys Ala Ala Thr Gln Asn Asn Ala Glu Ile Asp Ile Val

195 200 205

Ser Ala Phe Gln Ala Tyr Gly Gln Phe Leu Ser Gly Asp Ile Thr Glu

210	215	220	
Pro Gln Arg Phe Asp Ile Ile Arg Asn Ala Cys Pro Gly Gly Gly Ala			
225	230	235	240
Cys Gly Gly Met Tyr Thr Ala Asn Thr Met Ala Thr Ala Ile Glu Thr			
	245	250	255
Ile Gly Met Thr Leu Pro Gly Ser Ser Ser Asn Pro Ala Glu Ser Arg			
	260	265	270
Ala Lys Asp Leu Glu Cys Leu Ala Val Gly Gly Ala Ile Lys Lys Leu			
	275	280	285
Leu Lys Glu Asp Ile Arg Pro Arg Asp Ile Met Thr Arg Gln Ala Phe			
	290	295	300
Glu Asn Ala Met Val Val Val Asn Ile Thr Gly Gly Ser Thr Asn Ala			
305	310	315	320
Val Leu His Leu Ile Ala Ile Ala Asp Ser Val Gly Ile Lys Leu Asp			
	325	330	335
Ile Glu Asp Phe Gln Ser Val Ser Asp Arg Ile Pro Phe Leu Ala Asp			
	340	345	350
Leu Lys Pro Ser Gly Lys Tyr Val Met Ala Asp Met His Lys Ile Gly			
	355	360	365
Gly Thr Pro Ala Leu Leu Lys Phe Leu Leu Lys Glu Gly Leu Ile Asp			
	370	375	380
Gly Ser Gly Met Thr Val Thr Gly Glu Thr Leu Ala Lys Asn Leu Glu			
385	390	395	400
Lys Val Pro Asp Phe Pro Glu Asp Gln Lys Ile Ile Arg Pro Leu Ser			
	405	410	415
Asn Pro Ile Lys Glu Thr Gly His Ile Gln Ile Leu Lys Gly Ser Leu			
	420	425	430
Ala Pro Gly Gly Ser Val Gly Lys Ile Thr Gly Lys Glu Gly Thr Ser			
	435	440	445
Phe Thr Gly Lys Ala Arg Val Phe Asp Asp Glu Asp Asp Phe Ile Ala			
	450	455	460

Ala Leu Glu Arg Gly Glu Ile Lys Lys Glu Asp Lys Thr Val Val Val
465 470 475 480

Ile Arg Tyr Thr Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met Leu
485 490 495

Lys Pro Ser Ser Ala Leu Met Gly Tyr Gly Leu Gly Gln Ser Val Ala
500 505 510

Leu Ile Thr Asp Gly Arg Phe Ser Gly Gly Ser His Gly Phe Leu Ile
515 520 525

Gly His Ile Val Pro Glu Ala Ala Val Gly Gly Pro Ile Gly Leu Val
530 535 540

Lys Asp Gly Asp Val Ile Val Ile Asp Ala Glu Lys Arg Val Leu Asp
545 550 555 560

Leu Glu Val Asp Gln Glu Thr Leu Ala Glu Arg Arg Lys Gln Trp Glu
565 570 575

Ala Asp Lys Glu Ala Gly Lys Leu Pro Pro Thr Gly Leu Thr Met Arg
580 585 590

Gly Thr Leu Gly Lys Tyr Ala Arg Thr Val Lys Asp Ala Ser His Gly
595 600 605

Cys Ile Thr Asp Ala Leu Asp
610 615

<210> 85

<211> 1836

<212> DNA

<213> *Ajellomyces capsulatus*

<400> 85

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aagaagctca acagtgtttc ccaacatgia acgcaacca tttccaagg tgcctcacag 180

gccatgcttt acgctacggg cctaagccg gaggatatgt cgaaagctca agttggcatc 240

tctagcgtct ggtacaacgg aaaccctgc aacatgcac tectcgatct cagcaaccgt 300

gtgcggaag gtgtgcaaaa ggcgggactc ataggttacc agttcaacac tgttggcgtc 360

agtgacgcta tcagcatggg tacgtcaggt atgcgggtaca gtttgacagag tcgggatctc 420
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 cccgggtgtg acaagaatat gcctggcgtg gttatggcaa tgggaagagt aaaccggcca 540
 agtttgatgg tttatggcgg aacaattaag cccgggtgcg cggtaaccca aaacaacgcc 600
 gatatcgaca tcgtgtctgc gttccaggct tacggccaat tcataactgg tgagatcact 660
 gaggtctcagc gatacgacat catccgacat gcttgccctg gcggtggtgc ttgtgggggg 720

 atgtacactg caaacaccat ggcgtctgcg atcgaagtta tgggaatgac gttaccggga 780
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 cttcatacaa ttggtggtac tccctcatta ctcaagtcc tcttgaagga gggctctcatc 1140

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 gaattccctt cagatcagaa aatcattcga ccctcaaca accccatcaa gaaaactggg 1260
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 ggcgcggggc taggttcatc cgtcgcttg atcacagacg gccgtttcag tgggtggtctt 1560

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 aatcccgtta cggaatgaa aatgagaggg acgtgggaa aatatgctag atctgtcaag 1800
 gacgcaagtc acggatgcat caccgacgca ttatag 1836

<210> 86

<211> 611

<212> PRT

<213> *Ajellomyces capsulatus*

<400> 86

Met Leu Arg Leu Gln Ala Arg Gly Arg Met Pro Asn Cys Phe Lys Arg

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 Leu Leu Phe Pro Leu Ser Cys Arg Ala Leu Ser Ala Thr Pro Tyr Pro
 20 25 30
 Tyr Ser Ser Ser Ser Ser Gln Glu Lys Lys Leu Asn Ser Val Ser Gln
 35 40 45
 His Val Thr Gln Pro Ile Ser Gln Gly Ala Ser Gln Ala Met Leu Tyr
 50 55 60
 Ala Thr Gly Leu Met Pro Glu Asp Met Ser Lys Ala Gln Val Gly Ile

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

 130 135 140
 Ile Glu Thr Val Met Gly Gly Gln Trp Tyr Asp Ala Asn Ile Ser Ile
 145 150 155 160
 Pro Gly Cys Asp Lys Asn Met Pro Gly Val Val Met Ala Met Gly Arg
 165 170 175
 Val Asn Arg Pro Ser Leu Met Val Tyr Gly Gly Thr Ile Lys Pro Gly
 180 185 190
 Cys Ala Val Thr Gln Asn Asn Ala Asp Ile Asp Ile Val Ser Ala Phe

 195 200 205
 Gln Ala Tyr Gly Gln Phe Ile Thr Gly Glu Ile Thr Glu Ala Gln Arg
 210 215 220
 Tyr Asp Ile Ile Arg His Ala Cys Pro Gly Gly Gly Ala Cys Gly Gly
 225 230 235 240
 Met Tyr Thr Ala Asn Thr Met Ala Ser Ala Ile Glu Val Met Gly Met
 245 250 255

Thr Leu Pro Gly Ser Ser Ser Asn Pro Ala Glu Ser Lys Ala Lys Asp

260 265 270
Leu Glu Cys Leu Thr Ala Gly Glu Ala Ile Lys Thr Leu Leu Lys Glu

275 280 285
Asp Ile Arg Pro Thr Asp Ile Leu Thr Arg Gln Ala Phe Glu Asn Ala

290 295 300
Met Val Leu Val Asn Ile Thr Gly Gly Ser Thr Asn Ala Val Leu His
305 310 315 320

Leu Ile Ala Ile Ala Asp Ser Val Gly Ile Lys Leu Thr Ile Asp Asp

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

340 345 350
Ser Gly Lys Tyr Val Met Ala Asp Leu His Thr Ile Gly Gly Thr Pro
355 360 365

Ser Leu Leu Lys Phe Leu Leu Lys Glu Gly Leu Ile Asp Gly Ser Gly
370 375 380

Ile Thr Val Thr Gly Gln Thr Leu Ala Lys Asn Leu Glu Lys Val Pro

385 390 395 400
Glu Phe Pro Ser Asp Gln Lys Ile Ile Arg Pro Leu Asn Asn Pro Ile

405 410 415
Lys Lys Thr Gly His Ile Gln Ile Leu Arg Gly Ser Leu Ala Pro Glu
420 425 430

Gly Ser Val Gly Lys Ile Thr Gly Lys Glu Gly Thr Lys Phe Thr Gly
435 440 445

Lys Ala Lys Val Tyr Asp His Glu Asp Asp Phe Ile Thr Ala Leu Glu

450 455 460
Gln Asn Glu Ile Ser Lys Asp Glu Lys Thr Val Val Val Ile Arg Tyr

465 470 475 480
Thr Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met Leu Lys Pro Ser
485 490 495

Ser Ala Leu Met Gly Ala Gly Leu Gly Ser Ser Val Ala Leu Ile Thr

500 505 510
Asp Gly Arg Phe Ser Gly Gly Ser His Gly Phe Leu Ile Gly His Ile

515 520 525
Val Pro Glu Ala Ala Val Gly Gly Pro Ile Ala Leu Val His Asp Gly

530 535 540
Asp Val Ile Thr Ile Asp Ala Glu Lys Arg Leu Leu Asp Leu Asp Val

545 550 555 560
Ser Glu His Ile Leu Ala Gln Arg Arg Lys Glu Trp Ala Asp Arg Glu

565 570 575
Ser Lys Gly Leu Asn Pro Val Thr Gly Met Lys Met Arg Gly Thr Leu

580 585 590
Gly Lys Tyr Ala Arg Ser Val Lys Asp Ala Ser His Gly Cys Ile Thr

595 600 605
Asp Ala Leu

610

<210> 87

<211> 1845

<212> DNA

<213> *Coccidioides immitis*

<400> 87

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aaccggccga gtttgatggt atatggggga acgatcaggc cgggctgtgc tgcaacacaa 600

aacaatgctg atatcgatat cgtgtccgcc ttccaggcat acggccaatt cttgactggg 660

gagatctccg aggagcagcg atttgatatt atccgccatg cctgccctgg tgggtgtgca 720
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<210> 88

<211> 614

<212> PRT

<213> *Coccidioides immitis*

<400> 88

Met Leu Gln Leu Arg Pro Arg Gly His Met Pro Tyr Arg Gln Leu Leu

1 5 10 15

Thr Tyr Leu Ser His Arg Ala Phe Ser Ser Arg Ser Thr Phe Gln Gln

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Lys Ser Ser Ser Asn Pro Pro Ser Lys Ser Gly Lys Pro Leu Asn Glu

35 40 45

Val Ser Ser His Ile Thr Gln Pro Ile Ser Gln Gly Ala Ser Gln Ala

50 55 60

Met Leu Tyr Ala Thr Gly Leu Ser Thr Asp Asp Met Ser Lys Pro Gln

65 70 75 80

Val Gly Ile Ser Ser Val Trp Tyr Asn Gly Asn Pro Cys Asn Met His

85 90 95

Leu Leu Asp Leu Ser Asn Ile Val Arg Glu Gly Val Gln Lys Ala Gly

100 105 110

Leu Ile Gly Tyr Gln Phe Asn Thr Ile Gly Val Ser Asp Gly Ile Ser

115 120 125

Met Gly Thr Lys Gly Met Arg Tyr Ser Leu Gln Ser Arg Asp Leu Ile

130 135 140

Ala Asp Ser Ile Glu Thr Val Met Gly Gly Gln Trp Tyr Asp Ala Asn

145 150 155 160

Ile Ser Leu Pro Gly Cys Asp Lys Asn Met Pro Gly Val Ile Met Ala

165 170 175

Met Gly Arg Val Asn Arg Pro Ser Leu Met Val Tyr Gly Gly Thr Ile

180 185 190

Arg Pro Gly Cys Ala Ala Thr Gln Asn Asn Ala Asp Ile Asp Ile Val

195 200 205

Ser Ala Phe Gln Ala Tyr Gly Gln Phe Leu Thr Gly Glu Ile Ser Glu

210 215 220

Glu Gln Arg Phe Asp Ile Ile Arg His Ala Cys Pro Gly Gly Gly Ala

225 230 235 240

Cys Gly Gly Met Tyr Thr Ala Asn Thr Met Ala Ser Ala Ile Glu Val

245 250 255

Met Gly Met Thr Leu Pro Gly Ser Ser Ser Asn Pro Ala Glu Ser Lys

260 265 270

Ala Lys Lys Ala Glu Cys Leu Ala Ala Gly Glu Ala Ile Lys Asn Leu

275 280 285

Leu Ile Glu Asp Ile Arg Pro Ser Asp Ile Leu Thr Arg Thr Ala Phe

290 295 300
 Glu Asn Ala Met Ile Leu Val Asn Ile Thr Gly Gly Ser Thr Asn Ala

 305 310 315 320
 Val Leu His Leu Ile Ala Met Ala Asp Ser Val Gly Ile Lys Leu Thr
 325 330 335
 Ile Asp Asp Phe Gln Ala Val Ser Asp Arg Thr Pro Phe Leu Ala Asp
 340 345 350
 Leu Lys Pro Ser Gly Lys Tyr Val Met Ala Asp Leu His Asn Ile Gly
 355 360 365
 Gly Thr Pro Ser Leu Ile Lys Phe Leu Leu Lys Glu Gly Val Leu Asp

 370 375 380
 Gly Ser Gly Met Thr Val Thr Gly Gln Thr Leu Ala Lys Asn Val Glu
 385 390 395 400
 Asn Val Pro Asp Phe Pro Ser Asp Gln Lys Ile Ile Arg Pro Phe Ser
 405 410 415
 Asn Pro Ile Lys Lys Thr Gly His Leu Gln Ile Leu Arg Gly Ser Leu
 420 425 430
 Ala Pro Glu Gly Ser Val Gly Lys Ile Thr Gly Lys Glu Gly Thr Ser

 435 440 445
 Phe Thr Gly Lys Ala Arg Val Tyr Asp Asp Glu Asp Asp Phe Ile Ala
 450 455 460
 Ser Leu Glu Arg Asn Glu Ile Lys Lys Glu Glu Lys Thr Val Val Val
 465 470 475 480
 Ile Arg Tyr Thr Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met Leu
 485 490 495
 Lys Pro Ser Ser Ala Leu Met Gly Ala Gly Leu Gly Ser Ser Val Ala

 500 505 510
 Leu Ile Thr Asp Gly Arg Phe Ser Gly Gly Ser His Gly Phe Leu Ile
 515 520 525
 Gly His Ile Val Pro Glu Ala Ala Val Gly Gly Pro Ile Ala Leu Val
 530 535 540

Glu Asp Gly Asp Ile Ile Thr Ile Asp Ala Glu Lys Arg Val Leu Asp
 545 550 555 560
 Leu Glu Val Gly Glu Asp Val Leu Ala Gln Arg Arg Lys Lys Trp Gln

 565 570 575
 Glu Lys Gln Glu Ala Gly Leu Gly Arg Pro Thr Gly Leu Thr Met Arg
 580 585 590
 Gly Thr Leu Gly Lys Tyr Ala Arg Ala Val Thr Asp Ala Ser His Gly

 595 600 605
 Cys Ile Thr Asp Gly Val

610

<210> 89

<211> 1830

<212> DNA

<213> Botryotinia fuckeliana

<400> 89

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caatatgtgc gcctctctatc gtccacatcc tctctccgca catctccaa tgactcagaa 120

ccacagctca acagaacctc agctgctatc acacaacaa aatcacaagg tgcttcgcag 180

gcaatgttat atgccactgg tatgaccgag gaaagattaa acaaagcaca agttggtatc 240

tcttcagtat ggtaggtcggg aaatccttgc aacatgcac ttttggaaact caaccacaaa 300

glaaaggaag gagtagagag agccggtttg gtaggatatc aattcaacac cattggagtt 360

tcggacggta tttctatggg tacaaagggt atgagatata gtcttcagtc aagagatttg 420

attgcggata gtattgaaac tgtgatgggt ggtcaatggt atgatgcaa catctcgatt 480

cctggatgtg acaagaacat gcctgggtgtt atgatggcaa ttggcagagt caacagacca 540

gcccttatgg tttatggtgg ttctattaaa ccagggtgtg ccgcaacaca aaacaacgca 600

gatatcgata ttgtctccgc attccaagcc tacggacaat tcattactgg agagattaca 660

gaagaacaaa gattcgatgt tattcgtcat gcttgcccag gtcaaggtgc atgtggtgga 720

atgtataccg caaacacat ggcatcagct atcgaaatta tgggaatgac tcttcctgga 780

tcttctacca accccgcaga ttcaaaggcc aaattacttg aatgctacgc agctggtggt 840

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<210> 90

<211> 609

<212> PRT

<213> Botryotinia fuckeliana

<400> 90

Met Leu Ser Gln Leu Arg Thr Arg Ala Asn Ala Ser Leu Leu Thr Ser

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Arg Arg Ala Ser Gln Tyr Val Arg Ser Leu Ser Ser Thr Ser Ser Leu

20 25 30

Arg Thr Ser Ser Asn Asp Ser Glu Pro Gln Leu Asn Arg Thr Ser Ala

35 40 45

Ala Ile Thr Gln Pro Lys Ser Gln Gly Ala Ser Gln Ala Met Leu Tyr

50 55 60

Ala Thr Gly Met Thr Glu Glu Arg Leu Asn Lys Ala Gln Val Gly Ile

65 70 75 80

Ser Ser Val Trp Trp Ser Gly Asn Pro Cys Asn Met His Leu Leu Glu

85 90 95

Leu Asn His Lys Val Lys Glu Gly Val Glu Arg Ala Gly Leu Val Gly

100 105 110

Tyr Gln Phe Asn Thr Ile Gly Val Ser Asp Gly Ile Ser Met Gly Thr

115 120 125

Lys Gly Met Arg Tyr Ser Leu Gln Ser Arg Asp Leu Ile Ala Asp Ser

130 135 140

Ile Glu Thr Val Met Gly Gly Gln Trp Tyr Asp Ala Asn Ile Ser Ile

145 150 155 160

Pro Gly Cys Asp Lys Asn Met Pro Gly Val Met Met Ala Ile Gly Arg

165 170 175

Val Asn Arg Pro Ala Leu Met Val Tyr Gly Gly Ser Ile Lys Pro Gly

180 185 190

Cys Ala Ala Thr Gln Asn Asn Ala Asp Ile Asp Ile Val Ser Ala Phe

195 200 205

Gln Ala Tyr Gly Gln Phe Ile Thr Gly Glu Ile Thr Glu Glu Gln Arg

210 215 220

Phe Asp Val Ile Arg His Ala Cys Pro Gly Gln Gly Ala Cys Gly Gly

225 230 235 240

Met Tyr Thr Ala Asn Thr Met Ala Ser Ala Ile Glu Ile Met Gly Met

245 250 255

Thr Leu Pro Gly Ser Ser Thr Asn Pro Ala Asp Ser Lys Ala Lys Leu

260 265 270

Leu Glu Cys Tyr Ala Ala Gly Gly Ala Ile Lys Thr Leu Leu Lys Glu

275 280 285

Asp Ile Arg Pro Arg Asp Ile Met Thr Arg Gln Ala Phe Glu Asn Ala

290 295 300

Met Val Leu Val Thr Ile Thr Gly Gly Ser Thr Asn Ala Val Leu His

305 310 315 320

Leu Ile Ala Met Ala Asp Ala Val Gly Ile Lys Leu Thr Ile Asp Asp

325 330 335

Phe Gln Ala Val Ser Asp Arg Thr Pro Phe Leu Ala Asp Leu Lys Pro

340 345 350
 Ser Gly Lys Tyr Val Phe Asn Asp Leu Tyr Ser Ile Gly Gly Thr Pro

 355 360 365
 Ser Leu Ile Lys Leu Leu Ile Lys Glu Gly Val Ile Asp Gly Ser Gly
 370 375 380
 Met Thr Val Thr Gly Lys Thr Leu Ala Glu Asn Val Lys Asp Val Arg
 385 390 395 400
 Asp Phe Pro Ser Asp Gln Glu Ile Ile Arg Pro Phe Ser Asn Pro Ile
 405 410 415
 Lys Lys Ser Gly His Ile Gln Ile Leu Arg Gly Ser Leu Ala Pro Gly

 420 425 430
 Gly Ser Val Gly Lys Ile Thr Gly Lys Glu Gly Leu Arg Phe Val Gly
 435 440 445
 Lys Ala Lys Val Tyr Asp Ala Glu Asn Asp Phe Ile Glu Ala Leu Glu
 450 455 460
 Arg Gly Glu Ile Lys Lys Gly Glu Lys Thr Val Val Val Ile Arg Tyr
 465 470 475 480
 Glu Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met Leu Lys Pro Ser

 485 490 495
 Ser Ala Ile Met Gly Ala Gly Leu Gly Lys Asp Val Ala Leu Ile Thr
 500 505 510
 Asp Gly Arg Phe Ser Gly Gly Ser His Gly Phe Leu Ile Gly His Ile
 515 520 525
 Val Pro Glu Ala Gln Val Gly Gly Pro Ile Gly Leu Val Arg Asp Gly
 530 535 540
 Asp Thr Ile Val Ile Asp Ala Glu Thr Arg Val Leu Asp Leu Glu Val

 545 550 555 560
 Glu Gly Gly Glu Glu Glu Leu Glu Arg Arg Arg Lys Glu Phe Val Ala
 565 570 575
 Pro Pro Leu Lys Tyr Thr Lys Gly Thr Leu Ala Lys Tyr Ser Arg Leu
 580 585 590

Val Gln Asp Ala Ser His Gly Cys Ile Thr Asp Gly Glu Ile Val Glu

595

600

605

Ala

<210> 91

<211> 1692

<212> DNA

<213> Phaeosphaeria nodorum

<400> 91

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gtcaaagagg gtgtgcagcg ggctgggtctc ttgggcatgc agttcaacac cattggtgtg	240
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 aagggcacgc tgttcaagta tgcgcggttc gtcaaggacg ccagctcggg atgcgtgacg 1680

gactcggcat aa 1692

<210> 92

<211> 563

<212> PRT

<213> Phaeosphaeria nodorum

<400> 92

Met Ser Leu Ala Arg Phe Gly Gly Ala Leu Ser Arg Pro Lys Ser Gln

1 5 10 15

Gly Ala Ser Gln Ala Met Leu Tyr Ala Thr Gly Met Ser Glu Asp Asp

20 25 30

Met Asn Lys Ala Gln Val Gly Ile Ser Ser Val Trp Tyr Ser Gly Asn

35 40 45

Pro Cys Asn Met His Leu Met Asp Leu Asn Asn Lys Val Lys Glu Gly

50 55 60

Val Gln Arg Ala Gly Leu Leu Gly Met Gln Phe Asn Thr Ile Gly Val

65 70 75 80

Ser Asp Gly Ile Ser Met Gly Thr Lys Gly Met Arg Tyr Ser Leu Gln

85 90 95

Ser Arg Glu Ile Ile Ala Asp Ser Ile Glu Thr Val Met Gly Gly Gln

100 105 110

Trp Tyr Asp Ala Asn Ile Ser Ile Pro Gly Cys Asp Lys Asn Met Pro

115 120 125

Gly Val Ile Met Ala Met Gly Arg Val Asn Arg Pro Ser Leu Met Val

130 135 140

Tyr Gly Gly Thr Ile Gln Pro Gly Cys Ala Lys Thr Leu Asp Asn Gln

145 150 155 160

Ser Ile Asp Ile Val Ser Ala Phe Gln Ala Tyr Gly Gln Phe Ile Thr
165 170 175

Gly Glu Ile Thr Glu Asp Gln Arg Phe Asp Val Ile Arg His Ala Cys
180 185 190

Asn Gly Gln Gly Ala Cys Gly Gly Met Tyr Thr Ala Asn Thr Met Ala
195 200 205

Thr Ala Ile Glu Thr Met Gly Met Ser Leu Pro Gly Ser Ser Ser Asn
210 215 220

Pro Ala Asn Ser Gln Ala Lys Met Leu Glu Cys Leu Ala Ala Gly Gly
225 230 235 240

Ala Ile Lys Asn Leu Leu Lys Glu Asp Leu Arg Pro Ser Asp Ile Leu
245 250 255

Thr Arg Gln Ala Leu Glu Asn Ala Met Val Val Ile Ser Ile Thr Gly
260 265 270

Gly Ser Thr Asn Ala Val Leu His Leu Ile Ala Ile Ala Asp Ser Val
275 280 285

Gly Leu Lys Leu Thr Ile Asp Asp Phe Gln Ser Val Ser Asp Arg Ile
290 295 300

Pro Leu Leu Ala Asp Leu Lys Pro Ser Gly Lys Tyr Val Met Ala Asp
305 310 315 320

Val His Asp Ile Gly Gly Thr Pro Ala Leu Leu Lys Phe Leu Leu Lys
325 330 335

Glu Gly Leu Leu Asp Gly Ser Gln Met Thr Val Thr Gly Lys Thr Leu
340 345 350

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

Ile Arg Pro Leu Ser Glu Pro Leu Lys Thr Thr Gly His Leu Gln Ile
370 375 380

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

Lys Glu Gly Thr Ile Phe Thr Gly Lys Ala Lys Cys Tyr Asp Ala Glu

405 410 415
 Asp Asp Phe Ile Ser Ala Leu Glu Arg Gly Glu Ile Lys Lys Gly Glu
 420 425 430

Lys Thr Val Val Val Ile Arg Tyr Glu Gly Pro Lys Gly Gly Pro Gly
 435 440 445

Met Pro Glu Met Leu Lys Pro Ser Ser Ala Ile Met Gly Ala Gly Leu
 450 455 460

Gly Lys Asp Val Ala Leu Ile Thr Asp Gly Arg Phe Ser Gly Gly Ser
 465 470 475 480

His Gly Phe Leu Ile Gly His Ile Val Pro Glu Ala Gln Glu Gly Gly
 485 490 495

Pro Ile Gly Leu Val Gln Asp Gly Asp Glu Ile Thr Ile Asp Ser Glu
 500 505 510

Ser Asn Glu Leu Asn Ile Gly Val Ser Glu Gln Glu Leu Ala Glu Arg
 515 520 525

Arg Lys Ser Trp Lys Ala Pro Ala Leu Lys Tyr Gln Lys Gly Thr Leu
 530 535 540

Phe Lys Tyr Ala Arg Phe Val Lys Asp Ala Ser Ser Gly Cys Val Thr
 545 550 555 560

Asp Ser Ala

<210> 93

<211> 1797

<212> DNA

<213> Schizosaccharomyces pombe

<400> 93

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agtgaacaa tcaactgggcc gaagtctcag ggtgcttccc aagctatgtt atatgctact	180
ggacttaatg aggaggacat gaaaaaaccc caagtcggca ttgctagtgt ttggtatgaa	240
ggaaatcctt gcaatatgca ttactttgat ctcggtcgac gagtgaaaga aggtgtcaaa	300

aaggctggat tgaccggatt ccagtttaat actattgggtg ttagtgatgg tatttctatg 360

ggtactactg gtaigcgta tagtttgcaa tctcgtgaga ttattgcaga ctccattgag 420

accgtcatgc aaggteaag gtaigatgcc aacgtctcta ttctggctg tgacaaaaac 480

atgcctgggt gttaaatcgc tatgggaaga ttcaaccgcc ctagtattat ggtttacggc 540

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gcttttcaat cctatggga atttatcaca ggaataattg atgagccaac ccgtcatgac 660

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gttgacgaca ttaaacctcg cgacatcatg acacgttctg cttttgaaa tgctatggc 900

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aagatcatta gacctttgag caaccccatc aagaccgagg gtcattttacg tgcctccgt 1260

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gagttcaaga agggcgagaa gactgtcgtc attattcgtt ttgagggacc aaaaggtgga 1440

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gatgttgac ttttgactga cggtcgttct agtgggtggc ctcacggatt ttgattgga 1560

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agacgccga gtgtttggaa ggcacctcct ttgaagtacc aacaaggaac ctttttaaaa 1740

tatgctcgca acgttagcac tgcctccaag ggtgctgtta cagattcctt agagtaa 1797

<210> 94

<211> 598

<212> PRT

<213> Schizosaccharomyces pombe

<400> 94

Met Met Phe Cys Lys Leu Leu Arg Cys Gln Asn Gly Ile Ala Ser Lys

1 5 10 15
 Arg Ala Ala Leu Ser Leu Lys Gly Phe Lys Thr Ser Ser Ile Asn Leu

 20 25 30
 Val Glu Lys Lys Leu Asn Lys Tyr Ser Glu Thr Ile Thr Gly Pro Lys
 35 40 45
 Ser Gln Gly Ala Ser Gln Ala Met Leu Tyr Ala Thr Gly Leu Asn Glu
 50 55 60
 Glu Asp Met Lys Lys Pro Gln Val Gly Ile Ala Ser Cys Trp Tyr Glu
 65 70 75 80
 Gly Asn Pro Cys Asn Met His Leu Leu Asp Leu Gly Arg Arg Val Lys

 85 90 95
 Glu Gly Val Lys Lys Ala Gly Leu Thr Gly Phe Gln Phe Asn Thr Ile
 100 105 110
 Gly Val Ser Asp Gly Ile Ser Met Gly Thr Thr Gly Met Arg Tyr Ser
 115 120 125
 Leu Gln Ser Arg Glu Ile Ile Ala Asp Ser Ile Glu Thr Val Met Gln
 130 135 140
 Gly Gln Trp Tyr Asp Ala Asn Val Ser Ile Pro Gly Cys Asp Lys Asn

 145 150 155 160
 Met Pro Gly Cys Leu Ile Ala Met Gly Arg Phe Asn Arg Pro Ser Ile
 165 170 175
 Met Val Tyr Gly Gly Ser Ile Arg Ala Gly His Ser Pro Cys Gln Asn
 180 185 190
 Asn Ala Pro Ile Asp Ile Val Ser Ala Phe Gln Ser Tyr Gly Glu Phe
 195 200 205
 Ile Thr Gly Lys Ile Asp Glu Pro Thr Arg His Asp Ile Ile Arg His

 210 215 220
 Ala Cys Pro Gly Gly Gly Ala Cys Gly Gly Met Tyr Thr Ala Asn Thr
 225 230 235 240
 Met Ala Ser Cys Ala Glu Ala Met Gly Met Thr Leu Pro Gly Ser Ser
 245 250 255

Ser Tyr Leu Ala Gly Ser Pro Glu Lys Phe Ala Glu Cys Glu Ala Ala
260 265 270

Gly Ser Ala Ile Lys Arg Leu Leu Val Asp Asp Ile Lys Pro Arg Asp
275 280 285

Ile Met Thr Arg Ser Ala Phe Glu Asn Ala Met Val Leu Thr Met Thr
290 295 300

Leu Gly Gly Ser Thr Asn Ser Val Leu His Leu Ile Ala Ile Ala Lys
305 310 315 320

Ser Val Gly Ile Thr Leu Thr Leu Asp Asp Phe Gln Ala Val Ser Asn
325 330 335

Arg Thr Pro Phe Ile Ala Asp Met Lys Pro Ser Gly Lys Tyr Val Met
340 345 350

Glu Asp Leu Phe Ala Ile Gly Gly Ile Pro Ser Val Leu Lys Tyr Leu
355 360 365

His Ala Glu Gly Leu Ile Asp Gly Ser Asn Ile Thr Val Thr Gly Lys
370 375 380

Thr Leu Ala Glu Asn Leu Arg Gly Phe Lys Asp Leu Ala Glu Gly Gln
385 390 395 400

Lys Ile Ile Arg Pro Leu Ser Asn Pro Ile Lys Thr Glu Gly His Leu
405 410 415

Arg Val Leu Arg Gly Ser Leu Ala Pro Glu Gly Ser Val Ala Lys Ile
420 425 430

Thr Gly Lys Glu Gly Leu Asn Phe Thr Gly Lys Ala Arg Val Phe Asp
435 440 445

Ala Glu Asn Asp Phe Ile Ala Ala Leu Glu Arg Gly Glu Phe Lys Lys
450 455 460

Gly Glu Lys Thr Val Val Ile Ile Arg Phe Glu Gly Pro Lys Gly Gly
465 470 475 480

Pro Gly Met Pro Glu Met Leu Lys Pro Ser Ser Ala Ile Met Gly Ala
485 490 495

Gly Leu Gly Lys Asp Val Ala Leu Leu Thr Asp Gly Arg Phe Ser Gly

500 505 510
 Gly Ser His Gly Phe Leu Ile Gly His Val Asp Pro Glu Ala Gln Val
 515 520 525
 Gly Gly Pro Ile Ala Leu Val Gln Asp Gly Asp Val Ile Glu Ile Asn

530 535 540
 Ala Val Lys Asn Thr Leu Asp Leu Met Val Asp Glu Lys Glu Met Ala
 545 550 555 560
 Arg Arg Arg Ser Val Trp Lys Ala Pro Pro Leu Lys Tyr Gln Gln Gly
 565 570 575
 Thr Leu Leu Lys Tyr Ala Arg Asn Val Ser Thr Ala Ser Lys Gly Ala
 580 585 590
 Val Thr Asp Ser Leu Glu
 595

<210> 95

<211> 1758

<212> DNA

<213> Pichia guilliermondii

<400> 95

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atgttgtatg ctacgggctt tcaagatgaa gatttcgata aggcctcaaat tggagttgga	180
agtgtatggt ggtcaggaaa cccctgtaat atgcacttga tggacatgaa cgacagatgt	240
acagcttctg tgaacaaggc tggattgaaa ggaatgcaat tcaattccat tggagtttct	300
gatggtatca ccaacgggtac tgatggtatg agatattcat tacaatcgag agaaatcatt	360
gccgattcat ttgagacttt agtgatggcc cagatgtatg atggtaacat tgccattcca	420
tcgtgtgaca agaatatgcc tggactctt atggctatgg gtagacacaa tcgtccatcg	480
attatggttt atggtggtac tatcatgcct ggatctcctt cttgtggtgg tgcaaatgtt	540
cctgagaaga ttgatatcat tagtgctttc caatcttatg gtcaattttt gagggtgacag	600
atcaatgagg aacaaagaaa ggacattgta agacatgctt gtccagggtgc tgggtgcttgt	660
ggtggtatgt ataccgcaa caccatggct tctgctgctg aggtcatggg tatgtcactt	720
ccatactctt cttcagctcc tgccatttcg aaagaaaaag ctgatgagtg tgacaatgtt	780

ggttatgcc a tgaacattt attagaaatt gatttgaac ccaaggatat aatgactaaa 840
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cttgtctcg aagaaattct cgctgaaaga aagaagctgt ggtctctcc tgctccaaga 1680
tacacgagag gaaccttggc caagtactcc aaattggtta gtgatgttc caccggttgt 1740
gtaactgact tggactaa 1758

<210> 96

<211> 585

<212> PRT

<213> Pichia guilliermondii

<400> 96

Met Leu Ser Ala Arg Val His Ser Arg Leu Phe Ser Thr Ser Val Val

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Arg Cys Glu Lys Val Leu Asn Lys Tyr Ser Ser Ile Val Thr Gln Asp

20 25 30

Lys Ser Gln Gly Ala Ser Gln Ala Met Leu Tyr Ala Thr Gly Phe Gln

35 40 45

Asp Glu Asp Phe Asp Lys Ala Gln Ile Gly Val Gly Ser Val Trp Trp

50 55 60

Ser Gly Asn Pro Cys Asn Met His Leu Met Asp Met Asn Asp Arg Cys

65 70 75 80

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

Ile Gly Val Ser Asp Gly Ile Thr Asn Gly Thr Asp Gly Met Arg Tyr
100 105 110

Ser Leu Gln Ser Arg Glu Ile Ile Ala Asp Ser Phe Glu Thr Leu Val
115 120 125

Met Ala Gln Met Tyr Asp Gly Asn Ile Ala Ile Pro Ser Cys Asp Lys
130 135 140

Asn Met Pro Gly Thr Leu Met Ala Met Gly Arg His Asn Arg Pro Ser
145 150 155 160

Ile Met Val Tyr Gly Gly Thr Ile Met Pro Gly Ser Pro Ser Cys Gly
165 170 175

Gly Ala Asn Val Pro Glu Lys Ile Asp Ile Ile Ser Ala Phe Gln Ser
180 185 190

Tyr Gly Gln Phe Leu Ser Gly Gln Ile Asn Glu Glu Gln Arg Lys Asp
195 200 205

Ile Val Arg His Ala Cys Pro Gly Ala Gly Ala Cys Gly Gly Met Tyr
210 215 220

Thr Ala Asn Thr Met Ala Ser Ala Ala Glu Val Met Gly Met Ser Leu
225 230 235 240

Pro Tyr Ser Ser Ser Ala Pro Ala Ile Ser Lys Glu Lys Ala Asp Glu
245 250 255

Cys Asp Asn Val Gly Tyr Ala Met Lys His Leu Leu Glu Ile Asp Leu
260 265 270

Lys Pro Lys Asp Ile Met Thr Lys Lys Ser Phe Glu Asn Ala Ile Thr
275 280 285

Tyr Ile Ile Ala Thr Gly Gly Ser Thr Asn Ala Val Leu His Leu Ile
290 295 300

Ala Ile Ala His Ser Val Gly Ile Asp Leu Thr Val Asp Asp Phe Gln
305 310 315 320

Arg Ile Ser Asp Thr Thr Pro Leu Leu Ala Asp Phe Arg Pro Ser Gly

325 330 335
 Lys Tyr Val Met Ala Asp Leu Gln Gln Phe Gly Gly Thr Pro Ala Val
 340 345 350

 Met Lys Leu Leu Leu Glu Glu Gly Phe Leu Asp Gly Asp Gln Tyr Thr
 355 360 365
 Val Thr Gly Asn Thr Ile Lys Glu Asn Leu Ser Lys Val Lys Gly Leu
 370 375 380
 Pro Ala Ser Gln Asp Ile Val Arg Pro Val Ser Asn Pro Leu Lys Pro
 385 390 395 400
 Asn Gly His Leu Gln Ile Leu Lys Gly Thr Leu Ala Pro Gly Ser Ala
 405 410 415

 Val Gly Lys Ile Thr Gly Lys Glu Gly Thr Tyr Phe Lys Gly Ala Ala
 420 425 430
 Arg Val Phe Asp Asn Glu Glu Leu Phe Ile Lys Ala Leu Glu Lys Gly
 435 440 445
 Glu Ile Lys Lys Gly Glu Lys Thr Val Cys Val Ile Arg Tyr Glu Gly
 450 455 460
 Pro Lys Gly Gly Pro Gly Met Pro Glu Met Leu Lys Pro Ser Ser Ala
 465 470 475 480

 Leu Met Gly Tyr Gly Leu Gly Lys Asp Val Ala Leu Leu Thr Asp Gly
 485 490 495
 Arg Phe Ser Gly Gly Ser His Gly Phe Leu Ile Gly His Ile Val Pro
 500 505 510
 Glu Ala Ala Glu Gly Gly Pro Ile Ala Leu Val His Asp Gly Asp Glu
 515 520 525
 Ile Val Ile Asp Ala Glu Asn Asn Lys Ile Asp Leu Leu Val Ser Glu
 530 535 540

 Glu Ile Leu Ala Glu Arg Lys Lys Leu Trp Ser Pro Pro Ala Pro Arg
 545 550 555 560
 Tyr Thr Arg Gly Thr Leu Ala Lys Tyr Ser Lys Leu Val Ser Asp Ala
 565 570 575

Ser Thr Gly Cys Val Thr Asp Leu Asp

580

585

<210> 97

<211> 1782

<212> DNA

<213> Debaryomyces hansenii

<400> 97

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aagtcgcaag gggcatccca agcgatgttg tatgcgaccg ggtttgatga agaagatatg 180

aacaaggcac aggttggtgt tggatctgtc tggtggtcag gaaatccgtg caacatgcac 240

ttgatggaga tgaacaacaa ggtgaccgaa tctgttaaca gagccggttt gaaggggatg 300

cagttcaact cgattggtgt ctcggatggg atcactaatg gtactgatgg tatgagatac 360

tcgttgcaat cgcggtgaaat tattgctgac tcgtttgaga ccatgatgat ggcccagatg 420

tacgatgcc aacatcgcaat tccgctgtgt gacaagaaca tgccaggtac cttgatggct 480

atgggtagac acaacagacc atctattatg gtttacgggtg gtactattat gccaggttct 540

ccaacttgat gtaactcgat tattcctgac aagattgata tcattctctgc gttccaatcg 600

tatgggtcaat tcttatcgga ccagatcaat gagggcgaaa gaaaggatat cattaagaat 660

gcatgtcctg gtgctggtgc atgtggtggt atgtacactg ccaacaccat ggcctctgct 720

gctgaagttt taggtatgtc cttaccattt tegtccagtg cccagccat ttcgaaggaa 780

aaggcacatg aatgtgctac tgtcggtgat gccatcaaga atttgtagt ccttgacttg 840

aagccaatgg atatcatgac caagaaggct ttgaaaatg caatcactta tattatcgct 900

actggtggtt ctactaatgc cgttttacat ttgattgcc a tggcaaacac cgttggtgtt 960

gacttaactg tcgatgattt ccaaagaatt tcggactcca ctccattatt agccgatttc 1020

aagccaagtg gtaagtacgt tatggctgac ttacaaaagt acggtggtac cccagctgtc 1080

atgaagtgtg tattcgagga aggtttaatt gatggatctc aatatactgt cacaggttaag 1140

actatcaaag aaaatttgga atctgttaaa ggcttgccag ctgaacaaga aattgtcaga 1200

cccttatcta acccattaaa gccaaagtggc cacttacaaa ttttaaaggg tacttttagct 1260

ccaggtagtgcctgtcggtaa aattactggtaaggaaggta cttattttcaa gggtaaattct 1320

agagttttcg atgatgaaat ggcattcatt actgcttttag aaaatggcga aatcaagaaa 1380

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 gaagctgcag ttggtggacc aattgcgtta gtgcatgatg gtgatgaaat tgttattgac 1620
 gctgaaaaca atagaatcga cttattagta tctgaagata ttttagccga aagaaagaag 1680
 gaatggaccc caccaaagcc aagatataca agaggtacat tggctaaata ttctaagtta 1740
 gtcagtgatg cttcgttggg ttgtgttact gatttggat aa 1782

<210> 98

<211> 593

<212> PRT

<213> Debaryomyces hansenii

<400> 98

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

165 170 175
 Met Pro Gly Ser Pro Thr Cys Gly Asn Ser Ile Ile Pro Asp Lys Ile

 180 185 190
 Asp Ile Ile Ser Ala Phe Gln Ser Tyr Gly Gln Phe Leu Ser Asp Gln
 195 200 205
 Ile Asn Glu Gly Glu Arg Lys Asp Ile Ile Lys Asn Ala Cys Pro Gly
 210 215 220
 Ala Gly Ala Cys Gly Gly Met Tyr Thr Ala Asn Thr Met Ala Ser Ala
 225 230 235 240
 Ala Glu Val Leu Gly Met Ser Leu Pro Phe Ser Ser Ser Ala Pro Ala

 245 250 255
 Ile Ser Lys Glu Lys Ala His Glu Cys Ala Thr Val Gly Asp Ala Ile
 260 265 270
 Lys Asn Leu Leu Val Leu Asp Leu Lys Pro Met Asp Ile Met Thr Lys
 275 280 285
 Lys Ala Phe Glu Asn Ala Ile Thr Tyr Ile Ile Ala Thr Gly Gly Ser
 290 295 300
 Thr Asn Ala Val Leu His Leu Ile Ala Met Ala Asn Thr Val Gly Val

 305 310 315 320
 Asp Leu Thr Val Asp Asp Phe Gln Arg Ile Ser Asp Ser Thr Pro Leu
 325 330 335
 Leu Ala Asp Phe Lys Pro Ser Gly Lys Tyr Val Met Ala Asp Leu Gln
 340 345 350
 Lys Tyr Gly Gly Thr Pro Ala Val Met Lys Leu Leu Phe Glu Glu Gly
 355 360 365
 Leu Ile Asp Gly Ser Gln Tyr Thr Val Thr Gly Lys Thr Ile Lys Glu

 370 375 380
 Asn Leu Glu Ser Val Lys Gly Leu Pro Ala Glu Gln Glu Ile Val Arg
 385 390 395 400
 Pro Leu Ser Asn Pro Leu Lys Pro Ser Gly His Leu Gln Ile Leu Lys
 405 410 415

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

420 425 430

Gly Thr Tyr Phe Lys Gly Lys Ser Arg Val Phe Asp Asp Glu Met Ala

435 440 445

Phe Ile Thr Ala Leu Glu Asn Gly Glu Ile Lys Lys Gly Glu Lys Thr

450 455 460

Val Cys Val Ile Arg Tyr Glu Gly Pro Gln Gly Gly Pro Gly Met Pro

465 470 475 480

Glu Met Leu Lys Pro Ser Ser Ala Leu Met Gly Tyr Gly Leu Gly Gln

485 490 495

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

500 505 510

Phe Leu Ile Gly His Ile Val Pro Glu Ala Ala Val Gly Gly Pro Ile

515 520 525

Ala Leu Val His Asp Gly Asp Glu Ile Val Ile Asp Ala Glu Asn Asn

530 535 540

Arg Ile Asp Leu Leu Val Ser Glu Asp Ile Leu Ala Glu Arg Lys Lys

545 550 555 560

Glu Trp Thr Pro Pro Lys Pro Arg Tyr Thr Arg Gly Thr Leu Ala Lys

565 570 575

Tyr Ser Lys Leu Val Ser Asp Ala Ser Leu Gly Cys Val Thr Asp Leu

580 585 590

Val

<210> 99

<211> 1794

<212> DNA

<213> Lodderomyces elongisporus

<400> 99

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gacccttccc aaggagcatc gcaagcaatg ctctacgcca cagggttctc ctccgaggac 180

ttaaccgtg cacaatcgg tgctggatcc gtttggtgga ccgtaaccc ttgtaacatg 240

cacttgatgg agttaacaa tatgtgtgca gagtcatgca acaaggccgg tttaaaagca 300

atgcaattca actcaattgg tgtagtgat ggtatcacca acggtacaga gggtatgaaa 360

tactcattgc aatcacgtga aatcattgct gactcatttg aaacaatgac catggctcaa 420

ttatatgacg gtaatgttgc cateccaagt tgtgacaaga atatgcccgg tgtccttatg 480

gcaatgggta gacacaatag acccgccatt atggtgtacg gagtlacaat catgcccggc 540

tcaccaactt gcggtggctc aaagctgaat cccgccattg cagataagat tgacattatc 600

agtgctttcc aaagttaatg acaattcttg tccaaacaaa tcaacgagga agaaagaatt 660

gatattgtga aaaacgcatg tcttggacca ggtgcttgcg gtggtatgta cactgccaac 720

actatggcct ctgcagccga agtcttgggt ttaactttac ctttttcac atcggcacca 780

gcagtttcaa aagaaaaggc cgaagagtgt gccaacgttg ggtacgcat cagaaacttg 840

cttgaactcg acttgaaacc aagagacatt ttgacaaaa aatcatttga aaacgccatc 900

acatacatca ttgtaccggg tggctcaaca aatgcagttt tgcacatgat tgccattgct 960

tcaagcttcg atatcgaatt aactgttgac gatttccaaa gaatcagtga ctctactcca 1020

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ggtacaccag cagttaagaa gtttttgatg aatgaaggta tgattgatgg ttcgcaattg 1140

actgtgacag gtaagaccat tgctgaaaac ttggccaatg ttccagaatt gccaaagggt 1200

caagaaatca tccactcatt ggacaacca ttgaaacaa gcggtcactt gcaaactctg 1260

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caagatgttg cttatttgac cgatggtaga ttttctggtg gttcacacgg attcttgatt 1560

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gccaaagaa gagagcaatg gactccacct gaaccagat acaaaagagg tacattgttc 1740

aaatatgcca aattggtag tgatgcttcc aaaggatgtg ttactgactt gtaa 1794

<210> 100

<211> 597

<212> PRT

<213> Lodderomyces elongisporus

<400> 100

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 20 25 30
 Lys Tyr Ser Ser Val Val Thr Glu Asp Pro Ser Gln Gly Ala Ser Gln
 35 40 45
 Ala Met Leu Tyr Ala Thr Gly Phe Ser Ser Glu Asp Phe Asn Arg Ala
 50 55 60

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

Ile Ala Asp Ser Phe Glu Thr Met Thr Met Ala Gln Leu Tyr Asp Gly
 130 135 140
 Asn Val Ala Ile Pro Ser Cys Asp Lys Asn Met Pro Gly Val Leu Met
 145 150 155 160
 Ala Met Gly Arg His Asn Arg Pro Ala Ile Met Val Tyr Gly Gly Thr
 165 170 175
 Ile Met Pro Gly Ser Pro Thr Cys Gly Gly Ser Lys Leu Asn Pro Ala
 180 185 190

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

225 230 235 240
 Thr Met Ala Ser Ala Ala Glu Val Leu Gly Leu Thr Leu Pro Phe Ser
 245 250 255

 Ser Ser Ala Pro Ala Val Ser Lys Glu Lys Ala Glu Glu Cys Ala Asn
 260 265 270
 Val Gly Tyr Ala Ile Arg Asn Leu Leu Glu Leu Asp Leu Lys Pro Arg
 275 280 285
 Asp Ile Leu Thr Lys Lys Ser Phe Glu Asn Ala Ile Thr Tyr Ile Ile
 290 295 300
 Ala Thr Gly Gly Ser Thr Asn Ala Val Leu His Met Ile Ala Ile Ala
 305 310 315 320

 Ser Ser Phe Asp Ile Glu Leu Thr Val Asp Asp Phe Gln Arg Ile Ser
 325 330 335
 Asp Ser Thr Pro Leu Leu Ala Asp Phe Lys Pro Ser Gly Lys Tyr Val
 340 345 350
 Met Ala Asp Leu Gln Ala Ile Gly Gly Thr Pro Ala Val Met Lys Phe
 355 360 365
 Leu Met Asn Glu Gly Met Ile Asp Gly Ser Gln Leu Thr Val Thr Gly
 370 375 380

 Lys Thr Ile Ala Glu Asn Leu Ala Asn Val Pro Glu Leu Pro Lys Gly
 385 390 395 400
 Gln Glu Ile Ile His Ser Leu Asp Asn Pro Leu Lys Pro Ser Gly His
 405 410 415
 Leu Gln Ile Leu Lys Gly Thr Leu Ala Pro Gly Ser Ala Val Ala Lys
 420 425 430
 Ile Thr Gly Lys Glu Gly Thr Tyr Phe Lys Gly Lys Ala Arg Val Phe
 435 440 445

 Asp Glu Glu His Ala Phe Ile Thr Ala Leu Glu Asn Gly Glu Ile Lys
 450 455 460
 Lys Gly Glu Lys Thr Val Cys Val Ile Arg Tyr Glu Gly Pro Lys Gly
 465 470 475 480

Gly Pro Gly Met Pro Glu Met Leu Lys Pro Ser Ser Ala Leu Met Gly
485 490 495

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

Gly Gly Ser His Gly Phe Leu Ile Gly His Ile Val Pro Glu Ala Ala
515 520 525

Glu Gly Gly Pro Ile Ala Leu Val Glu Asp Gly Asp Glu Ile Val Ile
530 535 540

Asp Ala Asp Lys Asn Ile Ile Asp Leu Leu Val Ser Glu Asp Val Leu
545 550 555 560

Ala Lys Arg Arg Glu Gln Trp Thr Pro Pro Glu Pro Arg Tyr Lys Arg
565 570 575

Gly Thr Leu Phe Lys Tyr Ala Lys Leu Val Ser Asp Ala Ser Lys Gly
580 585 590

Cys Val Thr Asp Leu
595

<210> 101

<211> 1770

<212> DNA

<213> Candida albicans

<400> 101

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tcccaagcaa tgctttatgc cactggtttc agtgatgaag atttcgatcg tgcacaaatc 180
ggtgtcggtt ctgtttggtg gtcaggtaac ccatgtaaca tgcacttgat ggagttgaac 240

aacaggtggt ccgaatcagt caacaaggcc ggcttaaaag ccatgcaatt caactccatt 300
ggtgtgtcgg acggtatcac caacggaact gaaggtatga agtactcttt acagctgaga 360
gaaattatcg ccgactcctt tgaacctatg accatggccc aactatatga cggtaacatt 420
gccattcctt catgtgataa aaatatgccc ggggtattga tggctatggg aagacacaac 480
agacgtgcca ttatggtcta tgggtgtact atcttgctg gatctccaac ttgcggaacc 540
caaaacctg ctgtagccga caaatcgat atcattagt ctttccaatc ctacggacaa 600

tacttgtcaa aacaaatcaa caacgaagaa agaataagata ttgtcaaaca tgcctgtcca 660

gggcccggtg catgtgggtg tatgtacact gccaacacta tggcctctgc ctctgaagtc 720

ttgggggttga ccttaccatt ttctgcctcg tccccggcag tctccaaaga aaaagccgaa 780

gagtgtgcca acgtcgggtt cgccttaaag aatttgtag agttggactt gaaaccaaga 840

gatatgttca ccaaaaaatc atttgaaaac gctattgctt atatcattgc cactggtggt 900

tctactaatg ccgttttaca tcttattgcc attgcctctt catttgacat tactattact 960

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gaaaacttgg ctaaacttgc tgatttgcct gagggccaag acattgttag accagtatca 1200

aaccatttga agccaagtgg ccacttaciaa atcttgaaag gtactttggc tccagggctt 1260

gctgtcgcta aaatcacagg taaagaaggt acttatttca aaggtaaagc tagagtattc 1320

aacgacgaag gtgcatttat tgttgccttg gaaaatggcg agatcaaaaa aggcgaaaaa 1380

acagtttgtg tgatcagata cgaaggcca aaagtggtc caggtatgcc agaaatgttg 1440

aaaccttcgt ctgcattaat gggttacggg ttaggtaaag acgttgcttt gttgactgat 1500

ggtagatttt cgggtgggtc ccacgggttc cttattggcc acattgttcc tgaagccgct 1560

gaagggtggtc caattgcttt ggttgaagat ggcgatatta ttgtatcga cgcagacaat 1620

aacaaaatcg atttgttggg tgagccagac gtcttgaccg aaagaagaaa aactggacg 1680

cctccagaac caagatacaa aagaggtact ttggccaaat acgccaagtt ggtcagcgat 1740

gcatctaagg gatgtgttac agattataa 1770

<210> 102

<211> 589

<212> PRT

<213> Candida albicans

<400> 102

Met Ser Phe Val Lys Ser Cys Arg Gly Cys Leu Arg Thr Phe Ala Thr

1 5 10 15

Ser Thr Ile Lys His Glu Lys Lys Leu Asn Lys Tyr Ser Ser Ile Val

20 25 30

Thr Gly Asp Pro Ser Gln Gly Ala Ser Gln Ala Met Leu Tyr Ala Thr

35 40 45

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

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

 130 135 140
 Cys Asp Lys Asn Met Pro Gly Val Leu Met Ala Met Gly Arg His Asn
 145 150 155 160
 Arg Pro Ala Ile Met Val Tyr Gly Gly Thr Ile Leu Pro Gly Ser Pro
 165 170 175
 Thr Cys Gly Thr Gln Asn Pro Ala Val Ala Asp Lys Ile Asp Ile Ile
 180 185 190
 Ser Ala Phe Gln Ser Tyr Gly Gln Tyr Leu Ser Lys Gln Ile Asn Asn

 195 200 205
 Glu Glu Arg Ile Asp Ile Val Lys His Ala Cys Pro Gly Pro Gly Ala
 210 215 220
 Cys Gly Gly Met Tyr Thr Ala Asn Thr Met Ala Ser Ala Ser Glu Val
 225 230 235 240
 Leu Gly Leu Thr Leu Pro Phe Ser Ser Ser Ser Pro Ala Val Ser Lys
 245 250 255
 Glu Lys Ala Glu Glu Cys Ala Asn Val Gly Phe Ala Leu Lys Asn Leu

 260 265 270
 Leu Glu Leu Asp Leu Lys Pro Arg Asp Ile Val Thr Lys Lys Ser Phe
 275 280 285
 Glu Asn Ala Ile Ala Tyr Ile Ile Ala Thr Gly Gly Ser Thr Asn Ala

290 295 300
 Val Leu His Leu Ile Ala Ile Ala Ser Ser Phe Asp Ile Thr Ile Thr
 305 310 315 320
 Val Asp Asp Phe Gln Arg Ile Ser Asp Asn Thr Pro Leu Leu Ala Asp

 325 330 335
 Phe Lys Pro Ser Gly Lys Tyr Val Met Ala Asp Leu Gln Asn Val Gly
 340 345 350
 Gly Thr Pro Ala Val Met Lys Tyr Leu Ile Lys Glu Gly Ile Ile Asp
 355 360 365
 Gly Thr Gln Leu Ser Val Thr Gly Lys Thr Ile Asn Glu Asn Leu Ala
 370 375 380
 Lys Leu Ala Asp Leu Pro Glu Gly Gln Asp Ile Val Arg Pro Val Ser

 385 390 395 400
 Asn Pro Leu Lys Pro Ser Gly His Leu Gln Ile Leu Lys Gly Thr Leu
 405 410 415
 Ala Pro Gly Ser Ala Val Ala Lys Ile Thr Gly Lys Glu Gly Thr Tyr
 420 425 430
 Phe Lys Gly Lys Ala Arg Val Phe Asn Asp Glu Gly Ala Phe Ile Val
 435 440 445
 Ala Leu Glu Asn Gly Glu Ile Lys Lys Gly Glu Lys Thr Val Cys Val

 450 455 460
 Ile Arg Tyr Glu Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met Leu
 465 470 475 480
 Lys Pro Ser Ser Ala Leu Met Gly Tyr Gly Leu Gly Lys Asp Val Ala
 485 490 495
 Leu Leu Thr Asp Gly Arg Phe Ser Gly Gly Ser His Gly Phe Leu Ile
 500 505 510
 Gly His Ile Val Pro Glu Ala Ala Glu Gly Gly Pro Ile Ala Leu Val

 515 520 525
 Glu Asp Gly Asp Ile Ile Val Ile Asp Ala Asp Asn Asn Lys Ile Asp
 530 535 540

Leu Leu Val Glu Pro Asp Val Leu Thr Glu Arg Arg Lys His Trp Thr
 545 550 555 560
 Pro Pro Glu Pro Arg Tyr Lys Arg Gly Thr Leu Ala Lys Tyr Ala Lys
 565 570 575
 Leu Val Ser Asp Ala Ser Lys Gly Cys Val Thr Asp Leu

580 585

<210> 103

<211> 1815

<212> DNA

<213> *Pichia stipitis*

<400> 103

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gtggccagat cgttttctgt ctctgctact caatgtgaaa agaaattgaa caagtactct	120
tcgattgtca ctggtgatcc ctcccagggt gcttcgcaag ccatgctcta tgccacaggt	180
ttcgacgatg ccgacttcaa cagagcccag atcggtgtgg gctcagtttg gtggtcaggt	240
aatccttgca acatgcactt gatggagttg aacaacaagt gtactgaatc agtcaacaga	300
gctggtttga agggaatgca attcaactcg attggtattt ccgatgggat cactaacgga	360
actgaaggaa tgagatactc tcttcaatct cgtgaaatta ttgctgactc gttcgaatcc	420
atgatgcttg gtcaattgta cgatggtaac attgccattc catcctgtga caagaatatg	480
cctgggtgtct tgattgctat ggccagacac aacagacctt ctattatggt ctatggtggt	540
acaatcttgc caggtcaaac tacttgcgga accaacaacc cagctatcgc cgacaaaatt	600
gatatcatct cagctttcca gtcgtatgga cagtacttga ccaagtccat cactaacgaa	660
gaaagaaagg atatcgttag acacgcctgt cctggtcctg gtgcctgtgg tggatgtat	720
actgctaaca ccatggcatc tgcagctgaa tgccttggtg tgcctttgcc ctattcatct	780
tcggctccag ccgtctcaaa ggaaaaggat gctgagtggt ccaacatcgg tcaagccatc	840
aagcacttgt tggagatcga cttgaagccc cgtgatattt tgactaagaa atctttcgaa	900
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gccattgctt cctcagctga tattgatctt accgtagatg atttccagag aatctccgac	1020
tccactccgt tgttggcaga cttcaagcca tcgggacaat tcgtaatggc agacttacag	1080
aagtacggtg gtactccagc cgtgatgaaa ttcttgatga acgaaggctt cattgacgga	1140
gaccagtaca ctgtcactgg taagaccatc aaggaaaatt tggcttccgt caaggacttg	1200

cctgctgatac agcctatcat cagaccagtc agcaaccctt tgaagacaag cggtcacttg 1260
 caaatcttga agggttcctt ggctccaggt tctgctgtcg gtaagatcac cggttaaggaa 1320
 ggtacctact tcaagggtaa ggctcgtgtc ttgatgacg aaggagactt cattgtcgcc 1380
 ttggagaagg gtgagattaa gaagggtgaa aagaccgtct gtgtcatcag atacgaaggt 1440
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ttcttgattg ggcacattgt tcctgaagct gctgaagggt gacctatcgg ttgggtgtac 1620
 gatgggtgac aaatcgtcat tgatccgaa aacaacaaga tcgacttggt agtagacgaa 1680
 gctgtgttgg ctgaaagaag aaagtatgg actgctcctg agccaagata caccaggggt 1740
 actttggcca agtacgccag attggtcagt gacgcttctg ctggatgcgt taccgacttg 1800
 ccaataaaga attaa 1815

<210> 104

<211> 604

<212> PRT

<213> *Pichia stipitis*

<400> 104

Met Ser Phe Leu Phe Lys Ala Ala Ala Ala Arg Arg Val Ala Ser Lys

1 5 10 15
 Ser Pro Ala Ala Val Ala Arg Ser Phe Ser Val Ser Ala Thr Gln Cys

20 25 30
 Glu Lys Lys Leu Asn Lys Tyr Ser Ser Ile Val Thr Gly Asp Pro Ser

35 40 45
 Gln Gly Ala Ser Gln Ala Met Leu Tyr Ala Thr Gly Phe Asp Asp Ala

50 55 60
 Asp Phe Asn Arg Ala Gln Ile Gly Val Gly Ser Val Trp Trp Ser Gly

65 70 75 80
 Asn Pro Cys Asn Met His Leu Met Glu Leu Asn Asn Lys Cys Thr Glu

85 90 95
 Ser Val Asn Arg Ala Gly Leu Lys Gly Met Gln Phe Asn Ser Ile Gly

100 105 110
 Ile Ser Asp Gly Ile Thr Asn Gly Thr Glu Gly Met Arg Tyr Ser Leu

115 120 125

Gln Ser Arg Glu Ile Ile Ala Asp Ser Phe Glu Ser Met Met Leu Gly

130 135 140

Gln Leu Tyr Asp Gly Asn Ile Ala Ile Pro Ser Cys Asp Lys Asn Met

145 150 155 160

Pro Gly Val Leu Ile Ala Met Ala Arg His Asn Arg Pro Ser Ile Met

165 170 175

Val Tyr Gly Gly Thr Ile Leu Pro Gly Gln Thr Thr Cys Gly Thr Asn

180 185 190

Asn Pro Ala Ile Ala Asp Lys Ile Asp Ile Ile Ser Ala Phe Gln Ser

195 200 205

Tyr Gly Gln Tyr Leu Thr Lys Ser Ile Thr Asn Glu Glu Arg Lys Asp

210 215 220

Ile Val Arg His Ala Cys Pro Gly Pro Gly Ala Cys Gly Gly Met Tyr

225 230 235 240

Thr Ala Asn Thr Met Ala Ser Ala Ala Glu Cys Leu Gly Met Ser Leu

245 250 255

Pro Tyr Ser Ser Ser Ala Pro Ala Val Ser Lys Glu Lys Asp Ala Glu

260 265 270

Cys Ala Asn Ile Gly Gln Ala Ile Lys His Leu Leu Glu Ile Asp Leu

275 280 285

Lys Pro Arg Asp Ile Leu Thr Lys Lys Ser Phe Glu Asn Ala Ile Ala

290 295 300

Tyr Ile Ile Ala Thr Gly Gly Ser Thr Asn Ala Val Leu His Leu Ile

305 310 315 320

Ala Ile Ala Ser Ser Ala Asp Ile Asp Leu Thr Val Asp Asp Phe Gln

325 330 335

Arg Ile Ser Asp Ser Thr Pro Leu Leu Ala Asp Phe Lys Pro Ser Gly

340 345 350

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

355 360 365

Met Lys Phe Leu Met Asn Glu Gly Phe Ile Asp Gly Asp Gln Tyr Thr

370 375 380
 Val Thr Gly Lys Thr Ile Lys Glu Asn Leu Ala Ser Val Lys Asp Leu

 385 390 395 400
 Pro Ala Asp Gln Pro Ile Ile Arg Pro Val Ser Asn Pro Leu Lys Thr
 405 410 415
 Ser Gly His Leu Gln Ile Leu Lys Gly Ser Leu Ala Pro Gly Ser Ala
 420 425 430
 Val Gly Lys Ile Thr Gly Lys Glu Gly Thr Tyr Phe Lys Gly Lys Ala
 435 440 445
 Arg Val Phe Asp Asp Glu Gly Asp Phe Ile Val Ala Leu Glu Lys Gly

 450 455 460
 Glu Ile Lys Lys Gly Glu Lys Thr Val Cys Val Ile Arg Tyr Glu Gly
 465 470 475 480
 Pro Lys Gly Gly Pro Gly Met Pro Glu Met Leu Lys Pro Ser Ser Ala
 485 490 495
 Leu Met Gly Tyr Gly Leu Gly Lys Asp Val Ala Leu Leu Thr Asp Gly
 500 505 510
 Arg Phe Ser Gly Gly Ser His Gly Phe Leu Ile Gly His Ile Val Pro

 515 520 525
 Glu Ala Ala Glu Gly Gly Pro Ile Gly Leu Val Tyr Asp Gly Asp Glu
 530 535 540
 Ile Val Ile Asp Ala Glu Asn Asn Lys Ile Asp Leu Leu Val Asp Glu
 545 550 555 560
 Ala Val Leu Ala Glu Arg Arg Lys Leu Trp Thr Ala Pro Glu Pro Arg
 565 570 575
 Tyr Thr Arg Gly Thr Leu Ala Lys Tyr Ala Arg Leu Val Ser Asp Ala

 580 585 590
 Ser Ala Gly Cys Val Thr Asp Leu Pro Ile Lys Asn
 595 600
 <210> 105
 <211> 1705

<212> DNA

<213> Yarrowia lipolytica

<400> 105

ctacgtact aaggcgaca ctttgaacaa gttctccaag atcatcacgg agcccaagtc	60
gcaggagacc tctcaggcta tgctgtacgc ctgcggcttc aacgaggccg atctgggcaa	120
gccccagggtt ggtgtcgctt ccgtctgggtg gtccggaaac cctgcaaca tgcacctgct	180
tgatctcaac ttcaaggta aggagggcat cgagaagcac aacctcaagg ccatgcagtt	240
caacactatt ggtgtgtctg atggtatttc tatgggtacc aagggtatgc gatattctct	300
gcaatctcga gacatgattg ctgactccat tgagactctc atgatggccc agcactacga	360
cgccaacatc tccatcccgg gctgtgacaa gaacatgccc ggtgttctca tggccatggg	420
ccgagtcaac cgacctcca tcatgctgta cggaggaacc atccaccccg gaaaggccga	480
gactcgaag ggcgaggaca ttgatattgt ttccgccttc caggcctacg gacagtacat	540
tgccggcggc atctctgaga ccgagcgagc cgatgttatt cgacacgcct gccccggtca	600
gggagcctgt ggaggtatgt acactgctaa caccatggct tctgccgcag aggtgcttgg	660
tatgactctg cctggctcct cctccgctcc cgccatctcc aaggagaaga tggccgagtg	720
tgaggtcttg ggacctgcca tcaacaagct gctggagatg gacctcaagc ctaaggatat	780
catgacccga caggcctttg agaacgctat tgcttacatc attgccactg gaggtccac	840
caacgccgtt ctccatctgc tggctatcgc tcacaccgtc gacgttctt tgaccattga	900
cgacttcag cgaatctccg ataacactcc tctgctcgcc gacttcaagc cctccggagc	960
tcacgtcatg gccgatctgc agaagtgggg tggaaacccc gccgtcatca agatgtcat	1020
tgagcagggt ttcatgtatg gctctccat gacctgttcc ggagagtctc tcaaggacac	1080
cgctcgcaag taccctctc tcccaagga gcaggatata ttgcctctg ttgacgtcc	1140
cctcaagccc tctggctatc tgcagattct taagggtcc cttgctccc gtggatccgt	1200
cggaaagatc accggaaagg agggaaacatt cttcaagggt accgccgat gtttcgacga	1260
ggaggacctg ttcatgtagg ctctggagaa gggcgagatc aagaaggcg agaagacctg	1320
tgtcattatt cgatacgagg gcccgaaggg aggaccgggt atgcccaga tgctcaagcc	1380
ctcttctgcc ctgatgggat acggtctggg caaggatgtt gctctgctga ccgacggacg	1440
attctccgga ggatctcatg gtttctcat tggtcacatt gtccccgagg ctacgaggg	1500
aggtcccat ggtctggttg aggacggcga tgagatcatc atcgacgtg acaacaacat	1560
catcgacctg cttgttgatg agaagacat ggtgagcga aaggccaagt ggactcccc	1620
cgctcctcga tacacctg gaacctgca caagtactcc aagcttgtt ccgacgcctc	1680

cactggctgt atcactgacg cctaa

1705

<210> 106

<211> 567

<212> PRT

<213> Yarrowia lipolytica

<400> 106

Tyr Ala Thr Lys Ala His Thr Leu Asn Lys Phe Ser Lys Ile Ile Thr

1 5 10 15

Glu Pro Lys Ser Gln Gly Ala Ser Gln Ala Met Leu Tyr Ala Cys Gly

20 25 30

Phe Asn Glu Ala Asp Leu Gly Lys Pro Gln Val Gly Val Ala Ser Val

35 40 45

Trp Trp Ser Gly Asn Pro Cys Asn Met His Leu Leu Asp Leu Asn Phe

50 55 60

Lys Val Lys Glu Gly Ile Glu Lys His Asn Leu Lys Ala Met Gln Phe

65 70 75 80

Asn Thr Ile Gly Val Ser Asp Gly Ile Ser Met Gly Thr Lys Gly Met

85 90 95

Arg Tyr Ser Leu Gln Ser Arg Asp Met Ile Ala Asp Ser Ile Glu Thr

100 105 110

Leu Met Met Ala Gln His Tyr Asp Ala Asn Ile Ser Ile Pro Gly Cys

115 120 125

Asp Lys Asn Met Pro Gly Val Leu Met Ala Met Gly Arg Val Asn Arg

130 135 140

Pro Ser Ile Met Leu Tyr Gly Gly Thr Ile His Pro Gly Lys Ala Glu

145 150 155 160

Thr Arg Lys Gly Glu Asp Ile Asp Ile Val Ser Ala Phe Gln Ala Tyr

165 170 175

Gly Gln Tyr Ile Ala Gly Gly Ile Ser Glu Thr Glu Arg Ala Asp Val

180 185 190

Ile Arg His Ala Cys Pro Gly Gln Gly Ala Cys Gly Gly Met Tyr Thr

195 200 205
 Ala Asn Thr Met Ala Ser Ala Ala Glu Val Leu Gly Met Thr Leu Pro
 210 215 220
 Gly Ser Ser Ser Ala Pro Ala Ile Ser Lys Glu Lys Met Ala Glu Cys
 225 230 235 240
 Glu Ala Leu Gly Pro Ala Ile Asn Lys Leu Leu Glu Met Asp Leu Lys
 245 250 255
 Pro Lys Asp Ile Met Thr Arg Gln Ala Phe Glu Asn Ala Ile Ala Tyr
 260 265 270

 Ile Ile Ala Thr Gly Gly Ser Thr Asn Ala Val Leu His Leu Leu Ala
 275 280 285
 Ile Ala His Thr Val Asp Val Pro Leu Thr Ile Asp Asp Phe Gln Arg
 290 295 300
 Ile Ser Asp Asn Thr Pro Leu Leu Ala Asp Phe Lys Pro Ser Gly Ala
 305 310 315 320
 His Val Met Ala Asp Leu Gln Lys Trp Gly Gly Thr Pro Ala Val Ile
 325 330 335

 Lys Met Leu Ile Glu Gln Gly Phe Ile Asp Gly Ser Pro Met Thr Cys
 340 345 350
 Ser Gly Glu Ser Leu Lys Asp Thr Val Ala Lys Tyr Pro Ser Leu Pro
 355 360 365
 Lys Glu Gln Asp Ile Phe Ala Ser Val Asp Ala Pro Leu Lys Pro Ser
 370 375 380
 Gly His Leu Gln Ile Leu Lys Gly Ser Leu Ala Pro Gly Gly Ser Val
 385 390 395 400

 Gly Lys Ile Thr Gly Lys Glu Gly Thr Phe Phe Lys Gly Thr Ala Arg
 405 410 415
 Cys Phe Asp Glu Glu Asp Leu Phe Ile Glu Ala Leu Glu Lys Gly Glu
 420 425 430
 Ile Lys Lys Gly Glu Lys Thr Cys Val Ile Ile Arg Tyr Glu Gly Pro
 435 440 445

Lys Gly Gly Pro Gly Met Pro Glu Met Leu Lys Pro Ser Ser Ala Leu
450 455 460

Met Gly Tyr Gly Leu Gly Lys Asp Val Ala Leu Leu Thr Asp Gly Arg
465 470 475 480

Phe Ser Gly Gly Ser His Gly Phe Leu Ile Gly His Ile Val Pro Glu
485 490 495

Ala Tyr Glu Gly Gly Pro Ile Gly Leu Val Glu Asp Gly Asp Glu Ile
500 505 510

Ile Ile Asp Ala Asp Asn Asn Ile Ile Asp Leu Leu Val Asp Glu Lys
515 520 525

Thr Met Ala Glu Arg Lys Ala Lys Trp Thr Pro Pro Ala Pro Arg Tyr
530 535 540

Thr Ser Gly Thr Leu His Lys Tyr Ser Lys Leu Val Ser Asp Ala Ser
545 550 555 560

Thr Gly Cys Ile Thr Asp Ala
565

<210> 107

<211> 1752

<212> DNA

<213> Candida glabrata

<400> 107

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ctgaataaat acicatatat catcactgag cctaaggacc aaggtagcctc tcaggctatg 120

ttgtatgcca ctggtttcaa caaggatgat ttccagcaaag cgcaagttgg tgttggttct 180

tgttggtggt ctggtaaccc atgtaacatg catctattgg atttgaacca cagatgttcc 240

caatccatcg agaaagccgg tatgaaaggt atgcaattta acacaattgg tgtctctgac 300

ggtatctcga tgggtactaa aggtatgaga tattctttac aaagtagaga aattatcgca 360

gactctttcg agactatcat gatggcacia cactacgatg ccaatattgc tattccatcc 420

tgtgacaaga atatgcctgg tgttatgatg gctatgggta gacacaacag accatctatt 480

atggtttatg gtggtaccat tatgccaggt cacccaactt gtggctccaa gaacattcca 540

gagaacattg atgttgtctc tgctttccaa tcctacggtc aatacatctc gaagcaattc 600

aatgaagaag agagaagtga tgtttgtacaa cactcttgtc caggtcctgg ctcttgtggt 660
 ggtatgtaca ccgccaacac catggcctct gctgccgaag ttttaggtat cactatgcc 720
 aactcttctg ctttccagc tgtttctgct gaaaagattg ctgaatgtga caacattggt 780
 gctgctatca agaacactat ggaacttgggt attacccac gtcaaattctt caccaaggaa 840
 tcctttgaaa acgtatcac ttacgtcatt gctactggtg gttccactaa cgcagttctt 900
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atcagtgaca agacaccatt gctaggtgac ttcaagccat ctggtaagta tgtcatggcc 1020
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 aagggtctaa gtgaaactca agacattatt agaccattgt caaacccaat taagccaagt 1200
 ggccatctac aaattctata cggttctctt gctccaggtg gttctgttgg taagattact 1260
 ggtaaggaag gtacttactt caaaggtaag gctcgtgttt tcgaagaaga agacgctttc 1320
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tatgaaggtc caaagggtgg tccaggtatg ccagaaatgt tgaagccatc tagtgacta 1440
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 tctcatggtt tcttgattgg tcacattgtt ccagaagctg ccgaagggtg tccaattggt 1560
 ttggtcagag atggtgatga aattgtgatt gatgcagaca acaacaagat tgacctccta 1620
 atctctgaat ctgagatgac tcaacgtaag gccgaatgga aacctccagc cccacgttac 1680
 aacaggggta ctctatccaa atatgctaag ttagtctcta atgcctccca aggttgtgtt 1740
 acagacgctt aa 1752

<210> 108

<211> 583

<212> PRT

<213> Candida glabrata

<400> 108

Met Ser Ser Arg Leu Thr Phe Ala Arg Lys Phe Ser Ser Thr Arg Asn

1 5 10 15

Val Ala Lys Lys Leu Asn Lys Tyr Ser Tyr Ile Ile Thr Glu Pro Lys

20 25 30

Asp Gln Gly Ala Ser Gln Ala Met Leu Tyr Ala Thr Gly Phe Asn Lys

35 40 45

Asp Asp Phe Ser Lys Ala Gln Val Gly Val Gly Ser Cys Trp Trp Ser

50 55 60

Gly Asn Pro Cys Asn Met His Leu Leu Asp Leu Asn His Arg Cys Ser

65 70 75 80

Gln Ser Ile Glu Lys Ala Gly Met Lys Gly Met Gln Phe Asn Thr Ile

85 90 95

Gly Val Ser Asp Gly Ile Ser Met Gly Thr Lys Gly Met Arg Tyr Ser

100 105 110

Leu Gln Ser Arg Glu Ile Ile Ala Asp Ser Phe Glu Thr Ile Met Met

115 120 125

Ala Gln His Tyr Asp Ala Asn Ile Ala Ile Pro Ser Cys Asp Lys Asn

130 135 140

Met Pro Gly Val Met Met Ala Met Gly Arg His Asn Arg Pro Ser Ile

145 150 155 160

Met Val Tyr Gly Gly Thr Ile Met Pro Gly His Pro Thr Cys Gly Ser

165 170 175

Lys Asn Ile Pro Glu Asn Ile Asp Val Val Ser Ala Phe Gln Ser Tyr

180 185 190

Gly Gln Tyr Ile Ser Lys Gln Phe Asn Glu Glu Glu Arg Ser Asp Val

195 200 205

Val Gln His Ser Cys Pro Gly Pro Gly Ser Cys Gly Gly Met Tyr Thr

210 215 220

Ala Asn Thr Met Ala Ser Ala Ala Glu Val Leu Gly Ile Thr Met Pro

225 230 235 240

Asn Ser Ser Ala Phe Pro Ala Val Ser Ala Glu Lys Ile Ala Glu Cys

245 250 255

Asp Asn Ile Gly Ala Ala Ile Lys Asn Thr Met Glu Leu Gly Ile Thr

260 265 270

Pro Arg Gln Ile Phe Thr Lys Glu Ser Phe Glu Asn Ala Ile Thr Tyr

275 280 285

Val Ile Ala Thr Gly Gly Ser Thr Asn Ala Val Leu His Leu Val Ala

290 295 300
 Ile Ala His Ser Ala Gly Val Lys Ile Thr Pro Asp Asp Phe Gln Arg

 305 310 315 320
 Ile Ser Asp Lys Thr Pro Leu Leu Gly Asp Phe Lys Pro Ser Gly Lys
 325 330 335
 Tyr Val Met Ala Asp Leu Ile Lys Val Gly Gly Thr Gln Ser Val Ile
 340 345 350
 Lys Phe Leu Tyr Asp Asn Gly Phe Leu Tyr Gly Asp Ala Leu Thr Val
 355 360 365
 Thr Gly Glu Thr Leu Ala Glu Arg Ala Lys Lys Ala Lys Gly Leu Ser

 370 375 380
 Glu Thr Gln Asp Ile Ile Arg Pro Leu Ser Asn Pro Ile Lys Pro Ser
 385 390 395 400
 Gly His Leu Gln Ile Leu Tyr Gly Ser Leu Ala Pro Gly Gly Ser Val
 405 410 415
 Gly Lys Ile Thr Gly Lys Glu Gly Thr Tyr Phe Lys Gly Lys Ala Arg
 420 425 430
 Val Phe Glu Glu Glu Asp Ala Phe Ile Ser Ala Leu Glu Asn Gly Glu

 435 440 445
 Ile Lys Lys Gly Glu Lys Thr Val Val Ile Ile Arg Tyr Glu Gly Pro
 450 455 460
 Lys Gly Gly Pro Gly Met Pro Glu Met Leu Lys Pro Ser Ser Ala Leu
 465 470 475 480
 Met Gly Tyr Gly Leu Gly Lys Asp Val Ala Leu Leu Thr Asp Gly Arg
 485 490 495
 Phe Ser Gly Gly Ser His Gly Phe Leu Ile Gly His Ile Val Pro Glu

 500 505 510
 Ala Ala Glu Gly Gly Pro Ile Gly Leu Val Arg Asp Gly Asp Glu Ile
 515 520 525
 Val Ile Asp Ala Asp Asn Asn Lys Ile Asp Leu Leu Ile Ser Glu Ser
 530 535 540

Glu Met Ser Gln Arg Lys Ala Glu Trp Lys Pro Pro Ala Pro Arg Tyr
 545 550 555 560
 Asn Arg Gly Thr Leu Ser Lys Tyr Ala Lys Leu Val Ser Asn Ala Ser

565 570 575
 Gln Gly Cys Val Thr Asp Ala
 580

<210> 109

<211> 1764

<212> DNA

<213> Vanderwaltozyma polyspora

<400> 109

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aagaagtga ataagtactc ttatatcgtt acagaaccta aggaccaagg tgcatacaaa	120
gcgatgcttt atgcaactgg gttcaagaaa gaagatttta gtaaaggcca agttggtgta	180
ggatcatgtt gggtgctctg taatccatgt aatatgcatt tattggatct taatgataga	240
tgttcacgtt ctgtggagaa ggctggcttg aaagctatgc aatttaatac cattggtgtt	300
tccgatggta tttaaatggg tactaaaggt atgagatact ctttacagag tagagaaatc	360
attgctgatt cttttgaac tataatgatg gctcaacatt acgatgcaa tattgctatc	420
ccttcatgtg ataaaaacat gccgggtgtc atgatggcca tgggaagaca taacagacct	480
tctatcatgg tttatgggtg tactatttta cctggccatc caacctgtgg ttcttcaaaa	540
attccagaaa acattgatat agtatctgct ttccaatctt atggtcaata tatatctaaa	600
caattcagcg aacaagagag agaagatgtg gttgaacatg cttgtcctgg tccaggttct	660
tgtggtggta tgtatactgc taacactatg ggttctgtcg cagaagtgc aggtttgact	720
ttgccaaact cttctgcctt cccagcagtt tctcaagaaa agatgaatga atgtgattcc	780
attggtgaag ctattaagaa gacaatggaa ttaggtatca ctctcgtga tatcatgact	840
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caaagaatca gtgataagac cccattattg ggtgatttta aaccatcggg taaatacggt	1020
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<210> 110

<211> 587

<212> PRT

<213> Vanderwaltozyma polyspora

<400> 110

Met Thr Ile Ala Ser Lys Ala Leu Ser Ala Arg His Phe Ser Val Thr

1 5 10 15
Arg Asn Val Ser Lys Lys Leu Asn Lys Tyr Ser Tyr Ile Val Thr Glu

20 25 30
Pro Lys Asp Gln Gly Ala Ser Gln Ala Met Leu Tyr Ala Thr Gly Phe

35 40 45
Lys Lys Glu Asp Phe Ser Lys Gly Gln Val Gly Val Gly Ser Cys Trp

50 55 60
Trp Ser Gly Asn Pro Cys Asn Met His Leu Leu Asp Leu Asn Asp Arg

65 70 75 80
Cys Ser Arg Ser Val Glu Lys Ala Gly Leu Lys Ala Met Gln Phe Asn

85 90 95
Thr Ile Gly Val Ser Asp Gly Ile Ser Met Gly Thr Lys Gly Met Arg

100 105 110
Tyr Ser Leu Gln Ser Arg Glu Ile Ile Ala Asp Ser Phe Glu Thr Ile

115 120 125

Met Met Ala Gln His Tyr Asp Ala Asn Ile Ala Ile Pro Ser Cys Asp

130 135 140

Lys Asn Met Pro Gly Val Met Met Ala Met Gly Arg His Asn Arg Pro

145 150 155 160

Ser Ile Met Val Tyr Gly Gly Thr Ile Leu Pro Gly His Pro Thr Cys

165 170 175

Gly Ser Ser Lys Ile Pro Glu Asn Ile Asp Ile Val Ser Ala Phe Gln

180 185 190

Ser Tyr Gly Gln Tyr Ile Ser Lys Gln Phe Ser Glu Gln Glu Arg Glu

195 200 205

Asp Val Val Glu His Ala Cys Pro Gly Pro Gly Ser Cys Gly Gly Met

210 215 220

Tyr Thr Ala Asn Thr Met Gly Ser Val Ala Glu Val Leu Gly Leu Thr

225 230 235 240

Leu Pro Asn Ser Ser Ala Phe Pro Ala Val Ser Gln Glu Lys Met Asn

245 250 255

Glu Cys Asp Ser Ile Gly Glu Ala Ile Lys Lys Thr Met Glu Leu Gly

260 265 270

Ile Thr Pro Arg Asp Ile Met Thr Lys Gln Ala Phe Glu Asn Ala Ile

275 280 285

Thr Tyr Val Ile Ala Thr Gly Gly Ser Thr Asn Ala Val Leu His Leu

290 295 300

Val Ala Ile Ala His Ser Ala Gly Val Lys Ile Thr Pro Asp Asp Phe

305 310 315 320

Gln Arg Ile Ser Asp Lys Thr Pro Leu Leu Gly Asp Phe Lys Pro Ser

325 330 335

Gly Lys Tyr Val Met Ala Asp Leu Ile Lys Val Gly Gly Thr Gln Ser

340 345 350

Val Ile Lys Phe Leu Tyr Glu Asn Gly Phe Leu His Gly Asp Ala Ile

355 360 365

Thr Val Thr Gly Asp Thr Leu Ala Glu Arg Ala Ala Lys Thr Ser Gly

370 375 380
 Leu Pro Glu Gly Gln Asp Ile Ile Arg Pro Val Ser Gln Pro Ile Lys

 385 390 395 400
 Pro Asn Gly His Leu Gln Ile Leu Tyr Gly Ser Leu Ala Pro Gly Gly
 405 410 415
 Ala Val Gly Lys Ile Thr Gly Lys Glu Gly Thr Phe Phe Lys Gly Arg
 420 425 430
 Ala Arg Val Phe Glu Glu Glu Glu Ala Phe Ile His Ala Leu Glu Arg
 435 440 445
 Gly Glu Ile Lys Lys Gly Glu Lys Thr Val Val Val Ile Arg Tyr Glu

 450 455 460
 Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met Leu Lys Pro Ser Ser
 465 470 475 480
 Ala Leu Met Gly Tyr Gly Leu Gly Lys Asp Val Ala Leu Leu Thr Asp
 485 490 495
 Gly Arg Phe Ser Gly Gly Ser His Gly Phe Leu Ile Gly His Ile Val
 500 505 510
 Pro Glu Ala Ala Glu Gly Gly Pro Ile Gly Leu Val Lys Asp Gly Asp

 515 520 525
 Glu Ile Val Ile Asp Thr Asn Asn Asn Lys Ile Asp Leu Leu Val Ser
 530 535 540
 Glu Gln Glu Ile Ala Gln Arg Lys Ser Glu Trp Val Lys Pro Ala Pro
 545 550 555 560
 Arg Tyr Thr Arg Gly Thr Leu Ser Lys Tyr Ser Lys Leu Val Ser Asn
 565 570 575
 Ala Ser Asn Gly Cys Val Leu Asp Ala Asp Asn
 580 585

<210> 111

<211> 1758

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 111

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gccatgcttt atgccaccgg tttcaagaag gaagatttca agaagcctca agtcgggggtt	180
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tcagacggta tcctatggg tactaaaggt atgagatact cgtiacaaag tagagaaatc	360
attgcagact cctttgaaac catcatgatg gcacaacact acgatgctaa catcgccatc	420
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tccatcatgg tatatgggtg tactatcttg cccgggtcac caacatgtgg ttcttcgaag	540
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caattcactg aagaagaaag agaagatgtt gtggaacatg catgcccagg tcctggttct	660
tgtgggtgta tgtatactgc caacacaatg gcttctgccg ctgaagtgt aggtttgacc	720
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atggccgatt tgattaacgt tgggtgtacc caatctgtga ttaagtatct atatgaaaac	1080
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gccaacggtc acttgcaaat tctgtacggt tcattggcac caggtggagc tgtgggtaaa	1260
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cgttacacaa gaggtactct atccaagat gctaagttgg tttccaacgc ttccaacggt	1740
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<210> 112

<211> 585

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 112

Met Gly Leu Leu Thr Lys Val Ala Thr Ser Arg Gln Phe Ser Thr Thr

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Arg Cys Val Ala Lys Lys Leu Asn Lys Tyr Ser Tyr Ile Ile Thr Glu

20 25 30

Pro Lys Gly Gln Gly Ala Ser Gln Ala Met Leu Tyr Ala Thr Gly Phe

35 40 45

Lys Lys Glu Asp Phe Lys Lys Pro Gln Val Gly Val Gly Ser Cys Trp

50 55 60

Trp Ser Gly Asn Pro Cys Asn Met His Leu Leu Asp Leu Asn Asn Arg

65 70 75 80

Cys Ser Gln Ser Ile Glu Lys Ala Gly Leu Lys Ala Met Gln Phe Asn

85 90 95

Thr Ile Gly Val Ser Asp Gly Ile Ser Met Gly Thr Lys Gly Met Arg

100 105 110

Tyr Ser Leu Gln Ser Arg Glu Ile Ile Ala Asp Ser Phe Glu Thr Ile

115 120 125

Met Met Ala Gln His Tyr Asp Ala Asn Ile Ala Ile Pro Ser Cys Asp

130 135 140

Lys Asn Met Pro Gly Val Met Met Ala Met Gly Arg His Asn Arg Pro

145 150 155 160

Ser Ile Met Val Tyr Gly Gly Thr Ile Leu Pro Gly His Pro Thr Cys

165 170 175

Gly Ser Ser Lys Ile Ser Lys Asn Ile Asp Ile Val Ser Ala Phe Gln

180 185 190

Ser Tyr Gly Glu Tyr Ile Ser Lys Gln Phe Thr Glu Glu Glu Arg Glu

195 200 205

Asp Val Val Glu His Ala Cys Pro Gly Pro Gly Ser Cys Gly Gly Met

210 215 220

Tyr Thr Ala Asn Thr Met Ala Ser Ala Ala Glu Val Leu Gly Leu Thr

225 230 235 240

Ile Pro Asn Ser Ser Ser Phe Pro Ala Val Ser Lys Glu Lys Leu Ala

245 250 255

Glu Cys Asp Asn Ile Gly Glu Tyr Ile Lys Lys Thr Met Glu Leu Gly

260 265 270

Ile Leu Pro Arg Asp Ile Leu Thr Lys Glu Ala Phe Glu Asn Ala Ile

275 280 285

Thr Tyr Val Val Ala Thr Gly Gly Ser Thr Asn Ala Val Leu His Leu

290 295 300

Val Ala Val Ala His Ser Ala Gly Val Lys Leu Ser Pro Asp Asp Phe

305 310 315 320

Gln Arg Ile Ser Asp Thr Thr Pro Leu Ile Gly Asp Phe Lys Pro Ser

325 330 335

Gly Lys Tyr Val Met Ala Asp Leu Ile Asn Val Gly Gly Thr Gln Ser

340 345 350

Val Ile Lys Tyr Leu Tyr Glu Asn Asn Met Leu His Gly Asn Thr Met

355 360 365

Thr Val Thr Gly Asp Thr Leu Ala Glu Arg Ala Lys Lys Ala Pro Ser

370 375 380

Leu Pro Glu Gly Gln Glu Ile Ile Lys Pro Leu Ser His Pro Ile Lys

385 390 395 400

Ala Asn Gly His Leu Gln Ile Leu Tyr Gly Ser Leu Ala Pro Gly Gly

405 410 415

Ala Val Gly Lys Ile Thr Gly Lys Glu Gly Thr Tyr Phe Lys Gly Arg

420 425 430

Ala Arg Val Phe Glu Glu Glu Gly Ala Phe Ile Glu Ala Leu Glu Arg

435 440 445

Gly Glu Ile Lys Lys Gly Glu Lys Thr Val Val Val Ile Arg Tyr Glu

450 455 460
 Gly Pro Arg Gly Ala Pro Gly Met Pro Glu Met Leu Lys Pro Ser Ser

465 470 475 480
 Ala Leu Met Gly Tyr Gly Leu Gly Lys Asp Val Ala Leu Leu Thr Asp

 485 490 495
 Gly Arg Phe Ser Gly Gly Ser His Gly Phe Leu Ile Gly His Ile Val

 500 505 510
 Pro Glu Ala Ala Glu Gly Gly Pro Ile Gly Leu Val Arg Asp Gly Asp

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

530 535 540
 Asp Lys Glu Ile Ala Gln Arg Lys Gln Ser Trp Val Ala Pro Pro Pro

545 550 555 560
 Arg Tyr Thr Arg Gly Thr Leu Ser Lys Tyr Ala Lys Leu Val Ser Asn

 565 570 575
 Ala Ser Asn Gly Cys Val Leu Asp Ala

 580 585

<210> 113
 <211> 1752
 <212> DNA
 <213> Kluyveromyces lactis
 <400> 113

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tatgccacgg ggtttaagga agacgatttc ggcaaggctc aagttggtgt tggttcatgt 180

tgggtggtctg gtaatccatg taatatgcat ttgatggatt tcaacaacag aatcaccgaa 240

tccgttaaca aggctgggtt gaaaggtatg caattcaata ccattggtgt ttctgatggt 300

atttccatgg gtaccaaggg tatgagatat tctttgcaat ctagagaagt tattgctgat 360

tcgttcgaaa ccattatgat ggctcaacat tacgatgcca atatcgccat tccatcttgt 420

gataaaaaca tgcttggtgt tttgatggct atgggtagac ataacagacc ttccattatg 480

gtttatggtg gtaccatttt gccaggttct ccaacttgtg gttctgctaa gattccaaag 540

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ccagaagaag aaatcgctga acgtagaagt acatggactg ctccacctcc acgttatact 1680
agaggatgtt tatccaagta cgcaaaattg gtttcaaatg cttcccatgg ttgcgtgact 1740

gatttgaact aa 1752

<210> 114

<211> 583

<212> PRT

<213> Kluyveromyces lactis

<400> 114

Met Phe Ser Gln Ser Ala Val Arg Arg Phe Ser Thr Thr Arg Asn Val

1 5 10 15

Gly Lys Lys Leu Asn Lys Tyr Ser His Ile Ile Thr Glu Pro Lys Asp

20 25 30

Gln Gly Ala Ser Gln Ala Met Leu Tyr Ala Thr Gly Phe Lys Glu Asp

35	40	45
Asp Phe Gly Lys Ala Gln Val Gly Val Gly Ser Cys Trp Trp Ser Gly		
50	55	60
Asn Pro Cys Asn Met His Leu Met Asp Phe Asn Asn Arg Ile Thr Glu		
65	70	75
Ser Val Asn Lys Ala Gly Leu Lys Gly Met Gln Phe Asn Thr Ile Gly		
85	90	95
Val Ser Asp Gly Ile Ser Met Gly Thr Lys Gly Met Arg Tyr Ser Leu		
100	105	110
Gln Ser Arg Glu Val Ile Ala Asp Ser Phe Glu Thr Ile Met Met Ala		
115	120	125
Gln His Tyr Asp Ala Asn Ile Ala Ile Pro Ser Cys Asp Lys Asn Met		
130	135	140
Pro Gly Val Leu Met Ala Met Gly Arg His Asn Arg Pro Ser Ile Met		
145	150	155
Val Tyr Gly Gly Thr Ile Leu Pro Gly Ser Pro Thr Cys Gly Ser Ala		
165	170	175
Lys Ile Pro Lys Lys Ile Asp Val Val Ser Ala Phe Gln Ser Tyr Gly		
180	185	190
Gln Tyr Leu Ser Lys Glu Phe Thr Glu Thr Glu Arg Gln Asp Val Val		
195	200	205
Gln His Ala Cys Pro Gly Pro Gly Ser Cys Gly Gly Met Tyr Thr Ala		
210	215	220
Asn Thr Met Ala Ser Val Ala Glu Val Leu Gly Met Thr Leu Pro Asn		
225	230	235
Ser Ser Ser Phe Pro Ala Val Ser Lys Glu Lys Leu Asn Glu Cys Asp		
245	250	255
Thr Ile Gly Glu Ala Ile Lys Lys Thr Met Glu Leu Gly Ile Thr Pro		
260	265	270
Arg Asp Val Met Thr Lys Glu Ala Phe Glu Asn Ala Met Thr Tyr Val		
275	280	285

Ile Ala Thr Gly Gly Ser Thr Asn Ala Val Leu His Met Val Ala Val
290 295 300

Ala His Ser Ala Gly Val Lys Ile Thr Pro Asp Asp Phe Gln Arg Ile
305 310 315 320

Ser Asp Lys Thr Pro Leu Leu Gly Asp Phe Lys Pro Ser Gly Lys Tyr
325 330 335

Val Met Ala Asp Leu Ile Thr Val Gly Gly Thr Gln Ala Val Ile Lys
340 345 350

Tyr Leu Tyr Glu Glu Gly Phe Leu His Gly Asn Thr Ile Thr Ile Ser
355 360 365

Gly Asp Thr Leu Ala Glu Arg Ala Ala Lys Ala Val Ser Leu Lys Asp
370 375 380

Gly Gln Asp Ile Ile Arg Pro Leu Thr Asn Pro Ile Lys Thr Ser Gly
385 390 395 400

His Leu Gln Ile Leu Tyr Gly Ser Leu Ala Pro Gly Gly Ser Val Gly
405 410 415

Lys Ile Thr Gly Lys Glu Gly Thr Tyr Phe Lys Gly Lys Ala Arg Val
420 425 430

Phe Asn Asp Glu Pro Gly Phe Ile Ser Ala Leu Glu Asn Gly Glu Ile
435 440 445

Lys Lys Gly Glu Lys Thr Val Val Ile Ile Arg Tyr Glu Gly Pro Arg
450 455 460

Gly Gly Pro Gly Met Pro Glu Met Leu Lys Pro Ser Ser Ala Leu Met
465 470 475 480

Gly Tyr Gly Leu Gly Lys Asp Val Ala Leu Leu Thr Asp Gly Arg Phe
485 490 495

Ser Gly Gly Ser His Gly Phe Leu Ile Gly His Ile Val Pro Glu Ala
500 505 510

Ala Glu Gly Gly Pro Ile Gly Leu Val Arg Asp Gly Asp Glu Ile Ile
515 520 525

Ile Asp Ala Asp Asn Asn Lys Ile Asp Leu Leu Val Pro Glu Glu Glu

530 535 540
 Ile Ala Glu Arg Arg Ser Thr Trp Thr Ala Pro Pro Pro Arg Tyr Thr
 545 550 555 560

 Arg Gly Cys Leu Ser Lys Tyr Ala Lys Leu Val Ser Asn Ala Ser His
 565 570 575
 Gly Cys Val Thr Asp Leu Asn
 580
 <210> 115
 <211> 1746
 <212> DNA
 <213> Ashbya gossypii
 <400> 115

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gaaggccagg acatcattcg tcccgtgtcg cagccattga atcctagggg acatctccag 1200
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gactag 1746

<210> 116

<211> 581

<212> PRT

<213> Ashbya gossypii

<400> 116

Met Met Ser His Arg Arg Phe Ser Thr Ala Gln Arg Leu Arg Glu Gly

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Leu Asn Arg Tyr Ser Arg Val Ile Thr Glu Pro Arg Ala Gln Gly Ala

20 25 30
Ser Gln Ala Met Leu Tyr Ala Thr Gly Phe Gly Asp Gly Asp Phe Ala

35 40 45
Lys Ala Gln Val Gly Val Gly Ser Cys Trp Trp Ser Gly Asn Pro Cys

50 55 60
Asn Met His Leu Met Asp Leu Asn Asn Arg Val Ala Ala Ser Val Asp

65 70 75 80
Arg Ala Gly Leu Lys Ala Met Gln Phe Asn Thr Ile Gly Val Ser Asp

85 90 95
Gly Ile Ser Met Gly Thr Thr Gly Met Arg Tyr Ser Leu Gln Ser Arg

100 105 110
Glu Ile Ile Ala Asp Ser Phe Glu Thr Met Met Met Gly Gln His Tyr

115 120 125

Asp Gly Asn Val Ala Ile Pro Ser Cys Asp Lys Asn Met Pro Gly Val

130 135 140

Ile Met Ala Met Ala Arg His Asn Arg Pro Ser Ile Met Val Tyr Gly

145 150 155 160

Gly Thr Ile Met Ala Gly Ser Pro Cys Ser Gly Ser Thr Arg Leu Pro

165 170 175

Lys Lys Ile Asp Val Val Ser Ala Phe Gln Ala Tyr Gly Gln Tyr Leu

180 185 190

Ser Lys Gln Ile Thr Glu Glu Glu Ser Arg Asp Val Val Arg His Ala

195 200 205

Cys Pro Gly Pro Gly Ser Cys Gly Gly Met Tyr Thr Ala Asn Thr Met

210 215 220

Ala Ser Ala Ala Glu Val Leu Gly Leu Thr Leu Pro Asn Ser Ser Ala

225 230 235 240

Phe Pro Ala Ile Ser Glu Gln Lys Leu Ala Glu Cys Asp Ala Val Gly

245 250 255

Asp Ala Met Arg Lys Ala Leu Glu Leu Asn Ile Arg Pro Arg Asp Leu

260 265 270

Leu Thr Arg Glu Ala Phe Glu Asn Ala Ile Thr Tyr Val Ile Ala Thr

275 280 285

Gly Gly Ser Thr Asn Ala Val Leu His Leu Val Ala Ile Ala His Ser

290 295 300

Ala Gly Val Lys Leu Thr Pro Asp Asp Phe Gln Arg Ile Ser Asn Lys

305 310 315 320

Thr Pro Leu Leu Gly Asp Phe Lys Pro Ser Gly Lys Tyr Val Met Ala

325 330 335

Asp Leu Ile Glu Val Gly Gly Thr Gln Ala Val Ile Lys Phe Leu Tyr

340 345 350

Glu Asn Gly Phe Met His Gly Asp Ala Leu Thr Val Thr Gly Asp Thr

355 360 365

Leu Lys Glu Arg Ala Ala Lys Thr Ala Pro Leu Pro Glu Gly Gln Asp

370 375 380
Ile Ile Arg Pro Val Ser Gln Pro Leu Asn Pro Arg Gly His Leu Gln

385 390 395 400
Ile Leu Tyr Gly Ser Leu Ala Pro Gly Gly Ala Val Gly Lys Ile Thr

405 410 415
Gly Lys Glu Gly Thr Phe Phe Gln Gly Arg Ala Arg Val Phe Asp Glu

420 425 430
Glu Asn Ala Phe Ile Arg Ala Leu Glu Glu Gly Gln Ile Lys Lys Gly

435 440 445
Glu Lys Thr Val Val Val Ile Arg Tyr Glu Gly Pro Lys Gly Gly Pro

450 455 460
Gly Met Pro Glu Met Leu Lys Pro Ser Ser Ala Leu Met Gly Tyr Gly

465 470 475 480
Leu Gly Asn Asp Val Ala Leu Leu Thr Asp Gly Arg Phe Ser Gly Gly

485 490 495
Ser His Gly Phe Leu Ile Gly His Ile Val Pro Glu Ala Tyr Glu Gly

500 505 510
Gly Pro Ile Ala Leu Val Gln Asp Gly Asp Asp Ile Val Ile Asp Ala

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

530 535 540
Arg Arg Ala Arg Trp Thr Gln Pro Ala Pro Arg Tyr Lys Arg Gly Thr

545 550 555 560
Leu Ala Thr Tyr Ser Lys Leu Val Ser Asn Ala Ser Lys Gly Cys Val

565 570 575
Leu Asp Ser Asp Asp

580

<210

> 117

<211> 1704

<212> DNA

<213> Laccaria bicolor

<400> 117

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<210> 118

<211> 567

<212> PRT

<213> Laccaria bicolor

<400> 118

Met Asn Arg His Ser Arg Val Val Thr Gln Pro Lys Asp Gln Gly Ala

1 5 10 15

Ser Gln Ala Met Leu Tyr Ala Thr Asp Gly Ile Lys Thr Asp Asp Asp

20 25 30

Phe Asn Lys Ala Met Val Gly Val Ala Ser Val Trp Tyr Glu Gly Asn

35 40 45

Pro Cys Asn Lys His Leu Leu Gly Leu Gly Gln Glu Ile Lys Ala Ser

50 55 60

Leu Thr Lys Ser Gly Ile Ile Gly Tyr Gln Phe Gly Thr Val Gly Val

65 70 75 80

Ser Asp Gly Ile Ser Met Gly Thr Arg Gly Met Ser Tyr Ser Leu Gln

85 90 95

Ser Arg Asp Leu Ile Ala Asp Gln Val Glu Thr Ala Ala Gly Gly His

100 105 110

His Leu Asp Gly Met Val Val Val Pro Gly Cys Asp Lys Asn Met Pro

115 120 125

Gly Val Leu Met Ala Leu Gly Arg Leu Asn Arg Pro Gly Leu Met Val

130 135 140

Tyr Gly Gly Thr Ile Arg Ala Gly Ser Cys Glu Gly Ala Pro Gln Leu

145 150 155 160

Asp Ile Val Ser Ala Phe Gln Ser Tyr Gly Lys Tyr Leu Gln Asp Gly

165 170 175

Lys Thr Pro Glu Ala Glu Arg Glu Arg Tyr Asn Thr Val Arg His Ala

180 185 190

Cys Pro Gly Pro Gly Ala Cys Gly Gly Met Tyr Thr Ala Asn Thr Met

195 200 205

Ala Ser Ala Ala Glu Ala Leu Gly Met Thr Val Pro Gly Ser Ser Ser

210 215 220

Phe Pro Ala Glu Ser Leu Glu Lys His Asn Glu Cys Ala Ser Ile Gly

225 230 235 240

Lys Val Met Tyr Asn Leu Leu Glu Lys Asn Ile Leu Pro Arg Asp Ile

 245 250 255

Met Thr Arg Ser Ala Phe Glu Asn Ala Met Val Leu Thr Met Ile Leu

 260 265 270

Gly Gly Ser Thr Asn Ala Val Leu His Leu Ile Ala Met Ala His Ser

 275 280 285

Val Gly Ile Lys Leu Asp Ile Asp Asp Phe Gln Asn Val Ser Asp Arg

290 295 300

Thr Pro Phe Leu Ala Asp Ile Lys Pro Ser Gly Lys Tyr Val Met Glu

305 310 315 320

Asp Val Tyr Lys Ile Gly Gly Ile Pro Lys Ile Leu Ala Phe Leu Leu

 325 330 335

Lys Asn Lys Leu Ile Asp Gly Asn Asn Met Thr Val Thr Gly Arg Thr

 340 345 350

Leu Gly Glu Asn Leu Glu Glu Trp Thr His Arg Tyr Gly Glu Leu Asp

355 360 365

Ser Arg Gln Asp Val Ile Arg Pro Leu Asn Lys Pro Ile Lys Glu Thr

370 375 380

Gly His Ile Arg Ile Leu Lys Gly Asn Leu Ala Pro Gly Gly Ala Val

385 390 395 400

Ala Lys Ile Thr Gly Lys Glu Gly Leu Glu Phe Thr Gly Lys Ala Arg

 405 410 415

Thr Phe Asp Thr Glu Asp Asp Phe Val Lys Ala Val Glu Ser Gly Ser

420 425 430

Ile Lys Lys Gly Glu Lys Thr Val Val Ile Leu Arg Tyr Leu Gly Pro

435 440 445

Gln Gly Gly Pro Gly Met Pro Glu Met Leu Lys Pro Thr Ser Leu Ile

450 455 460

Met Gly Ala Gly Leu Gly Leu Asp Val Ala Cys Leu Thr Asp Gly Arg

465 470 475 480
Phe Ser Gly Gly Ser His Gly Phe Cys Ile Gly His Val Val Pro Glu

 485 490 495
Ala Gln Val Gly Gly Pro Ile Ala Leu Val Arg Asp Gly Asp Thr Ile

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

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

 530 535 540
Ser Gln Gly Thr Leu Tyr Lys Tyr Thr Lys Ser Val Thr Asp Ala Ser

545 550 555 560
His Gly Cys Val Thr Asp Ala

565

<210> 119

<211> 1797

<212> DNA

<213> Coprinopsis cinerea

<400> 119

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cccaaggacc agggagcaag tcaggctatg ctctatgcta cagatggcat aaagtcggac 180

gctgacttca acaagccgat ggtcgggtgc gccagcgtat ggtatgaggg caacccatgc 240

aacaagcacc ttctcggact tggccaggaa atcaaggctt cccttaccga ggcagacatc 300

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ggtcatcatc tcgatggcat ggtagtagtc cctgggtgcg acaagaatat gcctggtgtt 480

ctcatggctc ttggccgtct caaccgacca ggtctcatgg tctacggtgg aaccattcgc 540

gcaggctcgt gtgaaggcat gcctcaattg gatatcgttt ctgctttcca ggcctacgga 600

aaataccttc aagacggaag gacaccaag gctgaggaag aacgatacaa caccgttcga 660

cacgcctgtc ctggtcctgg tgcttgcggt ggcatgtaca ctgcaaacac aatggcaagt 720

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 tacaatacgc ccaaggttgt caccgatgcc agccatgggt gtgtcactga tgcttaa 1797

<210> 120

<211> 598

<212> PRT

<213> Coprinopsis cinerea

<400> 120

Met Pro Pro Lys Tyr Leu Pro Ile Arg Arg Gln Trp Leu Arg Ser Ala

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Arg Gly Leu Ser Thr Thr Ala Arg Cys Ser Asp Lys Pro Val Leu Asn			
20	25	30	
Arg Tyr Ser Arg Ile Ile Thr Gln Pro Lys Asp Gln Gly Ala Ser Gln			
35	40	45	
Ala Met Leu Tyr Ala Thr Asp Gly Ile Lys Ser Asp Ala Asp Phe Asn			
50	55	60	
Lys Pro Met Val Gly Val Ala Ser Val Trp Tyr Glu Gly Asn Pro Cys			

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

 130 135 140
 Asp Gly Met Val Val Val Pro Gly Cys Asp Lys Asn Met Pro Gly Val
 145 150 155 160
 Leu Met Ala Leu Gly Arg Leu Asn Arg Pro Gly Leu Met Val Tyr Gly
 165 170 175
 Gly Thr Ile Arg Ala Gly Ser Cys Glu Gly Met Pro Gln Leu Asp Ile
 180 185 190
 Val Ser Ala Phe Gln Ala Tyr Gly Lys Tyr Leu Gln Asp Gly Arg Thr

 195 200 205
 Pro Lys Ala Glu Glu Glu Arg Tyr Asn Thr Val Arg His Ala Cys Pro
 210 215 220
 Gly Pro Gly Ala Cys Gly Gly Met Tyr Thr Ala Asn Thr Met Ala Ser
 225 230 235 240
 Ala Ala Glu Ala Leu Gly Met Thr Leu Pro Gly Ser Ser Ser Phe Pro
 245 250 255
 Ala Gln Ser Glu Glu Lys His Leu Glu Thr Lys Ser Ile Gly Ser Val

 260 265 270
 Met Tyr Asn Leu Leu Glu Lys Asn Ile Leu Pro Arg Asp Ile Met Thr
 275 280 285
 Arg Ser Ala Phe Glu Asn Ala Met Val Leu Thr Val Ile Leu Gly Gly
 290 295 300
 Ser Thr Asn Ala Val Leu His Leu Ile Ala Ile Ala His Ser Val Gly
 305 310 315 320

Ile Lys Leu Asp Ile Asp Asp Phe Gln Lys Val Ser Asp Arg Ile Pro

325 330 335

Phe Leu Ala Asp Leu Lys Pro Ser Gly Lys Tyr Val Met Glu Asp Val

340 345 350

Tyr Lys Ile Gly Gly Ile Pro Lys Val Leu Ala Phe Leu Leu Lys Asn

355 360 365

Asn Leu Ile Asp Gly Asn Asn Met Thr Val Thr Gly Arg Thr Val Gly

370 375 380

Glu Asn Leu Asp Arg Trp Thr His Lys Tyr Gly Glu Leu His Phe Asp

385 390 395 400

Lys Gln Asp Val Ile Arg Pro Leu Asp Lys Pro Ile Lys Glu Thr Gly

405 410 415

His Ile Arg Ile Leu Lys Gly Asn Leu Ala Pro Gly Gly Ala Val Ala

420 425 430

Lys Ile Thr Gly Lys Glu Gly Leu Gly Phe Val Gly Lys Ala Arg Val

435 440 445

Phe Asp Ser Glu Asn Asp Phe Val Lys Ala Val Glu Ser Gly Ser Ile

450 455 460

Lys Lys Gly Glu Lys Thr Val Val Ile Leu Arg Tyr Leu Gly Pro Gln

465 470 475 480

Gly Gly Pro Gly Met Pro Glu Met Leu Lys Pro Thr Ser Leu Val Met

485 490 495

Gly Ala Gly Leu Gly Met Asp Val Ala Ile Leu Thr Asp Gly Arg Phe

500 505 510

Ser Gly Gly Ser His Gly Phe Cys Ile Gly His Val Val Pro Glu Ala

515 520 525

Gln Val Gly Gly Pro Ile Ala Leu Val Glu Asp Gly Asp Ile Ile Ser

530 535 540

Val Asp Ala Val Lys Asn Thr Ile Glu Leu Gln Val Pro Glu Pro Glu

545 550 555 560

Leu Ala Ala Arg Lys Ala Ala Trp Lys Ala Pro Pro Leu Lys Val Thr

565	570	575
Gln Gly Thr Leu Tyr Lys Tyr Ala Lys Val Val Thr Asp Ala Ser His		
580	585	590
Gly Cys Val Thr Asp Ala		
595		
<210> 121		
<211> 1791		
<212> DNA		
<213> Cryptococcus neoformans		
<400> 121		
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tacgcccag ctgttacga tgcttctcat ggatgtgtca cggatgctta a 1791

<210> 122

<211> 596

<212> PRT

<213> Cryptococcus neoformans

<400> 122

Met Leu Ser Arg Arg Ile Ala Thr Ala Ser Pro Ala Ala His Thr Arg

1 5 10 15

Ala Phe His Ala Ser Ala Ala Lys Ala Ser Lys Glu Val Ile Met Asn

20 25 30

Arg Tyr Ser Arg Thr Ile Thr Gln Pro Lys Ala Gln Gly Ala Ser Gln

35 40 45

Ala Met Leu Tyr Ala Thr Glu Gly Ile Val Asn Asp Glu Asp Phe Asn

50 55 60

Lys Ala Met Val Gly Val Ala Ser Val Trp Tyr Glu Gly Asn Pro Cys

65 70 75 80

Asn Arg His Ile Leu Gly Leu Gly Gln Arg Val Lys Lys Ser Leu Met

85 90 95

Asn Ala Gly Ile Val Gly Tyr Gln Phe Gly Thr Val Gly Val Ser Asp

100 105 110

Gly Ile Ser Met Gly Thr Ser Gly Met Ser Tyr Ser Leu Gln Ser Arg

115 120 125

Asp Leu Ile Ala Asp Ser Val Glu Thr Ala Ala Gly Gly His Trp Leu

130 135 140
 Asp Gly Met Val Val Leu Pro Gly Cys Asp Lys Asn Met Pro Gly Ala
 145 150 155 160
 Leu Ile Ala Leu Gly Arg Leu Asn Arg Pro Ser Met Met Val Tyr Gly
 165 170 175
 Gly Thr Ile Arg Pro Gly Ser Cys Gly Gly Glu Val Leu Asp Ile Val
 180 185 190
 Ser Ala Phe Gln Ser Tyr Gly Arg Tyr Leu Gln Glu Gly Gln Thr Pro

 195 200 205
 Glu Ala Glu Lys Thr Arg Tyr Asn Thr Ile Arg Asn Ala Cys Pro Gly
 210 215 220
 Pro Gly Ala Cys Gly Gly Met Tyr Thr Ala Asn Thr Ile Ala Ser Ala
 225 230 235 240
 Ser Glu Ala Leu Gly Met Thr Leu Pro Gly Ser Ser Ser Phe Pro Ala
 245 250 255
 Glu Tyr Pro Glu Lys His Ala Glu Cys Asp Ala Val Gly Glu Thr Met

 260 265 270
 Arg Lys Val Leu Glu Asp Asn Leu Leu Pro Arg Gln Ile Met Thr Arg
 275 280 285
 Gln Ala Phe Glu Asn Ala Met Ala Leu Thr Met Ala Leu Gly Gly Ser
 290 295 300
 Thr Asn Val Val Leu His Leu Ile Ala Ile Ala Arg Ser Val Gly Ile
 305 310 315 320
 Asn Leu Thr Ile Asp Asp Phe Gln Thr Val Ser Asp Arg Val Pro Leu

 325 330 335
 Leu Ala Asp Leu Lys Pro Ser Gly Lys Tyr Val Met Glu Asp Ile Asn
 340 345 350
 Thr Ile Gly Gly Thr Pro Ser Val Ile His Tyr Leu Ile Lys Asn Gly
 355 360 365
 Ile Met Thr Gly Asp Glu Met Thr Ile Thr Gly Lys Thr Leu Gly Glu
 370 375 380

Asn Cys Asp Arg Trp Val Glu Glu His Gly Ser Lys Trp Glu Gly Gln

385 390 395 400

Lys Ile Leu Arg Pro Ile Asn Asp Pro Leu Lys Ser Thr Gly His Ile

405 410 415

Arg Ile Leu Arg Gly Asn Leu Ala Pro Gly Gly Ala Val Ser Lys Ile

420 425 430

Thr Gly Lys Glu Gly Leu Arg Phe Thr Gly Lys Cys Arg Ala Phe Asp

435 440 445

Asp Glu Glu Gly Phe Val Lys Ala Val Glu Ser Gly Ser Ile Lys Lys

450 455 460

Gly Glu Lys Thr Val Val Val Leu Arg Tyr Leu Gly Pro Lys Gly Gly

465 470 475 480

Pro Gly Met Pro Glu Met Leu Lys Pro Thr Ser Leu Ile Met Gly Ala

485 490 495

Gly Leu Gly Tyr Asp Val Ala Cys Leu Thr Asp Gly Arg Phe Ser Gly

500 505 510

Gly Ser His Gly Phe Val Val Gly His Val Val Pro Glu Ala Gln Val

515 520 525

Gly Gly Pro Ile Ala Leu Val Gln Asp Gly Asp Val Ile His Ile Asp

530 535 540

Ala Val Ala Asn Thr Leu Ser Val Asp Val Ser Asp Glu Glu Met Ala

545 550 555 560

Arg Arg Lys Glu Asn Trp Val Ala Pro Pro Leu Lys Val Thr His Gly

565 570 575

Thr Leu Leu Lys Tyr Ala Arg Ala Val Thr Asp Ala Ser His Gly Cys

580 585 590

Val Thr Asp Ala

595

<210> 123

<211> 1833

<212> DNA

<213> Ustilago maydis

<400> 123

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cgccgcgttc tccacacctc ctacagccgt ctcaacacag agcgcgtcc gccgggcgt	120
ctaaacaagt actcgcgtat catcacccgg cccaaggatc agggagcatc gcaagccatg	180
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<210> 124

<211> 610

<212> PRT

<213> Ustilago maydis

<400> 124

Met Leu Arg Ser Ala Leu Ser Pro Ser Ala Arg Cys Val Leu Arg Gly

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Gly Leu Ala Ser Arg Arg Ala Leu His Thr Ser Ser Ala Ala Leu Asn

20 25 30
Thr Glu Arg Ala Pro Pro Gly Ala Leu Asn Lys Tyr Ser Arg Ile Ile

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

50 55 60
Asp Gly Ile Gln Ser Asp Glu Asp Leu Thr Arg Ala Met Val Gly Ile

65 70 75 80
Gly Ser Ile Trp Tyr Glu Gly Asn Pro Cys Asn Ala His Leu Leu Ala

85 90 95
Ile Ser Gln Arg Val Lys Lys Ser Val Gln Gln Ala Gly Leu Thr Gly

100 105 110
Tyr Gln Phe Gly Ser Val Gly Val Ser Asp Gly Ile Ser Met Gly Thr

115 120 125
Asp Ala Met Ser Tyr Ser Leu Pro Ser Arg Asp Leu Ile Ala Asp Ser

130 135 140
Val Glu Ser Ala Cys Gly Gly His Trp Leu Asp Gly Cys Val Val Ile

145 150 155 160
Pro Gly Cys Asp Lys Asn Met Pro Gly Val Leu Met Ala Leu Gly Arg

165 170 175
Leu Asn Arg Pro Gly Ile Met Leu Tyr Gly Gly Thr Ile Arg Pro Gly

180 185 190

Gly Cys Ala Ser Val Glu Gly Thr Leu Asp Ile Val Ser Ala Phe Gln

195 200 205

Ser Tyr Gly Gln Tyr Leu Ala Asn Gly Gly Ser Pro Ala Ala Glu Lys

210 215 220

Ile Arg Tyr Asp Thr Val Arg Asn Ala Cys Pro Gly Pro Gly Ala Cys

225 230 235 240

Gly Gly Met Tyr Thr Ala Asn Thr Met Ala Ser Cys Ala Glu Ala Leu

245 250 255

Gly Met Thr Leu Pro Gly Ser Ser Ser Phe Pro Ala Glu Tyr Pro Glu

260 265 270

Lys Ile Ala Glu Ala Glu Asn Met Gly Ala Ala Met Arg Leu Val Leu

275 280 285

Glu Lys Asp Ile Lys Pro Arg Asp Ile Met Thr Arg Ser Ala Phe Glu

290 295 300

Asp Ala Ile Ala Leu Thr Met Val Leu Gly Gly Ser Thr Asn Ala Val

305 310 315 320

Leu His Leu Ile Ala Val Ala His Ser Val Gly Ile Glu Leu Ser Ile

325 330 335

Asp Asp Phe Gln Arg Ile Ala Asp Val Thr Pro Phe Leu Ala Asp Leu

340 345 350

Lys Pro Ser Gly Lys Tyr Val Met Glu Asp Val His Ser Lys Leu Gly

355 360 365

Gly Ile Pro Thr Ile Ile Gln Tyr Cys Ile Glu Asn Lys Leu Met Lys

370 375 380

Gly Glu His Met Thr Val Thr Gly Arg Thr Leu Ala Glu Asn Val Asp

385 390 395 400

Arg Trp Thr His Glu Arg Gly Lys Leu Pro Ala Gly Gln Asp Val Leu

405 410 415

Arg Pro Ile Asp Lys Pro Leu Lys Ser Thr Gly His Ile Arg Ile Leu

420 425 430

Lys Gly Asn Leu Ala Pro Gly Gly Ala Val Ala Lys Ile Thr Gly Lys

435 440 445
Glu Gly Leu Arg Phe Thr Gly Lys Ala Arg Val Phe Asp Thr Glu Asp

450 455 460
Ala Met Val Gly Ala Val Glu Lys Gly Glu Ile Lys Lys Gly Glu Lys
465 470 475 480
Thr Val Ile Val Leu Arg Tyr Lys Gly Pro Lys Gly Gly Pro Gly Met
485 490 495
Pro Glu Met Leu Lys Pro Thr Ser Leu Ile Met Gly Ala Gly Leu Gly
500 505 510
Gln Asp Val Ala Cys Leu Thr Asp Gly Arg Phe Ser Gly Gly Ser His

515 520 525
Gly Phe Val Ile Gly His Val Val Pro Glu Ala Gln Val Gly Gly Pro
530 535 540
Ile Gly Leu Val Lys Asp Gly Asp Val Ile Ser Ile Asp Ala Glu Thr
545 550 555 560
Asn Thr Leu Glu Leu Val Gly Val Ser Ala Ala Asp Leu Glu Ser Arg
565 570 575
Arg Glu Ser Trp Lys Pro Leu Pro Leu Lys Pro Lys Ser Gly His Leu

580 585 590
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595 600 605
Asp Met

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<210> 125

<211> 1770

<212> DNA

<213> *Malassezia globosa*

<400> 125

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tatgccacgc acggaatcca gtcagatgag gatttacgac gtgccatggt tggcgtggcc	180

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 <210> 126
 <211> 589
 <212> PRT
 <213> *Malassezia globosa*

<400> 126

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Gln Gly Ala Ser Gln Ala Met Leu Tyr Ala Thr His Gly Ile Gln Ser
           35           40           45
Asp Glu Asp Leu Arg Arg Ala Met Val Gly Val Ala Ser Val Trp Tyr
           50           55           60

Glu Gly Asn Pro Cys Asn Ala His Leu Leu Gly Val Gly Gln Arg Ile
65           70           75           80
Arg Asp Ser Leu Asp Arg Ala Gly Leu Thr Gly Tyr Gln Phe Gly Thr
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Val Gly Val Ser Asp Gly Ile Ser Met Gly Thr Ser Ala Met Ser Tyr
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Ser Leu Pro Ser Arg Asp Leu Ile Ala Asp Ser Val Glu Ser Cys Met
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Gly Gly His Trp Leu Asp Gly Cys Val Val Val Pro Gly Cys Asp Lys
           130          135          140
Asn Met Pro Gly Val Leu Met Ala Leu Gly Arg Leu Asn Arg Pro Gly
145          150          155          160
Ile Met Val Tyr Gly Gly Thr Ile Arg Pro Gly His Cys Gly Ser Ile
           165          170          175
Thr Gly Thr Leu Asp Ile Val Ser Ala Phe Gln Ser Tyr Gly Gln Tyr
           180          185          190

Leu Ala Ser Gly Gly Thr Pro Asp Ala Glu Lys Ile Arg Tyr Asp Thr
           195          200          205
Val Arg His Ala Cys Pro Gly Pro Gly Ala Cys Gly Gly Met Tyr Thr
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Ala Asn Thr Met Ala Ser Cys Ala Glu Val Leu Gly Met Thr Leu Pro
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Gly Ser Ser Ser Phe Pro Ala Glu Tyr Asn Glu Lys Lys Ala Glu Cys

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Pro Arg Asp Ile Met Thr Arg Ser Ala Phe Glu Asp Ala Met Val Leu					
	275		280		285
Thr Met Val Leu Gly Gly Ser Thr Asn Ala Val Leu His Leu Leu Ala					
	290		295		300
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Val Ser Asp Ser Thr Pro Phe Leu Ala Asn Leu Lys Pro Ser Gly Gln					
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Tyr Val Met Glu Asp Val His Thr Val Leu Gly Gly Ile Pro Ser Val					
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Val His Tyr Leu Ile Glu Asn Lys Leu Met Lys Gly Glu His Met Thr					
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Val Thr Gly Arg Thr Leu Arg Glu Asn Cys Glu Gln Trp Val Ala Glu					
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Arg Gly Pro Met Pro Lys Asp Gln Asp Val Leu Arg Pro Ile Asp Lys					
385		390		395	400
Pro Ile Lys Arg Thr Gly His Ile Arg Val Leu Tyr Gly Asn Leu Ala					
	405		410		415
Pro Gly Gly Ala Ile Ala Lys Ile Thr Gly Lys Glu Gly Leu Glu Phe					
	420		425		430
Thr Gly Lys Ala Arg Val Phe Asp Thr Glu Asp Asp Met Val His Ala					
	435		440		445
Val Glu Gln Gly Thr Ile Lys Lys Gly Glu Lys Thr Val Val Ile Leu					
	450		455		460
Arg Tyr Lys Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met Leu Lys					
465		470		475	480
Pro Thr Ser Leu Ile Met Gly Ala Gly Leu Gly His Asp Val Ala Cys					
	485		490		495

Leu Thr Asp Gly Arg Phe Ser Gly Gly Ser His Gly Phe Val Ile Gly
500 505 510

His Val Val Pro Glu Ala Gln Glu Gly Gly Pro Ile Ala Leu Val Arg
515 520 525

Asp Gly Asp Glu Ile Thr Ile Asp Ala Val Asn Asn Ser Ile Gln Ile
530 535 540

Asn Asn Val Ser Asp Glu Glu Leu Ala Gln Arg Arg Ala Ala Trp Gln
545 550 555 560

Pro Arg Pro Leu Thr Val Asn Gln Gly Gly Leu Tyr Lys Tyr Thr Arg
565 570 575

Leu Val Ser Asn Ala Ser Gln Gly Cys Val Thr Asp Ala
580 585

<210> 127

<211> 1824

<212> DNA

<213> *Aspergillus clavatus*

<400> 127

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<210> 128

<211> 607

<212> PRT

<213> Aspergillus clavatus

<400> 128

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Asp	Ala	Lys	His
Asp	Asp	Gly	Thr
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Leu	Ala	Leu	Asn
Arg	Tyr	Ser	Ser
Tyr	Ile	Thr	Arg
Gly	His	Asp	Phe
35	40	45	
Pro	Gly	Ala	Arg
Ala	Met	Leu	Phe
Ala	Ala	Gly	Ile
Pro	Asp	Arg	Asp
50	55	60	
Ala	Met	Thr	Lys
Ser	Pro	Gln	Val
Gly	Val	Ala	Ser
Val	Trp	Trp	Glu

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Gly	Asn	Pro	Cys	Asn	Met	His	Leu	Leu	Asp	Leu	Gly	Lys	Thr	Val	Lys
85				90				95							
Lys	Ala	Val	Thr	Glu	Gln	Gly	Met	Ile	Gly	Trp	Gln	Tyr	Asn	Thr	Ile
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Gly	Val	Ser	Asp	Gly	Ile	Thr	Met	Gly	Ser	Asp	Gly	Met	Arg	Phe	Ser
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Leu	Gln	Thr	Arg	Glu	Ile	Ile	Ala	Asp	Ser	Val	Glu	Thr	Val	Thr	Cys
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Met	Ile	Tyr	Gly	Gly	Thr	Ile	Gln	Ile	Gly	Tyr	Ser	Asn	Leu	Leu	Arg
180				185				190							
Lys	Pro	Ile	Asn	Val	Ser	Ser	Cys	Phe	Glu	Ala	Ala	Gly	Ala	Tyr	Ala
195				200				205							
Tyr	Asp	Thr	Leu	Arg	Gln	Pro	Asp	Asp	Gly	Gly	Asp	Thr	Ser	Lys	Thr
210				215				220							
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225				230				235				240			
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245				250				255							
Glu	Ser	Met	Gly	Leu	Ser	Leu	Pro	Gly	Ser	Ser	Ser	Thr	Pro	Ala	Ser
260				265				270							
Ser	Pro	Ser	Lys	Met	Arg	Glu	Cys	Val	Lys	Ala	Ala	Glu	Ala	Ile	Lys
275				280				285							
Val	Cys	Met	Glu	Lys	Asn	Ile	Lys	Pro	Arg	Asp	Leu	Leu	Thr	Lys	Arg
290				295				300							
Ser	Phe	Glu	Asn	Ala	Leu	Val	Met	Thr	Met	Ala	Leu	Gly	Gly	Ser	Thr
305				310				315				320			

Asn Gly Val Leu His Phe Leu Ala Met Ala Arg Thr Ala Glu Val Asp

325 330 335

Leu Thr Leu Asp Asp Ile Gln Arg Val Ser Asn Lys Ile Pro Phe Ile

340 345 350

Ala Asp Leu Ala Pro Ser Gly Lys Tyr Tyr Met Ala Asp Leu Tyr Asp

355 360 365

Ile Gly Gly Ile Pro Ser Val Gln Lys Leu Leu Ile Ala Ala Gly Leu

370 375 380

Leu Asp Gly Asp Ile Pro Thr Val Thr Gly Lys Thr Leu Ala Glu Asn

385 390 395 400

Val Ala Ser Phe Pro Ser Leu Pro Gln Asp Gln Val Ile Ile Arg Pro

405 410 415

Leu Asp Lys Pro Ile Lys Ala Thr Gly His Leu Gln Ile Leu Arg Gly

420 425 430

Asn Leu Ala Pro Gly Gly Ala Val Ala Lys Ile Thr Gly Lys Glu Gly

435 440 445

Thr Lys Phe Thr Gly Lys Ala Arg Val Phe Asn Lys Glu His Gln Leu

450 455 460

Asn Asp Ala Val Thr Gln Gly Lys Ile Pro Arg Gly Glu Asn Leu Val

465 470 475 480

Leu Ile Val Arg Tyr Glu Gly Pro Lys Gly Gly Pro Gly Met Pro Glu

485 490 495

Gln Leu Lys Ala Ser Ala Ala Leu Met Gly Ala Lys Leu Asn Asn Val

500 505 510

Ala Leu Ile Thr Asp Gly Arg Tyr Ser Gly Ala Ser His Gly Phe Ile

515 520 525

Val Gly His Ile Val Pro Glu Ala Ala Val Gly Gly Pro Ile Ala Val

530 535 540

Val Arg Asp Gly Asp Val Ile Thr Ile Asp Ala Glu Thr Asn Thr Ile

545 550 555 560

Ser Met Asp Val Ser Asp Glu Glu Ile Arg Gln Arg Leu Lys Glu Trp

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595	600	605
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<212> DNA		
<213> Neosartorya fischeri		
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<210> 130

<211> 608

<212> PRT

<213> Neosartorya fischeri

<400> 130

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20 25 30

Thr Pro Ala Leu Asn Arg Tyr Ser Ser Tyr Ile Thr Arg Ser His Asp

35 40 45

Phe Pro Gly Ala Arg Ala Met Leu Phe Ala Ala Gly Ile Pro Asp Arg

50 55 60

Glu Ala Met Ala Lys Ser Pro Gln Val Gly Ile Ala Ser Val Trp Trp

65 70 75 80

Glu Gly Asn Pro Cys Asn Met His Leu Leu Asp Leu Gly Lys Thr Val

85 90 95

Lys Lys Ala Val Thr Asp Gln Gly Met Thr Gly Trp Gln Tyr Asn Thr

100 105 110

Ile Gly Val Ser Asp Ala Ile Ser Met Gly Ser Glu Gly Met Arg Phe

115 120 125

Ser Leu Gln Ser Arg Glu Ile Ile Ala Asp Ser Val Glu Thr Val Thr
130 135 140

Cys Ala Gln Tyr His Asp Ala Cys Ile Ala Ile Pro Gly Cys Asp Lys
145 150 155 160

Asn Met Pro Gly Val Val Met Gly Met Ala Arg His Asn Arg Pro Ser
165 170 175

Leu Met Ile Tyr Gly Gly Thr Ile Gln Ile Gly Tyr Ser Asn Leu Leu
180 185 190

Arg Lys Arg Val Asn Val Ser Thr Cys Phe Glu Ala Ala Gly Ala Tyr
195 200 205

Ala Tyr Asp Thr Leu Arg Gln Pro Asp Asp Gly Gly Asp Thr Ser Lys
210 215 220

Ser Lys Asp Glu Ile Met Asp Asp Ile Glu Arg His Ala Cys Pro Ser
225 230 235 240

Ala Gly Ala Cys Gly Gly Met Phe Thr Ala Asn Thr Met Ala Thr Ala
245 250 255

Ile Glu Ser Met Gly Leu Ser Leu Pro Gly Ser Ser Ser Thr Pro Ala
260 265 270

Ser Ser Pro Ser Lys Met Arg Glu Cys Val Lys Ala Ala Glu Ala Ile
275 280 285

Lys Ile Cys Met Glu Lys Asn Ile Lys Pro Arg Asp Leu Leu Thr Lys
290 295 300

Arg Ser Phe Glu Asn Ala Leu Val Met Thr Met Ala Leu Gly Gly Ser
305 310 315 320

Thr Asn Gly Val Leu His Phe Leu Ala Met Ala Arg Thr Ala Asp Val
325 330 335

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

Ile Ala Asp Leu Ala Pro Ser Gly Lys Tyr Tyr Met Ala Asp Leu Tyr
355 360 365

Asp Ile Gly Gly Ile Pro Ser Val Gln Lys Leu Leu Ile Ala Ala Gly

370

375

380

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

385 390 395 400

Asn Val Ala Ser Phe Pro Ser Leu Pro Gln Asp Gln Val Ile Ile Arg

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Pro Leu Asp Asn Pro Ile Lys Thr Thr Gly His Leu Gln Ile Leu Arg

420 425 430

Gly Asn Leu Ala Pro Gly Gly Ala Val Ala Lys Ile Thr Gly Lys Glu

435 440 445

Gly Thr Lys Phe Thr Gly Lys Ala Arg Val Phe Asn Lys Glu Phe Gln

450 455 460

Leu Asn Asp Ala Leu Thr Gln Gly Lys Ile Pro Arg Gly Glu Asn Leu

465 470 475 480

Val Leu Ile Val Arg Tyr Glu Gly Pro Lys Gly Gly Pro Gly Met Pro

485 490 495

Glu Gln Leu Lys Ala Ser Ala Ala Leu Met Gly Ala Lys Leu Asn Asn

500 505 510

Val Ala Leu Ile Thr Asp Gly Arg Tyr Ser Gly Ala Ser His Gly Phe

515 520 525

Ile Val Gly His Ile Val Pro Glu Ala Ala Ala Gly Gly Pro Ile Ala

530 535 540

Ile Val Arg Asp Asp Asp Val Ile Thr Ile Asp Ala Glu Thr Asn Thr

545 550 555 560

Ile Asn Met His Val Ser Asp Glu Glu Ile Gln Gln Arg Leu Lys Glu

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Trp Lys Pro Pro Val Pro His Val Thr Arg Gly Val Leu Ala Lys Tyr

580 585 590

Ala Arg Leu Val Gly Asp Ala Ser His Gly Ala Met Thr Asp Leu Phe

595 600 605

<210> 131

<211> 1827

<212> DNA

<213> *Aspergillus oryzae*

<400> 131

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accaacggtg tgctccactt ccttgccatg gctcggacag ctggcgtgga acttacttta	1020
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aaatactaca tggcggactt gtacgatatt ggcgggggtac cgtctgtcca aaagctgttg	1140
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aacgtggcat cattcccatc gttaccggac gatcaggtta ttattcgtcc tttggacaac	1260
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gtggccaaga tcaccggcaa ggagggcact aaatttatag gaaaggcacg agtgtttgat	1380
aaggagtatc aactcaatga tgactcaac cagggtaaaa taccgcgaga tgagaattta	1440
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gccagcgagg cattgatggg agccaagctt accaacgtgg cactgatcac tgatggaaga	1560
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cacggcgcaa tgacggacct tttctag 1827

<210> 132

<211> 608

<212> PRT

<213> Aspergillus oryzae

<400> 132

Met Asp Pro Ser Asn Pro Ala Val Ser Ala Thr Phe Gly Glu Ala Lys

1 5 10 15

Tyr Ile Glu Phe Pro Cys Leu Pro Glu Gly Thr Lys His Glu Asp Gly

20 25 30

Thr Pro Ala Leu Asn Arg Tyr Ser Ala Thr Ile Thr Arg Gly His Asp

35 40 45

Phe Pro Gly Ala Lys Ala Met Leu Tyr Ala Ala Gly Val Pro Asp Gln

50 55 60

Asn Ala Met Ala Lys Ser Pro Gln Val Gly Val Ala Ser Val Trp Trp

65 70 75 80

Glu Gly Asn Pro Cys Asn Met His Leu Leu Asp Met Gly Lys Thr Val

85 90 95

Lys Lys Ala Val Glu Gly Gln Gly Met Ile Gly Trp Gln Tyr Asn Thr

100 105 110

Ile Gly Val Ser Asp Ala Ile Thr Met Gly Ser Glu Gly Met Arg Phe

115 120 125

Ser Leu Gln Thr Arg Glu Ile Ile Ala Asp Ser Val Glu Thr Val Thr

130 135 140

Cys Ala Gln Tyr His Asp Ala Cys Ile Ala Ile Pro Gly Cys Asp Lys

145 150 155 160

Asn Met Pro Gly Val Val Met Gly Met Ala Arg His Asn Arg Pro Ser

165 170 175

Ile Met Ile Tyr Gly Gly Thr Ile Gln Ile Gly Tyr Ser Asn Leu Leu

180 185 190
 Arg Lys Pro Ile Asn Val Ser Ser Cys Phe Glu Ala Ala Gly Ala Tyr
 195 200 205
 Ser Tyr Asp Thr Leu Arg Gln Pro Asp Asp Gly Gly Asp Thr Ser Lys
 210 215 220
 Thr Lys Asp Glu Ile Met Asp Asp Leu Glu Arg His Ala Cys Pro Ser
 225 230 235 240
 Ala Gly Ala Cys Gly Gly Met Phe Thr Ala Asn Thr Met Ala Thr Ala

 245 250 255
 Ile Glu Ser Met Gly Leu Ser Leu Pro Gly Ser Ser Ser Thr Pro Ala
 260 265 270
 Thr Ser Pro Ser Lys Met Arg Glu Cys Val Lys Val Ala Glu Ala Ile
 275 280 285
 Lys Val Cys Met Glu Lys Asn Ile Arg Pro Arg Asp Leu Leu Thr Lys
 290 295 300
 Arg Ser Phe Glu Asn Ala Leu Val Met Thr Met Ala Leu Gly Gly Ser

 305 310 315 320
 Thr Asn Gly Val Leu His Phe Leu Ala Met Ala Arg Thr Ala Gly Val
 325 330 335
 Glu Leu Thr Leu Asp Asp Ile Gln Arg Val Ser Asn Lys Ile Pro Phe
 340 345 350
 Ile Ala Asp Leu Ser Pro Ser Gly Lys Tyr Tyr Met Ala Asp Leu Tyr
 355 360 365
 Asp Ile Gly Gly Val Pro Ser Val Gln Lys Leu Leu Ile Ala Gly Gly

 370 375 380
 Leu Leu Asp Gly Asp Ile Pro Thr Val Thr Gly Lys Thr Leu Ala Glu
 385 390 395 400
 Asn Val Ala Ser Phe Pro Ser Leu Pro Asp Asp Gln Val Ile Ile Arg
 405 410 415
 Pro Leu Asp Asn Pro Ile Lys Ala Thr Gly His Leu Gln Ile Leu Arg
 420 425 430

Gly Asn Leu Ala Pro Gly Gly Ala Val Ala Lys Ile Thr Gly Lys Glu

435 440 445

Gly Thr Lys Phe Ile Gly Lys Ala Arg Val Phe Asp Lys Glu Tyr Gln

450 455 460

Leu Asn Asp Ala Leu Asn Gln Gly Lys Ile Pro Arg Asp Glu Asn Leu

465 470 475 480

Val Ile Ile Val Arg Tyr Glu Gly Pro Lys Gly Gly Pro Gly Met Pro

485 490 495

Glu Gln Leu Lys Ala Ser Ala Ala Leu Met Gly Ala Lys Leu Thr Asn

500 505 510

Val Ala Leu Ile Thr Asp Gly Arg Tyr Ser Gly Ala Ser His Gly Phe

515 520 525

Ile Val Gly His Ile Val Pro Glu Ala Ala Val Gly Gly Pro Ile Ala

530 535 540

Val Val Arg Asp Gly Asp Val Val Thr Ile Asn Ala Glu Thr Asn Glu

545 550 555 560

Ile Ser Met Asp Val Ser Asp Glu Glu Ile Gln Gln Arg Leu Arg Glu

565 570 575

Trp Gln Pro Pro Ala Pro His Val Thr Arg Gly Val Leu Ala Lys Tyr

580 585 590

Ala Arg Leu Val Gly Asp Ala Ser His Gly Ala Met Thr Asp Leu Phe

595 600 605

<210> 133

<211> 1827

<212> DNA

<213> Aspergillus niger

<400> 133

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tctactatca ccaggggcca tgagttccct ggcgcggaagg ctatgctcta cgcggcaggc 180

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gaaggcaacc ctigcaacat gcacttggtg gacctggcca agacggtgaa gaaggcgatc 300
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gagtctgtaa cgigcgctca ataccatgac gcctgcattg ccatccccgg atgcgacaag 480
aacatgcctg gtgtggtgat gggatatggcg agacacaatc ggccctcgat catgctctac 540

ggtggtacta tcgaggttgg gtattcccag cttcttcgga agcgggtaag cgtttcgacg 600
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gataccagca agaccaagga cgagatcatg gatgatctgg agaggcatgc ctgcccgagc 720
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aacggagcca tgacggatct attttag 1827

<210> 134
<211> 608
<212> PRT
<213> Aspergillus niger

<400> 134

Met Asp Pro Ala Lys Pro Ala Val Ser Ser Thr Leu Gly Glu Ala Lys

1 5 10 15

Tyr Leu Glu Phe Pro Cys Val Pro Glu Gly Thr Lys His Glu Asp Gly

20 25 30

Thr Pro Val Leu Asn Arg Trp Ser Ser Thr Ile Thr Arg Gly His Glu

35 40 45

Phe Pro Gly Ala Lys Ala Met Leu Tyr Ala Ala Gly Ile Pro Asp His

50 55 60

Asn Ala Met Thr Lys Ser Pro Gln Val Gly Val Ala Ser Val Trp Trp

65 70 75 80

Glu Gly Asn Pro Cys Asn Met His Leu Leu Asp Leu Ala Lys Thr Val

85 90 95

Lys Lys Ala Ile Thr Asp Gln Gly Met Ile Gly Trp Gln Tyr Asn Thr

100 105 110

Ile Gly Val Ser Asp Ala Ile Gly Met Gly Ser Glu Gly Met Arg Phe

115 120 125

Ser Leu Gln Thr Arg Glu Ile Ile Ala Asp Ser Val Glu Ser Val Thr

130 135 140

Cys Ala Gln Tyr His Asp Ala Cys Ile Ala Ile Pro Gly Cys Asp Lys

145 150 155 160

Asn Met Pro Gly Val Val Met Gly Met Ala Arg His Asn Arg Pro Ser

165 170 175

Ile Met Leu Tyr Gly Gly Thr Ile Glu Val Gly Tyr Ser Gln Leu Leu

180 185 190

Arg Lys Arg Val Ser Val Ser Thr Cys Phe Glu Ala Ala Gly Ala Tyr

195 200 205

Thr Tyr Asn Thr Leu Arg Gln Pro Asp Asp Gly Gly Asp Thr Ser Lys

210 215 220

Thr Lys Asp Glu Ile Met Asp Asp Leu Glu Arg His Ala Cys Pro Ser

225 230 235 240

Ala Gly Ala Cys Gly Gly Met Phe Thr Ala Asn Thr Met Ala Thr Ala
245 250 255

Ile Glu Ser Met Gly Leu Ser Leu Pro Gly Ser Ser Ser Thr Pro Ala
260 265 270

Ser Ser Pro Thr Lys Met Arg Glu Cys Val Lys Ala Ala Glu Ala Ile
275 280 285

Lys Ile Cys Met Glu Lys Asn Ile Arg Pro Arg Asp Leu Leu Thr Lys
290 295 300

Arg Ala Phe Glu Asn Ala Leu Val Met Thr Met Ala Leu Gly Gly Ser
305 310 315 320

Thr Asn Gly Val Leu His Phe Leu Ala Met Ala Arg Thr Ala Gly Val
325 330 335

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

Ile Ala Asp Leu Ser Pro Ser Gly Lys Tyr Tyr Met Ala Asp Leu Tyr
355 360 365

Glu Val Gly Gly Ile Pro Ser Val Gln Lys Leu Leu Ile Ala Ala Gly
370 375 380

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

Asn Val Ala Ser His Pro Ser Leu Ser Ala Asp Gln Val Ile Ile Arg
405 410 415

Pro Leu Asp Asn Pro Ile Lys Ala Thr Gly His Leu Gln Ile Leu Arg
420 425 430

Gly Asn Leu Ala Pro Gly Gly Ala Val Ala Lys Ile Thr Gly Lys Glu
435 440 445

Gly Leu Arg Phe Thr Gly Lys Ala Arg Val Phe Asp Lys Glu His Gln
450 455 460

Leu Asn Glu Ala Leu Asn Gln Gly Lys Ile Pro His Gly Glu Asn Leu
465 470 475 480

Val Ile Val Val Arg Tyr Glu Gly Pro Lys Gly Gly Pro Gly Met Pro

485	490	495
Glu Gln Leu Lys Ala Ser Ala Ala Leu Met Gly Ala Lys Leu Thr Asn		
500	505	510
Val Ala Leu Ile Thr Asp Gly Arg Tyr Ser Gly Ala Ser His Gly Phe		
515	520	525
Ile Val Gly His Ile Val Pro Glu Ala Ala Val Gly Gly Pro Ile Ala		
530	535	540
Val Val Arg Asp Gly Asp Val Ile Thr Ile Asp Ala Glu Ser Asn Ala		
545	550	555
		560
Ile Thr Met Asp Val Ser Asp Glu Glu Val Gln Gln Arg Leu Arg Glu		
565	570	575
Trp Lys Pro Pro Ala Pro His Val Thr Arg Gly Val Leu Ala Lys Tyr		
580	585	590
Ala Arg Leu Val Gly Asp Ala Ser Asn Gly Ala Met Thr Asp Leu Phe		
595	600	605
<210> 135		
<211> 1773		
<212> DNA		
<213> Aspergillus terreus		
<400> 135		
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tgctttgagg cggcggggcg cttatgcctac gacacgtgc ggacgcccga cgacggcggc	660	

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ccccagcac ctcatgtcac gcggggcgtg ttggccaagt atgcccgtt ggtgggagat 1740

gcttcgcacg gtgcatgac cgacctgtt tag 1773

<210> 136

<211> 590

<212> PRT

<213> Aspergillus terreus

<400> 136

Met Asp Pro Ser Thr Pro Ala Val Ser Ser Thr Met Gly Glu Ala Lys

1 5 10 15

Tyr Ile Glu Phe Pro Ser Leu Pro Asp Asp Ala Lys His Pro Asp Gly

20 25 30

Thr Pro Ala Leu Asn Arg Tyr Ser Thr Thr Ile Thr Arg Gly His Asp

35 40 45

Phe Pro Gly Ala Lys Ala Met Leu Tyr Ala Ala Gly Ile Pro Asp Gln

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

 Ile Gly Val Ser Asp Ala Ile Thr Met Gly Ser Glu Gly Met Arg Phe
 115 120 125
 Ser Leu Gln Ser Arg Glu Ile Ile Ala Asp Ser Val Glu Thr Val Thr
 130 135 140
 Cys Ala Gln Tyr His Asp Ala Cys Ile Ala Ile Pro Gly Cys Asp Lys
 145 150 155 160
 Asn Met Pro Gly Val Val Met Gly Met Ala Arg His Asn Arg Pro Ser
 165 170 175

 Ile Met Ile Tyr Gly Gly Thr Ile Gln Ile Gly Tyr Ser Asn Leu Leu
 180 185 190
 Arg Lys Pro Ile Asn Val Ser Thr Cys Phe Glu Ala Ala Gly Ala Tyr
 195 200 205
 Ala Tyr Asp Thr Leu Arg Gln Pro Asp Asp Gly Gly Asp Thr Ser Lys
 210 215 220
 Thr Lys Asp Glu Ile Met Asp Glu Leu Glu Gln His Ala Cys Pro Ser
 225 230 235 240

 Ala Gly Ala Cys Gly Gly Met Phe Thr Ala Asn Thr Met Ala Thr Ala
 245 250 255
 Ile Glu Ser Met Gly Leu Ser Leu Pro Gly Ser Ser Ser Thr Pro Ala
 260 265 270
 Ser Ser Pro Ala Lys Met Arg Glu Cys Ala Lys Ala Ala Asp Ala Ile
 275 280 285
 Lys Arg Cys Leu Ala Leu Asn Leu Arg Pro Arg Asp Leu Leu Thr Lys
 290 295 300

Arg Ala Gly Arg Pro Pro Gly Gly Gly Pro Pro Pro Leu Arg Asp Ile
 305 310 315 320
 Pro Gly Gly Glu Ala Thr Ala Phe Pro Ser Leu Ala Thr Phe Trp Pro
 325 330 335
 Lys Gly Gln Ser Tyr Ser Met Gly Arg Ser Val Arg Arg Phe Gly Gly
 340 345 350
 Val Arg Ser Val Gln Glu Val Val Tyr Ser Gln Pro Ala Cys Leu Thr
 355 360 365

 Ala Pro Ser Pro Arg Ser Arg Ala Arg Pro Leu Ala Gly Glu Arg Gly
 370 375 380
 Leu Gly Gly Arg Pro Cys Pro Pro Thr Gln Val Ile Ile Arg Pro Leu
 385 390 395 400
 Asp Asn Pro Ile Lys Pro Thr Ser His Leu Gln Ile Leu Arg Gly Asn
 405 410 415
 Leu Ala Pro Gly Gly Ala Val Ala Lys Ile Thr Gly Lys Glu Gly Thr
 420 425 430

 Arg Phe Ser Gly Lys Ala Leu Val Phe Asp Lys Glu Tyr Gln Leu Asn
 435 440 445
 Asp Ala Leu Asn Gln Gly Gln Ile Pro Arg Gly Glu Asn Ile Val Ile
 450 455 460
 Val Val Arg Tyr Glu Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Gln
 465 470 475 480
 Leu Lys Ala Ser Ala Ala Leu Met Gly Ala Lys Leu Thr Asn Val Ala
 485 490 495

 Leu Ile Thr Asp Gly Arg Tyr Ser Gly Ala Ser His Gly Phe Ile Val
 500 505 510
 Gly His Ile Val Pro Glu Ala Ala Val Gly Gly Pro Ile Ala Val Val
 515 520 525
 Arg Ser Gly Asp Val Ile Thr Ile Asn Ala Glu Thr Asn Glu Ile Thr
 530 535 540
 Met Asp Val Ser Asp Glu Glu Ile Gln Gln Arg Leu Lys Glu Trp Lys

545	550	555	560
Pro Pro Ala Pro His Val Thr Arg Gly Val Leu Ala Lys Tyr Ala Arg			
	565	570	575
Leu Val Gly Asp Ala Ser His Gly Ala Met Thr Asp Leu Phe			
	580	585	590
<210> 137			
<211> 1827			
<212> DNA			
<213> <i>Coccidioides immitis</i>			
<400> 137			
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aatggtgcta tgactgacca gtttttag 1827

<210> 138

<211> 608

<212> PRT

<213> *Coccidioides immitis*

<400> 138

Met Ala Ser Gln Ala Pro Ile Ala Gln Asp Gly Pro Asn Glu Glu Ala

1 5 10 15

Lys Tyr Ile Asp Phe Pro Cys Leu Pro Asp Asp Ala Met Arg Asp Gly

20 25 30

Lys Pro Ala Leu Asn Lys Tyr Ser Gln Phe Ile Thr Lys Gly His Asp

35 40 45

Tyr Pro Gly Ala Gln Ala Met Leu Tyr Ala Ala Gly Val Pro Asp Arg

50 55 60

Asp Ala Met Lys Thr Ser Pro His Val Gly Ile Ala Ser Val Trp Trp

65 70 75 80

Glu Gly Asn Pro Cys Asn Met His Leu Leu Asp Leu Gly Lys Thr Val

85 90 95

Lys Lys Ala Val Ile Asp Gln Gly Met Leu Gly Trp Gln Tyr Asn Thr

100 105 110

Ile Gly Val Ser Asp Ala Ile Thr Met Gly His Glu Gly Met Arg Phe

115 120 125

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

370 375 380
 Leu Leu Asp Gly Gly Ile Pro Thr Val Thr Gly Lys Thr Leu Ala Glu
 385 390 395 400
 Asn Ile Ala Ser Phe Pro Ser Leu Pro Gln Asp Gln Ala Ile Ile His
 405 410 415
 Pro Leu Asp Asn Pro Ile Lys Ser Thr Gly His Leu Gln Val Leu Arg
 420 425 430
 Gly Asn Leu Ala Pro Gly Gly Ala Val Ala Lys Ile Thr Gly Lys Glu

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

 500 505 510
 Val Ala Leu Ile Thr Asp Gly Arg Tyr Ser Gly Ala Ser His Gly Phe
 515 520 525
 Ile Val Gly His Ile Val Pro Glu Ala Ala Val Gly Gly Pro Ile Ala
 530 535 540
 Val Val Gln Asp Gly Asp Thr Ile Thr Ile Asn Ala Asp Thr Asn Glu
 545 550 555 560
 Leu Thr Met Asp Val Ser Asp Glu Glu Ile Ala Gln Arg Leu Lys Gly

 565 570 575
 Trp Lys Pro Pro Lys Pro Arg Val Thr Arg Gly Val Leu Ala Lys Tyr
 580 585 590
 Ala Lys Leu Val Gly Asp Ala Ser Asn Gly Ala Met Thr Asp Gln Phe
 595 600 605
 <210> 139
 <211> 1788
 <212> DNA

<213> Paracoccidioides brasiliensis

<400> 139

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acagcgatgt tatatggcgc ggggtgccc gatcgtgaga gcatgaaaaa tagccccag	180
gtcggcattg cgacggtatg gtggaaggg aatgcctgta atatgcacct ttggatctg	240
gggaagacgg tcaaaaaagc catcacgat caggggatgc tgggctggca atataacacc	300
atcgggtgtc ccgatgctat ttccatgggt agtgaagta tgcgatactc cctccaatct	360
cgggagatca ttgcagacag catcgagaca gtagtaggtg ctcaatatca tgatgctgca	420
ttgcgattcc gtgcgacaa gaacatgcc ggctgcgtca tgggtatggc cagacataac	480
agaccgtctt tgatgatata cgggtgggaca attcaggtcg ggtactccaa gttactccgc	540
aggcgaatca acgtctctac ttgctacgaa gcagctggcg cgtacgtta caacacctta	600
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gctaccgca ttgagtcaat gggtttgact ctgccaggct cctcgtccac ccagctacg	780
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aagaacatta ggccgcgaga tctacttacg aaacgtcct ttgagaatgc gctggaata	900
accatggcgc tggcggggag cacgaacagc atcggtcacc tgatagcgat ggccagaacg	960
gccccggttg aattaacact cgatgattcc cagcgtgtga gcgacaaaat cccgtttatt	1020
gttgacttgg caccagttgg gaaatactac atggcagacc ttatgaaat tggcgggatt	1080
ccatctgtgc agaagctgtt gattgccgca ggcttgatgg acggtgacat cccacagta	1140
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gcgctaatta cggacgggag gtattcgggg gccagtcag ggtttattgt cgggcatatt	1560
gtgcctgagg cggcggttgg ggggcccatt gctgttgtgc acaatgggga tatgattacg	1620
attgatgcgg agagaaatga gattagtatg gcggtttcgg aggaggaggt tgcggagagg	1680
ttgaaggagt ggaggccgcc gaagccgcat gtgactaggg ggacgttggc caagtatgcg	1740

agacttggtg gagacgcgtc gcatggggct atgacggata tgttttga

1788

<210> 140

<211> 595

<212> PRT

<213> Paracoccidioides brasiliensis

<400> 140

Met Asn Pro Glu Glu Lys Val Asp Gly Phe Glu Glu Pro Arg Tyr Ile

1 5 10 15

Gln Phe Pro Cys Leu Pro Asp Asp Ala Thr Arg Asp Gly Lys Pro Val

20 25 30

Leu Asn Lys Tyr Ser Thr Phe Leu Thr Ala Met Leu Tyr Gly Ala Gly

35 40 45

Val Pro Asp Arg Glu Ser Met Lys Asn Ser Pro Gln Val Gly Ile Ala

50 55 60

Thr Val Trp Trp Glu Gly Asn Ala Cys Asn Met His Leu Leu Asp Leu

65 70 75 80

Gly Lys Thr Val Lys Lys Ala Ile Thr Asp Gln Gly Met Leu Gly Trp

85 90 95

Gln Tyr Asn Thr Ile Gly Val Ser Asp Ala Ile Ser Met Gly Ser Glu

100 105 110

Gly Met Arg Tyr Ser Leu Gln Ser Arg Glu Ile Ile Ala Asp Ser Ile

115 120 125

Glu Thr Val Val Gly Ala Gln Tyr His Asp Ala Ala Leu Arg Phe Arg

130 135 140

Cys Asp Lys Asn Met Pro Gly Cys Val Met Gly Met Ala Arg His Asn

145 150 155 160

Arg Pro Ser Leu Met Ile Tyr Gly Gly Thr Ile Gln Val Gly Tyr Ser

165 170 175

Lys Leu Leu Arg Arg Arg Ile Asn Val Ser Thr Cys Tyr Glu Ala Ala

180 185 190

Gly Ala Tyr Ala Tyr Asn Thr Leu Thr Gln Pro Asp Asp Gly Gly Asp

195 200 205
 Arg Ser Arg Thr Lys Asp Glu Ile Met Glu Asp Ile Glu Arg Asn Ala
 210 215 220
 Cys Pro Ser Ala Gly Ala Cys Ala Gly Met Tyr Thr Ala Asn Thr Leu
 225 230 235 240
 Ala Thr Ala Ile Glu Ser Met Gly Leu Thr Leu Pro Gly Ser Ser Ser

 245 250 255
 Thr Pro Ala Thr Val Pro Ala Lys Met Arg Glu Cys Val Lys Ala Ala
 260 265 270
 Asp Ala Ile Arg Ile Cys Met Glu Lys Asn Ile Arg Pro Arg Asp Leu
 275 280 285
 Leu Thr Lys Arg Ser Phe Glu Asn Ala Leu Val Ile Thr Met Ala Leu
 290 295 300
 Gly Gly Ser Thr Asn Ser Ile Val His Leu Ile Ala Met Ala Arg Thr

 305 310 315 320
 Ala Arg Val Glu Leu Thr Leu Asp Asp Ser Gln Arg Val Ser Asp Lys
 325 330 335
 Ile Pro Phe Ile Val Asp Leu Ala Pro Ser Gly Lys Tyr Tyr Met Ala
 340 345 350
 Asp Leu Tyr Glu Ile Gly Gly Ile Pro Ser Val Gln Lys Leu Leu Ile
 355 360 365
 Ala Ala Gly Leu Met Asp Gly Asp Ile Pro Thr Val Thr Gly Lys Thr

 370 375 380
 Leu Ala Glu Asn Ile Gln Ser Phe Pro Ser Leu Pro Gln Asp Gln Ala
 385 390 395 400
 Ile Ile His Pro Leu Ala Asn Pro Ile Lys Ser Thr Gly His Ile Gln
 405 410 415
 Ile Leu Lys Gly Asn Leu Ala Pro Gly Gly Ala Val Ala Lys Ile Thr
 420 425 430
 Gly Lys Glu Gly Thr Lys Phe Thr Gly Lys Ala Leu Val Phe Asn Lys

 435 440 445

Glu His Glu Leu Asp Glu Ala Leu Asn Lys Gly Leu Ile Pro Arg Gly
 450 455 460
 Glu Asn Leu Val Leu Ile Val Arg Tyr Glu Gly Pro Lys Gly Gly Pro
 465 470 475 480
 Gly Met Pro Glu Gln Leu Lys Ala Ser Ala Ala Leu Met Gly Ala Lys
 485 490 495
 Leu Thr Asn Val Ala Leu Ile Thr Asp Gly Arg Tyr Ser Gly Ala Ser

500 505 510
 His Gly Phe Ile Val Gly His Ile Val Pro Glu Ala Ala Val Gly Gly
 515 520 525
 Pro Ile Ala Val Val His Asn Gly Asp Met Ile Thr Ile Asp Ala Glu
 530 535 540
 Arg Asn Glu Ile Ser Met Ala Val Ser Glu Glu Glu Val Ala Glu Arg
 545 550 555 560
 Leu Lys Glu Trp Arg Pro Pro Lys Pro His Val Thr Arg Gly Thr Leu

565 570 575
 Ala Lys Tyr Ala Arg Leu Val Gly Asp Ala Ser His Gly Ala Met Thr
 580 585 590

Asp Met Phe

595

<210> 141

<211> 1635

<212> DNA

<213> Phaeosphaeria nodorum

<400> 141

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ccgcatctgc cagaggatgc catgcgagat ggcaagcctg cggtgaacaa atactcgtct	120
actcttactg ctggccataa ctttcggga gctcaggcca tgctttatgc ggctggtgtt	180
ccctcgaagg aagccatgaa gacacagcct cacgtaggca ttgcgagtgt atggtgggaa	240
ggcaacctat gcaaaactgc agtgctcgac ctgggaaagg agattaagaa aaacgtccag	300
gctgacaata tgctggcatg gcagtacaac actgtgggcg tgtcggatgg tattacgatg	360
ggtggagagg gcatgcgctt ctctctgcag actcgcgaga taatagcaga cagtattgag	420

acggtcacgt gcgcgaaca tcacgacgcg tgtattgcca ttcccggatg cgacaagaat 480
atgcctgggt tcatcatggc atttccccgt cacaaccgac catcgataat ggtatatggc 540
ggctccataa tgccaggcta ttccgagacg ctcaagaagc ccatcaacat ttcaacatgc 600

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tcgccagagg aaatcatgga tgacattgag cgcaatgcat gcccgggtgc tggcgcatgt 720
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gccaaagctg cagctgcat cgcgtctgc atggaaaaga acatcacgcc ccggaaacta 840
ctcaccaagg cctccttcga gaatgccctc gtcgatga tggtcctcgg cggtcgcacc 900
aacgccgtcc tgcacatgct cgccatggcc ggtacagcag gcgtccctt aacccttgac 960
gacttcagc gcgtgtccaa caaaattccc ttctcgcg acctcgcccc ctctggccgc 1020

tacatggctg ccgacctctt tgacattggc ggcatgccct ccgtcatgaa gctcctcgtc 1080
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gcgaaaaatca cggggaaaga gggcttgata ttccgcggta gggcgatggt atttgacaag 1320
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agtggtgcca gtcacgggtt tattgtcggg cacatgtgtc cagaagcggc cgtgggtggc 1560
ccattgtctg tggtaggga tgggatgtt atcactattg gtaagtcgtg ttgcaaagtc 1620
ggagagagat ggtga 1635

<210> 142

<211> 544

<212> PRT

<213> *Phaeosphaeria nodorum*

<400> 142

Met Asp Pro Arg Asn Leu Glu Lys Gln Arg Glu Pro Glu Glu Pro Arg

1 5 10 15

Phe Leu Thr Phe Pro His Leu Pro Glu Asp Ala Met Arg Asp Gly Lys

20 25 30

Pro Ala Leu Asn Lys Tyr Ser Ser Thr Leu Thr Ala Gly His Asn Phe

35	40	45	
Pro Gly Ala Gln Ala Met Leu Tyr Ala Ala Gly Val Pro Ser Lys Glu			
50	55	60	
Ala Met Lys Thr Gln Pro His Val Gly Ile Ala Ser Val Trp Trp Glu			
65	70	75	80
Gly Asn Pro Cys Lys Thr Ala Val Leu Asp Leu Gly Lys Glu Ile Lys			
85	90	95	
Lys Asn Val Gln Ala Asp Asn Met Leu Ala Trp Gln Tyr Asn Thr Val			
100	105	110	
Gly Val Ser Asp Gly Ile Thr Met Gly Gly Glu Gly Met Arg Phe Ser			
115	120	125	
Leu Gln Thr Arg Glu Ile Ile Ala Asp Ser Ile Glu Thr Val Thr Cys			
130	135	140	
Ala Gln His His Asp Ala Cys Ile Ala Ile Pro Gly Cys Asp Lys Asn			
145	150	155	160
Met Pro Gly Val Ile Met Ala Phe Ala Arg His Asn Arg Pro Ser Ile			
165	170	175	
Met Val Tyr Gly Gly Ser Ile Met Pro Gly Tyr Ser Glu Thr Leu Lys			
180	185	190	
Lys Pro Ile Asn Ile Ser Thr Cys Tyr Glu Lys His Gly Ala Tyr Ile			
195	200	205	
Tyr Lys Asn Leu Glu Ser Ala Glu Lys Gly Lys Phe Ser Pro Glu Glu			
210	215	220	
Ile Met Asp Asp Ile Glu Arg Asn Ala Cys Pro Gly Ala Gly Ala Cys			
225	230	235	240
Gly Gly Met Tyr Thr Ala Asn Thr Met Ser Thr Ser Ile Glu Ala Lys			
245	250	255	
Met Arg Glu Cys Ala Lys Ala Ala Ala Ala Ile Arg Val Cys Met Glu			
260	265	270	
Lys Asn Ile Thr Pro Arg Lys Leu Leu Thr Lys Ala Ser Phe Glu Asn			
275	280	285	

Ala Leu Val Met Met Met Val Leu Gly Gly Ser Thr Asn Ala Val Leu
290 295 300

His Met Leu Ala Met Ala Gly Thr Ala Gly Val Pro Leu Thr Leu Asp
305 310 315 320

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

Pro Ser Gly Arg Tyr Met Ala Ala Asp Leu Phe Asp Ile Gly Gly Met
340 345 350

Pro Ser Val Met Lys Leu Leu Val Ala Ala Gly Leu Leu Asp Gly Ser
355 360 365

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

Pro Ser Leu Pro Gln Asp Gln Val Leu Ile Arg Pro Leu Ser Asn Pro
385 390 395 400

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

Ala Gly Ala Val Ala Lys Ile Thr Gly Lys Glu Gly Leu Ile Phe Arg
420 425 430

Gly Arg Ala Met Val Phe Asp Lys Glu His Gln Leu Asp Lys Ala Leu
435 440 445

Asn Glu Gly Arg Ile Pro His Gly Glu Asn Ile Val Val Val Val Arg
450 455 460

Tyr Glu Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Gln Leu Lys Ala
465 470 475 480

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

Asp Gly Arg Tyr Ser Gly Ala Ser His Gly Phe Ile Val Gly His Met
500 505 510

Cys Pro Glu Ala Ala Val Gly Gly Pro Ile Ala Val Val Arg Asp Gly
515 520 525

Asp Val Ile Thr Ile Gly Lys Ser Cys Cys Lys Val Gly Glu Arg Trp

530 535 540

<210> 143

<211> 1803

<212> DNA

<213> *Gibberella zeae*

<400> 143

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cccggagctc aggctatgct ctacggagct ggtgtcaagg accagcacac aatgaagaac 180

gcgccccagg ttggtgttgc taccgtctgg tggcaaggaa acccgtgcaa taccatctc 240

cttgatcttg gccagatcgt caagaactcc atcgagaagg aaggcatgat cggtggcag 300

ttcaacaccg ttggtgtatc tgacccatc accatgggcg gcgagggcat gcgtttctct 360

cttcaaactc gagaaatcat tgctgattct atcgagtccg taacctgcgc ccagcatcat 420

gagccaaca tctccattcc cggtgtgac aagaacatgc ccggcacagt catggccgcc 480

gtctgtcaca accgcccctt catcatgac tacggcggta ccatccgcaa gggccactcc 540

aacctccttg agaagcccat caacatcagc acctgctacg aggcctcggg tgctttcaac 600

tacggtcgtc tgcatgcaa gacgaacccc ggcgagcctg gtcgcgagag ctccgatgtc 660

atggatgata tcgagaagca cgcttgtccc ggcgccggag cttgtggtgg catgtatata 720

gccaacacca tggtaccgc tatcgaggcc atgggcctta ctctgcctgg ttcacatcgc 780

tacctgccc agtctctga gaagcgtcgt gagtgtgagc gcgtgcca ggttatccga 840

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gtcggcggta caccctccgt catcaagatg ctctgcgcc gtggtcttct cgacggtagc 1140

atcatgacca ttaccggcaa gactctgcc gagaacgtcg cggactggcc tagtctggac 1200

cccggccagg acatcatccg tctcttgag aaccccatca aggactctgg ccacatccgc 1260

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ctgtccttca ccggcaaggc ccgtgtcttc aacaccgaga aggagctcaa cggcgactg 1380

aaccgaagcg agatcaagca gtccgatggt aacctcgtcg tcatcgtccg atacaggggc 1440

ccaaggcg gtcccgtat gcctgaacag ctcaaggctt ctgcagccat catgggtgcc 1500

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gagatggaga agcgaaggag tgagtgggaag cctcctgcgc cccgtgttac gaggggtgtg 1740
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tag 1803

<210> 144

<211> 600

<212> PRT

<213> *Gibberella zeae*

<400> 144

Met Ala Asp Gln Val Thr His Asp Pro Lys Gln Ser Ser Asp Tyr Ile

1 5 10 15

Pro Phe Pro Cys Leu Pro Pro Gly Gly Ala Leu Asn Arg Trp Ser Thr

20 25 30

Lys Ile Thr Arg Glu His Asp Tyr Pro Gly Ala Gln Ala Met Leu Tyr

35 40 45

Gly Ala Gly Val Lys Asp Gln His Thr Met Lys Asn Ala Pro Gln Val

50 55 60

Gly Val Ala Thr Val Trp Trp Gln Gly Asn Pro Cys Asn Thr His Leu

65 70 75 80

Leu Asp Leu Gly Gln Ile Val Lys Asn Ser Ile Glu Lys Glu Gly Met

85 90 95

Ile Gly Trp Gln Phe Asn Thr Val Gly Val Ser Asp Ala Ile Thr Met

100 105 110

Gly Gly Glu Gly Met Arg Phe Ser Leu Gln Thr Arg Glu Ile Ile Ala

115 120 125

Asp Ser Ile Glu Ser Val Thr Cys Ala Gln His His Asp Ala Asn Ile

130 135 140

Ser Ile Pro Gly Cys Asp Lys Asn Met Pro Gly Thr Val Met Ala Ala

145 150 155 160

Ala Arg His Asn Arg Pro Phe Ile Met Ile Tyr Gly Gly Thr Ile Arg

165 170 175
 Lys Gly His Ser Asn Leu Leu Glu Lys Pro Ile Asn Ile Ser Thr Cys
 180 185 190

 Tyr Glu Ala Ser Gly Ala Phe Asn Tyr Gly Arg Leu His Ala Lys Thr
 195 200 205
 Asn Pro Gly Glu Pro Gly Arg Glu Ser Ser Asp Val Met Asp Asp Ile
 210 215 220
 Glu Lys His Ala Cys Pro Gly Ala Gly Ala Cys Gly Gly Met Tyr Thr
 225 230 235 240
 Ala Asn Thr Met Ala Thr Ala Ile Glu Ala Met Gly Leu Thr Leu Pro
 245 250 255

 Gly Ser Ser Ser Tyr Pro Ala Glu Ser Pro Glu Lys Arg Arg Glu Cys
 260 265 270
 Glu Arg Ala Ala Gln Val Ile Arg Thr Thr Met Glu Lys Asp Leu Arg
 275 280 285
 Pro Arg Asp Ile Met Thr Arg Ala Ser Phe Glu Asn Ala Leu Val Leu
 290 295 300
 Thr Met Ile Leu Gly Gly Ser Thr Asn Gly Val Leu His Phe Leu Ala
 305 310 315 320

 Met Ala Asn Thr Ala Asp Val Pro Leu Thr Ile Asp Asp Ile Gln Arg
 325 330 335
 Ala Ser Asp Arg Thr Pro Phe Leu Ala Asp Leu Ala Pro Ser Gly Lys
 340 345 350
 Tyr Tyr Met Glu Asp Leu Tyr Lys Val Gly Gly Thr Pro Ser Val Ile
 355 360 365
 Lys Met Leu Val Ala Arg Gly Leu Leu Asp Gly Ser Ile Met Thr Ile
 370 375 380

 Thr Gly Lys Thr Leu Ala Glu Asn Val Ala Asp Trp Pro Ser Leu Asp
 385 390 395 400
 Pro Gly Gln Asp Ile Ile Arg Pro Leu Glu Asn Pro Ile Lys Asp Ser
 405 410 415

Gly His Ile Arg Ile Leu Lys Gly Asn Phe Ala Pro Gly Gly Ala Val

420 425 430

Ala Lys Ile Thr Gly Lys Glu Gly Leu Ser Phe Thr Gly Lys Ala Arg

435 440 445

Val Phe Asn Thr Glu Lys Glu Leu Asn Gly Ala Leu Asn Arg Ser Glu

450 455 460

Ile Lys Gln Ser Asp Gly Asn Leu Val Val Ile Val Arg Tyr Glu Gly

465 470 475 480

Pro Lys Gly Gly Pro Gly Met Pro Glu Gln Leu Lys Ala Ser Ala Ala

485 490 495

Ile Met Gly Ala Gly Leu Ser Asn Leu Ala Leu Val Thr Asp Gly Arg

500 505 510

Tyr Ser Gly Ala Ser His Gly Phe Ile Val Gly His Val Val Pro Glu

515 520 525

Ala Met Val Gly Gly Pro Ile Ala Leu Val Lys Asp Gly Asp Glu Ile

530 535 540

Thr Ile Asp Ala Ile Asn Asn Arg Ile Asp Val Asp Ile Thr Asp Glu

545 550 555 560

Glu Met Glu Lys Arg Arg Ser Glu Trp Lys Pro Pro Ala Pro Arg Val

565 570 575

Thr Arg Gly Val Leu Ala Lys Tyr Ala Arg Leu Val Gly Asp Ala Ser

580 585 590

His Gly Ala Val Thr Asp Gln Trp

595 600

<210> 145

<211> 1923

<212> DNA

<213> Neurospora crassa

<400> 145

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tccaccacca ccacgaccac caacgacaac agcgagcgca acttgcccaa agagggcgaa 120

tacatccaat ggcgtactct cccagctggc aaccccgacc agttgaaccg ctggtcgcac 180

tttttgactc gtgagcatga gtttcttga gctcaggcca tgctctacgg cgccggtgtc	240
ccgaataagg acatgatgaa gaaggcgccg catgtcggca ttgcgacggt ctggtgggag	300
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accgtgacgt gcgtcagca tcatgacgcc aacatctcca ttcccggtg cgacaagaac	540
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aaccgcgtct cagccaagac gccctttttg gctgacatgg cccctccgg caggtactac	1140
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agaaagaagg ggtggaaggc gccgaagatg aagccgacga ggggggcgtt ggccaagtat	1860
gcgaggttgg tgggggatgc gtcgcatggg gctgttactg atttgggtgg ggatgcctat	1920

tag

1923

<210> 146

<211> 640

<212> PRT

<213> Neurospora crassa

<400> 146

Met Ala Ser Asn Gln Asp Asn Lys Ala Val Ala Pro Asp Ala Ala Ala

1 5 10 15

Pro Ala Gly Gln Ser Thr Thr Thr Thr Thr Thr Asn Asp Asn Ser Glu

20 25 30

Arg Asn Leu Pro Lys Glu Gly Glu Tyr Ile Gln Trp Arg Thr Leu Pro

35 40 45

Ala Gly Asn Pro Asp Gln Leu Asn Arg Trp Ser His Phe Leu Thr Arg

50 55 60

Glu His Glu Phe Pro Gly Ala Gln Ala Met Leu Tyr Gly Ala Gly Val

65 70 75 80

Pro Asn Lys Asp Met Met Lys Lys Ala Pro His Val Gly Ile Ala Thr

85 90 95

Val Trp Trp Glu Gly Asn Pro Cys Asn Thr His Leu Leu Asp Leu Gly

100 105 110

Gln Lys Val Lys Lys Ala Val Glu Arg Glu Lys Met Leu Ala Trp Gln

115 120 125

Phe Asn Thr Ile Gly Val Ser Asp Gly Ile Thr Met Gly Gly Glu Gly

130 135 140

Met Arg Tyr Ser Leu Gln Ser Arg Glu Ile Ile Ala Asp Ser Ile Glu

145 150 155 160

Thr Val Thr Cys Ala Gln His His Asp Ala Asn Ile Ser Ile Pro Gly

165 170 175

Cys Asp Lys Asn Met Pro Gly Val Ile Met Ala Ala Ala Arg His Asn

180 185 190

Arg Pro Phe Val Met Ile Tyr Gly Gly Thr Met Arg Gly Gly His Ser

195 200 205

Glu Leu Leu Asp Arg Pro Ile Asn Ile Val Thr Cys Tyr Glu Ala Ser
 210 215 220
 Gly Ala Tyr Thr Tyr Gly Arg Leu Lys Pro Ala Cys Pro Asn Ser Thr
 225 230 235 240

 Ala Thr Pro Ser Asp Val Met Asp Asp Ile Glu Gln His Ala Cys Pro
 245 250 255
 Gly Ala Gly Ala Cys Gly Gly Met Tyr Thr Ala Asn Thr Met Ala Thr
 260 265 270
 Ala Ile Glu Ala Met Gly Leu Thr Ala Pro Gly Ser Ser Ser Phe Pro
 275 280 285
 Ala Ser Ser Pro Glu Lys Phe Arg Glu Cys Glu Lys Ala Ala Glu Tyr
 290 295 300

 Ile Lys Ile Cys Met Glu Lys Asp Ile Arg Pro Arg Asp Leu Leu Thr
 305 310 315 320
 Lys Ala Ser Phe Glu Asn Ala Leu Val Leu Thr Met Ile Leu Gly Gly
 325 330 335
 Ser Thr Asn Gly Val Leu His Tyr Leu Ala Met Ala Asn Ser Ala Asp
 340 345 350
 Val Asp Leu Thr Leu Asp Asp Ile Asn Arg Val Ser Ala Lys Thr Pro
 355 360 365

 Phe Leu Ala Asp Met Ala Pro Ser Gly Arg Tyr Tyr Met Glu Asp Leu
 370 375 380
 Tyr Lys Val Gly Gly Thr Pro Ala Val Leu Lys Met Leu Ile Ala Ala
 385 390 395 400
 Gly Tyr Ile Asp Gly Thr Ile Pro Thr Ile Thr Gly Lys Ser Leu Ala
 405 410 415
 Glu Asn Val Ser Asp Trp Pro Ser Leu Asp Pro Asp Gln Lys Ile Ile
 420 425 430

 Arg Pro Leu Asp Asn Pro Ile Lys Ser Gln Gly His Ile Arg Val Leu
 435 440 445
 Tyr Gly Asn Phe Ser Pro Gly Gly Ala Val Ala Lys Ile Thr Gly Lys

450 455 460
 Glu Gly Leu Ser Phe Thr Gly Lys Ala Arg Cys Phe Asn Lys Glu Phe
 465 470 475 480
 Glu Leu Asp Ala Ala Leu Lys Asn Ser Glu Ile Thr Leu Glu Gln Gly
 485 490 495

 Asn Gln Val Leu Ile Val Arg Tyr Glu Gly Pro Lys Gly Gly Pro Gly
 500 505 510
 Met Pro Glu Gln Leu Lys Ala Ser Ala Ala Ile Met Gly Ala Gly Leu
 515 520 525
 Thr Asn Val Ala Leu Val Thr Asp Gly Arg Tyr Ser Gly Ala Ser His
 530 535 540
 Gly Phe Ile Val Gly His Val Val Pro Glu Ala Ala Thr Gly Gly Pro
 545 550 555 560

 Ile Ala Leu Val Lys Asp Gly Asp Leu Ile Thr Ile Asp Ala Val Arg
 565 570 575
 Asn Arg Ile Asp Val Val Lys Thr Val Glu Gly Val Glu Gly Glu Glu
 580 585 590
 Glu Ile Ala Lys Val Leu Glu Glu Arg Lys Lys Gly Trp Lys Ala Pro
 595 600 605
 Lys Met Lys Pro Thr Arg Gly Ala Leu Ala Lys Tyr Ala Arg Leu Val
 610 615 620

 Gly Asp Ala Ser His Gly Ala Val Thr Asp Leu Gly Gly Asp Ala Tyr
 625 630 635 640

 <210> 147
 <211> 1575
 <212> DNA
 <213> Coprinopsis cinerea
 <400> 147

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 ttgatcttta ataccatcgg tgtcagtgat gccattacga tgggtacaga cggaatgcgg 180

tacagtctac ccagtcgaga cctcatcgcg gactccatcg aagcagtcgt catggcccag 240

cactacgacg gaaacatcgc tattcctgga tgcgacaaga acatgcccgg ctgcttcatg 300

gtgctgtcc gacacaaccg accgaccatt atcgtctatg gagggactat ccaacctggt 360

acccggcacg ttggtgcctt tactgtgggc aagatcaccg atgagcagag gttagcaggt 420

gtgcgacatg cctgtcctgg ccccgagacc tgcggcggaa tgtacactgc gaacacgatg 480

agttctgccc tcgaggctct cggtctgtcg ctcccgtatt cttcaagtat cccagcgatg 540

catccagaga aggtccaaga atgcttcagg gctgccaagt acatgaagaa gctgcttgag 600

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gcatattgtg attga 1575

<210> 148

<211> 524

<212> PRT

<213> Coprinopsis cinerea

<400> 148

Met Asp Lys Pro Gln Ile Gly Ile Ser Pro Val Trp Trp Glu Gly Asn

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Pro Cys Asn Phe His Leu Leu Asp Leu Ala Lys His Val Lys Lys Gly
 20 25 30
 Cys Gln Glu Glu Asp Gln Ile Gly Leu Ile Phe Asn Thr Ile Gly Val
 35 40 45
 Ser Asp Ala Ile Thr Met Gly Thr Asp Gly Met Arg Tyr Ser Leu Pro
 50 55 60
 Ser Arg Asp Leu Ile Ala Asp Ser Ile Glu Ala Val Val Met Ala Gln
 65 70 75 80
 His Tyr Asp Gly Asn Ile Ala Ile Pro Gly Cys Asp Lys Asn Met Pro
 85 90 95
 Gly Cys Phe Met Ala Ala Val Arg His Asn Arg Pro Thr Ile Ile Val
 100 105 110
 Tyr Gly Gly Thr Ile Gln Pro Gly Thr Arg His Val Gly Ala Phe Thr
 115 120 125
 Val Gly Lys Ile Thr Asp Glu Gln Arg Phe Asp Val Val Arg His Ala
 130 135 140
 Cys Pro Gly Pro Gly Ala Cys Gly Gly Met Tyr Thr Ala Asn Thr Met
 145 150 155 160
 Ser Ser Ala Leu Glu Val Leu Gly Leu Ser Leu Pro Tyr Ser Ser Ser
 165 170 175
 Ile Pro Ala Met His Pro Glu Lys Val Gln Glu Cys Phe Arg Ala Ala
 180 185 190
 Lys Tyr Met Lys Lys Leu Leu Glu Leu Asp Leu Lys Pro Arg Asp Ile
 195 200 205
 Leu Thr Lys Gln Ser Phe Leu Asn Ala Ile Val Ile Ile Thr Val Leu
 210 215 220
 Gly Gly Ser Thr Asn Ala Val Leu His Leu Leu Ala Met Ala Arg Ala
 225 230 235 240
 Ala Glu Ile Asp Leu Thr Ile Asp Asp Phe Gln Ala Val Ala Asp Arg
 245 250 255
 Thr Pro Phe Leu Ala Asp Leu Met Pro Ser Gly Arg Tyr Tyr Met Glu

260 265 270
 Asp Ile His Arg Ile Gly Gly Ile Pro Ala Ile Val Lys Tyr Leu Leu
 275 280 285
 Asn His Ser Asp Leu Ile Asp Gly Asn Gln Met Thr Val Thr Gly Lys

 290 295 300
 Thr Leu Ala Glu Asn Leu Ala Asp Val Pro Glu Leu Glu Phe His Asn
 305 310 315 320
 Gln Asp Val Phe Arg Pro Leu Asp Asn Pro Ile Lys Pro Thr Gly His
 325 330 335
 Ile Thr Ile Leu Arg Gly Asn Leu Ala Pro Glu Thr Ala Val Ala Lys
 340 345 350
 Leu Thr Gly Lys Glu Gly Leu Arg Phe Glu Gly Val Ala Arg Cys Phe

 355 360 365
 Asp Ser Leu Glu Lys Phe Tyr Pro Ala Leu Ala Ala Gly Glu Ile Lys
 370 375 380
 Pro Gly Thr Val Leu Ile Phe Arg Tyr Gln Gly Pro Lys Gly Ala Pro
 385 390 395 400
 Gly Met Pro Glu Met Leu Gly Met Ser Ala Ala Ser Arg Gly Pro Thr
 405 410 415
 Gly Ala Ile Ala Gly Ala Gly Leu Ala Asn Ser Thr Ala Leu Ile Thr

 420 425 430
 Asp Gly Arg Phe Ser Gly Ala Ser Arg Gly Phe Ile Ile Gly His Val
 435 440 445
 Val Pro Glu Ala Arg Val Gly Gly Pro Ile Ala Leu Val Lys Asp Gly
 450 455 460
 Asp Lys Ile Val Ile Asp Ala Glu Thr Arg Thr Ile Asn Trp Leu Val
 465 470 475 480
 Asp Glu Glu Glu Gln Ala Lys Arg Arg Lys Glu Trp Glu Ala Ser Asp

 485 490 495
 Asn Gly Lys Leu Asn Val Lys Arg Gly Val Leu Tyr Arg Tyr Ala Arg
 500 505 510

Asp Val Ala Pro Ala Ser Met Gly Ala Tyr Cys Asp

515	520	
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<211>	1767	
<212>	DNA	
<213>	Laccaria bicolor	
<400>	149	
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gcgatgcttt	acgtgtcggg tttagtgag gacgatatga acaagcctca gattgggatt	180
tctccagtgt	ggtgggaagg gaacccatgt aactctcacc ttcttgacct tgccaagcac	240
gtaaaggaag	gttgtaaagc agaggatctt gttggtctta tcttcaatac cattggcgtc	300
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gacaagaaca	tgccagggtg cttcatcgcc gcagtcgctc ataatcgacc aacgatcatt	480
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gcttgtggag	gcatgtacac tgccaacacc atgagttcag cccttgaggc tcttgggata	720
tctttgccct	attcatcgag cagccagcc ctgtaccccg agaaggttca agagtgtttt	780
cgagcagcaa	agtatttaaa acgtttgctt gaattagatc tgaagcccaa ggacattttg	840
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gcagttttgc	acttgctagc tatggctcgc gcagctgagg tagaactcac aatcgatgac	960
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gtagccaaac	tcacagggaa agaaggtctc aaatttgagg gaattgcgag atgctttgat	1320
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<210> 150

<211> 588

<212> PRT

<213> Laccaria bicolor

<400> 150

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20 25 30

Asn Lys Ile Arg Gly Gly Ala Gln Ala Met Leu Tyr Ala Val Gly Leu

35 40 45

Ser Glu Asp Asp Met Asn Lys Pro Gln Ile Gly Ile Ser Pro Val Trp

50 55 60

Trp Glu Gly Asn Pro Cys Asn Ser His Leu Leu Asp Leu Ala Lys His

65 70 75 80

Val Lys Glu Gly Cys Lys Ala Glu Asp Leu Val Gly Leu Ile Phe Asn

85 90 95

Thr Ile Gly Val Ser Asp Ala Ile Thr Met Gly Thr Asp Gly Met Arg

100 105 110

Tyr Ser Leu Pro Ser Arg Asp Ile Ile Ala Asp Ser Ile Glu Ala Ala

115 120 125

Gln His Tyr Asp Ala Asn Ile Ser Ile Pro Gly Cys Asp Lys Asn Met

130 135 140

Pro Gly Cys Phe Ile Ala Ala Val Arg His Asn Arg Pro Thr Ile Ile

145 150 155 160

Val Tyr Gly Gly Thr Ile Gln Pro Gly Val Arg His Val Asp Cys Pro

165 170 175
 Ser Met Gly Lys Glu Lys Gly Gly Ser Val Asn Ile Ser Asp Ala Phe

 180 185 190
 Glu Ser Tyr Gly Ala Phe Ala Val Gly Lys Ile Asn Asp Val Glu Arg
 195 200 205
 Phe Asp Val Val Arg His Ala Cys Pro Gly Ala Gly Ala Cys Gly Gly
 210 215 220
 Met Tyr Thr Ala Asn Thr Met Ser Ser Ala Leu Glu Ala Leu Gly Ile
 225 230 235 240
 Ser Leu Pro Tyr Ser Ser Ser Thr Pro Ala Leu Tyr Pro Glu Lys Val

 245 250 255
 Gln Glu Cys Phe Arg Ala Ala Lys Tyr Leu Lys Arg Leu Leu Glu Leu
 260 265 270
 Asp Leu Lys Pro Lys Asp Ile Leu Thr Arg Asn Ser Phe Leu Asn Ala
 275 280 285
 Ile Val Ile Ile Thr Val Leu Gly Gly Ser Thr Asn Ala Val Leu His
 290 295 300
 Leu Leu Ala Met Ala Arg Ala Ala Glu Val Glu Leu Thr Ile Asp Asp

 305 310 315 320
 Phe Gln Met Ile Ala Asp Lys Thr Pro Phe Leu Ala Asp Leu Met Pro
 325 330 335
 Ser Gly Arg Tyr Tyr Met Glu Asp Ile His Lys Ile Gly Gly Ile Pro
 340 345 350
 Ala Ile Leu Lys Tyr Leu Leu Asn His Thr Asp Leu Ile Asp Gly Thr
 355 360 365
 Gln Met Thr Val Thr Gly Arg Thr Leu Ala Glu Asn Leu Ala Asp Val

 370 375 380
 Pro Glu Leu Glu Phe Asp Lys Gln Asp Val Val Arg Ser Leu Ser Asn
 385 390 395 400
 Pro Ile Lys Lys Thr Gly His Ile Thr Ile Met Arg Gly Asn Leu Ala
 405 410 415

Pro Glu Thr Ala Val Ala Lys Leu Thr Gly Lys Glu Gly Leu Lys Phe

420 425 430

Glu Gly Ile Ala Arg Cys Phe Asp Ser Leu Asp Gly Phe Tyr Pro Ala

435 440 445

Leu Glu Ala Gly Glu Ile Lys Ala Gly Thr Val Leu Ile Phe Arg Tyr

450 455 460

Gln Gly Pro Lys Gly Ala Pro Gly Met Pro Glu Met Leu Gly Pro Thr

465 470 475 480

Gly Ala Ile Ala Gly Ala Gly Leu Ala Arg Ser Thr Ala Leu Ile Thr

485 490 495

Asp Gly Arg Phe Ser Gly Ala Ser Arg Gly Phe Ile Ile Gly His Val

500 505 510

Val Pro Glu Ala Arg Val Gly Gly Pro Ile Ala Leu Val Lys Asn Gly

515 520 525

Asp Arg Ile Val Ile Asp Ser Glu Thr Arg Thr Ile Asn Trp Leu Val

530 535 540

Asp Glu Asn Glu Gln Lys Leu Arg Lys Ala Glu Trp Asp Ala Ser Glu

545 550 555 560

Asn Ser Lys Phe Asn Val Gly Arg Gly Val Leu Leu Arg Tyr Ala Arg

565 570 575

Asp Val Ala Pro Ala Asn Leu Gly Ala Tyr Cys Asp

580 585

<210> 151

<211> 1794

<212> DNA

<213> Ustilago maydis

<400> 151

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 agggatgtac aaacgcttc cgagggtgtg gttactgatc gcgatctgtt ttga 1794

 <210> 152
 <211> 597
 <212> PRT
 <213> Ustilago maydis
 <400> 152

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20 25 30

Ser Ser Asp Lys Gly Ala Ala Gln Ser Met Leu His Ala Cys Gly Leu

35 40 45

Ser Val Gln Asp Leu Asp Lys Pro Gln Val Gly Ile Ser Ser Val Trp

50 55 60

Trp Glu Gly Asn Pro Cys Asn Thr His Leu Leu Glu Phe Gly Arg Lys

65 70 75 80

Ile Lys Gln Gly Cys Glu Ala Glu Gly Leu Val Gly Leu Gln Asn Asn

85 90 95

Thr Val Gly Val Ser Asp Ala Ile Thr Met Gly Gly Pro Gly Met Gln

100 105 110

Tyr Ser Leu Pro Ser Arg Glu Leu Ile Ala Asp Ser Ile Glu Thr Ile

115 120 125

Thr Leu Ala Gln Tyr His Asp Ala Asn Val Ser Ile Pro Gly Cys Asp

130 135 140

Lys Asn Met Pro Gly Cys Leu Ile Ala Cys Leu Arg His Asn Arg Pro

145 150 155 160

Ser Ile Ile Val Tyr Gly Gly Thr Ile Gln Pro Gly Lys His Gly Met

165 170 175

Asp Ile Pro Ala Leu Gly Arg Lys Lys Gly Asp Pro Cys Asn Val Ala

180 185 190

Asp Asn Phe Glu Ala Thr Gly Ala Tyr Ala Lys Gly Leu Ile Thr Ala

195 200 205

Glu Glu Arg Val Asp Leu Ile Arg Asn Ala Cys Pro Gly Pro Gly Ala

210 215 220

Cys Gly Gly Met Tyr Thr Ala Asn Thr Leu Ser Ile Ala Ile Glu Val

225 230 235 240

Met Gly Met Gly Leu Pro Leu Thr Ser Ser Thr Pro Ala Val Tyr Pro

245 250 255
 Glu Lys Met Gln Glu Cys Leu Arg Val Gly Ala Tyr Ile Lys Asn Leu

 260 265 270
 Leu Ala Lys Asp Ile Lys Pro Arg Asp Ile Met Thr Lys Lys Ala Phe
 275 280 285
 Glu Asn Ala Ile Val Met Thr His Val Leu Gly Gly Ser Thr Asn Ala
 290 295 300
 Val Leu His Leu Ile Ala Val Ala Arg Ala Gly Asp Ile Asp Ile Thr
 305 310 315 320
 Ile Asp Asp Phe Gln Arg Leu Gly Asp Lys Thr Pro Met Leu Ala Asp

 325 330 335
 Val Lys Pro Ser Gly Lys Tyr Tyr Met Glu Asp Ile His Lys Ile Gly
 340 345 350
 Gly Val Pro Arg Val Leu Lys Tyr Ile Leu Glu Asn Thr Asp Leu Leu
 355 360 365
 His Gly Asp Val Met Thr Val Thr Gly Lys Thr Met Arg Glu Asn Leu
 370 375 380
 Val Asp Val Glu Pro Leu Glu Phe Glu Thr Gln Asp Ile Ile Arg Pro

 385 390 395 400
 Leu Ser Asn Pro Ile Lys Ala Thr Gly His Leu Thr Ile Met Arg Gly
 405 410 415
 Ser Leu Cys Pro Gly Gly Ala Val Ser Lys Leu Thr Gly Lys Glu Gly
 420 425 430
 Leu Tyr Phe Asp Gly Ser Ala Val Val Phe Asp Ser Glu Asp Gly Ile
 435 440 445
 Thr Glu Ala Ile Ala Glu Gly Arg Val Lys Glu Gly Ser Val Val Val

 450 455 460
 Ile Arg Tyr Val Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met Leu
 465 470 475 480
 Gly Pro Thr Gly Ala Ile Met Gly Ala Gly Leu Gly Lys Thr Val Ala
 485 490 495

Leu Ile Thr Asp Gly Arg Phe Ser Gly Ala Ser His Gly Phe Cys Thr

500 505 510

Gly His Val Val Pro Glu Ala Ala Leu Gly Gly Pro Ile Ala Leu Val

515 520 525

Gln Asp Gly Asp Arg Ile Thr Val Asp Ala Asn Thr Arg Glu Ile Asn

530 535 540

Leu His Ile Ser Asp Glu Glu Met Glu Lys Arg Lys Gln Trp Trp Leu

545 550 555 560

Lys Glu Lys Lys Pro Thr Leu Thr Lys Lys His Lys Arg Gly Trp Leu

565 570 575

Tyr Lys Phe Ala Arg Asp Val Gln Asn Ala Ser Glu Gly Cys Val Thr

580 585 590

Asp Arg Asp Leu Phe

595

<210> 153

<211> 2337

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 153

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gctgaaaaca agaaggctaa ctgtgttaaa aatgtatata ctggtgaata caaagggtgt 1920
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aactttggtg aaggttcctc tcgtgaacac gctgctttgg aaccaagatt cttgggcgg 2040
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ccaaagaatg gtaagccatg ggatgctgtg ttgaccata ctttcaacga tgagcaaatt 2280
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<210> 154
<211> 778
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 154

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20 25 30

Leu Glu Asp His Ser Phe Ile Asn Tyr Lys Gln Asn Val Glu Thr Leu

35 40 45

Asp Ile Val Arg Lys Arg Leu Asn Arg Pro Phe Thr Tyr Ala Glu Lys

50 55 60

Ile Leu Tyr Gly His Leu Asp Asp Pro His Gly Gln Asp Ile Gln Arg

65 70 75 80

Gly Val Ser Tyr Leu Lys Leu Arg Pro Asp Arg Val Ala Cys Gln Asp

85 90 95

Ala Thr Ala Gln Met Ala Ile Leu Gln Phe Met Ser Ala Gly Leu Pro

100 105 110

Gln Val Ala Lys Pro Val Thr Val His Cys Asp His Leu Ile Gln Ala

115 120 125

Gln Val Gly Gly Glu Lys Asp Leu Lys Arg Ala Ile Asp Leu Asn Lys

130 135 140

Glu Val Tyr Asp Phe Leu Ala Ser Ala Thr Ala Lys Tyr Asn Met Gly

145 150 155 160

Phe Trp Lys Pro Gly Ser Gly Ile Ile His Gln Ile Val Leu Glu Asn

165 170 175

Tyr Ala Phe Pro Gly Ala Leu Ile Ile Gly Thr Asp Ser His Thr Pro

180 185 190

Asn Ala Gly Gly Leu Gly Gln Leu Ala Ile Gly Val Gly Gly Ala Asp

195 200 205

Ala Val Asp Val Met Ala Gly Arg Pro Trp Glu Leu Lys Ala Pro Lys

210 215 220

Ile Leu Gly Val Lys Leu Thr Gly Lys Met Asn Gly Trp Thr Ser Pro

225 230 235 240

Lys Asp Ile Ile Leu Lys Leu Ala Gly Ile Thr Thr Val Lys Gly Gly

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

Ala Ile Ala Gly Asp Leu Arg Phe Asn Pro Leu Thr Asp Lys Leu Lys
500 505 510

Asp Lys Asp Gly Asn Glu Phe Met Leu Lys Pro Pro His Gly Asp Gly
515 520 525

Leu Pro Gln Arg Gly Tyr Asp Ala Gly Glu Asn Thr Tyr Gln Ala Pro
530 535 540

Pro Ala Asp Arg Ser Thr Val Glu Val Lys Val Ser Pro Thr Ser Asp
545 550 555 560

Arg Leu Gln Leu Leu Lys Pro Phe Lys Pro Trp Asp Gly Lys Asp Ala
565 570 575

Lys Asp Met Pro Ile Leu Ile Lys Ala Val Gly Lys Thr Thr Thr Asp
580 585 590

His Ile Ser Met Ala Gly Pro Trp Leu Lys Tyr Arg Gly His Leu Glu
595 600 605

Asn Ile Ser Asn Asn Tyr Met Ile Gly Ala Ile Asn Ala Glu Asn Lys
610 615 620

Lys Ala Asn Cys Val Lys Asn Val Tyr Thr Gly Glu Tyr Lys Gly Val
625 630 635 640

Pro Asp Thr Ala Arg Asp Tyr Arg Asp Gln Gly Ile Lys Trp Val Val
645 650 655

Ile Gly Asp Glu Asn Phe Gly Glu Gly Ser Ser Arg Glu His Ala Ala
660 665 670

Leu Glu Pro Arg Phe Leu Gly Gly Phe Ala Ile Ile Thr Lys Ser Phe
675 680 685

Ala Arg Ile His Glu Thr Asn Leu Lys Lys Gln Gly Leu Leu Pro Leu
690 695 700

Asn Phe Lys Asn Pro Ala Asp Tyr Asp Lys Ile Asn Pro Asp Asp Arg
705 710 715 720

Ile Asp Ile Leu Gly Leu Ala Glu Leu Ala Pro Gly Lys Pro Val Thr
725 730 735

Met Arg Val His Pro Lys Asn Gly Lys Pro Trp Asp Ala Val Leu Thr

740	745	750
His Thr Phe Asn Asp Glu Gln Ile Glu Trp Phe Lys Tyr Gly Ser Ala		
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Leu Asn Lys Ile Lys Ala Asp Glu Lys Lys		
770	775	
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<211> 2718		
<212> DNA		
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<400> 155		
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gcctctgctc aaatggcctt gcttcagttt atgacgtgtg gtcttgaaaa aactatgatt	360	
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ccatgggagt taaaagctcc caaaatcatc ggtgtcaacc ttacgggcgc tatgtctggc	720	
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<210> 156

<211> 905

<212> PRT

<213> Schizosaccharomyces pombe

<400> 156

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 20 25 30
 Tyr Val Thr Pro Pro Tyr Glu Lys Leu Met Gly Lys Leu Gln Gln Val
 35 40 45
 Arg Lys Phe Leu Pro Gly Gln Lys Leu Thr Leu Ala Glu Lys Val Leu
 50 55 60

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

 Leu Ile Val Gly His Arg Gly Ala Asn Ser Asp Ile Pro Asp Ser Ile
 130 135 140
 Ala Asn Asn Lys Glu Ile Phe Asp Phe Leu Gln Ser Ala Ala Lys Lys
 145 150 155 160
 Tyr Gly Ile Gln Phe Trp Gly Pro Gly Ser Gly Ile Ile His Gln Ile
 165 170 175
 Val Leu Glu Asn Tyr Ala Ala Pro Gly Gly Met Met Leu Gly Thr Asp
 180 185 190

 Ser His Thr Pro Asn Ala Gly Gly Leu Gly Met Ile Ala Ile Gly Val
 195 200 205
 Gly Gly Ala Asp Ala Val Asp Ala Met Thr Asn Thr Pro Trp Glu Leu
 210 215 220
 Lys Ala Pro Lys Ile Ile Gly Val Asn Leu Thr Gly Ala Met Ser Gly
 225 230 235 240
 Trp Thr Thr Pro Lys Asp Leu Ile Leu His Leu Ala Gly Lys Leu Thr
 245 250 255

Val Arg Gly Gly Thr Gly His Ile Ile Glu Tyr Phe Gly Pro Gly Val
260 265 270

Ala Ser Leu Ser Cys Thr Gly Met Ala Thr Val Cys Asn Met Gly Ala
275 280 285

Glu Val Gly Ala Thr Thr Ser Ile Phe Pro Tyr Thr Asp Ser Met Arg
290 295 300

Arg Tyr Leu Ile Ala Thr His Arg Ala Glu Val Ala Asp Ala Ala Ser
305 310 315 320

Glu Val His Ser Glu Tyr Asn Tyr Leu Ala Ala Asp Thr Gly Ala Lys
325 330 335

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

Asn Gly Pro Phe Thr Pro Asp Leu Ser Thr Pro Val Ser Lys Phe Gly
355 360 365

Glu Ala Ile Glu Lys Asn Lys Trp Pro Lys Lys Leu Ser Ala Gly Leu
370 375 380

Ile Gly Ser Cys Thr Asn Ser Ser Tyr Gln Asp Met Thr Cys Val Val
385 390 395 400

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

Phe Leu Val Thr Pro Gly Ser Glu Gln Ile Arg Ala Thr Ile Glu Arg
420 425 430

Asp Gly Ile Thr Glu Arg Leu Glu Glu Ala Gly Ala Thr Val Leu Ala
435 440 445

Asn Ala Cys Gly Pro Cys Ile Gly Met Trp Lys Arg Thr Asp Asp Ile
450 455 460

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

Arg Ser Arg Asn Asp Gly Asn Pro Ser Thr Met Asn Phe Leu Thr Ser
485 490 495

Pro Val Ile Val Ala Ala Lys Ile Phe Ser Ser Asp Leu Ala Phe Asp

500 505 510
 Pro Thr His Asp Thr Leu Gln Thr Pro Asp Gly Lys Ala Phe Lys Phe
 515 520 525
 Arg Pro Pro Gln Gly Val Glu Leu Pro Ser Ala Gly Phe Ile Ala Gly
 530 535 540
 Asp Ser Ser Tyr Ile Pro Glu Pro Asn Pro Gln Pro Val Pro Glu Thr
 545 550 555 560
 Glu Val Thr Ile Asp Pro Lys Ser Asp Arg Leu Glu Ala Leu Glu Pro
 565 570 575

 Phe Glu Pro Tyr Gln Gly Gly Glu Met Glu Asn Leu Lys Val Ala Val
 580 585 590
 Lys Val Lys Gly Lys Cys Thr Thr Asp His Ile Ser Ala Ala Gly Lys
 595 600 605
 Trp Leu Lys Tyr Lys Gly His Leu Ser Asn Ile Cys Asn Asn Thr Leu
 610 615 620
 Ile Gly Ala Met Asn Ala Ala Thr Gly Glu Val Asn Arg Ala Tyr Asp
 625 630 635 640

 Asn Gly Lys Gly Met Thr Ile Pro Glu Leu Met Trp Lys Trp Lys Lys
 645 650 655
 Asp Gly Gln Pro Trp Leu Val Val Ala Glu His Asn Tyr Gly Glu Gly
 660 665 670
 Ser Ala Arg Glu His Ala Ala Leu Gln Pro Arg Ala Met Asn Gly Arg
 675 680 685
 Ile Ile Leu Thr Lys Ser Phe Ala Arg Ile His Glu Thr Asn Leu Lys
 690 695 700

 Lys Gln Gly Val Leu Pro Leu Thr Phe Val Asn Glu Ala Asp Tyr Glu
 705 710 715 720
 Lys Ile Asp Ala Glu Asp Lys Val Ser Thr Arg Gly Ile Glu Gln Leu
 725 730 735
 Leu Glu Gly Val Leu Asp Gln Pro Ile Thr Leu Val Val Thr Lys Lys
 740 745 750

Asp Gly Ser Val Val Glu Ile Pro Cys Lys His Thr Met Ser Lys Asp
755 760 765

Gln Ile Glu Phe Phe Lys Ala Gly Ser Ala Leu Asn Leu Ile Arg Glu
770 775 780

Lys Ala His Ser Gly Val Val Asn Gln Lys Val Ile Asp Ser Ile Lys
785 790 795 800

Gln Gln Pro Asp His Tyr Ala Asp Ala Tyr Ile Phe Asn Arg His Phe
805 810 815

Val Ile Ala Lys Gly Asp Gln Leu Gly Leu Pro Phe His Leu Lys Gly
820 825 830

Val Gln Val Gly Asp Thr Ile Arg Leu Asp Lys Ile Ala Ser Phe Gly
835 840 845

Ser Arg Asp Phe Thr Leu Phe Gly Asn Pro Tyr Val Asp Pro Ser Leu
850 855 860

Phe Thr Ile Glu Ala Val Val Leu Ser Phe Pro Lys Ser Ala Leu Ser
865 870 875 880

Val Arg Val Lys His Lys Arg Arg His Arg His Asp Arg Val Met Lys
885 890 895

His Lys Gln Thr Tyr Thr Ile Leu Arg
900 905

<210> 157

<211> 2337

<212> DNA

<213> Schizosaccharomyces pombe

<400> 157

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tatcagcgca tcaaagacaa tctcgagatt gttaagaagc gcttaaaccg tccttcacac	180
tattcagaaa aaatccttta cggtcacttg gacgatcccg taaatcagga tattgaacgt	240
ggtgtctctt acttgaagct tcgtctgat cgtgttgctt gtcaggatgc cactgcacaa	300
atggctatcc ttcaatttat gtccgcgggt atgccggagg tcgctgtccc cgtcactgtc	360

cattgtgacc acttgatcga agcctacgaa ggtggtccta tcgatctcga acgtgccaac 420
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gatggatctg ctgagtggtc taccaaactt aaccatacct ttaacaagga tcaaattgaa 2280

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<210> 158

<211> 778

<212> PRT

<213> Schizosaccharomyces pombe

<400> 158

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Phe Glu Lys Asn Lys Phe Ile Asn Tyr Gln Arg Ile Lys Asp Asn Leu

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Glu Ile Val Lys Lys Arg Leu Asn Arg Pro Leu Thr Tyr Ser Glu Lys

50 55 60

Ile Leu Tyr Gly His Leu Asp Asp Pro Val Asn Gln Asp Ile Glu Arg

65 70 75 80

Gly Val Ser Tyr Leu Lys Leu Arg Pro Asp Arg Val Ala Cys Gln Asp

85 90 95

Ala Thr Ala Gln Met Ala Ile Leu Gln Phe Met Ser Ala Gly Met Pro

100 105 110

Glu Val Ala Val Pro Val Thr Val His Cys Asp His Leu Ile Glu Ala

115 120 125

Tyr Glu Gly Gly Pro Ile Asp Leu Glu Arg Ala Asn Val Thr Asn Lys

130 135 140

Glu Val Tyr Asp Phe Leu Gln Thr Ala Cys Ala Lys Tyr Asn Ile Gly

145 150 155 160

Phe Trp Arg Pro Gly Ser Gly Ile Ile His Gln Ile Val Leu Glu Asn

165 170 175

Tyr Ala Phe Pro Gly Gly Leu Leu Ile Gly Thr Asp Ser His Thr Pro

180 185 190

Asn Ala Gly Gly Leu Gly Met Val Ala Ile Gly Val Gly Gly Ala Asp
 195 200 205
 Ala Val Asp Val Met Ala Asn Leu Pro Trp Glu Leu Lys Cys Pro Lys
 210 215 220
 Val Ile Gly Val Lys Leu Thr Gly Gln Leu Lys Gly Trp Thr Ser Pro
 225 230 235 240
 Lys Asp Val Ile Leu Lys Val Ala Gly Ile Leu Thr Val Lys Gly Gly
 245 250 255

 Thr Gly Ala Ile Val Glu Tyr Phe Gly Pro Gly Val Glu Ser Leu Ser
 260 265 270
 Cys Thr Gly Met Gly Thr Ile Cys Asn Met Gly Ala Glu Ile Gly Ala
 275 280 285
 Thr Thr Ser Ile Phe Pro Phe Asn Pro Arg Met Ser Glu Tyr Leu Arg
 290 295 300
 Ala Thr Asn Arg Ser Ala Ile Ala Asp Tyr Ala Glu Glu Phe Ala Pro
 305 310 315 320

 Ile Ile Ala Ala Asp Glu Asn Ala His Tyr Asp Gln Ile Ile Glu Ile
 325 330 335
 Asp Leu Asn Thr Leu Glu Pro His Leu Asn Gly Pro Phe Thr Pro Asp
 340 345 350
 Leu Ala Thr Pro Ile Ser Lys Phe Lys Glu Ala Val Lys Lys Asn Asp
 355 360 365
 Trp Pro Gln Glu Leu Lys Val Gly Leu Ile Gly Ser Cys Thr Asn Ser
 370 375 380

 Ser Tyr Glu Asp Met Ser Arg Ala Ala Ser Ile Cys Gln Gln Ala Ile
 385 390 395 400
 Asp Lys Gly Ile Lys Thr Lys Ser Leu Phe Thr Ile Thr Pro Gly Ser
 405 410 415
 Glu Gln Val Arg Ala Thr Leu Thr Arg Asp Gly Gln Leu Asp Thr Met
 420 425 430
 Arg Lys Ala Gly Gly Ile Val Leu Ala Asn Ala Cys Gly Pro Cys Ile

435 440 445
 Gly Gln Trp Lys Arg Thr Asp Val Lys Lys Gly Glu Lys Asn Ser Ile
 450 455 460
 Val Thr Ser Tyr Asn Arg Asn Phe Thr Gly Arg Asn Asp Ala Asn Pro
 465 470 475 480
 Ala Thr His Ala Phe Val Thr Ser Pro Asp Ile Val Thr Ala Met Val
 485 490 495
 Phe Ser Gly Asp Met Asn Phe Asn Pro Leu Thr Asp Thr Leu Lys Asp
 500 505 510

 Lys Asp Gly Asn Asp Phe Lys Phe Glu Pro Pro Thr Gly Ala Gly Leu
 515 520 525
 Pro Ser Lys Gly Tyr Asp Pro Gly Ser Asn Thr Tyr Val Ala Pro Ser
 530 535 540
 Ser Val Asn Val Lys Asp Val Ala Ile Asp Pro His Ser Lys Arg Leu
 545 550 555 560
 Gln Arg Leu Thr Pro Phe Lys Lys Trp Asp Gly Lys Asp Met Lys Gly
 565 570 575

 Leu Lys Ile Leu Ile Lys Ala Lys Gly Lys Cys Thr Thr Asp His Ile
 580 585 590
 Ser Ala Ala Gly Pro Trp Leu Lys Tyr Arg Gly His Leu Gln Asn Ile
 595 600 605
 Ser Asn Asn Tyr Met Ile Gly Ala Ile Asn Ala Glu Asn Gly Glu Ala
 610 615 620
 Asn Lys Leu Lys Asp Gln Leu Thr Gly Glu Tyr Lys Thr Val Pro Asn
 625 630 635 640

 Val Ala Ile Asp Tyr Arg Asp His Gly Ile Arg Trp Val Thr Leu Gly
 645 650 655
 Glu Gln Asn Phe Gly Glu Gly Ser Ser Arg Glu His Ala Ala Leu Glu
 660 665 670
 Pro Arg Tyr Leu Gly Gly Ala Ala Val Ile Thr Lys Ser Phe Ala Arg
 675 680 685

Ile His Glu Thr Asn Leu Lys Lys Gln Gly Leu Leu Pro Leu Thr Phe
690 695 700

Ala Asp Pro Ala Ala Tyr Asp Lys Ile Ser Pro Phe Asp Thr Val Asp
705 710 715 720

Ile Asp Gly Leu Thr Thr Phe Ala Pro Gly Lys Pro Leu Thr Leu Val
725 730 735

Val His Pro Ala Asp Gly Ser Ala Glu Trp Ser Thr Lys Leu Asn His
740 745 750

Thr Phe Asn Lys Asp Gln Ile Glu Trp Phe Lys Ala Gly Ser Ala Leu
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Asn His Met Ala Asn Met His Lys Gln Lys
770 775

<210> 159

<211> 2367

<212> DNA

<213> Kluyveromyces lactis

<400> 159

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ttggaagacc attccttcat taactataaa caaaacattg agtatgtcaa tatcgtcaga 180
gaaagactag gacgtccatt gacatacgca gaaaagattt tgtacggtca ttgggatgat 240
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gcttgtaag atgctaccgc tcaaatggct atcttgcaat tcatgtcagc aggtttacct 360
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gaaaaggatt tgaagagagc cattgataac aacaaggaag ttacgattt ctgggtact 480
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<210> 160

<211> 788

<212> PRT

<213> Kluyveromyces lactis

<400> 160

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Asp Ser Lys Val His Gln Asn Leu Leu Glu Asp His Ser Phe Ile Asn
35 40 45
Tyr Lys Gln Asn Ile Glu Tyr Val Asn Ile Val Arg Glu Arg Leu Gly
50 55 60
Arg Pro Leu Thr Tyr Ala Glu Lys Ile Leu Tyr Gly His Leu Asp Asp
65 70 75 80
Pro His Gly Gln Glu Ile Glu Arg Gly Val Ser Tyr Leu Lys Leu Arg
85 90 95
Pro Asp Arg Val Ala Cys Gln Asp Ala Thr Ala Gln Met Ala Ile Leu
100 105 110
Gln Phe Met Ser Ala Gly Leu Pro Gln Val Ala Lys Pro Leu Thr Val
115 120 125
His Cys Asp His Leu Ile Gln Ala Gln Ile Gly Gly Glu Lys Asp Leu
130 135 140
Lys Arg Ala Ile Asp Ile Asn Lys Glu Val Tyr Asp Phe Leu Ala Thr
145 150 155 160
Ala Thr Ala Lys Tyr Asn Met Gly Phe Trp Lys Pro Gly Ser Gly Ile
165 170 175
Ile His Gln Ile Val Leu Glu Asn Tyr Ala Phe Pro Gly Ala Leu Ile
180 185 190
Ile Gly Thr Asp Ser His Thr Pro Asn Ala Gly Gly Leu Gly Gln Leu
195 200 205
Ala Ile Gly Val Gly Gly Ala Asp Ala Val Asp Val Met Ser Asp Leu
210 215 220
Ala Trp Glu Leu Lys Ala Pro Lys Ile Met Gly Val Lys Leu Thr Gly
225 230 235 240
Arg Met Asn Gly Trp Thr Ser Pro Lys Asp Ile Ile Leu Lys Leu Ala

245 250 255
 Gly Ile Thr Thr Val Lys Gly Gly Thr Gly Lys Ile Val Glu Tyr Phe
 260 265 270
 Gly Asp Gly Val Asp Thr Phe Ser Ala Thr Gly Met Gly Thr Ile Cys
 275 280 285
 Asn Met Gly Ala Glu Ile Gly Ala Thr Thr Ser Val Phe Pro Phe Asn
 290 295 300
 Lys Ser Met Ile Asp Tyr Leu Asp Ala Thr Gly Arg Asp Lys Ile Ala

 305 310 315 320
 Gln Phe Ala Gln Leu Tyr His Lys Asp Leu Leu Ser Ala Asp Glu Gly
 325 330 335
 Ala Glu Tyr Asp Glu Ile Ile Glu Ile Asp Leu Asn Thr Leu Glu Pro
 340 345 350
 Tyr Val Asn Gly Pro Phe Thr Pro Asp Leu Ala Thr Pro Ile Ser Lys
 355 360 365
 Met Lys Asp Val Ala Val Lys Asn Asn Trp Pro Leu Glu Val Lys Val

 370 375 380
 Gly Leu Ile Gly Ser Cys Thr Asn Ser Ser Tyr Glu Asp Met Ser Arg
 385 390 395 400
 Ala Ala Ser Val Val Lys Asp Ala Ala Thr His Gly Leu Lys Ser Lys
 405 410 415
 Ser Ile Phe Thr Val Thr Pro Gly Ser Glu Gln Ile Arg Ala Thr Ile
 420 425 430
 Ala Arg Asp Gly Gln Leu Glu Thr Phe Lys Glu Phe Gly Gly Thr Val

 435 440 445
 Leu Ala Asn Ala Cys Gly Pro Cys Ile Gly Gln Trp Asp Arg Gln Asp
 450 455 460
 Ile Lys Lys Gly Asp Lys Asn Thr Ile Val Ser Ser Phe Asn Arg Asn
 465 470 475 480
 Phe Thr Ala Arg Asn Asp Gly Asn Pro Asp Thr His Ser Phe Val Ala
 485 490 495

Ser Pro Glu Ile Thr Thr Ala Phe Ala Ile Ala Gly Asp Leu Arg Phe

500 505 510

Asn Pro Leu Thr Asp Thr Leu Lys Asp Lys Asp Gly Asn Glu Phe Met

515 520 525

Leu Lys Pro Pro Thr Gly Val Gly Leu Pro Val Lys Gly Tyr Asp Pro

530 535 540

Gly Glu Asn Thr Tyr Gln Ala Pro Pro Lys Asp Arg Ser Ser Val Thr

545 550 555 560

Val Gln Val Ser Pro Thr Ser Asp Arg Leu Gln Leu Leu Lys Pro Phe

565 570 575

Lys Ala Trp Asp Gly Lys Asp Ala Phe Asp Met Pro Ile Leu Ile Lys

580 585 590

Ser Leu Gly Lys Thr Thr Thr Asp His Ile Ser Met Ala Gly Pro Trp

595 600 605

Leu Lys Tyr Arg Gly His Leu Glu Asn Ile Ser Asn Asn Tyr Met Ile

610 615 620

Gly Ala Ile Asn Ala Glu Asn Lys Lys Ala Asn Cys Val Lys His His

625 630 635 640

Tyr Thr Gly Glu Tyr Ala Gly Val Pro Asp Thr Ala Arg Ala Tyr Arg

645 650 655

Asp Ala Gly Ile Arg Trp Val Val Ile Gly Gly Glu Asn Phe Gly Glu

660 665 670

Gly Ser Ser Arg Glu His Ala Ala Leu Glu Pro Arg Phe Leu Gly Gly

675 680 685

Phe Ala Ile Ile Thr Lys Ser Phe Ala Arg Ile His Glu Thr Asn Leu

690 695 700

Lys Lys Gln Gly Met Leu Pro Leu Asn Phe Ala Glu Pro Ala Ala Tyr

705 710 715 720

Asp Lys Ile Asn Pro Asp Asp Thr Ile Asp Ile Leu Gly Leu Thr Thr

725 730 735

Leu Ala Pro Gly Lys Asn Leu Ile Met Arg Val His Pro Lys Glu Gly

740	745	750	
Glu Ala Trp Glu Thr Pro Leu Ser His Thr Phe Asn Ala Glu Gln Ile			
755	760	765	
Glu Trp Phe Lys Ala Gly Ser Ala Leu Asn Arg Leu Ala Asn Ala Lys			
770	775	780	
Lys Ala Lys Asn			
785			
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<211> 2376			
<212> DNA			
<213> Candida Albicans			
<400> 161			
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aagatattgt attcacattt atgcaatcca gaagaaagtc ttacttcac caatgtaagt			240
gataaaagg gccacaata ttggaattg caccagata gaggggccat gcaagatgct			300
tctgccaga tggcattgtt acaatttatg acatgtgga tgagttccac agcagttcca			360
gcctcaattc actgtgacca ttgattgtt ggtaaagatg gtgctgagga agatttagtt			420
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ggtgcaattg ccattgggtg tgggtgtgca gatgctgttg atgcattgac aggtaccct			660
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gccacaaga gatatttgat tgacacgcat agagcaccaa ttgccgaagc tgctgattcg			960
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gagataaatc tttctgaatt agaaccacat gtgaacgggc ctttactcc agatttgtct			1080
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<210> 162

<211> 791

<212> PRT

<213> Candida Albicans

<400> 162

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Leu Ala Thr Gln Ala Phe Asn Phe Ser Val Pro Pro Glu Tyr Gln Ser

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Arg Thr Pro Pro Tyr Ser Lys Leu Ile Asn Asn Leu Ser Thr Val Lys

35 40 45
 Lys Ile Leu Lys Asn Gln Pro Leu Thr Leu Ala Glu Lys Ile Leu Tyr
 50 55 60
 Ser His Leu Cys Asn Pro Glu Glu Ser Leu Thr Ser Ser Asn Val Ser
 65 70 75 80
 Asp Ile Arg Gly Gln Gln Tyr Leu Lys Leu His Pro Asp Arg Val Ala
 85 90 95
 Met Gln Asp Ala Ser Ala Gln Met Ala Leu Leu Gln Phe Met Thr Cys

 100 105 110
 Gly Met Ser Ser Thr Ala Val Pro Ala Ser Ile His Cys Asp His Leu
 115 120 125
 Ile Val Gly Lys Asp Gly Ala Glu Glu Asp Leu Val Lys Ser Ile Ala
 130 135 140
 Thr Asn Lys Glu Val Phe Asp Phe Leu Gln Ser Cys Gly Glu Lys Tyr
 145 150 155 160
 Gly Ile Gln Phe Trp Gly Pro Gly Ser Gly Ile Ile His Gln Ile Val

 165 170 175
 Leu Glu Asn Phe Ala Ala Pro Gly Leu Met Met Leu Gly Thr Asp Ser
 180 185 190
 His Thr Pro Asn Ala Gly Gly Leu Gly Ala Ile Ala Ile Gly Val Gly
 195 200 205
 Gly Ala Asp Ala Val Asp Ala Leu Thr Gly Thr Pro Trp Glu Leu Lys
 210 215 220
 Ala Pro Lys Ile Leu Gly Val Lys Leu Thr Gly Lys Leu Ser Gly Trp

 225 230 235 240
 Ser Ser Pro Lys Asp Val Ile Thr Thr Leu Ala Gly Ile Leu Thr Val
 245 250 255
 Arg Gly Gly Thr Gly Tyr Ile Val Glu Tyr Phe Gly Asp Gly Val Lys
 260 265 270
 Thr Leu Ser Cys Thr Gly Met Ala Thr Ile Cys Asn Met Gly Ala Glu
 275 280 285

Ile Gly Ala Thr Thr Ser Thr Phe Pro Tyr Gln Glu Ala His Lys Arg

290 295 300

Tyr Leu Ile Asp Thr His Arg Ala Pro Ile Ala Glu Ala Ala Asp Ser

305 310 315 320

Val Asn Ser Glu Phe Lys Phe Leu Gln Ala Asp Glu Gly Ala Glu Tyr

325 330 335

Asp Lys Val Ile Glu Ile Asn Leu Ser Glu Leu Glu Pro His Val Asn

340 345 350

Gly Pro Phe Thr Pro Asp Leu Ser Thr Pro Ile Ser Lys Phe Gly Glu

355 360 365

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

370 375 380

Gly Ser Cys Thr Asn Ser Ser Tyr Gln Asp Met Ser Arg Ala Val Ser

385 390 395 400

Ile Ile Lys Gln Ala Glu Ala Val Gly Leu Lys Pro Lys Ile Pro Phe

405 410 415

Phe Val Thr Pro Gly Ser Glu Gln Ile Arg Ala Thr Ile Glu Arg Asp

420 425 430

Gly Leu Ile Asn Thr Phe Glu Ser Asn Gly Ala Ile Val Leu Ala Asn

435 440 445

Ala Cys Gly Pro Cys Ile Gly Gln Trp Asp Arg Thr Asp Val Pro Lys

450 455 460

Thr Ser Thr Asp Phe Asn Ala Ile Phe Thr Ser Phe Asn Arg Asn Phe

465 470 475 480

Arg Ala Arg Asn Asp Gly Asn Arg Asn Thr Met Asn Phe Leu Thr Ser

485 490 495

Pro Asp Met Val Thr Ala Met Ile Tyr Ser Gly Asp Met Asn Phe Asn

500 505 510

Pro Val Thr Asp Ser Ile Glu Leu Pro Asn Gly Lys Glu Phe Arg Phe

515 520 525

Gln Pro Pro Gln Gly Lys Asp Leu Pro Gln Ser Gly Phe Ile Pro Gly

530 535 540
 Arg Ser Glu Phe Tyr Pro Glu Ala Asn Pro Gln Pro Lys Pro Glu Val

 545 550 555 560
 Glu Val Asn Val Ser Pro Ser Ser Asp Arg Leu Gln Leu Leu Glu Pro

 565 570 575
 Phe Gln Pro Trp Ser Gly Glu Glu Leu Ser Thr Thr Val Leu Leu Lys

 580 585 590
 Val Glu Gly Lys Cys Thr Thr Asp His Ile Ser Ala Ala Gly Val Trp

 595 600 605
 Leu Lys Tyr Lys Gly His Leu Glu Asn Ile Ser Tyr Asn Thr Leu Ile

 610 615 620
 Gly Ala Val Asn Lys Glu Thr Gly Glu Val Asn Lys Ala Tyr Asp Leu
 625 630 635 640
 Asn Gly Asp Ala Tyr Gly Ile Pro Glu Leu Met Ile Lys Trp Lys Asp

 645 650 655
 Glu Ser Arg Pro Trp Val Val Val Ala Glu His Asn Tyr Gly Glu Gly

 660 665 670
 Ser Ala Arg Glu His Ala Ala Leu Ser Pro Arg Phe Leu Gly Gly Ser

 675 680 685
 Val Ile Leu Val Lys Ser Phe Ala Arg Ile His Glu Thr Asn Leu Lys

 690 695 700
 Lys Gln Gly Met Leu Pro Leu Thr Phe Ala Asp Glu Ala Asp Tyr Asp
 705 710 715 720
 Lys Ile Ser Ser Gly Asp Leu Leu Thr Thr Ile Asp Leu Lys Asp Met

 725 730 735
 Ile Ala Lys Asp Gly Asn Asn Gly Gly Thr Leu Arg Val Lys Val Thr

 740 745 750
 Lys Arg Asp Gly Ser Glu Phe Glu Ile Leu Ala Lys His Thr Met Ser

 755 760 765
 Lys Asp Gln Val Glu Phe Phe Lys Ala Gly Ser Ala Ile Asn Tyr Ile

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Gly Asn Thr Lys Lys Gly Leu

785

790

<210> 163

<211> 2373

<212> DNA

<213> *Yarrowia lipolytica*

<400> 163

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gcgtccattc actgtgacca tctgattgtt ggccgagacg gtgccgatga tgatctgacc 420

cgatctatcg ctaccaacca ggagggtgtt gacttctgc agcaatgtgc cgagaagtac 480

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<210> 164

<211> 790

<212> PRT

<213> *Yarrowia lipolytica*

<400> 164

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Ala Arg Gly Leu Ala Thr Thr Ala Asn Ala Ser Gly Leu Ser Val Pro

20 25 30

Ala Asp Phe Lys Thr Arg Thr Pro Pro Tyr Ala Glu Leu Ile Asn Arg

35 40 45

Leu Asp Gln Val Lys Lys Ile Ile Asn Arg Asn Asp Leu Thr Leu Ala

50 55 60

Glu Lys Ile Leu Tyr Ser His Leu His Asn Pro Glu Glu Thr Pro Ser

65 70 75 80

Ile Thr Arg Gly Asp Thr Tyr Leu Lys Leu Asn Pro Asp Arg Val Ala
 85 90 95
 Met Gln Asp Ala Ser Ala Gln Met Ala Leu Leu Gln Phe Met Thr Cys
 100 105 110
 Gly Leu Pro Ser Thr Ala Val Pro Ala Ser Ile His Cys Asp His Leu
 115 120 125
 Ile Val Gly Arg Asp Gly Ala Asp Asp Asp Leu Thr Arg Ser Ile Ala
 130 135 140

 Thr Asn Gln Glu Val Phe Asp Phe Leu Gln Gln Cys Ala Glu Lys Tyr
 145 150 155 160
 Gly Ile Gln Phe Trp Gly Pro Gly Ser Gly Ile Ile His Gln Ile Val
 165 170 175
 Leu Glu Asn Phe Ser Val Pro Gly Leu Met Met Leu Gly Thr Asp Ser
 180 185 190
 His Thr Pro Asn Ala Gly Gly Leu Gly Ala Ile Ala Ile Gly Val Gly
 195 200 205

 Gly Ala Asp Ala Val Asp Ala Leu Thr Gly Thr Pro Trp Glu Leu Lys
 210 215 220
 Ala Pro Lys Ile Leu Gly Val Lys Leu Thr Gly Lys Leu Ser Gly Trp
 225 230 235 240
 Ala Ser Pro Lys Asp Val Ile Thr His Leu Ala Gly Lys Leu Thr Val
 245 250 255
 Arg Gly Gly Thr Gly Asn Ile Ile Glu Tyr His Gly Glu Gly Val Asp
 260 265 270

 Ser Leu Ser Cys Thr Gly Met Ala Thr Ile Cys Asn Met Gly Ala Glu
 275 280 285
 Val Gly Ala Thr Thr Ser Thr Phe Pro Phe Thr Glu Ser Met Arg Arg
 290 295 300
 Tyr Leu Glu Ala Thr Gly Arg Ala Pro Ile Ala Ala Ala Ala Ala Ala
 305 310 315 320
 Ala Arg Asp Arg Gly Phe Leu Ala Ala Asp Glu Gly Ala Gln Tyr Asp

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

Phe Asn Asn Gln Glu Leu Lys Leu Ser Val Leu Met Lys Val Glu Gly
580 585 590

Lys Cys Thr Thr Asp His Ile Ser Ala Ala Gly Ala Trp Leu Lys Tyr
595 600 605

Lys Gly His Leu Glu Asn Ile Ser Tyr Asn Thr Leu Ile Gly Ala Leu
610 615 620

Asn Lys Glu Thr Gln Lys Val Asn His Thr Ile Asp Ala Ala Asp Gly
625 630 635 640

Ser Glu Gln Ser Ile Pro Asp Leu Met Ile Lys Trp Lys Glu Gln Gly
645 650 655

Lys Pro Trp Ile Val Val Ala Glu His Asn Tyr Gly Glu Gly Ser Ala
660 665 670

Arg Glu His Ala Ala Leu Ser Pro Arg Phe Leu Gly Gly Gln Ala Ile
675 680 685

Leu Val Lys Ser Phe Ala Arg Ile His Glu Thr Asn Leu Lys Lys Gln
690 695 700

Gly Met Leu Pro Leu Thr Phe Glu Asn Glu Ala Asp Tyr Asp Lys Ile
705 710 715 720

Gln Ala Cys Asp Thr Leu Glu Thr Leu Asp Leu Leu Asp Met Leu Glu
725 730 735

Lys Gly Gly Asp Asn Gly Gly Phe Val Gln Met Arg Ala Thr Lys Ser
740 745 750

Asp Gly Ser Thr Tyr Asp Phe Arg Ala Arg His Thr Met Ser Ala Asp
755 760 765

Gln Val Asp Phe Phe Lys Ala Gly Ser Ala Ile Asn Phe Ile Gly Ala
770 775 780

Gln Lys Ala Ala Asn Lys
785 790

<210> 165

<211> 2343

<212> DNA

<213> Pichia stipitis

<400> 165

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aagaagcaac tcgagaacct cgacatcgtc aaggccagat tgaacagacc ttgacttat	180
gccgaaaagc ttctctacgg tcaattggac gacctcacg gacaagacat ccagagaggt	240
gtctctact tgaagttag accagatcgt gtcgcttgtc aagatgccac cgctcaaattg	300
gccattttgc aattcatgtc tgccggtttg cctcaagttg ccactccttc cactgtccac	360
tgtgaccatt tgatccaggc ccaaatgggt ggtgctaagg atttggccag agctattgac	420
ttgaacaagg aagtgtacga cttcttgtcg actgcctgtg ccaatacaa cttgggtttc	480
tggaaagccc gtccggtat catccatcag atcgatttgg aaaactacgc ctcccaggt	540
gctttgttga tcggtaccga ttgcacact cctaattgtg gtggtttggg tcaattggct	600
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gctccaaaga tcattgggtg caagttgacc ggtagaatgt ccggtggac ctgcctaaag	720
gatatcatct tgaagttggc tggatcacc actgtcaagg gtggtaccgg ttccattgtt	780
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tatttgaatg ccaattgtag atccaacatt gccgagtttg ccaacttgta caagaaggac	960
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aaggaaactg ccatcaagaa cggctggcca ttggaagtca aggttggttt gattggttct	1140
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taa 2343

<210> 166

<211> 780

<212> PRT

<213> *Pichia stipitis*

<400> 166

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20 25 30

Glu Ser His Ser Phe Ile Gln Tyr Lys Lys Gln Leu Glu Asn Leu Asp

35 40 45

Ile Val Lys Ala Arg Leu Asn Arg Pro Leu Thr Tyr Ala Glu Lys Leu

50 55 60

Leu Tyr Gly His Leu Asp Asp Pro His Gly Gln Asp Ile Gln Arg Gly

65 70 75 80

Val Ser Tyr Leu Lys Leu Arg Pro Asp Arg Val Ala Cys Gln Asp Ala

85 90 95

Thr Ala Gln Met Ala Ile Leu Gln Phe Met Ser Ala Gly Leu Pro Gln

100 105 110

Val Ala Thr Pro Ser Thr Val His Cys Asp His Leu Ile Gln Ala Gln

115 120 125
 Ile Gly Gly Ala Lys Asp Leu Ala Arg Ala Ile Asp Leu Asn Lys Glu
 130 135 140
 Val Tyr Asp Phe Leu Ser Thr Ala Cys Ala Lys Tyr Asn Leu Gly Phe
 145 150 155 160
 Trp Lys Pro Gly Ser Gly Ile Ile His Gln Ile Val Leu Glu Asn Tyr
 165 170 175
 Ala Phe Pro Gly Ala Leu Leu Ile Gly Thr Asp Ser His Thr Pro Asn

 180 185 190
 Ala Gly Gly Leu Gly Gln Leu Ala Ile Gly Val Gly Gly Ala Asp Ala
 195 200 205
 Val Asp Val Met Ala Asp Leu Ala Trp Glu Leu Lys Ala Pro Lys Ile
 210 215 220
 Ile Gly Val Lys Leu Thr Gly Arg Met Ser Gly Trp Thr Ser Pro Lys
 225 230 235 240
 Asp Ile Ile Leu Lys Leu Ala Gly Ile Thr Thr Val Lys Gly Gly Thr

 245 250 255
 Gly Ser Ile Val Glu Tyr Phe Gly Ser Gly Val Glu Thr Phe Ser Cys
 260 265 270
 Thr Gly Met Gly Thr Ile Cys Asn Met Gly Ala Glu Ile Gly Ala Thr
 275 280 285
 Thr Ser Val Phe Pro Phe Asn Asn Ser Met Val Asp Tyr Leu Asn Ala
 290 295 300
 Thr Gly Arg Ser Asn Ile Ala Glu Phe Ala Asn Leu Tyr Lys Lys Asp

 305 310 315 320
 Tyr Leu Ser Ala Asp Glu Gly Cys Glu Tyr Asp Gln Val Ile Glu Ile
 325 330 335
 Asp Leu Asn Thr Leu Glu Pro His Ile Asn Gly Pro Phe Thr Pro Asp
 340 345 350
 Leu Ala Thr Pro Val Ser Lys Met Lys Glu Thr Ala Ile Lys Asn Gly
 355 360 365

Trp Pro Leu Glu Val Lys Val Gly Leu Ile Gly Ser Cys Thr Asn Ser

370

375

380

Ser Tyr Glu Asp Met Thr Arg Ala Ala Ser Ile Ile Glu Asp Ala Ala

385

390

395

400

Thr His Gly Leu Lys Ser Lys Ala Ile Tyr Thr Val Ser Pro Gly Ser

405

410

415

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

420

425

430

Glu Asp Phe Gly Gly Val Val Met Ala Asn Ala Cys Gly Pro Cys Ile

435

440

445

Gly Gln Trp Asp Arg Gln Asp Ile Lys Lys Gly Asp Lys Asn Thr Ile

450

455

460

Val Ser Ser Phe Asn Arg Asn Phe Thr Ala Arg Asn Asp Gly Asn Pro

465

470

475

480

Ala Thr His Ala Phe Val Ala Ser Pro Glu Met Thr Thr Ala Phe Ala

485

490

495

Ile Ser Gly Asp Leu Gly Phe Asn Pro Ile Thr Asp Thr Leu Lys Asp

500

505

510

Ala Asn Gly Asn Glu Phe Lys Leu Lys Glu Pro Val Gly Val Gly Leu

515

520

525

Pro Val Asn Gly Tyr Asp Pro Gly Glu Asn Thr Tyr Gln Ala Pro Pro

530

535

540

Glu Asp Arg Ser Thr Val Gln Val Gln Ile Ala Pro Thr Ser Asp Arg

545

550

555

560

Leu Gln Lys Leu Thr Pro Phe Lys Pro Trp Asp Gly Lys Asp Ala Glu

565

570

575

Arg Leu Pro Ile Leu Ile Lys Ala Val Gly Lys Thr Thr Thr Asp His

580

585

590

Ile Ser Met Ala Gly Pro Trp Leu Lys Tyr Arg Gly His Leu Glu Asn

595

600

605

Ile Ser Asn Asn Tyr Met Ile Gly Ala Ile Asn Ala Glu Asn Gly Glu

610 615 620
Ala Asn Asn Val Lys Asn His Tyr Thr Gly Val Tyr Ser Gly Val Pro

625 630 635 640
Asp Thr Gly Ala Ala Tyr Arg Asp Ala Gly His Lys Trp Val Val Ile

645 650 655
Gly Asp Glu Asn Phe Gly Glu Gly Ser Ser Arg Glu His Ala Ala Leu

660 665 670
Glu Pro Arg Phe Leu Gly Gly Phe Ala Ile Ile Thr Lys Ser Phe Ala

675 680 685
Arg Ile His Glu Thr Asn Leu Lys Lys Gln Gly Leu Leu Pro Leu Asn

690 695 700
Phe Thr Asp Val Ala Ala Tyr Asp Lys Ile Gln Pro Glu Asp Glu Val

705 710 715 720
Asp Leu Leu Gly Leu Thr Glu Leu Ala Pro Gly Lys Asn Val Ile Leu

725 730 735
Arg Val His Pro Ala Asp Gly Ser Ala Thr Trp Glu Thr Glu Leu Ser

740 745 750
His Thr Tyr Asn Ile Glu Gln Ile Glu Trp Phe Lys Tyr Gly Ser Ala

755 760 765
Leu Asn Lys Met Ala Ala Val Ala Ala Glu Lys Lys

770 775 780

<210> 167

<211> 2358

<212> DNA

<213> Candida glabrata

<400> 167

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caggaagttt ttgatttcct ggagagctgt gcgaagagat acggcataca gtctctgggt	480
cctgggtccg gtattatcca tcaaatcgtg ctggagaact tctccgcgcc tggtttgatg	540
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aaggttctgg gtgttaaatt gaccggtaaa ctacacggct ggtcggctcc aaaggatgtc	720
atcccatgc ttgcaggtaa actaacgtt agaggtagta caggctacat tgtcgaatat	780
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ttcctaagag cggatgaagg tgctcaatat gacgaagtaa tagaaattaa cctatccgag	1020
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aaggctggtt tgaagcctcg cattcctttc ttgttactc caggatctga agctatcaga	1260
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ctgtcaaagg atcaaattga cttctttaag gctggatcag ctatcaactt cattggtgaa 2340

caacgtagaa accactga 2358

<210> 168

<211> 785

<212> PRT

<213> Candida glabrata

<400> 168

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Ile Pro Ser Val Pro Glu Asn Leu Arg Ala Tyr Thr Pro Pro Tyr Ala

20 25 30

Lys Leu Leu Asn Asn Leu Asp Lys Val Lys Gln Ile Leu Asn Asn Glu

35 40 45

Pro Leu Thr Leu Ala Glu Lys Ile Leu Tyr Ser His Leu Cys Asn Pro

50 55 60

Glu Glu Ser Leu Thr Ser Ser Arg Val Ala Asp Ile Arg Gly Gln Lys

65 70 75 80

Tyr Leu Lys Leu Asn Pro Asp Arg Val Ala Met Gln Asp Ala Ser Ala

85 90 95

Gln Met Ala Leu Leu Gln Phe Met Thr Thr Gly Leu Ser Glu Thr Ala

100 105 110

Val Pro Ala Ser Ile His Cys Asp His Leu Ile Val Gly Lys Asp Gly

115 120 125

Glu Thr Lys Asp Leu Arg Asn Ser Ile Lys Thr Asn Gln Glu Val Phe

130 135 140

Asp Phe Leu Glu Ser Cys Ala Lys Arg Tyr Gly Ile Gln Phe Trp Gly

145 150 155 160

Pro Gly Ser Gly Ile Ile His Gln Ile Val Leu Glu Asn Phe Ser Ala

165 170 175

Pro Gly Leu Met Met Leu Gly Thr Asp Ser His Thr Pro Asn Ala Gly
180 185 190

Gly Leu Gly Ala Ile Ala Ile Gly Val Gly Gly Ala Asp Ala Val Asp
195 200 205

Ala Leu Thr Gly Thr Pro Trp Glu Leu Lys Ala Pro Lys Val Leu Gly
210 215 220

Val Lys Leu Thr Gly Lys Leu His Gly Trp Ser Ala Pro Lys Asp Val
225 230 235 240

Ile Thr Met Leu Ala Gly Lys Leu Thr Val Arg Gly Gly Thr Gly Tyr
245 250 255

Ile Val Glu Tyr Phe Gly Glu Gly Val Glu Thr Leu Ser Cys Thr Gly
260 265 270

Met Ala Thr Ile Cys Asn Met Gly Ala Glu Ile Gly Ala Thr Thr Ser
275 280 285

Thr Phe Pro Tyr Gln Ala Ala His Lys Arg Tyr Leu Glu Ala Thr Gly
290 295 300

Arg Gly Phe Val Ala Thr Ala Ala Asp Ala Ala Leu Ala Asn Tyr Asn
305 310 315 320

Phe Leu Arg Ala Asp Glu Gly Ala Gln Tyr Asp Glu Val Ile Glu Ile
325 330 335

Asn Leu Ser Glu Leu Glu Pro His Val Asn Gly Pro Phe Thr Pro Asp
340 345 350

Leu Ser Thr Pro Ile Thr Lys Tyr Ala Glu Arg Ser Leu Glu Glu Lys
355 360 365

Trp Pro Gln Asn Ile Ser Ala Ala Leu Ile Gly Ser Cys Thr Asn Ser
370 375 380

Ser Tyr Gln Asp Met Ser Arg Val Ile Asp Leu Val Asn Gln Ala Glu
385 390 395 400

Lys Ala Gly Leu Lys Pro Arg Ile Pro Phe Phe Val Thr Pro Gly Ser
405 410 415

Glu Ala Ile Arg Ala Thr Leu Asp Arg Asp Gly Leu Ile Lys Lys Phe

				420				425				430			
Glu	Asp	Asn	Gly	Ala	Ile	Val	Leu	Ala	Asn	Ala	Cys	Gly	Pro	Cys	Ile
435				440				445							
Gly	Gln	Trp	Asp	Arg	Glu	Asp	Val	Pro	Lys	Glu	Ser	Ser	Glu	Thr	Asn
450				455				460							
Ser	Ile	Phe	Thr	Ser	Phe	Asn	Arg	Asn	Phe	Arg	Ala	Arg	Asn	Asp	Gly
465				470				475				480			
Asn	Arg	Asn	Thr	Met	Asn	Phe	Leu	Thr	Ser	Pro	Glu	Ile	Val	Thr	Ala
485				490				495							
Met	Ser	Tyr	Ser	Gly	Asn	Ala	Gln	Phe	Asn	Pro	Leu	Thr	Asp	Ala	Ile
500				505				510							
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Glu	Leu	Pro	Ser	Lys	Gly	Phe	Glu	His	Gly	Arg	Asp	Lys	Phe	Tyr	Pro
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Thr	Ser	Asp	Arg	Leu	Gln	Leu	Leu	Glu	Pro	Phe	Lys	Pro	Trp	Asn	Gly
565				570				575							
Lys	Glu	Leu	Arg	Thr	Asn	Val	Leu	Met	Lys	Val	Glu	Gly	Lys	Cys	Thr
580				585				590							
Thr	Asp	His	Ile	Ser	Ala	Ala	Gly	Val	Trp	Leu	Lys	Tyr	Lys	Gly	His
595				600				605							
Leu	Glu	Asn	Ile	Ser	Tyr	Asn	Thr	Leu	Ile	Gly	Ala	Gln	Asn	Lys	Glu
610				615				620							
Thr	Gly	Glu	Val	Asn	Lys	Ala	Tyr	Asp	Leu	Asp	Gly	Thr	Ala	Tyr	Asp
625				630				635				640			
Ile	Pro	Gly	Leu	Met	Met	Lys	Trp	Lys	Glu	Asp	Gly	Arg	Pro	Trp	Thr
645				650				655							
Val	Val	Ala	Glu	His	Asn	Tyr	Gly	Glu	Gly	Ser	Ala	Arg	Glu	His	Ala
660				665				670							

Ala Leu Ser Pro Arg Tyr Leu Gly Gly Gln Met Ile Leu Val Lys Ser
675 680 685

Phe Ala Arg Ile His Glu Thr Asn Leu Lys Lys Gln Gly Met Leu Pro
690 695 700

Leu Thr Phe Ala Asp Glu Ala Asp Tyr Asp Arg Ile Ser Gly Gly Asp
705 710 715 720

Thr Leu Glu Thr Val Gly Leu Ile Asp Leu Val Ala Gln Asp Gly Asn
725 730 735

Asn Gly Gly Phe Leu Asp Val Lys Val Thr Lys Pro Asn Gly Glu Ser
740 745 750

Phe Ile Ile Lys Thr Lys His Thr Leu Ser Lys Asp Gln Ile Asp Phe
755 760 765

Phe Lys Ala Gly Ser Ala Ile Asn Phe Ile Gly Glu Gln Arg Arg Asn
770 775 780

His

785

<210> 169

<211> 2334

<212> DNA

<213> Candida glabrata

<400> 169

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tacgtgaaa agatcctgta cggtcacttg gacgaccac acggacaaca gatcgagaga 240

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gacctaaata aggaagtcta cgacttcttg gcttctgcct ccgctaagta caacatcggt 480

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ccaaagaacg gtgaagcttg ggactgtgag ttgactcaca ctttcaacag cgagcaaadc 2280

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<210> 170

<211> 777

<212> PRT

<213> Candida glabrata

<400> 170

Met Leu Ser Ala Arg Thr Val Val Arg Asn Thr Gly Val Arg Arg Leu

1 5 10 15

Ala Thr Val Ser Asn Leu Thr Arg Asp Ser Lys Val Asn Gln Asn Leu

20 25 30

Leu Glu Asp His Ser Phe Ile Asn Tyr Lys Gln Asn Ile Glu Tyr Val

35 40 45

Asp Ile Val Arg Lys Arg Leu Gly Arg Pro Leu Thr Tyr Ala Glu Lys

50 55 60

Ile Leu Tyr Gly His Leu Asp Asp Pro His Gly Gln Gln Ile Glu Arg

65 70 75 80

Gly Val Ser Tyr Leu Lys Leu Arg Pro Asp Arg Val Ala Cys Gln Asp

85 90 95

Ala Thr Ala Gln Met Ala Ile Leu Gln Phe Met Ser Ala Gly Leu Pro

100 105 110

Glu Val Ala Arg Pro Val Thr Val His Cys Asp His Leu Ile Gln Ala

115 120 125

Gln Ile Gly Gly Glu Lys Asp Leu Lys Arg Ala Val Asp Leu Asn Lys

130 135 140

Glu Val Tyr Asp Phe Leu Ala Ser Ala Ser Ala Lys Tyr Asn Ile Gly

145 150 155 160

Phe Trp Lys Pro Gly Ser Gly Ile Ile His Gln Ile Val Leu Glu Asn

165 170 175

Tyr Ala Phe Pro Gly Ala Leu Ile Ile Gly Thr Asp Ser His Thr Pro

180 185 190

Asn Ala Gly Gly Leu Gly Gln Leu Ala Ile Gly Val Gly Gly Ala Asp

195 200 205

Ala Val Asp Val Met Ala Gly Leu Pro Trp Glu Leu Lys Ala Pro Lys

210 215 220

Ile Leu Gly Val Lys Leu Thr Gly Arg Met Asn Gly Trp Thr Ser Pro

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

Pro Gln Thr His Ala Phe Val Ala Ser Pro Glu Ile Val Thr Ala Phe
485 490 495

Ala Ile Ala Gly Asp Leu Arg Phe Asn Pro Leu Thr Asp Lys Leu Lys
500 505 510

Asp Lys Asp Gly Asn Glu Phe Lys Leu Lys Glu Pro Phe Gly Asn Gly
515 520 525

Leu Pro Glu Arg Gly Tyr Asp Pro Gly Glu Asn Thr Tyr Gln Ala Pro
530 535 540

Pro Lys Asp Arg Asn Ala Val Asp Val Lys Val Ala Pro Thr Ser Asp
545 550 555 560

Arg Leu Gln Val Leu Lys Pro Phe Lys Pro Trp Asp Gly Lys Asp Ala
565 570 575

Leu Asn Met Pro Ile Leu Ile Lys Ser Leu Gly Lys Thr Thr Thr Asp
580 585 590

His Ile Ser Met Ala Gly Pro Trp Leu Lys Tyr Arg Gly His Leu Glu
595 600 605

Asn Ile Ser Asn Asn Tyr Met Ile Gly Ala Ile Asn Ala Glu Asn Lys
610 615 620

Lys Ala Asn Ser Val Arg Asn Val Tyr Thr Gly Glu Tyr Lys Gly Val
625 630 635 640

Pro Asp Thr Ala Arg Asp Tyr Arg Asp Glu Gly Ile Lys Trp Val Val
645 650 655

Ile Gly Asp Glu Asn Phe Gly Glu Gly Ser Ser Arg Glu His Ala Ala
660 665 670

Leu Glu Pro Arg Phe Leu Gly Gly Phe Ala Ile Ile Thr Lys Ser Phe
675 680 685

Ala Arg Ile His Glu Thr Asn Leu Lys Lys Gln Gly Leu Leu Pro Leu
690 695 700

Asn Phe Lys Asn Pro Ala Asp Tyr Asp Lys Ile Asn Pro Asp Asp Lys
705 710 715 720

Ile Asp Ile Leu Gly Leu Thr Glu Leu Ala Pro Gly Lys Asn Val Thr

725	730	735	
Met Arg Val His Pro Lys Asn Gly Glu Ala Trp Asp Cys Glu Leu Thr			
740	745	750	
His Thr Phe Asn Ser Glu Gln Ile Glu Trp Phe Lys Tyr Gly Ser Ala			
755	760	765	
Leu Asn Lys Ile Lys Ala Asp Lys Ala			
770	775		

<210> 171

<211> 2070

<212> DNA

<213> Candida glabrata

<400> 171

atggtggtac tgcgtaggtc tttccacgta tatactcgac tgcagcgcgg tcagaacttg	60
actgagaaga ttgtgcagca atacagcgtc ggtcttgccc caggtaagcg agtgcactcc	120
ggtgactatg tctccatcaa gccagcacac gtcattgtccc atgacaactc ctggccagtg	180
gcattgaagt tcatgaacct cggtgcccgc acagtgaagg accccaggca gatagtcaac	240
acgtggacc acgacatcca gaacaagtcc gacaagaact tgaccaagta cagaaacatc	300
gagagcttcg ccaagaagca cggcatcgac ttctaccgag caggcagagg tatcggccac	360
cagatcatgg tcgaggaagg ctacgctttc ccattgaact tgaccgtggc ctcagactca	420
cactccaaca cttacgggtgg tatgggtgcc ctgggtaccc cagtgggtgag aacagacgcg	480
gctgccatct gggccacagg ccagacctgg tggcagatcc caccagtggc ccaagttgag	540
ttcaagggca agctacatga atcagtgtca ggtaaagaca tcatcgtcgc tctgtgcggt	600
gtcttcaaca aggatcaagt gctgaaccac gccatcgagt ttacaggaga tgccatcaag	660
cacctgcccc tggatttcag attacaata gccaatga cgacagaatg ggggtgccctt	720
tcaggcttat tcccagtaga tgacacctg atcaattggt acaagaatcg tctgaacata	780
gtcggtccta accaccaag gatcaatgag acaaccatca agaacttgga agacaaagcc	840
aaagtattca aggtgactc cgacgccgtc tacgctaaaa agctagtcac cgatctatcg	900
actttgactc aciatgtgtc aggtccaaat agcgtcaaag tctctaacac tgtccaggat	960
ctggctcgcg ataacataaa gatcaacaag gcttacctgg tgtcctgtac caacgctcgt	1020
ctctctgatt tggaatctgc cgctaaagtc gtttgcccaa cgggagacct ctccaaggtc	1080
aacaaagttg ctgacggtgt tgagttctac ttcgctgctg cttcttctga aattgagaaa	1140

gaagctgctg agaagggtat atggcaagca ctattggccg ctggctgtaa gcctctgcca 1200
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atcagtgcc aacacagaaa cttcaagggt agaatgggtt caaaggatgc ttggcctac 1320
ttggcctccc cagccgtggt tgccgcatct gctgtcttgg gtagaatcgg ttctccagct 1380
gaagtatggg gtattgagga cgtcaagtct tctggattac ttgccgagga gttagcatgc 1440

aacactgaaa cctcaaccgc cacaccagtt tctgaagggt ctgctgctaa ggttgaaatg 1500
ttagaaggct tcccagaaga gattgtaggt gaattgggtc tttgtgacgc cgacaacgta 1560
aataccgatg gtatttacc aggttaagtat acgtaccaag atgatgtctc tcgtgagact 1620
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gatattttgg tgagtggatt taactttggt accggttcct ccagagaaca agcagctact 1740
tctttacttg caaagggtat taatctggtg gttgcagggt ccttcagtaa cactttctcg 1800
agaaactcca tcaataacgc attgcttact ctggagattc caaccttagt tgaaaagcta 1860

cgttccaagt tcgagaatgc accaaaggaa ttgaccagaa gaactggatg gttcttaaaa 1920
tgggatgttc ctaacgctaa agtttatgtt acagaaggta gtccagatgg ccaagtccta 1980
ttagaacaaa aggtcgggtga actaggttaag aacttgcaag agattattat taaaggcgggt 2040
cttgaagggt gggccaagtc tcaattgtga 2070

<210> 172

<211> 689

<212> PRT

<213> Candida glabrata

<400> 172

Met Val Val Leu Arg Arg Ser Phe His Val Tyr Thr Arg Leu Gln Arg

1 5 10 15

Gly Gln Asn Leu Thr Glu Lys Ile Val Gln Gln Tyr Ser Val Gly Leu

20 25 30

Ala Pro Gly Lys Arg Val His Ser Gly Asp Tyr Val Ser Ile Lys Pro

35 40 45

Ala His Val Met Ser His Asp Asn Ser Trp Pro Val Ala Leu Lys Phe

50 55 60

Met Asn Leu Gly Ala Arg Thr Val Lys Asp Pro Arg Gln Ile Val Asn

65 70 75 80

Thr Leu Asp His Asp Ile Gln Asn Lys Ser Asp Lys Asn Leu Thr Lys
 85 90 95
 Tyr Arg Asn Ile Glu Ser Phe Ala Lys Lys His Gly Ile Asp Phe Tyr
 100 105 110
 Pro Ala Gly Arg Gly Ile Gly His Gln Ile Met Val Glu Glu Gly Tyr
 115 120 125
 Ala Phe Pro Leu Asn Leu Thr Val Ala Ser Asp Ser His Ser Asn Thr
 130 135 140

 Tyr Gly Gly Met Gly Ala Leu Gly Thr Pro Val Val Arg Thr Asp Ala
 145 150 155 160
 Ala Ala Ile Trp Ala Thr Gly Gln Thr Trp Trp Gln Ile Pro Pro Val
 165 170 175
 Ala Gln Val Glu Phe Lys Gly Lys Leu His Glu Ser Val Ser Gly Lys
 180 185 190
 Asp Ile Ile Val Ala Leu Cys Gly Val Phe Asn Lys Asp Gln Val Leu
 195 200 205

 Asn His Ala Ile Glu Phe Thr Gly Asp Ala Ile Lys His Leu Pro Val
 210 215 220
 Asp Phe Arg Leu Thr Ile Ala Asn Met Thr Thr Glu Trp Gly Ala Leu
 225 230 235 240
 Ser Gly Leu Phe Pro Val Asp Asp Thr Leu Ile Asn Trp Tyr Lys Asn
 245 250 255
 Arg Leu Asn Ile Val Gly Pro Asn His Pro Arg Ile Asn Glu Thr Thr
 260 265 270

 Ile Lys Asn Leu Glu Asp Lys Ala Lys Val Phe Lys Ala Asp Ser Asp
 275 280 285
 Ala Val Tyr Ala Lys Lys Leu Val Ile Asp Leu Ser Thr Leu Thr His
 290 295 300
 Tyr Val Ser Gly Pro Asn Ser Val Lys Val Ser Asn Thr Val Gln Asp
 305 310 315 320
 Leu Ala Arg Asp Asn Ile Lys Ile Asn Lys Ala Tyr Leu Val Ser Cys

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

Gln Ala Ala Thr Ser Leu Leu Ala Lys Gly Ile Asn Leu Val Val Ala
580 585 590

Gly Ser Phe Ser Asn Thr Phe Ser Arg Asn Ser Ile Asn Asn Ala Leu
595 600 605

Leu Thr Leu Glu Ile Pro Thr Leu Val Glu Lys Leu Arg Ser Lys Phe
610 615 620

Glu Asn Ala Pro Lys Glu Leu Thr Arg Arg Thr Gly Trp Phe Leu Lys
625 630 635 640

Trp Asp Val Pro Asn Ala Lys Val Tyr Val Thr Glu Gly Ser Pro Asp
645 650 655

Gly Gln Val Leu Leu Glu Gln Lys Val Gly Glu Leu Gly Lys Asn Leu
660 665 670

Gln Glu Ile Ile Ile Lys Gly Gly Leu Glu Gly Trp Val Lys Ser Gln
675 680 685

Leu

<210> 173

<211> 1728

<212> DNA

<213> artificial sequence

<220><223> codon optimized coding region

<400> 173

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gaaccaaagg accaggggtgc tagtcaagcc atgctttatg ccactggttt taaggaagac 120

gacttcggta aagcccaagt tggcgttagt tcttgttggg ggtctggtta tccgtgtaac 180

atgcatttaa tggattttta caacagaatt accgaaagtg ttaacaaagc tgggttaaag 240

ggaatgcaat tcaatactat tgggtgtctct gatggaatct ctatgggaac aaaggggaatg 300

agatatagtc tacaatcgag ggaggttatt gcagacagct tcgagacgat tatgatggca 360

cagcactatg atgcaaatat cgcgattcct tcttgtgata aaaacatgcc aggtgtccta 420

atggctatgg gacgtcaca caggccttca ataattggtt atggaggtac tatecttccc 480

ggttccccta catgtggaag tgctaagatc cccaaaaaga tagatgtcgt cagcgcattt 540

caatcttacg gtcaatatatt gtctaaagag ttacggaaa ctgaaagaca agacgtggtc 600
 caacatgctt gtccaggccc aggttcctgc ggcggatgt acactgcaa cacaatggca 660
 tccgtcgag aagtccttgg tatgacactt ccaaactcgt cctcgttccc tgcagtatcg 720
 aaagaaaaac ttaatgaatg tgacactatt ggagaagcaa taaagaagac aatggagtta 780
 ggtataacgc cactgacgt tatgaccaa gaagccttcg aaaacgcat gacttatgta 840
 attgctaccg gtggaagtac taatgctgtt cttcacatgg tcgtgttgc gcattccgct 900
 ggtgtaaaga tcacccaga cgactttcag agaatttcgg aaaaaacgcc cttgttgggt 960

gactttaagc cttctggcaa atatgttatg gccgacctta ttactgtcgg tggtagacaa 1020
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 ggtgacacac tggcggagag agctgcaaaa gctgtaagtt taaaggatgg tcaagacatc 1140
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 ctggccccag gtggctcagt aggaaaaata accggcaaag aagggactta cttcaaagga 1260
 aaggcaaggg ttttcaatga tgaacccggc ttcataatcg cattagagaa tggtgaaatc 1320
 aaaaagggtg aaaagaccgt agtcatcatt aggtatgagg gaccaagagg tggaccagga 1380

atgccagaaa tgttgaagcc atccagtgc ttaatgggtt atggtttagg taaggatgtt 1440
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 gtacctgagg cggtgaagg tgggccata ggttagtga gagacggtga tgagataatc 1560
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 cgtagtactt ggactgctcc acctccacgt tacaccagag gttgtttaag taaatatgcg 1680
 aaactggtga gcaatgcctc ccacggttgt gtaacggatc ttaactaa 1728

<210> 174

<211> 1674

<212> DNA

<213> Nitrosomonas europaea

<400> 174

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 tccgacggga tctccatggg taccgaaggc atgaagtatt ctctggttgc gcgcgaagtg 300
 atcgccgatt cgatcgaac ctgcgtacag gcggaaagta tggatggcgt catcgccatc 360

ggtgggttcg ataaaaacat gcctggcgcc atgatacgcg tggccagact gaacgtaccg 420

 tccatcttcg tctatggcgg taccatcaaa cctggccatt accagggcgg tgatctgacc 480
 atcgtaagcg ctttcgaagc tgtcggacag cataccgcgc acaagataga cgatcatgaa 540
 ctgctggaag tcgaacgcca tgcctgtccc ggcgccggtt cgtgcggtgg tatgtacaca 600
 gccaacacca tgtcatctgc catcgaggca atgggaatga gcctgcctta ctcttcacc 660
 atggcagcag aagatgagga aaaacggatc agcgccatac gctccgccga agtactggtg 720
 gacgcggtca aaaagcagat tctgccgcgc agcctgatca cccgcaaata catcgaaaat 780
 gcggtatctg tcgtcatggc ggtgggaggt tcgaccaatg ccgtgctgca cctgctggcc 840

 atcgcccatg cagccgaagt ggaattcagc atcgatgatt tcgaagccat tcgtgcacgc 900
 gtaccggtat tgtgcgatct gaaaccttcc ggacgctatg tagccacgga tctgcacaaa 960
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 cgtgccgatc aggatgtgat tcaaccctgg gacaatccgg tataatgaaca ggggcacctg 1140
 gcgatcctga aaggtaatct ttcacagaa ggtgcggttg ccaagatttc cggcatcaaa 1200
 aatccagta ttaccggtcc cgccagagtg ttcgattctg aagaacctg catggctgcc 1260

 attcttgaac gcaaaatcca gccaggtgat gtggtggtca tccgtacga aggccacag 1320
 ggcggaacccg gcatgcgcga aatgctttct ccacttcag cactgatcgg tgaagggtg 1380
 ggtgattcgg tcgggttgat taccgatggg cgtttctccg gtggtacctg cggaatggtg 1440
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 gattcgatta cgatcgatgc acaccgtcgc ctgctgcaac tgaatgttcc tgaagccgag 1560
 ctggaacgcc gccgggcagc ctggcatcca cctgcaccac gctacacag cggcgtactg 1620
 gcgaaatacg ccaagctggt atccactgcc agccgtggtg cagtaccga ttaa 1674

<210> 175

<211> 557

<212> PRT

<213> Nitrosomonas europaea

<400> 175

Met Pro Asp Asn Arg Arg Ser Gln Thr Ile Thr Gln Gly Ala Gln Arg

1 5 10 15

Thr Pro Asn Arg Ala Met Leu Arg Ala Val Gly Phe Gly Asp Gly Asp

20 25 30

Phe Asp Lys Pro Ile Val Gly Val Ala Asn Gly Phe Ser Thr Ile Thr
 35 40 45
 Pro Cys Asn Met Gly Leu Asp Thr Leu Ala Lys Cys Ala Glu His Ala
 50 55 60
 Leu Lys Thr Ala Gly Ala Met Pro Gln Met Phe Gly Thr Ile Thr Val
 65 70 75 80
 Ser Asp Gly Ile Ser Met Gly Thr Glu Gly Met Lys Tyr Ser Leu Val
 85 90 95
 Ser Arg Glu Val Ile Ala Asp Ser Ile Glu Thr Cys Val Gln Ala Glu
 100 105 110
 Ser Met Asp Gly Val Ile Ala Ile Gly Gly Cys Asp Lys Asn Met Pro
 115 120 125
 Gly Ala Met Ile Ala Leu Ala Arg Leu Asn Val Pro Ser Ile Phe Val
 130 135 140
 Tyr Gly Gly Thr Ile Lys Pro Gly His Tyr Gln Gly Arg Asp Leu Thr
 145 150 155 160
 Ile Val Ser Ala Phe Glu Ala Val Gly Gln His Thr Ala His Lys Ile
 165 170 175
 Asp Asp His Glu Leu Leu Glu Val Glu Arg His Ala Cys Pro Gly Ala
 180 185 190
 Gly Ser Cys Gly Gly Met Tyr Thr Ala Asn Thr Met Ser Ser Ala Ile
 195 200 205
 Glu Ala Met Gly Met Ser Leu Pro Tyr Ser Ser Thr Met Ala Ala Glu
 210 215 220
 Asp Glu Glu Lys Arg Ile Ser Ala Ile Arg Ser Ala Glu Val Leu Val
 225 230 235 240
 Asp Ala Val Lys Lys Gln Ile Leu Pro Arg Ser Leu Ile Thr Arg Lys
 245 250 255
 Ser Ile Glu Asn Ala Val Ser Val Val Met Ala Val Gly Gly Ser Thr
 260 265 270
 Asn Ala Val Leu His Leu Leu Ala Ile Ala His Ala Ala Glu Val Glu

275 280 285
 Phe Ser Ile Asp Asp Phe Glu Ala Ile Arg Ala Arg Val Pro Val Leu
 290 295 300
 Cys Asp Leu Lys Pro Ser Gly Arg Tyr Val Ala Thr Asp Leu His Lys

 305 310 315 320
 Ala Gly Gly Ile Pro Gln Val Met Lys Met Leu Leu Val His Asp Leu
 325 330 335
 Leu His Gly Asp Cys Leu Thr Ile Ser Gly Gln Thr Ile Ala Glu Val
 340 345 350
 Leu Lys Asp Ile Pro Glu Gln Pro Arg Ala Asp Gln Asp Val Ile Gln
 355 360 365
 Pro Trp Asp Asn Pro Val Tyr Glu Gln Gly His Leu Ala Ile Leu Lys

 370 375 380
 Gly Asn Leu Ser Ser Glu Gly Ala Val Ala Lys Ile Ser Gly Ile Lys
 385 390 395 400
 Asn Pro Ser Ile Thr Gly Pro Ala Arg Val Phe Asp Ser Glu Glu Thr
 405 410 415
 Cys Met Ala Ala Ile Leu Glu Arg Lys Ile Gln Pro Gly Asp Val Val
 420 425 430
 Val Ile Arg Tyr Glu Gly Pro Gln Gly Gly Pro Gly Met Arg Glu Met

 435 440 445
 Leu Ser Pro Thr Ser Ala Leu Ile Gly Glu Gly Leu Gly Asp Ser Val
 450 455 460
 Gly Leu Ile Thr Asp Gly Arg Phe Ser Gly Gly Thr Tyr Gly Met Val
 465 470 475 480
 Val Gly His Val Ala Pro Glu Ala Phe Ala Gly Gly Thr Ile Ala Leu
 485 490 495
 Val Gln Glu Gly Asp Ser Ile Thr Ile Asp Ala His Arg Arg Leu Leu

 500 505 510
 Gln Leu Asn Val Pro Glu Ala Glu Leu Glu Arg Arg Arg Ala Ala Trp
 515 520 525

His Pro Pro Ala Pro Arg Tyr Thr Arg Gly Val Leu Ala Lys Tyr Ala

530 535 540

Lys Leu Val Ser Thr Ala Ser Arg Gly Ala Val Thr Asp

545 550 555

<210> 176

<211> 1686

<212> DNA

<213> Synechocystis sp.

<400

> 176

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gccaacgggt acagcaccat taccctctgc aacatgggca ttaatgatct ggctctacgg	180
gccgagggcg gcttacggac agcggggggc atgcccgaat tgtttggcac taccaccatc	240
agtgacggta tttccatggg tacggaaggg atgaaatatt ccctagtctc cggggaagtg	300
attgctgatt ccatcgaaac agtatgcaat ggccaacgca tggacggagt tttggcgatc	360
gggggctgtg ataagaatat gccgggggca atgattgcca tggctcgcct caatattccc	420
tctatctttg tttacggtgg cactattaaa cccggacatt atgccgggga agatttaaca	480
gtggtcagtg ctttgaagc ggtgggccag tacagcgtg gcaaaattga tgaggaaacc	540
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gccaacacca tgcctccgc ctttgaagct atggggatga gcttgcccta tcttctacc	660
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gaagccatca aaaaacagat tttgccagc caaattctga cccggaaaagc ttttgaaaat	780
gccattgccg tgattatggc cgtggggggc tccactaatg cagtgtcca tctgtggcg	840
atgcccaaca ccattggggt gccctaagc ttggacgatt ttgaaacat tcgccacaaa	900
gtacctgtac tgtgcgacct caaaccttcc ggcaaatacg tcaccactaa tetccacgcc	960
gccggtggca ttccccaggt gatgaaaata ttgctggtca atggcattct ccacggtgac	1020
gctttaacga ttacaggaca gaccattgct gaagtttttag ccgatattcc tgaccaaccc	1080
cctgccggcc aggacgtaat ccattcctgg gatgaccctg tttatcaaga aggtcacctg	1140
gcagtgtca aaggtaacct ggccaccgaa ggcagtgtgg ctaaaatcag cgggtgttaa	1200
aagccggtga tactgtgtcc gcgcaagta tttgaatctg aagaagattg cctagaagcg	1260
attctagccg gcaaaattca agcaggagat gtggtggtcg tgcgctatga agggcccaaa	1320

gggtggcccg gtagcgga aatgctagcc cccacttctg ccatcattgg ggcagggttg 1380
 ggagactccg ttggccta at caccgatggc cgcttttctg gtggtaccta tggcttagtg 1440
 gtgggtcacg ttgccccga agcttatgtg ggaggggcga tgccttggg gcaagagggg 1500
 gatcaaatca ccatcgatgc tggcaagcgg ttactgcaac tcaacatcag tgaagaggaa 1560
 ttggcccaac ggcgggccca atggactcct cctcagcccc gctatccccg ggggatttta 1620
 gccaaagtatg ccaagttagt ttctccagc agccttggtg cagtgactga tatagacttg 1680

ttctaa 1686

<210> 177

<211> 561

<212> PRT

<213> Synechocystis sp.

<400> 177

Met Ser Asn Asn Pro Arg Ser Gln Val Ile Thr Gln Gly Thr Gln Arg

1 5 10 15

Ser Pro Asn Arg Ala Met Leu Arg Ala Val Gly Phe Gly Asp Asp Asp

20 25 30

Phe Thr Lys Pro Ile Val Gly Ile Ala Asn Gly Tyr Ser Thr Ile Thr

35 40 45

Pro Cys Asn Met Gly Ile Asn Asp Leu Ala Leu Arg Ala Glu Ala Gly

50 55 60

Leu Arg Thr Ala Gly Ala Met Pro Gln Leu Phe Gly Thr Ile Thr Ile

65 70 75 80

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

85 90 95

Ser Arg Glu Val Ile Ala Asp Ser Ile Glu Thr Val Cys Asn Gly Gln

100 105 110

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

115 120 125

Gly Ala Met Ile Ala Met Ala Arg Leu Asn Ile Pro Ser Ile Phe Val

130 135 140

Tyr Gly Gly Thr Ile Lys Pro Gly His Tyr Ala Gly Glu Asp Leu Thr

145 150 155 160

Val Val Ser Ala Phe Glu Ala Val Gly Gln Tyr Ser Ala Gly Lys Ile
165 170 175

Asp Glu Glu Thr Leu Tyr Gly Ile Glu Arg Asn Ala Cys Pro Gly Ala
180 185 190

Gly Ser Cys Gly Gly Met Phe Thr Ala Asn Thr Met Ser Ser Ala Phe
195 200 205

Glu Ala Met Gly Met Ser Leu Pro Tyr Ser Ser Thr Met Ala Ala Val
210 215 220

Asp Gly Glu Lys Ala Asp Ser Thr Glu Glu Ser Ala Lys Val Leu Val
225 230 235 240

Glu Ala Ile Lys Lys Gln Ile Leu Pro Ser Gln Ile Leu Thr Arg Lys
245 250 255

Ala Phe Glu Asn Ala Ile Ala Val Ile Met Ala Val Gly Gly Ser Thr
260 265 270

Asn Ala Val Leu His Leu Leu Ala Ile Ala Asn Thr Ile Gly Val Pro
275 280 285

Leu Ser Leu Asp Asp Phe Glu Thr Ile Arg His Lys Val Pro Val Leu
290 295 300

Cys Asp Leu Lys Pro Ser Gly Lys Tyr Val Thr Thr Asn Leu His Ala
305 310 315 320

Ala Gly Gly Ile Pro Gln Val Met Lys Ile Leu Leu Val Asn Gly Ile
325 330 335

Leu His Gly Asp Ala Leu Thr Ile Thr Gly Gln Thr Ile Ala Glu Val
340 345 350

Leu Ala Asp Ile Pro Asp Gln Pro Pro Ala Gly Gln Asp Val Ile His
355 360 365

Ser Trp Asp Asp Pro Val Tyr Gln Glu Gly His Leu Ala Val Leu Lys
370 375 380

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

Lys Pro Val Ile Thr Gly Pro Ala Lys Val Phe Glu Ser Glu Glu Asp

405 410 415
Cys Leu Glu Ala Ile Leu Ala Gly Lys Ile Gln Ala Gly Asp Val Val
420 425 430

Val Val Arg Tyr Glu Gly Pro Lys Gly Gly Pro Gly Met Arg Glu Met
435 440 445

Leu Ala Pro Thr Ser Ala Ile Ile Gly Ala Gly Leu Gly Asp Ser Val
450 455 460

Gly Leu Ile Thr Asp Gly Arg Phe Ser Gly Gly Thr Tyr Gly Leu Val
465 470 475 480

Val Gly His Val Ala Pro Glu Ala Tyr Val Gly Gly Ala Ile Ala Leu
485 490 495

Val Gln Glu Gly Asp Gln Ile Thr Ile Asp Ala Gly Lys Arg Leu Leu
500 505 510

Gln Leu Asn Ile Ser Glu Glu Glu Leu Ala Gln Arg Arg Ala Gln Trp
515 520 525

Thr Pro Pro Gln Pro Arg Tyr Pro Arg Gly Ile Leu Ala Lys Tyr Ala
530 535 540

Lys Leu Val Ser Ser Ser Ser Leu Gly Ala Val Thr Asp Ile Asp Leu
545 550 555 560

Phe

<210> 178

<211> 1716

<212> DNA

<213> Streptococcus mutans

<400> 178

atgactgaca aaaaaactct taaagactta agaaatcgta gttctgttta cgattcaatg	60
gttaaatacac ctaatcgtgc tatgttgcgt gcaactggta tgcaagatga agactttgaa	120
aaacctatcg tcggtgtcat ttcaacttgg gctgaaaaca caccttgtaa tatccactta	180
catgactttg gtaaactagc caaagtcggt gttaaggaag ctggtgcttg gccagttcag	240
ttcggaacaa tcacggtttc tgatggaatc gccatgggaa cccaaggaat gcgtttctcc	300

ttgacatctc gtgatattat tgcagattct attgaagcag ccatgggagg tcataatgcg 360

gatgcttttg tagccattgg cggtttgat aaaaacatgc ccggttctgt tatcgctatg 420

gctaacatgg atatccagc catttttgc taccggcgaa caattgcacc tggtaattta 480

gacggcaaag atacgattt agtcctctgtc ttgaaggtg tcggccattg gaaccacggc 540

gatatgacca aagaagaagt taaagctttg gaatgtaatg cttgtcccgg tcctggaggc 600

tgcggtggtg tgtatactgc taacacaatg gcgacagcta ttgaagtttt gggacttagc 660

cttccgggtt catcttctca cccggctgaa tccgcagaaa agaaagcaga tattgaagaa 720

gctggtcgcg ctgttgtcaa aatgctcgaa atgggcttaa aaccttctga cattttaacg 780

cgatgaagctt ttgaagatgc tattactgia actatggctc tgggaggttc aaccaactca 840

acccttcacc tcttagctat tgcccatgct gctaattgtg aattgacact tgatgatttc 900

aatactttcc aagaaaaagt tcctcatttg gctgatttga aaccttctgg tcaatatgta 960

ttccaagacc ttacaaggt cggaggggta ccagcagtta tgaaatatct ccttaaaaat 1020

ggcttccttc atggtgaccg taccacttgi actggcaaaa cagtcgctga aaatttgaag 1080

gcttttgatg atttaacacc tggcctaaaag gttattatgc cgcttgaaaa tcctaaacgt 1140

gaagatggtc cgctcattat tctccatggt aacttggctc cagacggtgc cgttgcaaaa 1200

gtttctgggt taaaagtgcg tcgtcatgtc ggtcctgcta aggtctttaa ttctgaagaa 1260

gaagccattg aagctgtctt gaatgatgat attgttgatg gtgatgttgt tgtcgtacgt 1320

ttttaggtac caaagggcgg tcctggatg cctgaaatgc tttcccttcc atcaatgatt 1380

gttggtaaag ggcaaggtga aaaagttgcc cttctgacag atggccgctt ctcaggtggt 1440

acttatggtc ttgtcgtggg tcatatcgct cctgaagcac aagatggcgg tccaatcgcc 1500

tacctgcaaa caggagacat agtcactatt gaccaagaca ctaaggaatt acactttgat 1560

atctccgatg aagagttaaa acatcgtcaa gagaccattg aattgccacc gctctattca 1620

cgcggtatcc ttggtaaata tgctcacatc gtttcgtctg cttctagggg agccgtaaca 1680

gacttttga agcctgaaga aactggcaaa aatga 1716

<210> 179

<211> 571

<212> PRT

<213> Streptococcus mutans

<400> 179

Met Thr Asp Lys Lys Thr Leu Lys Asp Leu Arg Asn Arg Ser Ser Val

1

5

10

15

Tyr Asp Ser Met Val Lys Ser Pro Asn Arg Ala Met Leu Arg Ala Thr
 20 25 30
 Gly Met Gln Asp Glu Asp Phe Glu Lys Pro Ile Val Gly Val Ile Ser
 35 40 45
 Thr Trp Ala Glu Asn Thr Pro Cys Asn Ile His Leu His Asp Phe Gly
 50 55 60
 Lys Leu Ala Lys Val Gly Val Lys Glu Ala Gly Ala Trp Pro Val Gln
 65 70 75 80
 Phe Gly Thr Ile Thr Val Ser Asp Gly Ile Ala Met Gly Thr Gln Gly
 85 90 95
 Met Arg Phe Ser Leu Thr Ser Arg Asp Ile Ile Ala Asp Ser Ile Glu
 100 105 110
 Ala Ala Met Gly Gly His Asn Ala Asp Ala Phe Val Ala Ile Gly Gly
 115 120 125
 Cys Asp Lys Asn Met Pro Gly Ser Val Ile Ala Met Ala Asn Met Asp
 130 135 140
 Ile Pro Ala Ile Phe Ala Tyr Gly Gly Thr Ile Ala Pro Gly Asn Leu
 145 150 155 160
 Asp Gly Lys Asp Ile Asp Leu Val Ser Val Phe Glu Gly Val Gly His
 165 170 175
 Trp Asn His Gly Asp Met Thr Lys Glu Glu Val Lys Ala Leu Glu Cys
 180 185 190
 Asn Ala Cys Pro Gly Pro Gly Gly Cys Gly Gly Met Tyr Thr Ala Asn
 195 200 205
 Thr Met Ala Thr Ala Ile Glu Val Leu Gly Leu Ser Leu Pro Gly Ser
 210 215 220
 Ser Ser His Pro Ala Glu Ser Ala Glu Lys Lys Ala Asp Ile Glu Glu
 225 230 235 240
 Ala Gly Arg Ala Val Val Lys Met Leu Glu Met Gly Leu Lys Pro Ser
 245 250 255
 Asp Ile Leu Thr Arg Glu Ala Phe Glu Asp Ala Ile Thr Val Thr Met

260 265 270
 Ala Leu Gly Gly Ser Thr Asn Ser Thr Leu His Leu Leu Ala Ile Ala
 275 280 285
 His Ala Ala Asn Val Glu Leu Thr Leu Asp Asp Phe Asn Thr Phe Gln

 290 295 300
 Glu Lys Val Pro His Leu Ala Asp Leu Lys Pro Ser Gly Gln Tyr Val
 305 310 315 320
 Phe Gln Asp Leu Tyr Lys Val Gly Gly Val Pro Ala Val Met Lys Tyr
 325 330 335
 Leu Leu Lys Asn Gly Phe Leu His Gly Asp Arg Ile Thr Cys Thr Gly
 340 345 350
 Lys Thr Val Ala Glu Asn Leu Lys Ala Phe Asp Asp Leu Thr Pro Gly

 355 360 365
 Gln Lys Val Ile Met Pro Leu Glu Asn Pro Lys Arg Glu Asp Gly Pro
 370 375 380
 Leu Ile Ile Leu His Gly Asn Leu Ala Pro Asp Gly Ala Val Ala Lys
 385 390 395 400
 Val Ser Gly Val Lys Val Arg Arg His Val Gly Pro Ala Lys Val Phe
 405 410 415
 Asn Ser Glu Glu Glu Ala Ile Glu Ala Val Leu Asn Asp Asp Ile Val

 420 425 430
 Asp Gly Asp Val Val Val Val Arg Phe Val Gly Pro Lys Gly Gly Pro
 435 440 445
 Gly Met Pro Glu Met Leu Ser Leu Ser Ser Met Ile Val Gly Lys Gly
 450 455 460
 Gln Gly Glu Lys Val Ala Leu Leu Thr Asp Gly Arg Phe Ser Gly Gly
 465 470 475 480
 Thr Tyr Gly Leu Val Val Gly His Ile Ala Pro Glu Ala Gln Asp Gly

 485 490 495
 Gly Pro Ile Ala Tyr Leu Gln Thr Gly Asp Ile Val Thr Ile Asp Gln
 500 505 510

Asp Thr Lys Glu Leu His Phe Asp Ile Ser Asp Glu Glu Leu Lys His
 515 520 525
 Arg Gln Glu Thr Ile Glu Leu Pro Pro Leu Tyr Ser Arg Gly Ile Leu
 530 535 540
 Gly Lys Tyr Ala His Ile Val Ser Ser Ala Ser Arg Gly Ala Val Thr

545 550 555 560
 Asp Phe Trp Lys Pro Glu Glu Thr Gly Lys Lys
 565 570

<210> 180

<211> 1719

<212> DNA

<213> Streptococcus thermophilus

<400> 180

atggaggaaa acatcgtgtc tgaaaataac atgaaacacc gttcttctgt ctacgatagc	60
atggttaaat cacctaaccg tgctatgctt cgtgcgactg ggatgacgga tgatagtttt	120
gaaaagccta ttgttggggt tatctcaact tgggctgaga acacgccatg taatatccac	180
ttgcacggtt ttggtcaaat tgccaaagag ggtgtcaaag atgcgggtgc ttggccagtt	240
caatttggtg caattaccgt tgcagatggt attgccatgg ggacaccagg gatgcgtttc	300
tcattgacat ctctgatgat tatttctgac tcaatcgaag ctgctatggg tggtcacaat	360
gtcgaatgct ttgttgctat tgggtggctgt gataagaaca tgccagggtc aatgattgct	420
attgccaaca tggatatcc agctattttt gcttacggtg gtacgattgc accgggtaat	480
cttaacggta aggatatcga cttggtttct gttttcgaag gtatcggtaa atggaaccac	540
ggagatatga ctgccgaaga gggttaaaaat cttgaatgta atgcttgccc tggccctggt	600
ggttgttggtg gtatgtatag tgctaacaca atggcaacag caattgaggt tatggggatg	660
agccttccag gatcatcatc tcaccctgca gaatcagctg agaagaaggc tgatatcgaa	720
gaagcaggtc gtgcagttgt aaaaatgcta gaaatgggac ttaagccatc agatatcttg	780
acacgtgaag ctttgaaga tgccatcaca gttacaatgg cgcttggtgg ttcaacaaat	840
gccactcttc acttgcttgc tatcgctcat gcggctaacg ttgatttaac gcttgaagac	900
ttcaacgatt tccaagagcg cgtgcctcac ttggctgact tgaagccttc aggtcaatat	960
gtcttccaag acctttacaa gtgttggtggt gtgccagccg ttatgaaata tcttcttaag	1020
aatgggtttc ttcacgggtg tcgtatcacg tgtactggta agactgttgc agaaaatttg	1080

gaagctttcg atgatttgac accaggtcaa aaagttatca tgccacttga aaatcctaaa 1140
 cgtgccgatg gtccattgat tatcttgaag ggtaacttgg cccagaagg tgctgttgcc 1200
 aaagtatcag gtgttaaagt gcgtaacatt actggctctg ctaaagtatt tgactcagaa 1260
 gaagatgcca tcgaggcagt tctttctgac gaaatcgttg acggcgatgt agttgttgta 1320
 cgtttttagt gtcctaaggg tggctctggt atgccagaaa tgttgtcatt gtcacatg 1380
 attgttggtg aaggacaagg agacaagggt gccctcttga ctgatggacg tttctcaggt 1440
 ggtacttacg gacttgttgt aggtcatatt gctcctgaag ctcaagttgg tggaccgatt 1500

gcctacctcc gtacaggatg tatggttaca gttgaccagg ataccagaaga aatcactatg 1560
 catgtaccag acgaagagtt ggcgaacgt aaagcagaaa ctgagttacc accactttat 1620
 agccgtgggtg tcctcggtaa gtatgctcac atcgtttcat cagcatcacg tgggtcggtt 1680
 actgacttct ggaatatgga taaatcaggt aaagcttaa 1719

<210> 181

<211> 572

<212> PRT

<213> Streptococcus thermophilus

<400> 181

Met Glu Glu Asn Ile Val Ser Glu Asn Asn Met Lys His Arg Ser Ser

1 5 10 15

Val Tyr Asp Ser Met Val Lys Ser Pro Asn Arg Ala Met Leu Arg Ala

20 25 30

Thr Gly Met Thr Asp Asp Ser Phe Glu Lys Pro Ile Val Gly Val Ile

35 40 45

Ser Thr Trp Ala Glu Asn Thr Pro Cys Asn Ile His Leu His Gly Phe

50 55 60

Gly Gln Ile Ala Lys Glu Gly Val Lys Asp Ala Gly Ala Trp Pro Val

65 70 75 80

Gln Phe Gly Thr Ile Thr Val Ala Asp Gly Ile Ala Met Gly Thr Pro

85 90 95

Gly Met Arg Phe Ser Leu Thr Ser Arg Asp Ile Ile Ala Asp Ser Ile

100 105 110

Glu Ala Ala Met Gly Gly His Asn Val Asp Ala Phe Val Ala Ile Gly

115 120 125

Gly Cys Asp Lys Asn Met Pro Gly Ser Met Ile Ala Ile Ala Asn Met
130 135 140

Asp Ile Pro Ala Ile Phe Ala Tyr Gly Gly Thr Ile Ala Pro Gly Asn
145 150 155 160

Leu Asn Gly Lys Asp Ile Asp Leu Val Ser Val Phe Glu Gly Ile Gly
165 170 175

Lys Trp Asn His Gly Asp Met Thr Ala Glu Glu Val Lys Asn Leu Glu
180 185 190

Cys Asn Ala Cys Pro Gly Pro Gly Gly Cys Gly Gly Met Tyr Thr Ala
195 200 205

Asn Thr Met Ala Thr Ala Ile Glu Val Met Gly Met Ser Leu Pro Gly
210 215 220

Ser Ser Ser His Pro Ala Glu Ser Ala Glu Lys Lys Ala Asp Ile Glu
225 230 235 240

Glu Ala Gly Arg Ala Val Val Lys Met Leu Glu Met Gly Leu Lys Pro
245 250 255

Ser Asp Ile Leu Thr Arg Glu Ala Phe Glu Asp Ala Ile Thr Val Thr
260 265 270

Met Ala Leu Gly Gly Ser Thr Asn Ala Thr Leu His Leu Leu Ala Ile
275 280 285

Ala His Ala Ala Asn Val Asp Leu Thr Leu Glu Asp Phe Asn Asp Phe
290 295 300

Gln Glu Arg Val Pro His Leu Ala Asp Leu Lys Pro Ser Gly Gln Tyr
305 310 315 320

Val Phe Gln Asp Leu Tyr Asn Val Gly Gly Val Pro Ala Val Met Lys
325 330 335

Tyr Leu Leu Lys Asn Gly Phe Leu His Gly Asp Arg Ile Thr Cys Thr
340 345 350

Gly Lys Thr Val Ala Glu Asn Leu Glu Ala Phe Asp Asp Leu Thr Pro
355 360 365

Gly Gln Lys Val Ile Met Pro Leu Glu Asn Pro Lys Arg Ala Asp Gly

370 375 380
Pro Leu Ile Ile Leu Lys Gly Asn Leu Ala Pro Glu Gly Ala Val Ala
385 390 395 400

Lys Val Ser Gly Val Lys Val Arg Asn Ile Thr Gly Pro Ala Lys Val
405 410 415
Phe Asp Ser Glu Glu Asp Ala Ile Glu Ala Val Leu Ser Asp Glu Ile
420 425 430
Val Asp Gly Asp Val Val Val Val Arg Phe Val Gly Pro Lys Gly Gly
435 440 445
Pro Gly Met Pro Glu Met Leu Ser Leu Ser Ser Met Ile Val Gly Lys
450 455 460

Gly Gln Gly Asp Lys Val Ala Leu Leu Thr Asp Gly Arg Phe Ser Gly
465 470 475 480
Gly Thr Tyr Gly Leu Val Val Gly His Ile Ala Pro Glu Ala Gln Val
485 490 495
Gly Gly Pro Ile Ala Tyr Leu Arg Thr Gly Asp Met Val Thr Val Asp
500 505 510
Gln Asp Thr Lys Glu Ile Thr Met His Val Pro Asp Glu Glu Leu Ala
515 520 525

Lys Arg Lys Ala Glu Thr Glu Leu Pro Pro Leu Tyr Ser Arg Gly Val
530 535 540
Leu Gly Lys Tyr Ala His Ile Val Ser Ser Ala Ser Arg Gly Ala Val
545 550 555 560
Thr Asp Phe Trp Asn Met Asp Lys Ser Gly Lys Ala
565 570

<210> 182

<211> 1674

<212> DNA

<213> Ralstonia metallidurans

<400> 182

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60

tcgatgtact acgcgctcgg ctacaagaag gaagacttcg acaagccgat ggtgggtatc 120
gccaacggcc actcgacgat caccacctgc aacgccggcc tgcagcgctt gccggacgcg 180
gccgtggatg cgatcaaggc ctccgacgcc aaccgcgaga tcttcggcac gccgacgatc 240
tccgacggca tctcgatggg caccgagggc atgaagtact cgctgatctc gcgtgaagtc 300
attgccgact gcatcgaac cgctgcccag ggccagtggg tggacggcgt ggtcgtgatc 360
ggcggctgcg acaagaacat gcccggcggc atgatcgac tggcgcgac caacgtgccg 420
ggcatctacg tctacggcgg caccatccgc ccgggtaact ggaagggcaa ggacctgacc 480

atcgtgtcgt cgttcgaggc cgtgggcgaa ttcaccgccg gccgcatgag cgaggaagac 540
ttcgaggcgg tggagaagaa cgcctgcccg agcaccggct cgtgcggtgg catgtacacc 600
gccaacacaa tgagctcgtc gttcgaggcg ctgggcatgt cgctgctgaa ttcgtcgacg 660
atggccaacc cggaccagga aaaggtggac agcgccgccg aatcgcccg cgtgctggtg 720
gaagccatca agaaggacat caagccgcgc gacatcatca cgcgcaaac gatcgagaac 780
gccgtgacgc tgatcatggc caccggcggg tccaccaacg cggtagtgca ttacctggcc 840
atgcccact cgccgaagt ggaatggacc atcgacgatt tcgagcgcat ccgccgccgc 900

gtgccggtga tctgcaacct gaagccgtcg ggccgctacg tggccaccga cctgcaccgc 960
gccggtggca ttccgcaagt gatgaagatc ctgctgaacg ccggtctgct gcatggcgac 1020
tgctgacga tcacggggcg cacgtggcc gaggagctcg agcacgttcc caatgagccg 1080
cgtaccgacc aggacgtgat cctgccgatc tcgaggccc tgtacaagca aggccacctg 1140
gccatcctga agggcaacct cgccaggaa ggcgagtg ccaaaatcac cggcctgaag 1200
aaccgggtca tcaccggccc ggcccgcgtg ttcgaggacg aacagagcg catggaagcg 1260
atcctggcgg acaagatcaa cgctggcgac atcctggtgc tgcgtacct tggcccgaag 1320

ggcgcccg gcatgcctga aatgctggcg ccgacttcgg cgatcatcgg caagggtctc 1380
ggcgaatcgg ttggtttcat caccgacggc cgcttctcgg ggggcacctg ggcatggtg 1440
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gactcgatca cgatcgacgc gcaccagctg ctgctgcaac tgaatgtggc cgacgacgag 1560
ctggcccgcc gccgcgtgc ctggaacag ccggcgccgc gctacacgc cggcgtactg 1620
gcgaagtctg cgaggctggc ctccacggcc agcaaggcg ccgtgacgga ctga 1674

<210> 183
<211> 557
<212> PRT
<213> Ralstonia metallidurans

<400> 183

Met Ala Tyr Asn Lys Arg Ser Gln His Ile Thr Gln Gly Val Ala Arg

1 5 10 15

Ser Pro Asn Arg Ser Met Tyr Tyr Ala Leu Gly Tyr Lys Lys Glu Asp

20 25 30

Phe Asp Lys Pro Met Val Gly Ile Ala Asn Gly His Ser Thr Ile Thr

35 40 45

Pro Cys Asn Ala Gly Leu Gln Arg Leu Ala Asp Ala Ala Val Asp Ala

50 55 60

Ile Lys Ala Ser Asp Ala Asn Pro Gln Ile Phe Gly Thr Pro Thr Ile

65 70 75 80

Ser Asp Gly Met Ser Met Gly Thr Glu Gly Met Lys Tyr Ser Leu Ile

85 90 95

Ser Arg Glu Val Ile Ala Asp Cys Ile Glu Thr Ala Ala Gln Gly Gln

100 105 110

Trp Met Asp Gly Val Val Val Ile Gly Gly Cys Asp Lys Asn Met Pro

115 120 125

Gly Gly Met Ile Ala Leu Ala Arg Thr Asn Val Pro Gly Ile Tyr Val

130 135 140

Tyr Gly Gly Thr Ile Arg Pro Gly Asn Trp Lys Gly Lys Asp Leu Thr

145 150 155 160

Ile Val Ser Ser Phe Glu Ala Val Gly Glu Phe Thr Ala Gly Arg Met

165 170 175

Ser Glu Glu Asp Phe Glu Gly Val Glu Lys Asn Ala Cys Pro Ser Thr

180 185 190

Gly Ser Cys Gly Gly Met Tyr Thr Ala Asn Thr Met Ser Ser Ser Phe

195 200 205

Glu Ala Leu Gly Met Ser Leu Leu Asn Ser Ser Thr Met Ala Asn Pro

210 215 220

Asp Gln Glu Lys Val Asp Ser Ala Ala Glu Ser Ala Arg Val Leu Val

225 230 235 240

Glu Ala Ile Lys Lys Asp Ile Lys Pro Arg Asp Ile Ile Thr Arg Lys

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

Val Gln Glu Gly Asp Ser Ile Thr Ile Asp Ala His Gln Leu Leu Leu
500 505 510

Gln Leu Asn Val Ala Asp Asp Glu Leu Ala Arg Arg Arg Ala Ala Trp
515 520 525

Lys Gln Pro Ala Pro Arg Tyr Thr Arg Gly Val Leu Ala Lys Phe Ala
530 535 540

Arg Leu Ala Ser Thr Ala Ser Lys Gly Ala Val Thr Asp
545 550 555

<210> 184

<211> 1674

<212> DNA

<213> Ralstonia eutropha

<400> 184

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tcgatgtact acgccctggg ctaccagaag gaagacttcg acaagcccat ggtcggcatc 120

gccaacggcc actcgacgat caccgcgtgc aacgccggcc tgcagcgctt ggccgacgcc 180

gcgatcgacg ccgtgaaggg ctccgacgcc aatccgcagg tattcggcac gccgacgac 240

tccgacggca tgtcgatggg caccgagggc atgaagtact cgctgatctc gcgcgaagtc 300

attgccgact gcatcgagac cgccgccag ggccagtggg tggacggcgt ggtggtgatc 360

ggcggctcgc acaagaacat gccgggcggc atgatcgcgc tcgcgcgcac caatgtgccg 420

ggcatctacg tctatggcgg caccatcaag cccggcaact ggaagggcaa ggacctgacc 480

atcgtgtcgt cgctcgaggg cgtgggcgaa ttcaccgccg gccgcatgag cgaagaagat 540

ttcgagggcg tggaaaggaa cgcttggtccg tcgaccggat cgtgcggcgg catgtacacc 600

gccaatacga tgagctcgtc gtccgagggc cttgggatgt cgctgctgta ttcgtcgacg 660

atggccaacc ccgatcagga aaaggtcgat agcgtgccg aatcggcgcg cgtgctggtc 720

gaggcgatca agaaggacat caagccgcgc gacatcatca cgcgcaagtc gatcgaaaac 780

gccgtcgcgc tgatcatggc caccgtggc tcgaccaacg cgggtctgca ctacctggcc 840

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gtgcctgtga tctgcaacct gaagccgtcg ggccagtacg tggccaccga cctgcacaag 960

gcgggcggca tcccgcaggt catgaagatc ctgctgaagg ccggactgct gcatggcgac 1020

tgccctgacca tcacaggccg caccgtggct gaagagctgg aacacgtgcc ggaccagccg 1080

cgggcccacc aggacgtgat catgccaatc gagaaggcgc tctatgcgga ggggcatctg 1140
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gattcgatca cgatcgatgc gcacaagctg gtgttgagg tgaatgtgtc ggataggagg 1560
ttggctcgcc gccgggctga gtggaacaa cctgttgcgc gttatacacg gggggtattg 1620
gccaaagtttg ctgactggc gtcgacggcc agtaaggggg cggtgacgga ttga 1674

<210> 185

<211> 557

<212> PRT

<213> *Ralstonia eutropha*

<400> 185

Met Ala Phe Asn Lys Arg Ser Arg Asn Ile Thr Gln Gly Val Ala Arg

1 5 10 15

Ser Pro Asn Arg Ser Met Tyr Tyr Ala Leu Gly Tyr Gln Lys Glu Asp

20 25 30

Phe Asp Lys Pro Met Val Gly Ile Ala Asn Gly His Ser Thr Ile Thr

35 40 45

Pro Cys Asn Ala Gly Leu Gln Arg Leu Ala Asp Ala Ala Ile Asp Ala

50 55 60

Val Lys Ala Ser Asp Ala Asn Pro Gln Val Phe Gly Thr Pro Thr Ile

65 70 75 80

Ser Asp Gly Met Ser Met Gly Thr Glu Gly Met Lys Tyr Ser Leu Ile

85 90 95

Ser Arg Glu Val Ile Ala Asp Cys Ile Glu Thr Ala Ala Gln Gly Gln

100 105 110

Trp Met Asp Gly Val Val Val Ile Gly Gly Cys Asp Lys Asn Met Pro

115 120 125

Gly Gly Met Ile Ala Leu Ala Arg Thr Asn Val Pro Gly Ile Tyr Val
 130 135 140
 Tyr Gly Gly Thr Ile Lys Pro Gly Asn Trp Lys Gly Lys Asp Leu Thr
 145 150 155 160
 Ile Val Ser Ser Phe Glu Ala Val Gly Glu Phe Thr Ala Gly Arg Met
 165 170 175
 Ser Glu Glu Asp Phe Glu Gly Val Glu Arg Asn Ala Cys Pro Ser Thr
 180 185 190

 Gly Ser Cys Gly Gly Met Tyr Thr Ala Asn Thr Met Ser Ser Ser Phe
 195 200 205
 Glu Ala Leu Gly Met Ser Leu Leu Tyr Ser Ser Thr Met Ala Asn Pro
 210 215 220
 Asp Gln Glu Lys Val Asp Ser Ala Ala Glu Ser Ala Arg Val Leu Val
 225 230 235 240
 Glu Ala Ile Lys Lys Asp Ile Lys Pro Arg Asp Ile Ile Thr Arg Lys
 245 250 255

 Ser Ile Glu Asn Ala Val Ala Leu Ile Met Ala Thr Gly Gly Ser Thr
 260 265 270
 Asn Ala Val Leu His Tyr Leu Ala Ile Ala His Ser Ala Glu Val Glu
 275 280 285
 Trp Thr Ile Asp Asp Phe Glu Arg Ile Arg Arg Lys Val Pro Val Ile
 290 295 300
 Cys Asn Leu Lys Pro Ser Gly Gln Tyr Val Ala Thr Asp Leu His Lys
 305 310 315 320

 Ala Gly Gly Ile Pro Gln Val Met Lys Ile Leu Leu Lys Ala Gly Leu
 325 330 335
 Leu His Gly Asp Cys Leu Thr Ile Thr Gly Arg Thr Leu Ala Glu Glu
 340 345 350
 Leu Glu His Val Pro Asp Gln Pro Arg Ala Asp Gln Asp Val Ile Met
 355 360 365
 Pro Ile Glu Lys Ala Leu Tyr Ala Glu Gly His Leu Ala Ile Leu Lys

370	375	380	
Gly Asn Leu Ala Glu Glu Gly Ala Val Ala Lys Ile Thr Gly Leu Lys			
385	390	395	400
Asn Pro Val Ile Thr Gly Pro Ala Arg Val Phe Glu Asp Glu Gln Ser			
	405	410	415
Ala Met Glu Ala Ile Leu Ala Asp Lys Ile Asn Ala Gly Asp Val Leu			
	420	425	430
Val Leu Arg Tyr Leu Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met			
	435	440	445
Leu Ala Pro Thr Ser Ala Ile Ile Gly Lys Gly Leu Gly Glu Ser Val			
	450	455	460
Gly Phe Ile Thr Asp Gly Arg Phe Ser Gly Gly Thr Trp Gly Met Val			
465	470	475	480
Val Gly His Val Ala Pro Glu Ala Tyr Val Gly Gly Asn Ile Ala Leu			
	485	490	495
Val Arg Glu Gly Asp Ser Ile Thr Ile Asp Ala His Lys Leu Val Leu			
	500	505	510
Gln Val Asn Val Ser Asp Glu Glu Leu Ala Arg Arg Arg Ala Glu Trp			
	515	520	525
Lys Gln Pro Val Ala Arg Tyr Thr Arg Gly Val Leu Ala Lys Phe Ala			
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Arg Leu Ala Ser Thr Ala Ser Lys Gly Ala Val Thr Asp			
545	550	555	
<210> 186			
<211> 1713			
<212> DNA			
<213> Lactococcus lactis			
<400> 186			
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ttgacacaag acccaacaca gccagcgacc caagccatgc actatggcat tggttttaaa			120
gatgaggact tcaaaaaagc tcaggtcgga atcgtcagca tggattggga cggaaatccc			180

tgtaacatgc acttgggcac actcggtagt aaaatcaaaa attctgtcaa tcaaactgac 240
 ggactgattg ggcttcaatt tcacacgatt ggggtttctg acggaattgc caacggaaag 300
 cttggcatga gatattcctt ggtcagtcgt gaagtatttg ctgacagtat tgaaccaac 360
 gctggcgccg aatattacga tgcaattgtc gctgttcccg gttgtgacaa aaatatgcca 420
 ggctcaatca ttggcatggc tcggctcaat cgtccgtcaa ttatggttta tgggtgaacg 480

 attgaacatg gcgaatacaa aggcgaaaag ttaaataattg tttcggcttt tgaagcgctt 540
 ggacaaaaaa tcaactgaaa tatttccgag gaagattatc acggcgtcat ttgtaatgcc 600
 attccgggac aggggtgcttg tgggggcatg tatacagcaa atacactggc ttcggcaatt 660
 gaaactttgg gaatgagttt gccttattcg gcttcaaatc cagcggtcag tcaagaaaaa 720
 gaagacgaat gtgatgaaat tggctctggca atcaaaaatt tgctagaaaa agacatcaaa 780
 ccaagcgata tcatgaccaa ggaagctttt gaaaatgcca taacgatcgt catggttctc 840
 ggtgggttcaa ctaatgtctg gcttcataatc attgccatgg ctaatgccat cgggtgtcgaa 900

 attacgcaag atgattttca acgtatttcc gatgtcacgc ctgtgcttgg cgacttcaag 960
 ccaagtggca agtacatgat ggaagatttg caaaaaattg gtggcgtgcc tgctgttttg 1020
 aaatatattg tcaaagaggg caagcttcat ggcgactgtt tgacagttac tggtaaaact 1080
 ctagctgaaa atgttgaaac agcactggat ttggactttg acagccaaga cattattcga 1140
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 gaaggtgggt ctgtggcaaa aatttctgga aaagaagggg aatttttcaa aggaacagct 1260
 cgtgtctttg atggcgaaca acattttatt gacggaattg agtcaggtcg ttgacacgca 1320

 ggagatgtcg ctgtcattcg taatatcggc ccagtcggag gccaggaat gccagaaatg 1380
 ttaaaaccga cctcagcctt gattggagca ggtcttgga aatcttgtgc ttgtattact 1440
 gacggacgtt tctctggtgg cacacatggc tttgtggttg gccacattgt ccccgaagcg 1500
 gttgagggtg gattgattgg cttggtcgaa gatgatgata ttatcgagat tgatgcggtc 1560
 aataacagca ttagtttgaa agttctgtac gatgagattg ctagacgacg tgccaattat 1620
 caaaaacctg ctctaaagc aacgcgtggg gttcttgcta aatttgctaa actcacgcgc 1680
 ccagccagtg aaggctgtgt gactgattta tag 1713

<210> 187

<211> 570

<212> PRT

<213> Lactococcus lactis

<400> 187

Met Glu Phe Lys Tyr Asn Gly Lys Val Glu Ser Ile Glu Leu Asn Lys
1 5 10 15
Tyr Ser Lys Thr Leu Thr Gln Asp Pro Thr Gln Pro Ala Thr Gln Ala
 20 25 30
Met His Tyr Gly Ile Gly Phe Lys Asp Glu Asp Phe Lys Lys Ala Gln
 35 40 45
Val Gly Ile Val Ser Met Asp Trp Asp Gly Asn Pro Cys Asn Met His

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

 115 120 125
Ile Val Ala Val Pro Gly Cys Asp Lys Asn Met Pro Gly Ser Ile Ile
 130 135 140
Gly Met Ala Arg Leu Asn Arg Pro Ser Ile Met Val Tyr Gly Gly Thr
145 150 155 160
Ile Glu His Gly Glu Tyr Lys Gly Glu Lys Leu Asn Ile Val Ser Ala
 165 170 175
Phe Glu Ala Leu Gly Gln Lys Ile Thr Gly Asn Ile Ser Glu Glu Asp

 180 185 190
Tyr His Gly Val Ile Cys Asn Ala Ile Pro Gly Gln Gly Ala Cys Gly
 195 200 205
Gly Met Tyr Thr Ala Asn Thr Leu Ala Ser Ala Ile Glu Thr Leu Gly
 210 215 220
Met Ser Leu Pro Tyr Ser Ala Ser Asn Pro Ala Val Ser Gln Glu Lys
225 230 235 240
Glu Asp Glu Cys Asp Glu Ile Gly Leu Ala Ile Lys Asn Leu Leu Glu

245 250 255
 Lys Asp Ile Lys Pro Ser Asp Ile Met Thr Lys Glu Ala Phe Glu Asn
 260 265 270
 Ala Ile Thr Ile Val Met Val Leu Gly Gly Ser Thr Asn Ala Val Leu
 275 280 285
 His Ile Ile Ala Met Ala Asn Ala Ile Gly Val Glu Ile Thr Gln Asp
 290 295 300
 Asp Phe Gln Arg Ile Ser Asp Val Thr Pro Val Leu Gly Asp Phe Lys

 305 310 315 320
 Pro Ser Gly Lys Tyr Met Met Glu Asp Leu His Lys Ile Gly Gly Val
 325 330 335
 Pro Ala Val Leu Lys Tyr Leu Leu Lys Glu Gly Lys Leu His Gly Asp
 340 345 350
 Cys Leu Thr Val Thr Gly Lys Thr Leu Ala Glu Asn Val Glu Thr Ala
 355 360 365
 Leu Asp Leu Asp Phe Asp Ser Gln Asp Ile Ile Arg Pro Leu Glu Asn

 370 375 380
 Pro Ile Lys Ala Thr Gly His Leu Gln Ile Leu Tyr Gly Asn Leu Ala
 385 390 395 400
 Glu Gly Gly Ser Val Ala Lys Ile Ser Gly Lys Glu Gly Glu Phe Phe
 405 410 415
 Lys Gly Thr Ala Arg Val Phe Asp Gly Glu Gln His Phe Ile Asp Gly
 420 425 430
 Ile Glu Ser Gly Arg Leu His Ala Gly Asp Val Ala Val Ile Arg Asn

 435 440 445
 Ile Gly Pro Val Gly Gly Pro Gly Met Pro Glu Met Leu Lys Pro Thr
 450 455 460
 Ser Ala Leu Ile Gly Ala Gly Leu Gly Lys Ser Cys Ala Leu Ile Thr
 465 470 475 480
 Asp Gly Arg Phe Ser Gly Gly Thr His Gly Phe Val Val Gly His Ile
 485 490 495

Val Pro Glu Ala Val Glu Gly Gly Leu Ile Gly Leu Val Glu Asp Asp

500	505	510	
Asp Ile Ile Glu Ile Asp Ala Val Asn Asn Ser Ile Ser Leu Lys Val			
515	520	525	
Ala Asp Asp Glu Ile Ala Arg Arg Arg Ala Asn Tyr Gln Lys Pro Ala			
530	535	540	
Pro Lys Ala Thr Arg Gly Val Leu Ala Lys Phe Ala Lys Leu Thr Arg			
545	550	555	560
Pro Ala Ser Glu Gly Cys Val Thr Asp Leu			
565	570		

<210> 188

<211> 1674

<212> DNA

<213> *Flavobacterium johnsoniae*

<400> 188

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gtcagcatgg gttatgatgg taatacttgc aatatgcact taaatgattt agcaaaagat	180
gttaaaaaag gtgtttggga tgctggtctg gtcggactta tttttaatac cattggtgta	240
agtgacggaa ttictaacgg tacagaagga atgcgttatt cattagtffc tcgtgatgta	300
atcgacagatt ctattgaaac tgtagccggt gcacaatggt acgatagtat tattgcaatt	360
cctggetcgc ataaaaatat gcctggagca ttaatcgcaa tgggaagatt aaaccgtccg	420
tcaatgatgg tttatggagg atctatccac tcaggaaaat ggaaaggtga atctctaaac	480
atcgtttctg cttttgaagc tttaggaaaa aaagtaaaag gcgaaattac tccggaagat	540
tttaaagggtg ttattcaaaa tgcttgctct ggagctggtg cctgcggtgg tatgtatact	600
gcaaacacta tgccttctgc aattgaagca ttaggtatga gtatgcctta cagttcttct	660
aaccctgctt tgagtcagga aaaaagagac gaatgtattg ctgccggaga agctattaaa	720
gttttattag aaaaagatat taagccaaga gatattatga ctctgaaagc tttcgaaaat	780
gctattacaa ttgtagcagt ttaggaggt tctacaaacg cagttatgca cttaatgca	840
atggcacact ctgttggtat tacaattact ctgtgatgatt ttcaggcaat taacgacaga	900
acacctgttc ttgccgatat gaaaccaagt ggtaaataata tgatggaaga cattcacgaa	960

gtgggaggta ttccgggtgt aatgaaatat ttattgaaag tgggacttat ccacggagat 1020
 tgtttaacag taactggaaa aacagttgct gaaaacttag cttctacacc ggatttacia 1080
 gacggacaag aagtaattca tgaaattcaa aaagcgtaa aaccaacagg aaatattcag 1140
 gttttatacg gaaaccttgc ttctgaagga gctgtggcaa aaatcagcgg aaaagaaggg 1200

gaatatattcg aaggaccagc tgttgtatgt gaagggaat ttgaagtaat tccaggcttg 1260
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 ggtccgggaa tgctgaaat gctaaaaccg acatctgcca ttattggtgc aggattagga 1380
 agcagctgtg cacttattac agacggcaga ttctccggag gttcacacgg attcgtggtg 1440
 ggacacgtaa caccagaggc ttatgatgga ggtggatttg cactagtaaa agatggagat 1500
 ttaattgcta tcgatgctgt aaaaaataca atcgacctga aaatatctga cgaagaattt 1560
 gcagctcgta aagcggcttg ggttcaacca gcgctaaaag ttgacagagg ggttttactt 1620

aaatacgcaa gatcggtttc tagtgcttca acaggctgtg ttaccgataa ttaa 1674

<210> 189

<211> 557

<212> PRT

<213> Flavobacterium johnsoniae

<400> 189

Met Glu Leu Asn Lys Tyr Ser Lys Thr Ile Thr Gln Asp Gln Thr Gln

1 5 10 15

Pro Ala Ala Gln Ala Met Leu Tyr Gly Ile Gly Leu Thr Glu Glu Asp

20 25 30

Leu Lys Lys Ala Gln Val Gly Ile Val Ser Met Gly Tyr Asp Gly Asn

35 40 45

Thr Cys Asn Met His Leu Asn Asp Leu Ala Lys Asp Val Lys Lys Gly

50 55 60

Val Trp Asp Ala Gly Leu Val Gly Leu Ile Phe Asn Thr Ile Gly Val

65 70 75 80

Ser Asp Gly Ile Ser Asn Gly Thr Glu Gly Met Arg Tyr Ser Leu Val

85 90 95

Ser Arg Asp Val Ile Ala Asp Ser Ile Glu Thr Val Ala Gly Ala Gln

100 105 110

Trp Tyr Asp Ser Ile Ile Ala Ile Pro Gly Cys Asp Lys Asn Met Pro
115 120 125

Gly Ala Leu Ile Ala Met Gly Arg Leu Asn Arg Pro Ser Met Met Val
130 135 140

Tyr Gly Gly Ser Ile His Ser Gly Lys Trp Lys Gly Glu Ser Leu Asn
145 150 155 160

Ile Val Ser Ala Phe Glu Ala Leu Gly Lys Lys Val Lys Gly Glu Ile
165 170 175

Thr Pro Glu Asp Phe Lys Gly Val Ile Gln Asn Ala Cys Pro Gly Ala
180 185 190

Gly Ala Cys Gly Gly Met Tyr Thr Ala Asn Thr Met Ser Ser Ala Ile
195 200 205

Glu Ala Leu Gly Met Ser Met Pro Tyr Ser Ser Ser Asn Pro Ala Leu
210 215 220

Ser Gln Glu Lys Arg Asp Glu Cys Ile Ala Ala Gly Glu Ala Ile Lys
225 230 235 240

Val Leu Leu Glu Lys Asp Ile Lys Pro Arg Asp Ile Met Thr Arg Lys
245 250 255

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

Asn Ala Val Met His Leu Ile Ala Met Ala His Ser Val Gly Ile Thr
275 280 285

Ile Thr Leu Asp Asp Phe Gln Ala Ile Asn Asp Arg Thr Pro Val Leu
290 295 300

Ala Asp Met Lys Pro Ser Gly Lys Tyr Met Met Glu Asp Ile His Glu
305 310 315 320

Val Gly Gly Ile Pro Gly Val Met Lys Tyr Leu Leu Lys Val Gly Leu
325 330 335

Ile His Gly Asp Cys Leu Thr Val Thr Gly Lys Thr Val Ala Glu Asn
340 345 350

Leu Ala Ser Thr Pro Asp Leu Gln Asp Gly Gln Glu Val Ile His Glu

355 Ile Gln Lys Ala Leu Lys Pro Thr Gly Asn Ile Gln Val Leu Tyr Gly
 370 375 380
 Asn Leu Ala Ser Glu Gly Ala Val Ala Lys Ile Ser Gly Lys Glu Gly
 385 390 395 400
 Glu Tyr Phe Glu Gly Pro Ala Val Val Phe Glu Gly Glu Phe Glu Val
 405 410 415
 Ile Pro Gly Leu Gln Ala Gly Lys Ile Lys Pro Gly Asn Val Val Val
 420 425 430

 Ile Arg Gly Cys Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met Leu
 435 440 445
 Lys Pro Thr Ser Ala Ile Ile Gly Ala Gly Leu Gly Ser Ser Cys Ala
 450 455 460
 Leu Ile Thr Asp Gly Arg Phe Ser Gly Gly Ser His Gly Phe Val Val
 465 470 475 480
 Gly His Val Thr Pro Glu Ala Tyr Asp Gly Gly Gly Ile Ala Leu Val
 485 490 495

 Lys Asp Gly Asp Leu Ile Ala Ile Asp Ala Val Lys Asn Thr Ile Asp
 500 505 510
 Leu Lys Ile Ser Asp Glu Glu Phe Ala Ala Arg Lys Ala Ala Trp Val
 515 520 525
 Gln Pro Ala Leu Lys Val Asp Arg Gly Val Leu Leu Lys Tyr Ala Arg
 530 535 540
 Ser Val Ser Ser Ala Ser Thr Gly Cys Val Thr Asp Asn
 545 550 555

 <210>
 190
 <211> 2364
 <212> DNA
 <213> Clostridium butyricum
 <400> 190

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60

ttaaagtcta aaccatgtgt tgaatcagaa agagcaatat taataacaga atcatttaaa	120
caaacagaag gccagccagc aattttaaga agagcattgg cattgaaaca cataactgaa	180
aatatcccta taacaattag agatcaagaa cttatagtgg gaagttaac taaagaacca	240
aggtcttcac aagtatttcc tgagtittct aataagtggt tacaagatga attggataga	300
ttaaataaga gaactggaga tgcattccaa atttcagaag aaagtaaaga aaaattaaaa	360
gatgtctttg agtattggaa tggaaagaca acaagtgagt tagcaacttc atatatgaca	420
gaggaaacaa gagaggcagt aaattgtgat gtatttactg taggaaacta ctattataat	480
ggcgtaggac atgtatctgt agattatgga aaagtattaa gggttggatt taatgggatt	540
ataaatgagg ctaaggaaca attagaaaaa aacaggagta tagatcctga tttataaag	600
aaagaaaaat tcctaaatag tgttattatc tcatgcgaag ctgcaataac atatgtaaat	660
agatatgcta aaaaggctaa agagattgca gataatacaa gtgatgcaa aagaaaagct	720
gaattaaatg aaatagcaaa aatttgttca aaagtttcag gagagggagc taaatctttc	780
tatgaagcat gtcaattatt ttggtttatt catgcaataa taaatataga atctaattgga	840
cattctattt ctccagctag atttgatcaa tacatgtatc catattatga aaatgataaa	900
aatataacag ataagtttgc tcaagaatta atagattgta tctggattaa attaatgat	960
attaataaag taagagatga gatttcaact aaacattttg gtggttacc aatgtatcaa	1020
aacttaattg ttgggggtca aaattcagaa ggaaaagatg caactaataa agtatcatat	1080
atggcattag aagcagctgt ccatgtaaag ttgcctcagc catctttgtc agtaagaata	1140
tggaataaga ctccagatga atttttgctt agagcagcag aattaactag agaagggtta	1200
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ataaattctg gatttgataa aaataaacag attggaccta aaactcaaaa ttttgaagaa	1440
atgaaatcct ttgatgaatt catgaaagct tataaaagctc aaatggagta ttttgtaaaa	1500
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gcagaatata acttcagtgg accacaaggt gttggagtag ctaatatagg agattcatta	1680
gttgcagtta aaaaaattgt gtttgatgaa aataagatta ctcttcaga attaaagaaa	1740
acattaaata atgattttta aaattcagaa gaaatacaag cttactaaa aaatgctcct	1800
aagtttggaa atgatatgta tgaagttagt aatttagcta gagagggtgc attagtatac	1860
tgtagagaag ttaataaata tacaatcca aggggaggaa attttcaacc aggattatat	1920

ccatcttcaa ttaatgtata ttttgaagc ttaacaggtg ctactccaga tggaaggaaa 1980
 tccggacaac cattagctga tggggtttct ccatcaagag gctgtgatgt atctggacct 2040

actgcagctt gtaactcagt tagtaaatta gatcatttta tagcttcaaa tggaacttta 2100
 tttaatcaaa aattccatcc gtcagcatta aaaggtgata atggattaat gaatttatca 2160
 tcattaataa gaagttatct tgatcaaaag ggatttcattg ttcaatttaa tgtaatagat 2220
 aaaaaaatat tacttgcagc acaaaaaaat cctgaaaaat atcaagattt aattgttaga 2280
 gttgcaggat atagtgcaca gttcatttct ttagataaat ctattcaaaa tgatattatt 2340
 gcaagaactg aacatgttat gtaa 2364

<210> 191
 <211> 787
 <212> PRT
 <213> Clostridium butyricum

<400> 191
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 Ile Leu Ile Thr Glu Ser Phe Lys Gln Thr Glu Gly Gln Pro Ala Ile
 35 40 45
 Leu Arg Arg Ala Leu Ala Leu Lys His Ile Leu Glu Asn Ile Pro Ile
 50 55 60

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

Lys Thr Thr Ser Glu Leu Ala Thr Ser Tyr Met Thr Glu Glu Thr Arg
 130 135 140

Glu Ala Val Asn Cys Asp Val Phe Thr Val Gly Asn Tyr Tyr Tyr Asn
 145 150 155 160
 Gly Val Gly His Val Ser Val Asp Tyr Gly Lys Val Leu Arg Val Gly
 165 170 175
 Phe Asn Gly Ile Ile Asn Glu Ala Lys Glu Gln Leu Glu Lys Asn Arg
 180 185 190

 Ser Ile Asp Pro Asp Phe Ile Lys Lys Glu Lys Phe Leu Asn Ser Val
 195 200 205
 Ile Ile Ser Cys Glu Ala Ala Ile Thr Tyr Val Asn Arg Tyr Ala Lys
 210 215 220
 Lys Ala Lys Glu Ile Ala Asp Asn Thr Ser Asp Ala Lys Arg Lys Ala
 225 230 235 240
 Glu Leu Asn Glu Ile Ala Lys Ile Cys Ser Lys Val Ser Gly Glu Gly
 245 250 255

 Ala Lys Ser Phe Tyr Glu Ala Cys Gln Leu Phe Trp Phe Ile His Ala
 260 265 270
 Ile Ile Asn Ile Glu Ser Asn Gly His Ser Ile Ser Pro Ala Arg Phe
 275 280 285
 Asp Gln Tyr Met Tyr Pro Tyr Tyr Glu Asn Asp Lys Asn Ile Thr Asp
 290 295 300
 Lys Phe Ala Gln Glu Leu Ile Asp Cys Ile Trp Ile Lys Leu Asn Asp
 305 310 315 320

 Ile Asn Lys Val Arg Asp Glu Ile Ser Thr Lys His Phe Gly Gly Tyr
 325 330 335
 Pro Met Tyr Gln Asn Leu Ile Val Gly Gly Gln Asn Ser Glu Gly Lys
 340 345 350
 Asp Ala Thr Asn Lys Val Ser Tyr Met Ala Leu Glu Ala Ala Val His
 355 360 365
 Val Lys Leu Pro Gln Pro Ser Leu Ser Val Arg Ile Trp Asn Lys Thr
 370 375 380

 Pro Asp Glu Phe Leu Leu Arg Ala Ala Glu Leu Thr Arg Glu Gly Leu

385 390 395 400
 Gly Leu Pro Ala Tyr Tyr Asn Asp Glu Val Ile Ile Pro Ala Leu Val
 405 410 415
 Ser Arg Gly Leu Thr Leu Glu Asp Ala Arg Asp Tyr Gly Ile Ile Gly
 420 425 430
 Cys Val Glu Pro Gln Lys Pro Gly Lys Thr Glu Gly Trp His Asp Ser
 435 440 445

 Ala Phe Phe Asn Leu Ala Arg Ile Val Glu Leu Thr Ile Asn Ser Gly
 450 455 460
 Phe Asp Lys Asn Lys Gln Ile Gly Pro Lys Thr Gln Asn Phe Glu Glu
 465 470 475 480
 Met Lys Ser Phe Asp Glu Phe Met Lys Ala Tyr Lys Ala Gln Met Glu
 485 490 495
 Tyr Phe Val Lys His Met Cys Cys Ala Asp Asn Cys Ile Asp Ile Ala
 500 505 510

 His Ala Glu Arg Ala Pro Leu Pro Phe Leu Ser Ser Met Val Asp Asn
 515 520 525
 Cys Ile Gly Lys Gly Lys Ser Leu Gln Asp Gly Gly Ala Glu Tyr Asn
 530 535 540
 Phe Ser Gly Pro Gln Gly Val Gly Val Ala Asn Ile Gly Asp Ser Leu
 545 550 555 560
 Val Ala Val Lys Lys Ile Val Phe Asp Glu Asn Lys Ile Thr Pro Ser
 565 570 575

 Glu Leu Lys Lys Thr Leu Asn Asn Asp Phe Lys Asn Ser Glu Glu Ile
 580 585 590
 Gln Ala Leu Leu Lys Asn Ala Pro Lys Phe Gly Asn Asp Ile Asp Glu
 595 600 605
 Val Asp Asn Leu Ala Arg Glu Gly Ala Leu Val Tyr Cys Arg Glu Val
 610 615 620
 Asn Lys Tyr Thr Asn Pro Arg Gly Gly Asn Phe Gln Pro Gly Leu Tyr
 625 630 635 640

Pro Ser Ser Ile Asn Val Tyr Phe Gly Ser Leu Thr Gly Ala Thr Pro
645 650 655
Asp Gly Arg Lys Ser Gly Gln Pro Leu Ala Asp Gly Val Ser Pro Ser
660 665 670
Arg Gly Cys Asp Val Ser Gly Pro Thr Ala Ala Cys Asn Ser Val Ser
675 680 685
Lys Leu Asp His Phe Ile Ala Ser Asn Gly Thr Leu Phe Asn Gln Lys
690 695 700

Phe His Pro Ser Ala Leu Lys Gly Asp Asn Gly Leu Met Asn Leu Ser
705 710 715 720
Ser Leu Ile Arg Ser Tyr Phe Asp Gln Lys Gly Phe His Val Gln Phe
725 730 735
Asn Val Ile Asp Lys Lys Ile Leu Leu Ala Ala Gln Lys Asn Pro Glu
740 745 750
Lys Tyr Gln Asp Leu Ile Val Arg Val Ala Gly Tyr Ser Ala Gln Phe
755 760 765

Ile Ser Leu Asp Lys Ser Ile Gln Asn Asp Ile Ile Ala Arg Thr Glu
770 775 780

His Val Met

785

<210> 192

<211> 915

<212> DNA

<213> Clostridium butyricum

<400> 192

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cttgttattg aaggaaggaa ttacagtgtt gaagacgtta taaaggaatt gaaaaaagat 360
agtgttcaat atagaagatc aaacgggtgga attacactat ctggagggga agtattactt 420

caaccagatt ttgcagtga gcttttaaaa gagtgtaa catatggctg gcacactgcc 480
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ctggctatga ttgatataaa aagtatgaat gatgaaatcc ataggaaatt tacaggagtg 600
agtaacgaaa taatattaca aaacattaaa ttaagtgatg aattagctaa agaaataata 660

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ggagaaaata agtatcaagc aattggaaga gagtattctt tgaaagaact aaaatcacct 840
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<210> 193

<211> 304

<212> PRT

<213> Clostridium butyricum

<400> 193

Met Ser Lys Glu Ile Lys Gly Val Leu Phe Asn Ile Gln Lys Phe Ser

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Leu	His	Asp	Gly
Pro	Gly	Ile	Arg
Thr	Ile	Val	Phe
Phe	Lys	Gly	Cys
20	25	30	
Ser	Met	Ser	Cys
Leu	Trp	Cys	Ser
Asn	Pro	Glu	Ser
Gln	Asp	Ile	Lys
35	40	45	
Pro	Gln	Val	Met
Phe	Asn	Lys	Asn
Leu	Cys	Thr	Lys
Cys	Gly	Arg	Cys
50	55	60	
Lys	Ser	Gln	Cys
Lys	Ser	Ala	Ala
Ile	Asp	Met	Asn
Ser	Glu	Tyr	Arg

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

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