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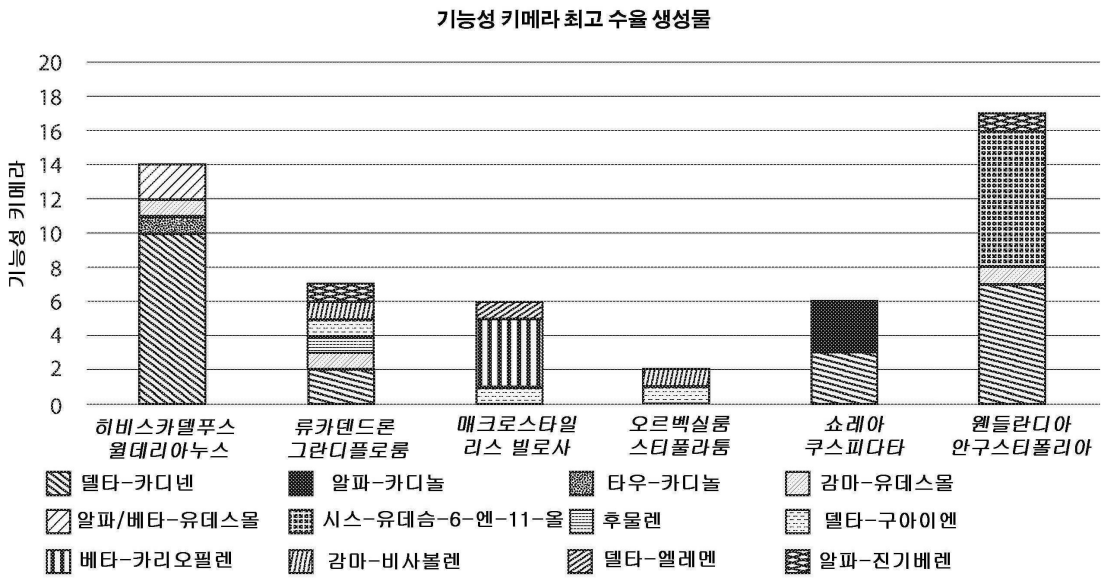
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(54) 발명의 명칭 **키메라 테르펜 합성효소**

(57) 요 약

본원에는 키메라 테르펜 합성효소, 키메라 테르펜 합성효소를 제조하는 방법, 및 이 합성효소를 사용하여 테르펜을 제조하는 방법이 기술되어 있다.

대 표 도



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명 세 서

청구범위

청구항 1

서열번호 1 내지 52로 구성되는 군으로부터 선택된 아미노산 서열과 적어도 90% 동일한 아미노산 서열을 포함하는 키메라 테르펜 합성효소.

청구항 2

제1항에 있어서, 키메라 테르펜 합성효소가 서열번호 1 내지 52로 구성되는 군으로부터 선택된 아미노산 서열과 동일한 아미노산 서열을 포함하는 것인 키메라 테르펜 합성효소.

청구항 3

제1항 또는 제2항의 키메라 테르펜 합성효소를 코딩하는 핵산 분자.

청구항 4

제3항의 핵산 분자를 포함하는 벡터.

청구항 5

제4항에 있어서, 벡터가 바이러스 벡터, 일시적 발현을 위한 벡터, 또는 유도성 발현을 위한 벡터인 벡터.

청구항 6

제4항 또는 제5항에 있어서, 벡터가 렌티바이러스 벡터, 레트로바이러스 벡터, 아데노바이러스 벡터, 아데노 관련 벡터, 갈락토스 유도성 벡터, 또는 독시사이클린 유도성 벡터인 벡터.

청구항 7

제3항의 핵산 분자를 포함하는 숙주 세포.

청구항 8

제4항 내지 제6항 중 어느 한 항의 벡터에 의해 형질전환된 숙주 세포.

청구항 9

제7항 또는 제8항에 있어서, 세포가 진균 세포인 숙주 세포.

청구항 10

제9항에 있어서, 진균 세포가 효모 세포인 숙주 세포.

청구항 11

제10항에 있어서, 효모 세포가 *사카로마이세스*(*Saccharomyces*), *피키아*(*Pichia*), *클루이베로마이세스*(*Kluyveromyces*), *한세눌라*(*Hansenula*), 또는 *야로위아*(*Yarrowia*) 세포인 숙주 세포.

청구항 12

제11항에 있어서, 세포가 *사카로마이세스 세레비지애*(*Saccharomyces cerevisiae*) 세포인 숙주 세포.

청구항 13

제7항 또는 제8항에 있어서, 세포가 식물 세포인 숙주 세포.

청구항 14

제7항 또는 제8항에 있어서, 세포가 세균 세포인 숙주 세포.

청구항 15

키메라 테르펜 합성효소를 코딩하는 핵산 분자로서, 서열번호 67 내지 118로 구성되는 군으로부터 선택된 뉴클레오타이드 서열과 적어도 90% 동일한 서열을 포함하는 핵산 분자.

청구항 16

제15항에 있어서, 핵산 분자가 서열번호 67 내지 118로 기재된 서열을 포함하는 것인 핵산 분자.

청구항 17

제15항 또는 제16항에 있어서, 핵산 분자가 TATA 박스 서열을 추가로 포함하는 것인 핵산 분자.

청구항 18

제3항에 있어서, 핵산 분자 서열의 적어도 40%가 멸종 식물로부터 유래된 것인 핵산 분자.

청구항 19

제1항 내지 제18항 중 어느 한 항에 있어서, 키메라 테르펜 합성효소가 키메라 세스퀴테르펜 합성효소인 키메라 테르펜 합성효소, 핵산 분자 또는 숙주 세포.

청구항 20

제19항에 있어서, 키메라 테르펜 합성효소가 알파-구아이엔(alpha-guaiene) 합성효소인 키메라 테르펜 합성효소, 핵산 분자 또는 숙주 세포.

청구항 21

제20항에 있어서, 알파-구아이엔 합성효소가 서열번호 17, 22 또는 29와 적어도 90% 동일한 서열을 포함하는 것인 키메라 테르펜 합성효소, 핵산 분자 또는 숙주 세포.

청구항 22

제21항에 있어서, 알파-구아이엔 합성효소가 서열번호 17, 22 또는 29를 포함하는 것인 키메라 테르펜 합성효소, 핵산 분자 또는 숙주 세포.

청구항 23

제18항에 있어서, 알파-구아이엔 합성효소가 서열번호 17, 22 또는 29로 구성되는 것인 키메라 테르펜 합성효소, 핵산 분자 또는 숙주 세포.

청구항 24

제18항에 있어서, 멸종 식물이 *히비스카델푸스 윌데리아누스*(*Hibiscadelphus wilderianus*), *류카덴드론 그란디플로룸*(*Leucadendron grandiflorum*), *매크로스타일리스 빌로사*(*Macrostylis villosa*), *오르벡실룸 스티풀라툼*(*Orbexilum stipulatum*), *쇼레아 쿠스피다타*(*Shorea cuspidata*) 및 *웬들란디아 안구스티폴리아*(*Wendlandia angustifolia*)로 구성되는 군으로부터 선택된 것인 핵산 분자.

청구항 25

하나 이상의 세스퀴테르펜을 제조하는 방법으로서, 하나 이상의 세스퀴테르펜을 제조하기에 적합한 조건 하에서 제3항, 제15항 내지 제18항 및 제24항 중 어느 한 항의 핵산을 포함하는 숙주 세포를 배양하는 단계를 포함하는 방법.

청구항 26

제25항의 방법에 의해 제조된 하나 이상의 세스퀴테르펜을 포함하는 조성물.

청구항 27

제26항에 있어서, 하나 이상의 세스퀴테르펜 중 적어도 하나가 아로마 화합물인 조성물.

청구항 28

향수를 제조하는 방법으로서, 하나 이상의 세스퀴테르펜을 제조하기에 적합한 조건 하에서 제3항, 제15항 내지 제18항 및 제24항 중 어느 한 항의 핵산을 포함하는 숙주 세포를 배양하는 단계; 및 하나 이상의 세스퀴테르펜을 추출하는 단계를 포함하는 방법.

청구항 29

알파-구아이엔을 생성할 수 있는 키메라 테르펜 합성효소로서, 키메라 테르펜 합성효소의 아미노산 서열의 적어도 40%가 멸종 식물로부터 유래된 것인 키메라 테르펜 합성효소.

청구항 30

알파-구아이엔을 생성할 수 있는 키메라 테르펜 합성효소를 코딩하는 핵산 분자로서, 상기 핵산 분자 서열의 적어도 40%가 멸종 식물로부터 유래된 것인 핵산 분자.

청구항 31

제30항의 핵산을 발현하는 숙주 세포.

청구항 32

알파-구아이엔을 생성할 수 있는 키메라 테르펜 합성효소를 발현하는 숙주 세포.

청구항 33

제31항 또는 제32항의 숙주 세포를 배양하는 단계를 포함하는, 알파-구아이엔을 제조하는 방법.

청구항 34

제33항에 있어서, 숙주 세포에 의해 생성된 알파-구아이엔을 모으는 단계를 추가로 포함하는 방법.

청구항 35

제31항 또는 제32항에 있어서, 세포가 진균 세포인 숙주 세포.

청구항 36

제31항 또는 제32항에 있어서, 세포가 식물 세포인 숙주 세포.

청구항 37

제31항 또는 제32항에 있어서, 세포가 세균 세포인 숙주 세포.

청구항 38

제31항, 제32항 및 제35항 중 어느 한 항에 있어서, 세포가 효모 세포인 숙주 세포.

청구항 39

제38항에 있어서, 효모 세포가 *사카로마이세스, 피키아, 클루이베로마이세스, 한세눌라*, 또는 *야로위아* 세포인 숙주 세포.

청구항 40

제39항에 있어서, 효모 세포가 *사카로마이세스 세레비지애* 세포인 숙주 세포.

청구항 41

서열번호 119 내지 357로 구성되는 군으로부터 선택된 서열을 포함하는 키메라 테르펜 합성효소.

발명의 설명

기 술 분 야

[0001] **관련 출원**

[0002] 본원은 35 U.S.C. § 119(e) 하에 2018년 2월 14일자로 제출된 발명의 명칭이 "키메라 테르펜 합성효소(CHIMERIC TERPENE SYNTHASES)"인 미국 가출원 연속 번호 62/630,640의 이익을 주장한 것이며, 상기 가출원은 그의 전체 내용이 본 명세서에 참고 인용된다.

[0003] **발명의 분야**

[0004] 본 개시내용은 키메라 테르펜 합성효소, 키메라 테르펜 합성효소를 제조하는 방법, 및 그 합성효소를 사용하여 테르펜을 제조하는 방법에 관한 것이다.

배 경 기 술

[0005] 테르펜은 5개의 탄소 형성 블록들로부터 형성된 다양한 부류의 유기 화합물이고 적어도 400가지 상이한 구조적 패밀리들을 포괄한다. 그의 구조적 다양성을 고려할 때, 테르펜은 페로몬, 항산화제 및 항균제로서의 작용을 포함하는 다수의 역할을 가진다. 테르펜 합성효소가 원핵생물 및 진핵생물 둘 다에서 테르펜을 생성하지만, 테르펜 이성질체들의 폭 넓은 배열은 종종 천연 발생 공급원으로부터의 고수율 추출을 방해한다. 더구나, 테르펜의 구조적 복잡성은 종종 드 노보 화학적 합성을 제한한다.

발명의 내용

[0006] 본 개시내용의 양태는 서열번호 1 내지 52로 구성되는 군으로부터 선택된 아미노산 서열과 적어도 90% 동일한 아미노산 서열을 포함하는 키메라 테르펜 합성효소에 관한 것이다. 일부 실시양태에서, 키메라 테르펜 합성효소는 서열번호 1 내지 52로 구성되는 군으로부터 선택된 아미노산 서열과 적어도 91%, 적어도 92%, 적어도 93%, 적어도 94%, 적어도 95%, 적어도 96%, 적어도 97%, 적어도 98%, 또는 적어도 99% 동일한 아미노산 서열을 포함한다. 일부 실시양태에서, 키메라 테르펜 합성효소는 서열번호 1 내지 52로 구성되는 군으로부터 선택된 아미노산 서열과 동일한 아미노산 서열을 포함한다.

[0007] 본 개시내용의 추가 양태는 본원에 기재된 키메라 테르펜 합성효소를 코딩하는 핵산 분자에 관한 것이다. 일부 실시양태에서, 핵산 분자는 서열번호 67 내지 118로 구성되는 군으로부터 선택된 뉴클레오타이드 서열과 적어도 90% 동일한 서열을 포함한다. 일부 실시양태에서, 핵산 분자는 서열번호 67 내지 118로 구성되는 군으로부터 선택된 서열을 포함한다.

[0008] 본 개시내용의 추가 양태는 본원에 기재된 핵산 분자를 포함하는 벡터에 관한 것이다. 일부 실시양태에서, 벡터는 바이러스 벡터, 일시적 발현을 위한 벡터, 또는 유도성 발현을 위한 벡터이다. 일부 실시양태에서, 벡터는 렌티바이러스 벡터, 레트로바이러스 벡터, 아데노바이러스 벡터, 아데노 관련 벡터, 갈락토스 유도성 벡터 또는 독시사이클린 유도성 벡터이다.

[0009] 본 개시내용의 추가 양태는 본원에 기재된 핵산 또는 본원에 기재된 벡터를 포함하는 숙주 세포에 관한 것이다.

[0010] 일부 실시양태에서, 숙주 세포는 진균 세포이다. 일부 실시양태에서, 세포는 효모 세포이다. 일부 실시양태에서, 세포는 *사카로마이세스*(*Saccharomyces*), *피키아*(*Pichia*), *클루이베로마이세스*(*Kluyveromyces*), *한세눌라*(*Hansenula*), 또는 *야로위아*(*Yarrowia*) 세포이다. 일부 실시양태에서, 세포는 *사카로마이세스 세레비지애*(*Saccharomyces cerevisiae*) 세포이다.

[0011] 일부 실시양태에서, 숙주 세포는 식물 세포이다.

[0012] 일부 실시양태에서, 숙주 세포는 세균 세포이다.

[0013] 본 개시내용의 추가 양태는 키메라 테르펜 합성효소를 코딩하는 핵산 분자에 관한 것이며, 여기서 핵산 분자 서열 또는 아미노산 서열의 적어도 10%는 희귀 또는 멸종 식물로부터 유래한다. 일부 실시양태에서, 핵산 분자 서열 또는 아미노산 서열의 적어도 40%는 희귀 또는 멸종 식물로부터 유래한다.

[0014] 일부 실시양태에서, 핵산 분자 서열 또는 아미노산 서열의 적어도 20%, 적어도 30%, 적어도 40%, 적어도 50%,

적어도 60%, 적어도 70%, 적어도 80%, 또는 적어도 90%는 희귀 또는 멸종 식물로부터 유래한다. 일부 실시양태에서, 핵산 분자 서열 또는 아미노산 서열의 적어도 90%, 적어도 91%, 적어도 92%, 적어도 93%, 적어도 94%, 또는 적어도 95%는 희귀 또는 멸종 식물로부터 유래한다.

[0015] 일부 실시양태에서, 키메라 테르펜 합성효소는 키메라 세스퀴테르펜(sesquiterpene) 합성효소이다. 일부 실시양태에서, 희귀 또는 멸종 식물은 *히비스카델푸스 윌데리아누스(Hibiscadelphus wilderianus)*, *류카덴드론 그란디플로룸(Leucadendron grandiflorum)*, *매크로스타일리스 빌로사(Macrostylis villosa)*, *오르벡실룸 스티풀라툼(Orbexilum stipulatum)*, *쇼레아 쿠스피다타(Shorea cuspidata)* 및 *웬들란디아 안구스티폴리아(Wendlandia angustifolia)*로 구성되는 군으로부터 선택된다.

[0016] 본 개시의 추가 양태는 키메라 테르펜 합성효소를 코딩하는 핵산 분자에 관한 것이다. 일부 실시양태에서, 핵산 분자 서열 또는 아미노산 서열의 적어도 10%는 희귀 또는 멸종 식물로부터 유래한다. 일부 실시양태에서, 핵산 분자 서열의 적어도 20%, 적어도 30%, 적어도 40%, 적어도 50%, 적어도 60%, 적어도 70%, 적어도 80%, 또는 적어도 90%는 희귀 또는 멸종 식물로부터 유래한다. 일부 실시양태에서, 핵산 분자 서열의 적어도 90%, 적어도 91%, 적어도 92%, 적어도 93%, 적어도 94%, 또는 적어도 95%는 희귀 또는 멸종 식물로부터 유래한다.

[0017] 일부 실시양태에서, 핵산 분자는 TATA 박스 서열을 추가로 포함한다.

[0018] 본 개시내용의 추가 양태는 하나 이상의 세스퀴테르펜을 제조하는 방법으로서, 하나 이상의 세스퀴테르펜을 제조하기에 적합한 조건 하에서 본원에 기재된 숙주 세포를 배양하는 단계를 포함하는 방법에 관한 것이다.

[0019] 본 개시내용의 추가 양태는 본원에 기재된 방법에 의해 제조된 하나 이상의 세스퀴테르펜을 포함하는 조성물에 관한 것이다.

[0020] 한 실시양태에서, 하나 이상의 세스퀴테르펜 중 적어도 하나는 아로마 화합물이다.

[0021] 본 개시내용의 추가 양태는 향수를 제조하는 방법으로서, 하나 이상의 세스퀴테르펜을 제조하기에 적합한 조건 하에서 본원에 기재된 숙주 세포를 배양하는 단계; 및 하나 이상의 세스퀴테르펜을 추출하는 단계를 포함하는 방법에 관한 것이다.

[0022] 본원에 기재된 조성물 및 방법의 제한사항들 각각은 다양한 기재된 실시양태들을 포괄할 수 있다. 따라서, 어느 한 요소 또는 요소들의 조합을 수반하는 본 발명의 제한사항들 각각은 본 발명의 각각의 양태에 포함될 수 있을 것으로 예상된다. 이러한 본 개시내용은 후술하는 설명에 기재되어 있거나 도면에 예시된 성분들의 구성 및 배열의 세부사항에 대한 그의 적용에서 제한되지 않는다.

도면의 간단한 설명

[0023] 첨부된 도면은 실제 크기로 도시하고자 의도된 것이 아니다. 도면은 본 개시내용을 예시하기 위한 것일 뿐 본 개시내용의 실현 가능성을 위해 요구하지 않는다. 간결성을 목적으로 하여, 모든 구성요소들이 모든 도면에서 표지되어 있지 않을 수 있다. 도면은 다음과 같다:

도 1은 *에이치. 윌데리아누스(H. wilderianus)*로부터의 희귀 서열을 함유하는 세스퀴테르펜 합성효소(SQTS)를 사용함으로써 생성되는 확인된 세스퀴테르펜의 구조를 도시하는 일련의 도면이다.

도 2는 *엘. 그란디플로룸(L. grandiflorum)*으로부터의 희귀 서열을 함유하는 SQTS를 사용함으로써 생성되는 확인된 세스퀴테르펜의 구조를 도시하는 일련의 도면이다.

도 3은 *엠. 빌로사(M. villosa)*로부터의 희귀 서열을 함유하는 SQTS를 사용함으로써 생성되는 세스퀴테르펜의 구조를 도시하는 일련의 도면이다.

도 4는 *오. 스티풀라툼(O. stipulatum)*으로부터의 희귀 서열을 함유하는 SQTS를 사용함으로써 생성된 세스퀴테르펜의 구조를 도시하는 일련의 도면이다.

도 5는 *에스. 쿠스피다타(S. cuspidata)*로부터의 희귀 서열을 함유하는 SQTS를 사용함으로써 생성되는 확인된 세스퀴테르펜의 구조를 도시하는 일련의 도면이다.

도 6은 *더블유. 안구스티폴리아(W. angustifloia)*로부터의 희귀 서열을 함유하는 SQTS를 사용함으로써 생성되는 확인된 세스퀴테르펜의 구조를 도시하는 일련의 도면이다.

도 7은 키메라 생성물 분포 대 식물 종을 보여주는 그래프이다. 키메라는 가장 높은 수율로 생성된 세스퀴테르

펜에 근거하여 범주화된다.

도 8a 내지 8f는 희귀 식물의 종을 도시하는 일련의 사진을 포함한다. 도 8a는 *히비스카델푸스 윌데리아누스(Hibiscadelphus wilderianus)*를 도시한다(Radlkofer et al., New and Noteworthy Hawaiian Plants. Hawaiian Board of Agriculture and Forestry Botanical Bulletin. 1911;(1):1-15). 도 8b는 *류카덴드론 그란디플로룸(Leucadendron grandiflorum)*을 도시한다(Salisbury et al., The Paradisus Londinensis or Coloured Figures of Plants Cultivated in the Vicinity of the Metropolis. 1805; (Volume 1, part 2): 105). 도 8c는 *매크로스타일리스 빌로사(Macrostylis villosa)* 아종 빌로사를 도시한다("Red List of South African Plants: Macrostylis villosa subsp. villosa," 2007). 도 8d는 *오르벡실룸 스티폴라툼(Orbexilum stipulatum)*을 도시한다(Short, "Orbexilum stipulatum collected at Falls of the Ohio," 1840 from The Philadelphia Herbarium at the Academy of Natural Sciences). 도 8e는 *쇼레아 쿠스피다타(Shorea cuspidata)*를 도시한다("Kew Royal Botanical Gardens: Shorea cuspidata specimen K000700460," 1962). 도 8f는 *웬들란디아 안구스티폴리아(Wendlandia angustifolia)*를 도시한다("Kew Royal Botanical Gardens: Wendlandia angustifolia K000030921," collection date not recorded).

도 9는 *에이치. 윌데리아누스* 키메라 스크리닝 데이터(표 4)로부터의 선택된 기체 크로마토그래피-질량 분광측정(GC/MS) 크로마토그램을 도시하는 일련의 도면이다.

도 10은 *엘. 그란디플로룸* 키메라 스크리닝 데이터(표 5)로부터의 선택된 GC/MS 크로마토그램을 도시하는 일련의 도면이다.

도 11은 *엘. 그란디플로룸* 키메라 스크리닝 데이터(표 5)로부터의 선택된 GC/MS 크로마토그램을 도시하는 일련의 도면이다.

도 12는 *엠. 빌로사* 키메라 스크리닝 데이터(표 6)로부터의 선택된 GC/MS 크로마토그램을 도시하는 일련의 도면이다.

도 13은 *에스. 쿠스피다타* 키메라 스크리닝 데이터(표 8)로부터의 선택된 GC/MS 크로마토그램을 도시하는 일련의 도면이다.

도 14는 *더블유. 안구스티폴리아* 키메라 스크리닝 데이터(표 9)로부터의 선택된 GC/MS 크로마토그램을 도시하는 일련의 도면이다.

도 15는 *더블유. 안구스티폴리아* 키메라 스크리닝 데이터(표 9)로부터의 선택된 GC/MS 크로마토그램을 도시하는 일련의 도면이다.

발명을 실시하기 위한 구체적인 내용

[0024] 테르펜은 향료 산업에서 널리 사용되지만, 천연 공급원으로부터의 테르펜의 정제 및 드 노보 화학적 합성은 종종 높은 생산 비용 및 낮은 수율을 가진다. 본 개시내용은 적어도 하나의 희귀 또는 멸종 식물로부터의 테르펜 합성효소 서열의 부분을 포함하는 키메라 테르펜 합성효소가 다양한 세스퀴테르펜들을 생성하는 데 활용될 수 있다는 예상치 못한 발견을 부분적으로 전제로 한다. 따라서, 본원은 키메라 테르펜 합성효소, 키메라 테르펜 합성 효소를 제조하는 방법, 및 기재된 키메라 테르펜 합성효소를 사용하여 테르펜을 제조하는 방법을 제공한다. 일부 실시양태에서, 키메라 테르펜 합성효소는 키메라 세스퀴테르펜 합성효소이다.

[0025] 본 발명은 상세한 설명에 기재된 성분들의 구성 및 배열의 세부사항에 대한 그의 적용에서 제한되지 않는다. 본 발명은 다른 실시양태들을 구현할 수 있고 다양한 방식들로 실시될 수 있거나 수행될 수 있다. 추가로, 본원에서 사용된 어구 및 용어는 설명하기 위한 것이고 제한으로서 간주되어서는 안 된다. 본원에서 "포괄하는", "포함하는", "가진", "함유하는", "수반하는" 및 이들의 어미변화와 같은 용어의 사용은 이후에 나열된 항목들 및 이들의 균등물뿐만 아니라 추가 항목도 포괄하기 위한 것이다.

[0026] *키메라 테르펜 합성효소*

[0027] 본 개시내용의 양태는 적어도 2개의 테르펜 합성효소들로부터의 단편(예를 들면, 서열)을 포함하는 키메라 테르펜 합성효소에 관한 것으로서, 여기서 2개 이상의 테르펜 합성효소들 중 적어도 하나는 희귀 또는 멸종 식물로부터 유래한다. 예를 들면, 키메라 테르펜 합성효소의 서열은 적어도 2종, 적어도 3종, 적어도 4종, 적어도 5종, 적어도 6종, 적어도 7종, 적어도 8종, 적어도 9종 또는 적어도 10종의 테르펜 합성효소들로부터의 하나 이상의 단편(예를 들면, 전체 서열의 하나 이상의 부분)을 포함할 수 있다. 본원에 기재된 키메라 테르펜 합성효

소는 합성 키메라 테르펜 합성효소일 수 있다는 것을 인식해야 한다. 따라서, 합성 키메라 테르펜 합성효소를 포함하는, 본원에 기재된 키메라 테르펜 합성효소는 하나 초과의 테르펜 합성효소들로부터 유래된 서열을 포함하고, 여기서 상기 테르펜 합성효소들 중 적어도 하나는 희귀 또는 멸종 식물로부터 유래한다. 일부 실시양태에서, 키메라 테르펜 합성효소는 키메라 세스퀴테르펜 합성효소이다.

[0028] 테르펜 합성효소는 이소프레노이드 디포스페이트 기질로부터의 테르펜의 형성을 촉매작용하는 효소이다. 적어도 두 유형의 테르펜 합성효소들이 특징규명되어 있다: 고전적 테르펜 합성효소 및 이소프레닐 디포스페이트 합성효소 유형의 테르펜 합성효소. 고전적 테르펜 합성효소는 원핵생물(예를 들면, 세균) 및 진핵생물(예를 들면, 식물, 진균 및 아메바)에서 발견되는 반면, 이소프레닐 디포스페이트 합성효소 유형의 테르펜 합성효소는 곤충에서 발견된다(예를 들면, 본 목적을 위해 전체적으로 본원에 참고로 포함된 문헌(Chen *et al.*, Terpene synthase genes in eukaryotes beyond plants and fungi: Occurrence in social amoebae. *Proc Natl Acad Sci U S A*. 2016;113(43):12132-12137) 참조). 여러가지 고도로 보존된 구조적 모티프들은 기질 결합을 조화시키는데 관여하는 아스파르테이트 농후 "DDxx(x)D/E" 모티프 및 "NDxxSxxxD/E"(서열번호 55) 모티프를 포함하여 고전적 테르펜 합성효소에서 보고되었다(예를 들면, 본 목적을 위해 전체적으로 본원에 각각 참고로 포함된 문헌(Starks *et al.*, Structural basis for cyclic terpene biosynthesis by tobacco 5-epi-aristolochene synthase. *Science*. 1997 Sep 19;277(5333):1815-20); 및 문헌(Christianson *et al.*, Unearthing the roots of the terpenome. *Curr Opin Chem Biol*. 2008 Apr;12(2):141-50) 참조).

[0029] 테르펜 합성효소는 그 자신이 생성하는 테르펜의 유형에 의해 분류될 수 있다. 본원에서 사용된 바와 같이, 달리 표시되어 있지 않은 한, 테르펜은 이소프렌(즉, C_5H_8) 유닛 및 이의 유도체를 포함하는 유기 화합물이다. 예를 들면, 테르펜은 분자식 $(C_5H_8)_n$을 가진 순수 탄화수소를 포함하고, 여기서 n은 이소프렌 서브유닛의 수를 나타낸다. 테르펜은 산소첨가된 화합물(종종 테르페노이드로서 지칭됨)도 포함한다. 테르펜은 구조적으로 다양한 화합물들이고, 예를 들면, 환형(예를 들면, 단환형 화합물, 다환형 화합물, 동종환형 화합물 및 이종환형 화합물), 또는 비환형(예를 들면, 선형 화합물 및 분지형 화합물)일 수 있다. 일부 실시양태에서, 테르펜은 향을 가질 수 있다. 본원에서 사용된 바와 같이, 아로마 화합물은 향을 가진 화합물을 지칭한다. 질량 분광측정(예를 들면, 기체 크로마토그래피-질량 분광측정(GC/MS, 하기 실시예 2에 나타냄)을 포함하는, 당분야에서 공지된 임의의 방법을 이용하여 관심 있는 테르펜을 확인할 수 있다.

[0030] 테르펜 합성효소는, 예를 들면 모노테르펜 합성효소, 디테르펜 합성효소 및 세스퀴테르펜 합성효소를 포함할 수 있다. 모노테르펜 합성효소 및 세스퀴테르펜 합성효소의 일부 비제한적 예들이, 예를 들면, 본 목적을 위해 전체적으로 본원에 참고로 포함된 문헌(Degenhardt *et al.*, Monoterpene and sesquiterpene synthases and the origin of terpene skeletal diversity in plants. *Phytochemistry*. 2009 Oct-Nov;70(15-16):1621-37)에서 확인될 수 있다.

[0031] 모노테르펜 합성효소는 10-탄소 모노테르펜의 형성을 촉매작용한다. 일반적으로, 모노테르펜 합성효소는 게라닐 디포스페이트(GPP)를 기질로서 사용한다. 모노테르펜 합성효소의 비제한적 예는 미르센(Myrcene) 합성효소(UniprotKB 식별기호: O24474), (R)-리모넨(limonene) 합성효소(UniprotKB 식별기호: Q2XSC6), (E)-베타-오시멘(ocimene) 합성효소(UniprotKB 식별기호: Q5CD81) 및 리모넨 합성효소(UniprotKB 식별기호: Q9FV72)를 포함한다. 모노테르펜의 비제한적 예는 리모넨, 사비넨(sabinene), 투젠(thujene), 카렌(carene), 보르네올(borneol), 유칼립톨(eucalyptol) 및 캄펜(camphene)을 포함하나 이들로 제한되지 않는다.

[0032] 디테르펜 합성효소는 20-탄소 디테르펜의 형성을 촉진한다. 일반적으로, 디테르펜 합성효소는 게라닐게라닐 디포스페이트를 기질로서 사용한다. 디테르펜 합성효소의 비제한적 예는 시스-아비에놀(cis-abienol) 합성효소(UniprotKB 식별기호: H8ZM73), 스클라레올(sclareol) 합성효소(UniprotKB 식별기호: K4HYB0) 및 아비에타디엔(abietadiene) 합성효소(Q38710)를 포함한다. 예를 들면, 본 목적을 위해 전체적으로 본원에 참고로 포함된 문헌(Gong *et al.*, Diterpene synthases and their responsible cyclic natural products. *Nat Prod Bioprospect*. 2014;4(2):59-72)을 참조할 수 있다. 디테르펜의 비제한적 예는 셈브렌(cembrene) 및 스클라레올을 포함하나 이들로 제한되지 않는다.

[0033] 세스퀴테르펜 합성효소는 15-탄소 세스퀴테르펜의 형성을 촉매작용한다. 일반적으로, 세스퀴테르펜 합성효소는 파르네실 디포스페이트(FDP)를 세스퀴테르펜으로 전환시킨다. 세스퀴테르펜 합성효소의 비제한적 예는 (+)-델타-카디넨(cadinene) 합성효소(UniprotKB 식별기호: Q9SAN0), UniprotKB 식별기호: A0A067FTE8, 베타-유데스몰(eudesmol) 합성효소(UniprotKB 식별기호: B1B1U4), (+)-델타-카디넨 합성효소 이소자임 XC14(UniprotKB 식별기호: Q39760), (+)-델타-카디넨 합성효소 이소자임 XC1(UniprotKB 식별기호: Q39761), (+)-델타-카디넨 합성

효소 이소자임 A(UniprotKB 식별기호: Q43714), 세스퀴테르펜 합성효소 2(UniprotKB 식별기호: Q9FQ26), 잠정적 델타-구아이엔(guaiene) 합성효소(UniprotKB 식별기호: A0A0A0QUT9), 델타-구아이엔 합성효소 1(UniprotKB 식별기호: D0VMR6), 알파-진기베렌(zingiberene) 합성효소(UniprotKB 식별기호: Q5SBP4), (Z)-감마-바사볼렌(bisabolene) 합성효소 1(UniprotKB 식별기호: Q9T0J9), A0A067D5M4, 델타-엘레멘(elemene) 합성효소(UniprotKB 식별기호: A0A097ZIE0), ShoBecSQTS1, A0A068UHT0, 테르펜 합성효소(UniprotKB 식별기호: G5CV47), A0A068VE40 및 A0A068VI46을 포함한다.

[0034] 일부 실시양태에서, 세스퀴테르펜 합성효소는 알파-구아이엔 합성효소이다. 본원에서 사용된 바와 같이, 알파-구아이엔 합성효소는 알파-구아이엔의 형성을 촉매작용할 수 있다. 일부 실시양태에서, 알파-구아이엔 합성효소는 (2E,6E)-파르네실 디포스페이트를 기질로서 사용한다. 알파-구아이엔 합성효소의 비제한적 예는 UniprotKB 식별기호: D0VMR6, UniprotKB 식별기호: D0VMR7, UniprotKB 식별기호: D0VMR8, UniprotKB 식별기호: Q49SP3을 포함한다. 본원에 개시된 바와 같이, 알파-구아이엔 합성효소는 서열번호 17, 22 또는 29와 적어도 50%(예를 들면, 수치들 사이의 모든 값들을 포함하는, 적어도 55%, 60%, 65%, 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%, 99% 또는 99% 초과) 동일한 서열을 포함할 수 있다. 일부 실시양태에서, 알파-구아이엔 합성효소는 서열번호 17, 22 또는 29를 포함한다. 일부 실시양태에서, 알파-구아이엔 합성효소는 서열번호 17, 22 또는 29로 구성된다.

[0035] 본원에서 사용된 바와 같이, 달리 표시되어 있지 않은 한, 세스퀴테르펜은 세스퀴테르펜 탄화수소 및 세스퀴테르펜 알코올(세스퀴테르페놀)을 포함한다. 세스퀴테르펜의 비제한적 예는 델타-카디넨, 에피-쿠베놀, 타우-카디놀, 알파-카디놀, 감마-셀리넨, 10-에피-감마-유데스몰, 감마-유데스몰, 알파/베타-유데스몰, 주니퍼 캄포르, 7-에피-알파-유데스몰, 크립토메리디올 이성질체 1, 크립토메리디올 이성질체 2, 크립토메리디올 이성질체 3, 후물렌, 알파-구아이엔, 델타-구아이엔, 진기베렌, 베타-비사볼렌, 베타-파르네센, 베타-세스퀴펠란드렌, 쿠베놀, 알파-바사보롤, 알파-쿠르쿠멘, 트랜스-네롤리돌, 감마-비사볼렌, 베타-카리오필렌, 트랜스-세스퀴사비넨 수화물, 델타-엘레멘, 시스-유데슴-6-엔-11-올, 다우센, 이소다우센, 트랜스-베르가모텐, 알파-진기베렌, 세스퀴사비넨 수화물, 및 8-이소프로페닐-1,5-디메틸-1,5-사이클로데카디엔을 포함하나 이들로 제한되지 않는다.

[0036] 본 개시내용은 다기능성(예를 들면, 하나 초과의 세스퀴테르펜을 생성할 수 있는) 키메라 테르펜 합성효소도 포괄한다. 일부 실시양태에서, 키메라 테르펜 합성효소는 델타-카디넨 및 알파-카디놀을 생성할 수 있다. 일부 실시양태에서, 키메라 테르펜 합성효소는 델타-카디넨, 타우-카디놀 및 알파-카디놀을 생성할 수 있다. 일부 실시양태에서, 키메라 테르펜 합성효소는 알파-구아이엔 및 델타-구아이엔을 생성할 수 있다. 일부 실시양태에서, 키메라 테르펜 합성효소는 베타-카리오필렌 및 후물렌을 생성할 수 있다.

[0037] 일부 실시양태에서, 본 개시의 키메라 테르펜 합성효소(예를 들면, 키메라 세스퀴테르펜 합성효소)는 서열번호 1 내지 52로 구성되는 군으로부터 선택된 서열과 적어도 50%(예를 들면, 수치들 사이의 모든 값들을 포함하는, 적어도 55%, 60%, 65%, 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%, 99% 또는 99% 초과) 동일한 아미노산 서열을 포함한다. 일부 실시양태에서, 키메라 테르펜 합성효소는 서열번호 1 내지 52로 제공된 아미노산 서열을 포함한다.

[0038] 일부 실시양태에서, 키메라 테르펜 합성효소는 서열번호 119 내지 357로 제공된 하나 이상의 서열을 포함한다.

[0039] 당분야에서 공지된 바와 같이, 용어 "서열 동일성"은, 서열 비교(정렬)에 의해 결정된, 2개의 폴리펩타이드들 또는 폴리뉴클레오타이드들의 서열들 사이의 관련성을 지칭한다. 당분야에서, 동일성은 일련의 2개 이상의 잔기들(예를 들면, 핵산 또는 아미노산 잔기들) 사이의 일치의 수에 의해 결정된, 2개의 서열들 사이의 서열 관련성의 정도를 의미하기도 한다. 동일성은 특정 수학적 모델 또는 컴퓨터 프로그램(예를 들면, "알고리즘")에 의해 주소지정된 갭 정렬(존재하는 경우)로 2개 이상의 서열들 중 더 작은 서열들 사이의 동일한 일치의 퍼센트를 측정한다.

[0040] 관련된 폴리펩타이드들의 동일성은 당분야에서 통상의 기술을 가진 자에게 공지된 방법들 중 임의의 방법에 의해 용이하게 계산될 수 있다. 2개의 서열들(예를 들면, 핵산 또는 아미노산 서열들)의 "퍼센트 동일성"은, 예를 들면 문헌(Karlin and Altschul *Proc. Natl. Acad. Sci. USA* 90:5873-77, 1993)에서와 같이 변형된, 문헌(Karlin and Altschul *Proc. Natl. Acad. Sci. USA* 87:2264-68, 1990)의 알고리즘을 이용함으로써 결정될 수 있다. 이러한 알고리즘은 문헌(Altschul et al., *J. Mol. Biol.* 215:403-10, 1990)의 NBLAST® 및 XBLAST® 프

로그램(버전 2.0) 내로 내포되어 있다. 본 발명의 단백질 분자와 상동한 아미노산 서열을 수득하기 위한 BLAST® 단백질 검색은, 예를 들면 XBLAST 프로그램, 점수=50, 단어길이=3을 사용함으로써 수행될 수 있다. 2개의 서열들 사이에 갭이 존재하는 경우에는, 예를 들면 문헌(Altschul *et al.*, *Nucleic Acids Res.* 25(17):3389-3402, 1997)에 기재된 바와 같이, Gapped BLAST®를 이용할 수 있다. BLAST® 및 Gapped BLAST® 프로그램을 이용할 때에는, 각각의 프로그램(예를 들면, XBLAST® 및 NBLAST®)의 디폴트 파라미터를 이용할 수 있거나, 당분야에서 통상의 기술을 가진 자에 의해 이해될 수 있는 바와 같이 그 파라미터를 적절히 조절할 수 있다.

[0041] 이용될 수 있는 또 다른 국소적 정렬 기법은, 예를 들면 스미스-워터만(Smith-Waterman) 알고리즘(Smith, T.F. & Waterman, M.S. (1981) "Identification of common molecular subsequences." *J. Mol. Biol.* 147:195-197)에 기반한다. 이용될 수 있는 일반적인 전반적 정렬 기법은, 예를 들면 동적 프로그래밍에 기반한 니들만-운쉬(Needleman-Wunsch) 알고리즘(Needleman, S.B. & Wunsch, C.D. (1970) "A general method applicable to the search for similarities in the amino acid sequences of two proteins." *J. Mol. Biol.* 48:443-453)이다. 보다 최근에는, 알려진 바에 의하면 니들만-운쉬 알고리즘을 포함하는, 다른 최적 전반적 정렬 방법들보다 더 빨리 핵산 및 아미노산 서열들의 전반적 정렬을 생성하는 신속 최적 전반적 서열 정렬 알고리즘(FOGSAA)이 개발되었다.

[0042] 본 개시내용은 본원에 기재된 키메라 테르펜 합성효소들(예를 들면, 세스퀴테르펜 합성효소들) 중 어느 한 키메라 테르펜 합성효소에 의해 생성된 하나 이상의 테르펜(예를 들면, 세스퀴테르펜)을 포함하는 조성물도 포괄한다. 일부 실시양태에서, 조성물은 아로마 화합물인 적어도 하나의 테르펜(예를 들면, 세스퀴테르펜)을 포함한다. 일부 실시양태에서, 조성물은 (예를 들면, 단일 향료 또는 혼합 향료를 포함하는) 퍼퓸이다. 일부 실시양태에서, 조성물은 조성물의 휘발성을 감소시키기 위해 고정제(즉, 안정화제)를 추가로 포함한다. 비제한적 예는 레시노이드(예를 들면, 벤조인(benzoin), 올리바눔(olibanum), 스토락스(storax), 랍다눔(labdanum), 미르(myrrh) 및 톨루 발삼(tolu balsam)) 및 벤질 벤조에이트를 포함하는 고정제를 포함한다. 일부 실시양태에서, 조성물은 에틸 알코올을 추가로 포함한다. 일부 실시양태에서, 조성물은 증류수를 추가로 포함한다.

[0043] 일부 실시양태에서, 본 개시내용의 테르펜 합성효소(예를 들면, 세스퀴테르펜 합성효소)는 수치들 사이의 임의의 값을 포함하는 적어도 1%, 적어도 2%, 적어도 3%, 적어도 4%, 적어도 5%, 적어도 6%, 적어도 7%, 적어도 8%, 적어도 9%, 적어도 10%, 적어도 15%, 적어도 20%, 적어도 30%, 적어도 40%, 적어도 50%, 적어도 60%, 70%, 적어도 80%, 적어도 90%, 적어도 95% 또는 100%의 특정 테르펜, 예컨대 세스퀴테르펜을 포함하는 테르펜(예를 들면, 세스퀴테르펜) 조성물을 생성한다. 세스퀴테르펜의 비제한적 예는 델타-카디넨, 에피-쿠베놀, 타우-카디놀, 알파-카디놀, 감마-셀리넨, 10-에피-감마-유데스몰, 감마-유데스몰, 알파/베타-유데스몰, 주니퍼 캄포르, 7-에피-알파-유데스몰, 크립토메리디올 이성질체 1, 크립토메리디올 이성질체 2, 크립토메리디올 이성질체 3, 후물렌, 알파-구아이엔, 델타-구아이엔, 진기베렌, 베타-비사볼렌, 베타-파르네센, 베타-세스퀴펠란드렌, 쿠베놀, 알파-바사보롤, 알파-쿠르쿠멘, 트랜스-네롤리돌, 감마-비사볼렌, 베타-카리오필렌, 트랜스-세스퀴사비넨 수화물, 델타-엘레멘, 시스-유데슴-6-엔-11-올, 다우센, 이소다우센, 트랜스-베르가모텐, 알파-진기베렌, 세스퀴사비넨 수화물 및 8-이소프로페닐-1,5-디메틸-1,5-사이클로데카디엔을 포함한다. 비제한적 예로서, 테르펜 합성효소는 숙주 세포에서 이종 발현될 수 있고, 재조합 숙주 세포에 의해 생성된 세스퀴테르펜은 추출될 수 있고, 조성물 중의 세스퀴테르펜의 유형은 기체 크로마토그래피-질량 분광측정을 이용함으로써 측정될 수 있다. 일부 실시양태에서, 테르펜 합성효소는 재조합 발현될 수 있고 정제된다. 일부 실시양태에서, 정제된 테르펜 합성효소에 의해 생성된 세스퀴테르펜은 추출될 수 있고, 조성물 중의 세스퀴테르펜의 유형은 기체 크로마토그래피-질량 분광측정을 이용함으로써 측정될 수 있다.

[0044] 일부 실시양태에서, 알파-구아이엔 합성효소는 수치들 사이의 임의의 값을 포함하는 적어도 1%, 적어도 2%, 적어도 3%, 적어도 4%, 적어도 5%, 적어도 6%, 적어도 7%, 적어도 8%, 적어도 9%, 적어도 10%, 적어도 15%, 적어도 20%, 적어도 30%, 적어도 40%, 적어도 50%, 적어도 60%, 적어도 70%, 적어도 80%, 적어도 90%, 적어도 95% 또는 100%의 알파-구아이엔을 포함하는 세스퀴테르펜 조성물을 생성할 수 있다. 일부 실시양태에서, 알파-구아이엔 합성효소는 수치들 사이의 임의의 값을 포함하는 1% 내지 10%, 5% 내지 20%, 15% 내지 20%, 16% 내지 20%, 17% 내지 20%, 18% 내지 20%, 19% 내지 20%, 20% 내지 25%, 20% 내지 24%, 20% 내지 23%, 20% 내지 22%, 20% 내지 21%, 20% 내지 30%, 30% 내지 40%, 40% 내지 50%, 50% 내지 60%, 60% 내지 70%, 70% 내지 80%, 80% 내지 90%, 또는 90% 내지 100%의 알파-구아이엔을 포함하는 세스퀴테르펜 조성물을 생성할 수 있다.

[0045] *희귀 식물 및 멸종 식물*

[0046] 본원에 개시된 키메라 테르펜 합성효소의 서열의 적어도 한 부분은 희귀 또는 멸종 식물로부터 유래한다. 본원에서 사용된 바와 같이, 용어 "희귀 식물" 또는 "희귀 식물들"은 흔하지 않고/않거나, 드물고/드물거나, 드물게 접하고/접하거나, 위기에 처해(예를 들면, 위험에 처해)있고/있거나, 취약하고/하거나, 개인 채집으로만 이용 가능하고/하거나, 특산지에서 발견되지 않고/않거나, 경작으로만 이용 가능하고/하거나, 멸종된 식물들을 포괄한다. 일부 실시양태에서, 희귀 식물은 드물게 접하는(예를 들면, 몇몇 장소, 예컨대, 1개, 2개, 3개, 4개 또는 5개의 장소에서만 접하는) 식물이다. 일부 실시양태에서, 희귀 식물은 멸종 식물이다. 본원에서 사용된 바와 같이, 멸종 식물은 살아있는 구성원을 갖지 않거나; 살아있는 구성원을 갖지 않는 것으로서 분류되거나; 당분야에서 통상의 기술을 가진 자에 의해 살아있는 구성원을 갖지 않을 것으로 예측되는 식물의 종을 지칭한다. 비제한적 예로서, 위험에 처한 종들의 국제자연보호연합(IUCN) 적색 목록을 이용하여 식물의 보존 상태를 결정하고 희귀 식물을 확인할 수 있다. 예를 들면, IUCN 적색 목록 상에서, 멸종된 식물, 야생에서 멸종된 식물, 결정적으로 위험에 처한 식물, 위험에 처한 식물, 취약한 식물, 및 거의 위험에 처한 식물로서 분류된 식물들은 희귀 식물로서 간주될 수 있다.

[0047] 희귀 식물의 비제한적 예는 *류카덴드론 그란디플로룸*, *쇼레아 쿠스피다타*, *매크로스타일리스 빌로사*, *오르벡실룸 스티풀라툼*, *미르시아 스켈딩기이*(*Myrcia skeldingii*), *네시오타 엘립티카*(*Nesiota Elliptica*), *매크로스타일리스 빌로사*, *웬들란디아 안구스토폴라*(*Wendlandia angustofola*), *에리카 피라미달리스*(*Erica Pyramidalis*), *스테노카르푸스 둠베엔시스*(*Stenocarpus dumbeensis*), *프라도시아 글라지오비이*(*Pradosia glaziovii*), *크라술라 수부라타*(*Crassula subulata*), *히비스카델푸스 윌데리아누스* 및 *에리카 폴리아세아*(*Erica foliacea*)를 포함한다.

[0048] 일부 실시양태에서, 희귀 식물은 *히비스카델푸스 윌데리아누스*일 수 있다. *히비스카델푸스* 속은 히비스세아(Hibisceae) 족(말바세아(Malvaceae))에 속하고, 상기 속의 구성원들은 하부 꽃잎이 상부 3개의 꽃잎들보다 종종 더 짧은 관형 구조를 형성하는 꽃잎을 종종 갖는다(예를 들면, 전체적으로 본원에 참고로 포함된 문헌(Oppenheimer *et al.*, A new species of Hibiscadelphus Rock (Malvaceae, Hibisceae) from Maui, Hawaiian Islands; *PhytoKeys*, 2014;(39):65-75) 참조). *히비스카델푸스* 속은 하와이 특산 식물이고, 적어도 8가지 종들이 기재되어 있다. 이 종들 중 4가지 종들(*히비스카델푸스 봄비시누스*(*Hibiscadelphus bombycinus*), *히비스카델푸스 크루시브락테아투스*(*Hibiscadelphus crucibracteatus*), *히비스카델푸스 윌데리아누스* 및 *히비스카델푸스 우디이*(*Hibiscadelphus woodii*)를 포함함)은 멸종 상태이고, 이 종들 중 2가지 종들(*히비스카델푸스 기파르디아누스*(*Hibiscadelphus giffardianus*) 및 *히비스카델푸스 후알라라이엔시스*(*Hibiscadelphus hualalaiensis*))은 경작으로만 존속되고, 2가지 종들(*히비스카델푸스 디스탄스*(*Hibiscadelphus distans*) 및 *히비스카델푸스 스텔라투스*(*Hibiscadelphus stellatus*))은 야생에서 잔존한다.

[0049] *히비스카델푸스 윌데리아누스*(*Hibiscadelphus wilderianus*)는 1910년에 하와이 내의 마우이 섬의 아우와히의 용암원 상에서 2,600 피트의 고도에서 마지막으로 관찰된 멸종 나무 종이다(예를 들면, 전체적으로 본원에 각각 참고로 포함된 문헌(Radlkofer *et al.*, New and Noteworthy Hawaiian Plants; Hawaiian Board of Agriculture and Forestry Botanical Bulletin, 1911;(1):1-15); 및 문헌("The IUCN Red List of Threatened Species: Hibiscadelphus wilderianus," World Conservation Monitoring Centre, 1998) 참조). *히비스카델푸스 윌데리아누스*라는 라틴어 기재는 라들코퍼(Radlkofer *et al.*)의 최초 보고서에서 발견될 수 있다. 잎과 열매를 가진 나무 가지의 사진은 라들코퍼의 최초 보고서에 포함되었고, 도 8a에 재현되어 있다.

[0050] 일부 실시양태에서, 희귀 식물은 *류카덴드론 그란디플로룸*일 수 있다. *류카덴드론*은 프로테아과에 속하는 자웅이체 속이고 남아프리카 특산 식물이다. *류카덴드론* 속 내의 종은 상록 관목을 포함하고, 종종 원뿔 모양의 과서(종자 머리)를 갖는다. *류카덴드론* 속 내에는 *엘. 알붐*(*L. album*), *엘. 아르쿠아툼*(*L. arcuatum*), *엘. 아르겐테움*(*L. argenteum*), *엘. 바르케라*(*L. barkerae*), *엘. 보늄*(*L. bonum*), *엘. 브루니오이데스*(*L. brunioides*), *엘. 부르켈리이*(*L. burchellii*), *엘. 카덴스*(*L. cadens*), *엘. 카멜라에아*(*L. chamelaea*), *엘. 시네레움*(*L. cinereum*), *엘. 코모숨*(*L. comosum*), *엘. 콘카붐*(*L. concavum*), *엘. 코니쿰*(*L. conicum*), *엘. 코니페룸*(*L. coniferum*), *엘. 코르다툼*(*L. cordatum*), *엘. 코리아세움*(*L. coriaceum*), *엘. 코림보숨*(*L. corymbosum*), *엘. 크립토세팔룸*(*L. cryptocephalum*), *엘. 다프노이데스*(*L. daphnoides*), *엘. 디에몬티아눔*(*L. diemontianum*), *엘. 디스컬러*(*L. discolor*), *엘. 드레게이*(*L. dregei*), *엘. 두비움*(*L. dubium*), *엘. 엘리멘세*(*L. elimense*), *엘. 에리시폴리움*(*L. ericifolium*), *엘. 유칼립티폴리움*(*L. eucalyptifolium*), *엘. 플렉수오숨*(*L. flexuosum*), *엘. 플로리둠*(*L. floridum*), *엘. 포에둠*(*L. foedum*), *엘. 갈피니이*(*L. galpinii*), *엘. 간도게리*(*L. gandogeri*), *엘. 글라베리뭄*(*L. glaberrimum*), *엘. 글로보숨*(*L. globosum*), *엘. 그란디플로룸*, *엘. 기도엔세*(*L. gydoense*), *엘. 임모데라툼*(*L. immoderatum*), *엘. 라니게룸*(*L. lanigerum*), *엘. 라우레올룸*(*L.

laureolum), *엘. 락숨*(*L. laxum*), *엘. 레비사누스*(*L. levisanus*), *엘. 리니폴리움*(*L. linifolium*), *엘. 로에리엔세*(*L. loeriense*), *엘. 로란티폴리움*(*L. loranthifolium*), *엘. 마코와니이*(*L. macowanii*), *엘. 메리디아눔*(*L. meridianum*), *엘. 메이에리아눔*(*L. meyerianum*), *엘. 마이크로세팔룸*(*L. microcephalum*), *엘. 모데스튬*(*L. modestum*), *엘. 뮤이리이*(*L. muirii*), *엘. 네르보숨*(*L. nervosum*), *엘. 니티둠*(*L. nitidum*), *엘. 노바일*(*L. nobile*), *엘. 올렌스*(*L. olens*), *엘. 오리엔탈레*(*L. orientale*), *엘. 오스보르네이*(*L. osbornei*), *엘. 플라티스페르뭄*(*L. platyspermum*), *엘. 폰도엔세*(*L. pondoense*), *엘. 프로세룸*(*L. procerum*), *엘. 푸베센스*(*L. pubescens*), *엘. 푸비브락테오락튬*(*L. pubibracteolatum*), *엘. 라디아튬*(*L. radiatum*), *엘. 레모튬*(*L. remotum*), *엘. 로오디이*(*L. roodii*), *엘. 로우르케이*(*L. rourkei*), *엘. 루브룸*(*L. rubrum*), *엘. 살리시폴리움*(*L. salicifolium*), *엘. 살리그눔*(*L. salignum*), *엘. 세리세움*(*L. sericeum*), *엘. 세사일*(*L. sessile*), *엘. 쉐일라*(*L. sheilae*), *엘. 싱굴라르*(*L. singular*), *엘. 소로세팔로데스*(*L. sorocephalodes*), *엘. 스피랄레*(*L. spirale*), *엘. 스피시폴리움*(*L. spissifolium*), *엘. 스텔라레*(*L. stellare*), *엘. 스텔리게룸*(*L. stelligerum*), *엘. 스트로빌리눔*(*L. strobilinum*), *엘. 테레티폴리움*(*L. teretifolium*), *엘. 티미폴리움*(*L. thymifolium*), *엘. 틴크튬*(*L. tinctum*), *엘. 트라도우웬세*(*L. tradouwense*), *엘. 울리기노숨*(*L. uliginosum*), *엘. 베르티실라튬*(*L. verticillatum*) 및 *엘. 잔토코누스*(*L. xanthoconus*)를 포함하는 적어도 80종이 있다.

[0051] *류카덴드론 그란디플로룸*은 윈베르그 콘부쉬(Wynberg Conebush)로서도 일반적으로 공지되어 있고, 1806년에 남아프리카 클라팜에서 마지막으로 관찰되었다. *류카덴드론 그란디플로룸*의 기록된 목격은 윈베르그 산 상에서 일어났고, 이 종은 축축한 화강암 토양 상의 윈베르그 언덕의 남쪽 경사지에 존재하였을 수 있다(예를 들면, 전체적으로 본원에 참고로 포함된 문헌(T. Rebelo, "Wynberg Conebush – extinct for 200 years," iSpot, 25 July 2015) 참조). *류카덴드론 그란디플로룸*은 내용이 전체적으로 본원에 각각 참고로 포함된 문헌(Salisbury et al., The Paradisus Londinensis or Coloured Figures of Plants Cultivated in the Vicinity of the Metropolis. 1805; (Volume 1, part 2): 105); 및 웹사이트(www -dot- biodiversitylibrary.org-backslash-ia/mobot31753000575172#page/248/mode/1up)에 기재 및 기술되어 있다. *류카덴드론 그란디플로룸*의 현재 채집물은 기록되어 있지 않고, 이 종은 1800년대 초까지 거의 없어졌거나 멸종된 것으로 간주된다(예를 들면, 문헌(T. Rebelo, "Wynberg Conebush – extinct for 200 years," iSpot, 25 July 2015; Catalogue of Life: Leucadendron grandiflorum (Salisb.) R. Br., 20 December 2017) 참조). 자매 종은 *엘. 글로보숨* 및 *엘. 엘리멘세*를 포함한다. 도 8b는 *류카덴드론 그란디플로룸*을 도시한다.

[0052] 일부 실시양태에서, 희귀 식물은 *매크로스타일리스 빌로사*일 수 있다. *매크로스타일리스* 속은 운향과에 속하고 적어도 10가지 종들(예를 들면, *매크로스타일리스 바르비게라*(*Macrostylis barbigera*), *매크로스타일리스 카시오포이데스*(*Macrostylis cassiopoides*), *매크로스타일리스 카울리플로라*(*Macrostylis cauliflora*), *매크로스타일리스 크라시폴리아*(*Macrostylis crassifolia*), *매크로스타일리스 데시피엔스*(*Macrostylis decipiens*), *매크로스타일리스 히르타*(*Macrostylis hirta*), *매크로스타일리스 라물로사*(*Macrostylis ramulosa*), *매크로스타일리스 사쿠아로사*(*Macrostylis squarrosa*), *매크로스타일리스 테누이스*(*Macrostylis tenuis*) 및 *매크로스타일리스 빌로사*)을 포함한다.

[0053] *매크로스타일리스 빌로사*의 2가지 인정된 아종, 즉 *매크로스타일리스 빌로사* (Thunb.) Sond. 아종 마이너 및 *매크로스타일리스 빌로사*(Thunb.) Sond. 아종 빌로사가 있다. *매크로스타일리스 빌로사*(Thunb.) Sond. 아종 마이너는 그의 서식지가 농지로 전환되었고 생존 식물을 재배치하기 위한 광범위한 조사가 실패하였기 때문에 멸종된 아종으로서 분류된다. 이것은 과거에 남아프리카의 웨스턴 케이프에서 발견되었고 경사지 상의 자갈 및 점토 토양에서 서식하였다(예를 들면, 전체적으로 본원에 참고로 포함된 문헌("Red List of South African Plants: Macrostylis villosa subsp. minor," 2005)을 참조할 수 잇다). *매크로스타일리스 빌로사*(Thunb.) Sond. 아종 빌로사는 도시 확장으로부터의 집단 상실, 외래 식물 침습 및 농지로의 서식지의 전환으로 인해 멸종 위기에 처한 것으로 간주되었다. *매크로스타일리스 빌로사*(Thunb.) Sond. 아종 빌로사의 사진은 도 8c에 재현되어 있다(예를 들면, 전체적으로 본원에 참고로 포함된 문헌("Red List of South African Plants: Macrostylis villosa subsp. villosa," 2007) 참조)

[0054] 일부 실시양태에서, 희귀 식물은 *오르벡실룸 스티풀라튬*(*소랄레아 스티풀라타*(*Psoralea stipulata*))일 수 있다. *오르벡실룸*은 콩과에 속하고 이 속의 구성원들은 주름지고 털이 없는 특징적인 꼬투리 벽을 종종 갖는다. *오르벡실룸*은 그의 "드문 화후증대 꽃받침"에 의해 구별될 수도 있다(예를 들면, 전체적으로 본원에 참고로 포함된 문헌(Turner, Revision of the genus Orbexilum (Fabaceae: Psoraleeae). Lundellia. 2008; (11):1-7) 참). *오르벡시룸* 종은 *오. 키아파사눔*(*O. chiapasanum*), *오. 그라실*(*O. gracile*), *오. 루피넬룸*(*O. lupinellum*), *오. 매크로필룸*(*O. macrophyllum*), *오. 멜라노카르품*(*O. melanocarpum*), *오. 올리간튬*(*O. oliganthum*), *오. 오*

노브리키스(*O. onobrychis*), *오. 페둔쿨라툼*(*O. pedunculatum*), *오. 심플렉스*(*O. simplex*), *오. 스티풀라툼* 및 *오. 비르가툼*(*O. virgatum*)을 포함한다.

[0055] "라르게스티풀 리더-루트(Largestipule Leather-root)" 또는 "폴스-오프-더-오하이오 스쿠르프페아(Falls-of-the-Ohio Scurfpea)"로서도 공지된 *오. 스티풀라툼*은 켄터키주 록 아일랜드에서만 발견되었다. *오. 스티풀라툼*의 마지막 기록된 관찰은 이 섬의 재포장 및 홍수 전에 1881년에 있었다. 켄터키주 및 오하이오 강의 인디애나 해안 둘 다에서, 1998년의 집중적인 조사를 포함하는, 유사한 서식지의 수 많은 조사에도 불구하고, 이 종은 재배치되지 않았다. 따라서, 이 종은 멸종된 종으로서 분류되었다(예를 들면, 전체적으로 본원에 각각 참고로 포함된 문헌(NatureServe Explorer: Orbexilum stipulatum - (Torr. & Gray) Rydb., 2016) 및 전술된 문헌(Baskin *et al.*) 참조).

[0056] *오. 스티풀라툼*은 다년생 허브이었고 각각 길이가 약 2 cm인 3개의 소엽들로 나누어진 잎을 가졌다. 상기 종은 잎의 기부에서 지속성 종자를 가졌고, 꽃받침 너머로 확장되지 않은 꽃부리 통을 가진 것으로서도 기재되었다. 이 식물이 5월 말 내지 6월 중순에 개화하였으나, 종자가 자연에서 관찰되지 않았을 가능성이 있다(예를 들면, 전체적으로 본원에 각각 참고로 포함된 문헌("NatureServe Explorer: Orbexilum stipulatum - (Torr. & Gray) Rydb.," 2016); 및 문헌(Baskin *et al.*, Geographical origin of the specimens of Orbexilum stipulatum (T. & G.) Rydb. (Psoralea stipulata T. & G.). Castanea. 1986;(51): 207-210) 참조). *오. 스티풀라툼*의 사진은 문헌(Short, "Orbexilum stipulatum collected at Falls of the Ohio," 1840 from The Philadelphia Herbarium at the Academy of Natural Sciences)에서 확인될 수 있고, 도 8d에 재현되어 있다.

[0057] 일부 실시양태에서, 희귀 식물은 *쇼레아 쿠스피다타*일 수 있다. *쇼레아*는 이우시과 내의 속이고, 남동아시아의 많은 특산 열대우림 나무들을 포함한다. 많은 *쇼레아* 종들은 속씨식물(개화 식물)이다. *쇼레아* 종의 비제한적 예는 *쇼레아 아피니스*(*Shorea affinis*), *쇼레아 콘게스티플로라*(*Shorea congestiflora*), *쇼레아 코르디폴리아*(*Shorea cordifolia*), *쇼레아 디스티카*(*Shorea disticha*), *쇼레아 메기스토필라*(*Shorea megistophylla*), *쇼레아 트라페지폴리아*(*Shorea trapezifolia*), *쇼레아 제일라니카*(*Shorea zeylanica*), *쇼레아 아쿠미나티시마*(*Shorea acuminatissima*), *쇼레아 알루타세아*(*Shorea alutacea*), *쇼레아 안구스티폴리아*(*Shorea angustifolia*), *쇼레아 바코엔시스*(*Shorea bakoensis*), *쇼레아 발라노카르포이데스*(*Shorea balanocarpoides*), *쇼레아 카이아나*(*Shorea chaiana*), *쇼레아 콜라리스*(*Shorea collaris*), *쇼레아 쿠스피다타*, *쇼레아 파구에티아나*(*Shorea faguetiana*), *쇼레아 파구에티오이데스*(*Shorea faguetioides*), *쇼레아 깁보사*(*Shorea gibbosa*), *쇼레아 호페이폴리아*(*Shorea hopeifolia*), *쇼레아 일리아시이*(*Shorea iliasii*), *쇼레아 인듀플리카타*(*Shorea induplicata*), *쇼레아 쿠다텐시스*(*Shorea kudatensis*), *쇼레아 락사*(*Shorea laxa*), *쇼레아 롱기플로라*(*Shorea longiflora*), *쇼레아 롱기스페르마*(*Shorea longisperma*), *쇼레아 매크로발라노스*(*Shorea macrobalanos*), *쇼레아 뮤존겐시스*(*Shorea mujongensis*), *쇼레아 물티플로라*(*Shorea multiflora*), *쇼레아 오보보이데아*(*Shorea obovoidea*), *쇼레아 파토이엔시스*(*Shorea patoiensis*), *쇼레아 펠타타*(*Shorea peltata*), *쇼레아 폴리안드라*(*Shorea polyandra*), *쇼레아 리케티아*(*Shorea richetia*), *쇼레아 서브실린드리카*(*Shorea subcylindrica*), *쇼레아 테누이라물로사*(*Shorea tenuiramulosa*) 및 *쇼레아 잔토필라*(*Shorea xanthophylla*)를 포함할 수 있다.

[0058] 이러한 분류 이후에 바코 국립공원, 람비르 국립공원 및 세멩고 수목원에서 *에스. 쿠스피다타*의 몇몇 보고된 목격이 있었지만(전체적으로 본원에 각각 참고로 포함된 문헌(Ashton, Shorea cuspidata. Tree Flora of Sabah and Sarawek. 2004;(5):246-247); 문헌(Ling et al., Diversity of the tree flora in Semenggoh Arboretum, Sarawak, Borneo. Gardens' Bulletin Singapore. 2012; (64):139-169)), *에스. 쿠스피다타*는 IUCN 적색 목록(전체적으로 본원에 참고로 포함된 문헌("The IUCN Red List: Shorea cuspidata," 1998))에서 멸종된 종으로서 현재 분류된 말레이시아 특산 나무이다. *쇼레아 쿠스피다타*는 희귀 식물로서 간주될 수 있다. *쇼레아 쿠스피다타*는 제2의 엷은 라임-황색 꽃잎을 가진 꽃을 가진 중간 크기의 나무로서 특징규명되어 있다(예를 들면, 문헌(Ashton, Man. Dipt. Brun. 1968: f. 10, pl. 14 (stem-base)) 참조). *쇼레아 쿠스피다타* 표본의 사진은 도 8e에 재현되어 있다(전체적으로 본원에 참고로 포함된 문헌("Kew Royal Botanical Gardens: Shorea cuspidata specimen K000700460," 1962)).

[0059] 일부 실시양태에서, 희귀 식물은 *웬들란디아 안구스티폴리아*일 수 있다. *웬들란디아*는 꼭두서니과에 속하는 개화 식물의 한 속이다. *웬들란디아* 종의 비제한적 예는 *웬들란디아 아베란스*(*Wendlandia aberrans*), *웬들란디아 아쿠미나타*(*Wendlandia acuminata*), *웬들란디아 아모카나*(*Wendlandia amocana*), *웬들란디아 안다마니카*(*Wendlandia andamanica*), *웬들란디아 안구스티폴리아*, *웬들란디아 아펜디쿨라타*(*Wendlandia appendiculata*), *웬들란디아 아라비카*(*Wendlandia arabica*), *웬들란디아 아르보레센스*(*Wendlandia arborescens*), *웬들란디아 아우구스티니*(*Wendlandia augustini*), *웬들란디아 바시스타미네아*(*Wendlandia basistaminea*), *웬들란디아 비쿠스*

피다타(*Wendlandia bicuspidata*), *웬들란디아 보우바르디오이데스*(*Wendlandia bouvardioides*), *웬들란디아 브라키안타*(*Wendlandia brachyantha*), *웬들란디아 브레비파니쿨라타*(*Wendlandia brevipaniculata*), *웬들란디아 브레비투바*(*Wendlandia brevituba*) 및 *웬들란디아 부들레아세아*(*Wendlandia buddleacea*)를 포함할 수 있다.

[0060] *더블유. 안구스티폴리아*는 IUCN 적색 목록(전체적으로 본원에 참고로 포함된 문헌("The IUCN Red List: Shorea cuspidata," 1998) 참조)에서 멸종된 종으로서 현재 분류된 인도 특산 식물이다. 이러한 분류 이후에, *더블유. 안구스티폴리아*는 보고에 의하면 인도의 칼라카드 문단타라이 호랑이 보존지에서 관찰되었다(전체적으로 본원에 참고로 포함된 문헌(Viswanathan *et al.*, Rediscovery of Wendlandia Angustifolia Wight Ex Hook.f. (Rubiaceae), from Tamil Nadu, a Species Presumed Extinct. Journal of The Bombay Natural History Society. 2000 97(2):311-313)). *더블유. 안구스티폴리아*는 희귀 식물로서 간주될 수 있다. *더블유. 안구스티폴리아*는 세 갈래의 윤생 잎 및 선형-창끝모양 잎을 가진 관목 또는 나무로서 기재되었다(예를 들면, 전체적으로 본원에 참고로 포함된 문헌(Viswanathan *et al.*, Rediscovery of Wendlandia Angustifolia Wight Ex Hook.f. (Rubiaceae), from Tamil Nadu, a Species Presumed Extinct, Journal of The Bombay Natural History Society. 2000; 97(2):311-313) 참조). 표본의 사진은 도 8f에 재현되어 있다(전체적으로 본원에 참고로 포함된 문헌("Kew Royal Botanical Gardens: Wendlandia Angustifolia K000030921," collection date not recorded)).

[0061] *키메라 테르펜 합성효소 및 테르펜의 제조 방법*

[0062] 키메라 테르펜 합성효소를 코딩하는 핵산 분자도 본원에 기재되어 있다. 일부 실시양태에서, 이러한 키메라 테르펜 합성효소를 코딩하는 핵산 분자의 적어도 10%(예를 들면, 수치들 사이의 모든 값들을 포함하는, 적어도 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 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%, 99% 또는 99% 초과)는 희귀 또는 멸종 식물로부터 유래할 수 있다.

[0063] 일부 경우, 키메라 테르펜 합성효소를 코딩하는 핵산 분자는 서열번호 67 내지 118로 구성되는 군으로부터 선택된 서열과 적어도 50%(예를 들면, 수치들 사이의 모든 값들을 포함하는, 적어도 55%, 60%, 65%, 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%, 99% 또는 99% 초과) 동일한 뉴클레오타이드 서열을 포함한다. 일부 경우, 키메라 테르펜 합성효소를 코딩하는 핵산 분자는 서열번호 67 내지 118로 구성되는 군으로부터 선택된 서열과 동일한 뉴클레오타이드 서열을 포함한다. 일부 경우, 키메라 테르펜 합성효소를 코딩하는 핵산 분자는 뉴클레오타이드 서열 TATA(TATA 박스 서열)을 추가로 포함한다. 일부 경우, 키메라 테르펜 합성효소를 코딩하는 핵산 분자는 서열번호 67 내지 118로 구성되는 군으로부터 선택된 서열의 N-말단에 위치하는 뉴클레오타이드 서열 TATA(TATA 박스 서열)를 포함한다. 일부 경우, 키메라 테르펜 합성효소를 코딩하는 핵산 분자는 서열번호 119 내지 357로 기재된 서열을 코딩하는 뉴클레오타이드 서열을 포함한다.

[0064] 일부 실시양태에서, 키메라 테르펜 합성효소(예를 들면, 키메라 세스퀴테르펜 합성효소)의 아미노산 서열의 적어도 10%(예를 들면, 수치들 사이의 모든 값들을 포함하는, 적어도 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 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%, 99% 또는 99% 초과)는 희귀 또는 멸종 식물로부터 유래할 수 있다. 일부 경우, 키메라 테르펜 합성효소는 서열번호 119 내지 357로 기재된 하나 이상의 서열을 포함한다.

[0065] 알파-구아이엔을 생성할 수 있는 키메라 테르펜 합성효소도 본원에 기재되어 있다. 일부 실시양태에서, 이러한 키메라 테르펜 합성효소를 코딩하는 핵산 분자의 적어도 10%(예를 들면, 수치들 사이의 모든 값들을 포함하는, 적어도 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 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%, 99% 또는 99% 초과)는 희귀 또는 멸종 식물로부터 유래할 수

있다.

[0066] 일부 실시양태에서, 알파-구아이엔을 생성할 수 있는 키메라 테르펜 합성효소의 아미노산 서열의 적어도 10%(예를 들면, 수치들 사이의 모든 값들을 포함하는, 적어도 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 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%, 99% 또는 99% 초과)는 희귀 또는 멸종 식물로부터 유래할 수 있다.

[0067] 일부 경우, 키메라의 구성은 관심 있는 적어도 2개의 테르펜 합성효소들 사이의 서열(예를 들면, 핵산 서열 및/또는 아미노산 서열) 정렬을 포함할 수 있다. 예를 들면, 서열 정렬 분석을 이용하여, 특정 테르펜 합성효소의 단편(예를 들면, 도메인)을 키메라 테르펜 합성효소에 포함시켜야 하는지를 확인할 수 있다. 일부 실시양태에서, 키메라 테르펜 합성효소는 키메라 세스퀴테르펜 합성효소이다. 분석의 비제한적 예는 실시예 2에 기재된 blastn-mapdamage 및 tblastn 파이프라인에 기재된 유형을 포함할 수 있다.

[0068] 일부 실시양태에서, 키메라 테르펜 합성효소 코딩 서열은 기준 키메라 테르펜 합성효소 코딩 서열에 상응하는 1개, 2개, 3개, 4개 또는 5개 이상의 위치에서 돌연변이를 포함한다. 일부 실시양태에서, 키메라 테르펜 합성효소 코딩 서열은 기준 키메라 테르펜 합성효소 코딩 서열에 비해 코딩 서열의 1개, 2개, 3개, 4개 또는 5개 이상의 코돈에서 돌연변이를 포함한다. 당분야에서 통상의 기술을 가진 자에 의해 이해될 수 있는 바와 같이, 코돈 내의 돌연변이는 유전 코드의 축퇴성으로 인해 코돈에 의해 코딩된 아미노산을 교체할 수 있거나 교체하지 않을 수 있다. 일부 실시양태에서, 코딩 서열 내의 하나 이상의 돌연변이는 기준 키메라 테르펜 합성효소의 아미노산 서열에 비해 키메라 테르펜 합성효소의 아미노산 서열을 변경시키지 않는다.

[0069] 일부 실시양태에서, 키메라 테르펜 합성효소 서열 내의 하나 이상의 돌연변이는 기준 키메라 테르펜 합성효소의 아미노산 서열에 비해 키메라 테르펜 합성효소의 아미노산 서열을 변경시킨다. 일부 실시양태에서, 하나 이상의 돌연변이는 기준 키메라 테르펜 합성효소의 아미노산 서열에 비해 키메라 테르펜 합성효소의 아미노산 서열을 변경시키고 기준 키메라 테르펜 합성효소에 비해 키메라 테르펜 합성효소의 활성을 변경(향상 또는 감소)시킨다.

[0070] 숙련된 당업자는 또한 키메라 테르펜 합성효소 코딩 서열 내의 돌연변이가 보존적 아미노산 치환을 형성하여, 상기 폴리펩타이드의 기능적으로 동등한 변이체, 예를 들면 상기 폴리펩타이드의 활성을 보유하는 변이체를 제공할 수 있다는 것도 인식할 수 있을 것이다. 본원에서 사용된 바와 같이, "보존적 아미노산 치환"은 아미노산 치환이 이루어지는 단백질의 상대적 전하 또는 크기 특성 또는 기능적 활성을 변경시키지 않는 아미노산 치환을 지칭한다.

[0071] 일부 경우, 아미노산은 그의 R 기(예를 들면, 표 1 참조)를 특징으로 한다. 예를 들면, 아미노산은 비극성 지방족 R 기, 양으로 하전된 R 기, 음으로 하전된 R 기, 비극성 방향족 R 기 또는 극성 비하전된 R 기를 포함할 수 있다. 비극성 지방족 R 기를 포함하는 아미노산의 비제한적 예는 알라닌, 글리신, 발린, 류신, 메티오닌 및 이소류신을 포함한다. 양으로 하전된 R 기를 포함하는 아미노산의 비제한적 예는 라이신, 아르기닌 및 히스티딘을 포함한다. 음으로 하전된 R 기를 포함하는 아미노산의 비제한적 예는 아스파르트산 및 글루탐산을 포함한다. 비극성 방향족 R 기를 포함하는 아미노산의 비제한적 예는 페닐알라닌, 티로신 및 트립토판을 포함한다. 극성 비하전된 R 기를 포함하는 아미노산의 비제한적 예는 세린, 트레오닌, 시스테인, 프롤린, 아스파라긴 및 글루타민을 포함한다.

[0072] 변이체는 당분야에서 통상의 기술을 가진 자에게 공지된 폴리펩타이드 서열을 변경시키는 방법, 예컨대 그러한 방법을 편집한 참고 문헌들, 예를 들면 문헌(Molecular Cloning: A Laboratory Manual, J. Sambrook, et al., eds., Fourth Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 2012) 또는 문헌(Current Protocols in Molecular Biology, F.M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York, 2010)에서 확인된 방법에 따라 제조될 수 있다.

[0073] 폴리펩타이드의 기능적으로 동등한 변이체의 비제한적 예는 본원에 개시된 단백질의 아미노산 서열의 보존적 아미노산 치환을 포함할 수 있다. 아미노산의 보존적 치환은 다음의 군들 내의 아미노산들 중에서 이루어진 치환을 포함한다: (a) M, I, L, V; (b) F, Y, W; (c) K, R, H; (d) A, G; (e) S, T; (f) Q, N; 및 (g) E, D. 일부 실시양태에서, 변이체 폴리펩타이드를 제조할 때 1개, 2개, 3개, 4개, 5개, 6개, 7개, 8개, 9개, 10개, 11개,

12개, 13개, 14개, 15개, 16개, 17개, 18개, 19개, 20개 또는 20개 초과의 잔기들이 변경될 수 있다. 일부 실시양태에서, 아미노산은 보존적 아미노산 치환에 의해 대체된다.

[0074] [표 1]

보존적 아미노산 치환의 비제한적 예

원래의 잔기	R 기 유형	보존적 아미노산 치환
Ala	비극성 지방족 R 기	Cys, Gly, Ser
Arg	양으로 하전된 R 기	His, Lys
Asn	극성 비하전된 R 기	Asp, Gln, Glu
Asp	음으로 하전된 R 기	Asn, Gln, Glu
Cys	극성 비하전된 R 기	Ala, Ser
Gln	극성 비하전된 R 기	Asn, Asp, Glu
Glu	음으로 하전된 R 기	Asn, Asp, Gln
Gly	비극성 지방족 R 기	Ala, Ser
His	양으로 하전된 R 기	Arg, Tyr, Trp
Ile	비극성 지방족 R 기	Leu, Met, Val
Leu	비극성 지방족 R 기	Ile, Met, Val
Lys	양으로 하전된 R 기	Arg, His
Met	비극성 지방족 R 기	Ile, Leu, Phe, Val
Pro	극성 비하전된 R 기	
Phe	비극성 방향족 R 기	Met, Trp, Tyr
Ser	극성 비하전된 R 기	Ala, Gly, Thr
Thr	극성 비하전된 R 기	Ala, Asn, Ser
Trp	비극성 방향족 R 기	His, Phe, Tyr, Met
Tyr	비극성 방향족 R 기	His, Phe, Trp
Val	비극성 지방족 R 기	Ile, Leu, Met, Thr

[0075]

[0076] 원하는 특성 및/또는 활성을 가진 키메라 테르펜 합성효소(예를 들면, 키메라 세스퀴테르펜 합성효소) 변이체를 생성하기 위한 폴리펩타이드의 아미노산 서열의 아미노산 치환은 키메라 테르펜 합성효소(예를 들면, 키메라 세스퀴테르펜 합성효소)의 코딩 서열의 변경에 의해 이루어질 수 있다. 유사하게, 폴리펩타이드의 기능적으로 동등한 변이체를 생성하기 위한 폴리펩타이드의 아미노산 서열의 보존적 아미노산 치환은 전형적으로 키메라 테르펜 합성효소(예를 들면, 키메라 세스퀴테르펜 합성효소)의 코딩 서열의 변경에 의해 이루어진다.

[0077] 돌연변이(예를 들면, 치환)는 당분야에서 통상의 기술을 가진 자에게 공지된 다양한 방법들에 의해 뉴클레오타이드 서열에서 이루어질 수 있다. 예를 들면, 돌연변이는 PCR 지정 돌연변이, 쿤켈(Kunkel)의 방법(Kunkel, *Proc. Nat. Acad. Sci. U.S.A.* 82: 488-492, 1985)에 따른 부위 지정 돌연변이유발, 또는 폴리펩타이드를 코딩하는 유전자의 화학적 합성에 의해 이루어질 수 있다.

[0078] 원형 순열(Yu and Lutz, *Trends Biotechnol.* 2011 Jan;29(1):18-25)을 포함하는 임의의 적합한 방법을 이용하여 변이체를 생성할 수 있다. 원형 순열에서, 폴리펩타이드의 선형 일차 서열은 (예를 들면, 서열의 N-말단과 C-말단을 연결함으로써) 원형화될 수 있고, 폴리펩타이드는 상이한 위치에서 절단될("쪼개질") 수 있다. 따라서, 새로운 폴리펩타이드의 선형 일차 서열은 선형 서열 정렬 방법(예를 들면, Clustal Omega 또는 BLAST)에 의해 측정될 때 낮은(예를 들면, 수치들 사이의 모든 값들을 포함하는, 80% 미만, 75% 미만, 70% 미만, 65% 미만, 60% 미만, 55% 미만, 50% 미만, 45% 미만, 40% 미만, 35% 미만, 30% 미만, 25% 미만, 20% 미만, 15% 미만, 10% 미만 또는 5% 미만의) 서열 동일성을 가질 수 있다. 그러나, 2개의 단백질들의 위상학적 분석은 2개의 폴리펩타이드들의 삼차 구조가 유사하거나 유사하지 않다는 것을 보여줄 수 있다. 특정 이론에 의해 구속받고자 하지는 않지만, 기준 폴리펩타이드의 원형 순열을 통해 생성되고 기준 폴리펩타이드와 유사한 삼차 구조를 가진 변이체 폴리펩타이드는 유사한 기능적 특성(예를 들면, 효소 활성, 효소 반응속도론, 기질 특이성 또는 생성물 특이성)을 공유할 수 있다. 일부 경우, 원형 순열은 이차 구조, 삼차 구조 또는 사차 구조를 변경시킬 수 있고 상이한 기능적 특성(예를 들면, 증가된 또는 감소된 효소 활성, 상이한 기질 특이성 또는 상이한 생성물 특이성)을 가진 효소를 생성할 수 있다. 예를 들면, 문헌(Yu and Lutz, *Trends Biotechnol.* 2011 Jan;29(1):18-25)을 참조할 수 있다.

[0079] 원형 순열을 겪은 단백질에서 단백질의 선형 아미노산 서열은 원형 순열을 겪지 않은 기준 단백질과 상이한 것으로 이해되어야 한다. 그러나, 당분야에서 통상의 기술을 가진 자는, 예를 들면 서열들을 정렬시키고 보존된 모티프를 검출하고/하거나, 단백질의 구조 또는 예측된 구조를, 예를 들면 상동성 모델링으로 비교함으로써, 원형 순열을 겪은 단백질의 어느 잔기가 원형 순열을 겪지 않은 기준 단백질의 잔기에 상응하는지를 용이하게 결정할 수 있을 것이다.

[0080] 본 개시내용의 양태는 효소를 코딩하는 유전자, 이의 기능적 변형체 및 변이체의 재조합 발현에 관한 것일뿐만 아니라, 이와 관련된 용도에 관한 것이기도 하다.

[0081] 본원에 기재된 키메라 테르펜 합성효소들 중 임의의 키메라 테르펜 합성효소를 코딩하는 핵산은 당분야에서 공지된 임의의 방법을 통해 임의의 적절한 벡터 내로 혼입될 수 있다. 예를 들면, 벡터는 바이러스 벡터(예를 들면, 렌티바이러스, 레트로바이러스, 아데노바이러스 또는 아데노 관련 바이러스 벡터), 일시적 발현에 적합한 임의의 벡터, 또는 유도성 발현을 위한 임의의 벡터(예를 들면, 갈락토스 유도성 또는 독시사이클린 유도성 벡터)를 포함하나 이들로 제한되지 않는 발현 벡터일 수 있다. 키메라 테르펜 합성효소(예를 들면, 키메라 세스퀴테르펜 합성효소)의 발현을 위한 벡터의 비제한적 예는 하기 실시예 2에 기재되어 있다.

[0082] 일부 실시양태에서, 벡터는 세포에서 자율적으로 복제한다. 벡터는 본원에 기재된 유전자를 함유하는 핵산을 삽입하고 라이게이션시켜, 세포에서 복제할 수 있는 재조합 벡터를 생성하는 제한 엔도뉴클레아제(endonuclease)에 의해 절단되는 하나 이상의 엔도뉴클레아제 제한 부위를 함유할 수 있다. RNA 벡터도 사용될 수 있지만, 벡터는 전형적으로 DNA로 구성된다. 클로닝 벡터는 플라스미드, 포스미드, 파지미드, 바이러스 게놈 및 인공 염색체를 포함하나, 이들로 제한되지 않는다. 본원에서 사용된 바와 같이, 용어 "발현 벡터" 또는 "발현 구축물"은 숙주 세포(예를 들면, 미생물), 예컨대, 효모 세포에서 특정 핵산의 전사를 허용하는 일련의 특정된 핵산 요소들을 가진, 재조합 또는 합성으로 생성된 핵산 구축물을 지칭한다. 일부 실시양태에서, 본원에 기재된 유전자의 핵산 서열은 조절 서열에 작동가능하게 연결되고, 일부 실시양태에서, RNA 전사체로서 발현되도록 클로닝 벡터 내로 삽입된다. 일부 실시양태에서, 벡터는 재조합 벡터에 의해 형질전환 또는 형질감염된 세포를 확인하기 위해 하나 이상의 마커, 예컨대 본원에 기재된 선택가능한 마커를 함유한다.

[0083] 일부 실시양태에서, 벡터는 숙주 세포의 게놈 내로 통합될 수 있다.

[0084] 코딩 서열과 조절 서열은 코딩 서열과 조절 서열이 공유결합되고 코딩 서열의 발현 또는 전사가 조절 서열의 영향 또는 제어 하에 있을 때 "작동가능하게 연결되어" 또는 "작동가능하게 결합되어" 있다고 기재된다. 코딩 서열이 기능성 단백질로 번역되어야 하는 경우, 코딩 서열과 조절 서열은 5' 조절 서열 내의 프로모터의 유도가 코딩 서열을 전사하는 경우, 및 코딩 서열과 조절 서열 사이의 결합의 성질이 (1) 프레임-시프트 돌연변이의 도입을 야기하지 않거나, (2) 코딩 서열의 전사를 지시하는 프로모터 영역의 능력을 방해하지 않거나, (3) 단백질로 번역되는 상응하는 RNA 전사체의 능력을 방해하지 않는 경우 작동가능하게 연결되어 있거나 결합되어 있다고 기재된다. 따라서, 프로모터 영역이 코딩 서열을 전사하고 전사체가 관심 있는 단백질 또는 폴리펩타이드로 번역될 수 있는 경우 프로모터 영역은 코딩 서열에 작동가능하게 연결되어 있거나 결합되어 있다.

[0085] 일부 실시양태에서, 본원에 기재된 단백질들 중 임의의 단백질을 코딩하는 핵산은 조절 서열(예를 들면, 인핸서 서열)의 제어 하에 있다. 일부 실시양태에서, 핵산은 프로모터의 제어 하에서 발현된다. 프로모터는 유전자의 발현의 정상적 조절을 제공하는 천연 프로모터, 예를 들면, 그의 내생성 환경 내의 유전자의 프로모터일 수 있다. 대안적으로, 프로모터는 유전자의 천연 프로모터와 상이한 프로모터일 수 있고, 예를 들면, 프로모터는 그의 내생성 환경 내의 유전자의 프로모터와 상이하다. 본원에서 사용된 바와 같이, "이종 프로모터" 또는 "재조합 프로모터"는 그에 작동가능하게 연결되거나 결합되는 DNA 서열의 전사와 천연적으로 또는 정상적으로 관련되어 있지 않거나 이러한 전사를 천연적으로 또는 정상적으로 제어하지 않는 프로모터이다. 일부 실시양태에서, 뉴클레오타이드 서열은 이종 프로모터의 제어 하에 있다.

[0086] 일부 실시양태에서, 프로모터는 진핵 프로모터이다. 진핵 프로모터의 비제한적 예는 당분야에서 통상의 기술을 가진 자에게 공지되어 있는 TDH3, PGK1, PKC1, TDH2, PYK1, TPI1, AT1, CMV, EF1a, SV40, PGK1(인간 또는 마우스), Ubc, 인간 베타 액틴, CAG, TRE, UAS, Ac5, 폴리헤드린, CaMKIIa, GAL1, GAL10, TEF1, GDS, ADH1, CaMV35S, Ubi, H1, U6을 포함한다(예를 들면, 애드진(Addgene) 웹사이트: blog.addgene.org/plasmids-101-the-promoter-region 참조). 일부 실시양태에서, 프로모터는 원핵생물 프로모터(예를 들면, 박테리오파지 또는 세균 프로모터)이다. 박테리오파지 프로모터의 비제한적 예는 Pls1con, T3, T7, SP6 및 PL을 포함한다. 세균 프로모터의 비제한적 예는 Pbad, PmgrB, Ptrc2, Plac/ara, Ptac, Pm을 포함한다.

[0087] 일부 실시양태에서, 프로모터는 유도성 프로모터이다. 본원에서 사용된 바와 같이, "유도성 프로모터"는 분자의 존재 또는 부재에 의해 제어되는 프로모터이다. 유도성 프로모터의 비제한적 예는 화학적으로 조절되는 프로모터 및 물리적으로 조절되는 프로모터를 포함한다. 화학적으로 조절되는 프로모터의 경우, 전사 활성은 하나 이상의 화합물, 예컨대, 알코올, 테트라사이클린, 갈락토스, 스테로이드, 금속 또는 다른 화합물에 의해 조절될 수 있다. 물리적으로 조절되는 프로모터의 경우, 전사 활성은 광 또는 온도와 같은 현상에 의해 조절될 수 있다. 테트라사이클린에 의해 조절되는 프로모터의 비제한적 예는 안하이드로테트라사이클린(aTc) 반응성 프로모터 및 다른 테트라사이클린 반응성 프로모터 시스템(예를 들면, 테트라사이클린 리프레서 단백질(tetR), 테트라사이클린 오퍼레이터 서열(tetO) 및 테트라사이클린 트랜스활성화제 융합 단백질(tTA))을 포함한다. 스테로이드에 의해 조절되는 프로모터의 비제한적 예는 래트 글루코코르티코이드 수용체, 인간 에스트로겐 수용체, 나방 엑디손(ecdysone) 수용체, 및 스테로이드/레티노이드/갑상선 수용체 수퍼패밀리로부터의 프로모터에 기반한 프로모터를 포함한다. 금속에 의해 조절되는 프로모터의 비제한적 예는 메탈로티오네인(금속 이온에 결합하여 이를 격리시키는 단백질) 유전자로부터 유래한 프로모터를 포함한다. 병원론에 의해 조절되는 프로모터의 비제한적 예는 살리실산, 에틸렌 또는 벤조티아디아졸(BTH)에 의해 유도되는 프로모터를 포함한다. 온도/열 유도성 프로모터의 비제한적 예는 열 충격 프로모터를 포함한다. 광에 의해 조절되는 프로모터의 비제한적 예는 식물 세포로부터의 광 반응성 프로모터를 포함한다. 일부 실시양태에서, 유도성 프로모터는 갈락토스 유도성 프로모터이다. 일부 실시양태에서, 유도성 프로모터는 하나 이상의 생리학적 조건(예를 들면, pH, 온도, 방사선, 삼투압, 식염수 구배, 세포 표면 결합, 또는 하나 이상의 외인성 또는 내인성 유도 작용제의 농도)에 의해 유도된다. 외인성 유도제 또는 유도 작용제의 비제한적 예는 아미노산 및 아미노산 유사체, 사카라이드 및 폴리사카라이드, 핵산, 단백질 전사 활성화제 및 리프레서, 사이토카인, 독소, 석유계 화합물, 금속 함유 화합물, 염, 이온, 효소 기질 유사체, 호르몬 또는 이들의 임의의 조합을 포함한다.

[0088] 일부 실시양태에서, 프로모터는 구성적 프로모터이다. 본원에서 사용된 바와 같이, "구성적 프로모터(constitutive promoter)"는 유전자의 연속적 전사를 가능하게 하는 비조절된 프로모터를 지칭한다. 구성적 프로모터의 비제한적 예는 CP1, CMV, EF1a, SV40, PGK1, Ubc, 인간 베타 액틴, CAG, Ac5, 폴리헤드린, TEF1, GDS, CaM35S, Ubi, H1 및 U6을 포함한다.

[0089] 당분야에서 통상의 기술을 가진 자에게 공지된 다른 유도성 프로모터 또는 구성적 프로모터도 본원에서 고려된다.

[0090] 유전자 발현을 위해 필요한 조절 서열의 정확한 성질은 종들 또는 세포 유형들 사이에 상이할 수 있으나, 일반적으로, 필요에 따라, 각각 전사 및 번역의 시작과 관련된 5' 비전사 서열 및 5' 비번역 서열, 예컨대, TATA 박스, 캡핑 서열, CAAT 서열 등을 포함한다. 구체적으로, 이러한 5' 비전사 조절 서열은 작동가능하게 연결되어 있거나 결합된 유전자의 전사 제어를 위한 프로모터 서열을 포함하는 프로모터 영역을 포함할 것이다. 조절 서열은 인핸서 서열 또는 업스트림 활성화제 서열도 포함할 수 있다. 본원에 개시된 벡터는 5' 리더 또는 신호 서열을 포함할 수 있다. 조절 서열은 터미네이터 서열도 포함할 수 있다. 일부 실시양태에서, 터미네이터 서열은 전사 동안 DNA에서 유전자의 말단을 표시한다. 이종 유기체에서 본원에 기재된 하나 이상의 유전자의 발현을 유도하기에 적합한 하나 이상의 적절한 벡터의 선택 및 디자인은 당분야에서 통상의 기술을 가진 자의 능력 및 재량 내에 있다.

[0091] 발현을 위해 필요한 요소를 함유하는 발현 벡터는 상업적으로 입수될 수 있고 당분야에서 통상의 기술을 가진 자에게 공지되어 있다(예를 들면, 문헌(Sambrook et al., Molecular Cloning: A Laboratory Manual, Fourth Edition, Cold Spring Harbor Laboratory Press, 2012) 참조).

[0092] 진핵생물 세포 또는 원핵생물 세포를 포함하는 임의의 적합한 숙주 세포를 사용하여 본원에 개시된 키메라 테르펜 합성효소들 중 임의의 키메라 테르펜 합성효소를 생성할 수 있다. 적합한 숙주 세포는 진균 세포(예를 들면, 효모 세포) 및 세균 세포(예를 들면, *이. 콜라이* 세포)를 포함한다. 발현을 위한 효모의 속의 비제한적 예는 *사카로마이세스*(예를 들면, *사카로마이세스 세레비지애*), *피키아*, *클루이베로마이세스*(예를 들면, *클루이베로마이세스 락티스*), *한세눌라* 및 *야로위아*를 포함한다. 일부 실시양태에서, 효모 균주는 산업적 배수체 효모 균주이다. 진균 세포의 다른 비제한적 예는 *아스퍼길루스*(*Aspergillus*) 종, *페니실리움*(*Penicillium*) 종, *푸사리움*(*Fusarium*) 종, *리조푸스*(*Rhizopus*) 종, *아크레모니움*(*Acremonium*) 종, *뉴로스포라*(*Neurospora*) 종, *소르다리아*(*Sordaria*) 종, *마그나포르테*(*Magnaporthe*) 종, *알로마이세스*(*Allomyces*) 종, *우스틸라고*(*Ustilago*) 종, *보트리티스*(*Botrytis*) 종 및 *트리코데르마*(*Trichoderma*) 종으로부터 수득된 세포를 포함한다.

[0093] 본원에서 사용된 바와 같이, 용어 "세포"는 단일 세포 또는 세포의 집단, 예컨대, 동일한 세포주 또는 균주에

속하는 세포의 집단을 지칭할 수 있다. 단수형 용어 "세포"의 사용은 세포의 집단보다는 오히려 단일 세포를 명확히 지칭하기 위한 것으로 해석되어서는 안 된다.

[0094] 본원에 기재된 키메라 테르펜 합성효소들(예를 들면, 키메라 세스퀴테르펜 합성효소들) 중 임의의 키메라 테르펜 합성효소를 코딩하는 벡터는 당분야에서 공지된 임의의 방법을 이용함으로써 적합한 숙주 세포 내로 도입될 수 있다. 효모 형질전환 프로토콜의 비제한적 예는 하기 실시예 2, 및 본 목적을 위해 전체적으로 본원에 참고로 포함된 문헌(Gietz *et al.*, Yeast transformation by the LiAc/SS Carrier DNA/PEG method. *Methods Mol Biol*. 2006;313:107-20)에 기재되어 있다. 숙주 세포는 당분야에서 통상의 기술을 가진 자에 의해 이해될 수 있는 바와 같이 적합한 임의의 조건 하에서 배양될 수 있다. 예를 들면, 당분야에서 공지된 임의의 배지, 온도 및 항온처리 조건이 이용될 수 있다. 유도성 벡터를 보유하는 숙주 세포의 경우, 세포를 적절한 유도 작용제제와 함께 배양하여 발현을 촉진할 수 있다.

[0095] 본원에 개시된 세포들 중 임의의 세포는 핵산의 접촉 및/또는 통합 전에, 중에 및/또는 후에 임의의 유형(농후 또는 최소) 및 임의의 조성의 배지에서 배양될 수 있다. 배양 조건 또는 배양 공정은 당분야에서 통상의 기술을 가진 자에 의해 이해되는 바와 같이 통상적인 실험을 통해 최적화될 수 있다. 일부 실시양태에서, 선택된 배지는 다양한 성분들로 보충된다. 일부 실시양태에서, 보충 성분의 농도 및 양은 최적화된다. 일부 실시양태에서, 배지 및 성장 조건(예를 들면, pH, 온도 등)의 다른 양태는 통상적인 실험을 통해 최적화된다. 일부 실시양태에서, 배지가 하나 이상의 보충 성분으로 보충되는 빈도, 및 세포가 배양되는 시간의 양은 최적화된다.

[0096] 본원에 기재된 세포의 배양은 당분야에서 공지되고 이용되는 배양 용기에서 수행될 수 있다. 일부 실시양태에서, 통기 반응 용기(예를 들면, 교반형 탱크 반응기)를 이용하여 세포를 배양한다. 일부 실시양태에서, 생물반응기 또는 발효기를 이용하여 세포를 배양한다. 따라서, 일부 실시양태에서, 세포를 발효에서 사용한다. 본원에서 사용된 바와 같이, 용어 "생물반응기" 및 "발효기"는 교환가능하게 사용되고, 살아있는 유기체 또는 살아있는 유기체의 부분을 포함하는, 생물학적, 생화학적 및/또는 화학적 반응이 일어나는 밀폐된 공간 또는 부분적으로 밀폐된 공간을 지칭한다. "대규모 생물반응기" 또는 "산업적 규모 생물반응기"는 상업적 또는 준상업적 규모로 생성물을 생성하는 데 이용되는 생물반응기이다. 대규모 생물반응기는 전형적으로 수십 리터, 수백 리터 또는 수천 리터 이상의 부피를 가진다.

[0097] 일부 실시양태에서, 생물반응기는 세포(예를 들면, 효모 세포) 또는 세포 배양물(예를 들면, 효모 세포 배양물), 예컨대, 본원에 기재된 세포 또는 세포 배양물을 포함한다. 일부 실시양태에서, 생물반응기는 포자 및/또는 휴면 세포 유형의 단리된 미생물(예를 들면, 건조된 상태의 휴면 세포)을 포함한다.

[0098] 생물반응기의 비제한적 예는 교반형 탱크 발효기, 회전형 혼합 디바이스에 의해 교반되는 생물반응기, 케모스타트(chemostat), 진탕 디바이스에 의해 교반되는 생물반응기, 에어리프트 발효기, 팩킹된-층 반응기, 고정된-층 반응기, 유동화된 층 생물반응기, 파동에 의해 유도된 교반을 이용하는 생물반응기, 원심분리 생물반응기, 롤러병, 및 중공형 섬유 생물반응기, 롤러 장치(예를 들면, 벤치탑(benchtop), 카트-장착된 및/또는 자동화된 변종), 수직으로 적층된 플레이트, 스피너 플라스크, 교반 또는 락킹 플라스크, 진탕 다중-웰 플레이트, MD 병, T-플라스크, 럭스(Roux) 병, 다중-표면 조직 배양 증식기, 변형된 발효기, 및 코팅된 비드(예를 들면, 세포 부착을 방지하기 위해 혈청 단백질, 니트로셀룰로스 또는 카복시메틸 셀룰로스로 코팅된 비드)를 포함한다.

[0099] 일부 실시양태에서, 생물반응기는 세포(예를 들면, 효모 세포)가 이동 액체 및/또는 기체 버블과 접촉하는 세포 배양 시스템을 포함한다. 일부 실시양태에서, 세포 또는 세포 배양물은 현탁액에서 성장한다. 다른 실시양태에서, 세포 또는 세포 배양물은 고체상 담체에 부착된다. 담체 시스템의 비제한적 예는 마이크로담체(예를 들면, 중합체 구, 마이크로비드, 및 다공성 또는 비다공성일 수 있는 마이크로디스크), 특정 화학적 기(예를 들면, 삼차 아민 기)에 의해 하전된 교차결합된 비드(예를 들면, 덱스트란), 비다공성 중합체 섬유에 포획된 세포를 포함하는 2D 마이크로담체, 3D 담체(예를 들면, 담체 섬유, 중공형 섬유, 다중카트리지 반응기, 및 다공성 섬유를 포함할 수 있는 반투과성 막), 감소된 이온 교환 능력을 가진 마이크로담체, 캡슐화 세포, 모세관 및 응집체를 포함한다. 일부 실시양태에서, 담체는 덱스트란, 젤라틴, 유리 또는 셀룰로스와 같은 물질로부터 제작된다.

[0100] 일부 실시양태에서, 산업적 규모 공정은 연속적, 반연속적 또는 불연속적 방식으로 작동된다. 작동 방식의 비제한적 예는 회분, 유가, 연장된 회분, 반복적 회분, 배출/충전, 회전-벽, 스피닝 플라스크 및/또는 관주 작동 방식이다. 일부 실시양태에서, 생물반응기는 기질 스톡, 예를 들면, 탄수화물 공급원의 연속적 또는 반연속적 보충, 및/또는 생물반응기로부터의 생성물의 연속적 또는 반연속적 분리를 가능하게 한다.

[0101] 일부 실시양태에서, 생물반응기 또는 발효기는 반응 파라미터를 측정하고/하거나 조절하기 위해 센서 및/또는

제어 시스템을 포함한다. 반응 파라미터의 비제한적 예는 생물학적 파라미터(예를 들면, 성장률, 세포 크기, 세포 수, 세포 밀도, 세포 유형 또는 세포 상태 등), 화학적 파라미터(예를 들면, pH, 산화환원 전위, 반응 기질 및/또는 생성물의 농도, 용해된 기체의 농도, 예컨대, 산소 농도 및 CO_2 농도, 영양분 농도, 대사물질 농도, 올리고펩타이드의 농도, 아미노산의 농도, 비타민의 농도, 호르몬의 농도, 첨가제의 농도, 혈청 농도, 이온 강도, 이온의 농도, 상대 습도, 몰농도, 오스몰농도, 다른 화학물질, 예를 들면, 완충제, 보조제 또는 반응 부산물의 농도), 물리적/기계적 파라미터(예를 들면, 밀도, 전도성, 교반 정도, 압력, 및 유속, 전단 응력, 전단률, 점도, 색상, 혼탁도, 광 흡수, 혼합률, 전환율), 및 열역학적 파라미터, 예컨대, 온도, 광 강도/질 등)를 포함한다. 본원에 기재된 파라미터를 측정하기 위한 센서는 관련 기계 및 전자 분야에서 통상의 기술을 가진 자에게 잘 공지되어 있다. 본원에 기재된 센서로부터의 입력물에 근거하여 생물반응기에서 파라미터를 조절하기 위한 제어 시스템은 생물반응기 공학 분야에서 통상의 기술을 가진 자에게 잘 공지되어 있다.

[0102] 본원에 개시된 숙주 세포들 중 임의의 숙주 세포에 의해 생성된 테르펜은 당분야에서 공지된 임의의 방법을 이용함으로써 추출될 수 있다. 세스퀴테르펜 추출 방법의 비제한적 예는 실시예 2에 제공되어 있다. 본원에 기재된 방법, 조성물 또는 숙주 세포로부터 생성된 테르펜들 중 임의의 테르펜이 예를 들면, 피부, 모발, 의류 또는 가정용품에의 국소 적용에 적합한 조성물(예를 들면, 퍼퓸)에 사용될 수 있다. 본원에서 사용된 바와 같이, 용어 "퍼퓸"은 사람의 모발, 피부 또는 의류, 또는 가정용품에의 적용에 적합한 임의의 향료 제제이다. 이 용어는 오 드 코롱(eau de cologne), 오 드 뚜왈렛(eau de toilette), 오 드 빠르퓸(eau de parfum), 퍼퓸 추출물 또는 추출액을 포함하나 이들로 제한되지 않는다. 이러한 퍼퓸은, 본 발명의 하나 이상의 테르펜을 포함한다는 것 이외에, 예를 들면, 하나 이상의 천연 오일, 고정제, 연화제 또는 용매를 포함할 수 있다.

[0103] 퍼퓸 제제에 사용될 수 있는 천연 오일의 예는 아미리스 오일; 안젤리카씨 오일; 안젤리카 뿌리 오일; 아니스씨 오일; 발레리안 오일; 바실 오일; 베이 오일; 쑥 오일; 벤조인 수지; 베르가못 오일; 자작나무 타르 오일; 비터 아몬드 오일; 사보리 오일; 부코-잎 오일; 카브로바 오일; 캐드 오일; 칼라무스 오일; 캄포르 오일; 카낭가 오일; 카다멈 오일; 카스카릴라 오일; 카시아 오일; 캐스토리움 앱솔루트(castoreum absolute); 삼나무-잎 오일; 삼나무목재 오일; 시스투스 오일; 시트로넬라 오일; 레몬 오일; 코파이바 발삼 오일; 고수 오일; 코스터스루트 오일; 쿠민 오일; 사이프레스 오일; 다바나 오일; 딜 오일; 딜씨 오일; 엘레미 오일; 타라곤 오일; 유칼립투스 시트리오도라 오일; 유칼립투스 오일; 펜넬 오일; 피르 오일; 갈바눔 오일; 제라늄 오일; 포도 오일; 유창목 오일; 거전 발삼 오일; 헬리크리섬 오일; 생강 오일; 아이리스 뿌리 오일; 칼라무스 오일; 청캐모마일 오일; 로마 캐모마일 오일; 당근씨 오일; 캐스카릴라 오일; 솔잎 오일; 스피어민트 오일; 캐러웨이 오일; 랍다넘 오일; 라반딘 오일; 라벤더 오일; 레몬그라스 오일; 러비지 오일; 라임 오일(예를 들면, 증류된 또는 압축된 라임 오일); 리나로에 오일; 리트세아 쿠베바 오일; 베이 잎 오일; 메이스 오일; 마조람 오일; 만다린 오일; 마소이 껍질 오일; 암브레트 오일; 클라리 세이지 오일; 미리스티카 오일; 미르 오일; 머틀 오일; 클로브 잎 오일; 클로브 꽃 오일; 네롤리 오일; 올리바넘 오일; 오포파낙스 오일; 오랜지 오일; 오리가넘 오일; 팔마로사 오일; 파출리 오일; 페릴라 오일; 페루 발삼 오일; 파슬리 잎 오일; 파슬리씨 오일; 페티그레인 오일; 페퍼민트 오일; 후추 오일; 피망 오일; 소나무 오일; 페니로얄 오일; 로즈우드 오일; 장미 오일; 로즈마리 오일; 달마시안 세이지 오일; 스패니쉬 세이지 오일; 샌달우드 오일; 셀러리씨 오일; 스파이크 라벤더 오일; 일본 아니스씨 오일; 스티락스 오일; 타게테스 오일; 전나무 오일; 티트리 오일; 터펜틴 오일; 타임 오일; 튜버로스 앱솔루트; 바닐라 추출물; 바이올렛 잎 앱솔루트; 버베나 오일; 베티버 오일; 주니퍼 오일; 와인-리스 오일; 약쑥 오일; 윈터그린 오일; 일랑 오일; 히솝 오일; 시벳 앱솔루트; 시나몬 잎 오일; 시나몬 껍질 오일뿐만 아니라; 이들의 분획 또는 이들로부터 단리된 구성성분; 및 이들의 조합도 포함하나 이들로 제한되지 않는다.

[0104] 퍼퓸 제제에 사용될 수 있는 화합물의 다른 예는 우드 모스(wood moss) 앱솔루트; 비스왁스 앱솔루트; 카시아 앱솔루트; 오 드 브로트(eau de brouts) 앱솔루트; 오크모스(oakmoss) 앱솔루트; 갈바넘 수지; 헬리크리섬 앱솔루트; 아이리스 뿌리 앱솔루트; 자스민 앱솔루트; 랍다넘 앱솔루트; 랍다넘 수지; 라반딘 앱솔루트; 라벤더 앱솔루트; 미모사 앱솔루트; 사향의 팅크제; 미르 앱솔루트; 올리바넘 앱솔루트; 오랜지 꽃 앱솔루트; 장미 앱솔루트; 톨루(Tolu) 발삼; 톤카(Tonka) 앱솔루트뿐만 아니라; 이들의 분획 또는 이들로부터 단리된 구성성분; 및 이들의 조합도 포함할 수 있다.

[0105] 본원에서 사용된 바와 같이, 용어 "연화제"는 조직 수분 함량을 증가시키는(그리고, 예를 들면, 피부를 더 부드럽고 더 유연하게 만들 수 있는) 지방 또는 유성 물질을 의미한다. 본 화합물 및 방법과 함께 사용할 연화제는 임의의 적절한 동물 지방/오일, 식물성 오일 및/또는 왁스를 포함할 수 있다. 비제한적 세트의 예로서, 본 조성물 및 방법과 함께 사용할 연화제는 천연 또는 합성 유래의 연화제일 수 있고, 냉압착 아몬드 오일, 호호바 오일, 해바라기 오일, 올리브 오일, 헤이즐넛 오일, 아보카도 오일, 홍화 오일, 포도씨 오일, 코코넛 오일, 맥아

오일, 살구씨 오일, 천연 왁스 및 "버터"(예를 들면, 비정련된 밀랍, 시어 버터, 호호바 버터 및/또는 코코아 버터), Schercemol™ LL 에스테르, Schercemol™ 1818 에스테르, 부틸렌 글리콜, 카프릭/카프릴릭 트리글리세라이드, 세테아레쓰-20, 하나 이상의 지방 알코올(예를 들면, 세테아릴 알코올, 세틸 알코올 및/또는 코코넛 지방산), 하나 이상의 실리콘(예를 들면, 사이클로메티콘, 디메티콘 및/또는 사이클로펜타실록산), 유화 왁스, 석유젤리, 지방산, 글리세릴 스테아레이트, 수소첨가된 오일, 이소프로필 미리스테이트, 광유, 옥틸 팔미테이트, 파라핀, 스쿠알렌, 스테아르산, 팔미토일 프롤린 또는 마그네슘 팔미토일 글루타메이트를 포함할 수 있다.

[0106] 본원에서 사용된 바와 같이, 용어 "고정제"는 퍼퓸에서 하나 이상의 화합물의 증기압(및 이로써 휘발성 물질)을 등등하게 만드는 데 사용된 화합물을 의미한다. 비제한적 세트의 예로서, 본원에 기재된 화합물 및 퍼퓸과 함께 사용할 고정제는 디프로필렌 글리콜, 디에틸 프탈레이트, Hedione®, 로진(Rosin)의 Abalyn™ D-E 메틸 에스테르, 호호바(예컨대, 플로라에스테르스(Floraesters) K-100 호호바 또는 플로라에스테르스 K-20W 호호바), 세피사이드(Sepicide) LD 및/또는 Foralyn™ 5020-F CG 수소첨가된 로지네이트일 수 있다.

[0107] 본원에서 사용된 바와 같이, 용어 "용매"는 퍼퓸을 제조하는 데 사용되는 희석제이다. 비제한적 예로서, 용매는 알코올(예를 들면, 에틸 알코올), 1,2-헥산디올, 1,2-헵탄디올, 중성향 오일(예를 들면, 분획화된 코코넛 오일 또는 호호바 오일), 또는 하나 이상의 휘발성 실리콘일 수 있다. 비제한적 예로서, 조향사의 알코올(에틸 알코올의 일종)이 사용될 수 있다. 조향사의 알코올은 매우 소량의 부틸 알코올, 데나토늄 벤조에이트(Britex) 및/또는 헥실렌 글리콜을 함유할 수 있는 200 프루프 에틸 알코올로부터 제조된다. SDA 40B 200 프루프 및 SDA-B 200 프루프를 포함하는 다양한 등급의 조향사의 알코올이 사용될 수 있다.

[0108] 본 개시내용에 따른 퍼퓸 조성물에 사용할 추가 화합물 또는 항료 물질은 당분야에서 통상적으로 사용되는 임의의 화합물을 포함할 수 있다.

[0109] 본 발명은 어떠한 방식으로든 제한으로서 해석되어서는 안 되는 하기 실시예에 의해 더 예시된다. 본원 전체에 걸쳐 인용된 (모든 참고문헌들, 발행된 특허들, 공개된 특허출원들 및 동시계류 중인 특허출원들을 포함하는) 모든 참고문헌들의 전체 내용은 명확히 본원에 참고로 포함된다.

[0110] **실시예**

[0111] **실시예 1. 키메라 테르펜 합성효소의 기능성 특징규명**

[0112] 12개의 멸종된 식물 샘플들로부터의 게놈 DNA를 서열분석하였다(표 2). 7개의 식물들로부터 세스퀴테르펜 합성효소(SQTS) 단편을 회수하였으나(표 11), 서열분석에서의 갭은 전체 길이 유전자의 재구축을 방해하였다. (서열 갭을 채우기 위해 현존 식물로부터의 세스퀴테르펜 합성효소로부터의 서열을 함유하는) 2,738개의 테르펜 합성효소 키메라들을 포함하는 라이브러리를 스크리닝하였다. 6개의 희귀 식물들(표 2)로부터의 52개의 SQTS 키메라들(표 10에 제공된 서열)의 발현은 스크리닝 균주에서 세스퀴테르펜의 생성으로 이어졌다. 이 실시예에 기재된 절차들 각각을 위한 방법 및 재료는 실시예 2에서 확인될 수 있다.

[0113] [표 2]

[0114]

과	속	종	대륙	위치	멸종 년도
돌나물과	*크라술라*	*수부라타*	아프리카	남아프리카	1900
철쭉과	*에리카*	*퍼라미달리스*	아프리카	남아프리카	1910
아욱과	***히비스카델푸스***	***윌데리아누스***	**오세아니아**	**하와이**	**1910**
프로테아과	***류카덴드론***	***그란디플로룸***	**아프리카**	**남아프리카**	**1806**
운향과	***매크로스타일리스***	***빌로사***	**아프리카**	**남아프리카**	**1980**
도금양과	*미르시아*	*스켈딘기이*	아메리카	자마이카	1972
갈매나무과	*네시오타*	*엘립티카*	아프리카	세인트 헬레나	2003
콩과	***오르벡실룸***	***스티풀라툼***	**아메리카**	**켄터키**	**1881**
사포타과	*프라도시아*	*글라지오비이*	아메리카	브라질	1997
이우시과	***쇼레아***	***쿠스피다타***	**아시아**	**말레이시아**	**1996**
프로테아과	*스테노카르푸스*	*둠베엔시스*	오세아니아	뉴칼레도니아	1905
꼭두서니과	***웬들란디아***	***안구스티폴리아***	**아시아**	**인도**	**1997**

[0115] 개시에서는 기체 크로마토그래피-질량 분광측정(GC/MS) 데이터에 근거하여 기능성 SQTS 키메라에 의해 생성된 테르펜을 확인하였다. 일부 경우에는, 질량 스펙트럼 및 보유 시간에 근거한 식별을 확인하기 위해서, 특징규명

된 세스퀴테르펜을 함유하는 인증된 표준물 또는 정유(essential oil)를 사용할 수 있었다. 다른 경우, 표준물을 사용할 수 없었고, 질량 스펙트럼 분석에만 근거하여 구조를 확인하였다. 구조를 확인하는 데 이용된 상이한 방법들은 표 3에 상세히 기재되어 있고, 각각의 세스퀴테르펜을 확인하는 데 이용된 구체적인 방법은 표 4 내지 9에 표시되어 있다. 일부 경우, 생성물은 "세스퀴테르펜" 또는 "세스퀴테르페놀"로서만 확인되었다. 한 경우, 질량 스펙트럼은 회수되었으나, NIST/내부 데이터베이스에서의 일치를 제공하지 않았다. 이 세스퀴테르페놀은 "확인되지 않은 세스퀴테르페놀"로서 생성물 표에서 확인되었고, 추가 특징규명을 이용하여 그의 구조를 확인할 수 있다.

[0116] *히비스카델푸스 윌데리아누스*로부터 유래한 14개의 SQTS 키메라들은 1개 이상의 세스퀴테르펜을 생성하였다(도 1, 표 3). *류카덴드론 그란디플로룸*으로부터 유래한 7개의 SQTS 키메라들도 세스퀴테르펜을 생성하였고(도 2, 표 5), *매크로스타일리스 빌로사*로부터 유래한 6개의 SQTS 키메라들도 세스퀴테르펜을 생성하였고(도 3, 표 6), *오르벡실룸 스티폴라툼*으로부터 유래한 2개의 SQTS 키메라들도 세스퀴테르펜을 생성하였고(도 4, 표 7), *쇼레아 쿠스피다타*로부터 유래한 6개의 SQTS 키메라들도 세스퀴테르펜을 생성하였고(도 5, 표 8), *웬들란디아 안구스티폴리아*로부터 유래한 17개의 SQTS 키메라들도 세스퀴테르펜을 생성하였다(도 6, 표 9). SQTS는 1개 내지 9개의 상이한 테르펜을 생성하는 것으로 확인되었다. 식물 SQTS 키메라의 생성물 프로파일은 기능성 SQTS 키메라가 가장 높은 수율로 생성된 테르펜에 의해 나누어졌을 때 상이하였다(도 7). 델타-카디넨 합성효소는 총 22개로 기능성 키메라가 가장 많은 군이었고, 상기 식물들 중 4개의 식물들로부터 유래하였다. *히비스카델푸스 윌데리아누스*로부터의 14개의 상기 합성효소들 중 10개의 합성효소들은 이 품종의 합성효소이었다. 알파-카디놀은 델타-카디넨 합성효소의 소수 생성물로서 빈번히 검출되었으나; *쇼레아 쿠스피다타*로부터의 3개의 SQTS 키메라들은 델타-카디넨보다 알파-카디놀을 더 많이 생성하였다. *쇼레아 쿠스피다타*로부터 유래한 이 6개의 SQTS 키메라들은 매우 유사한 생성물 혼합물을 생성하였다(표 8, 도 13).

[0117] 2,738-구성원 키메라 세스퀴테르펜 합성효소 라이브러리의 스크리닝은 52개의 기능성 키메라 세스퀴테르펜 합성효소(SQTS)의 성공적인 발현을 결과로 얻었다. 14개의 합성효소들은 100년 이상 전에 하와이에서 멸종된 나무인 *히비스카델푸스 윌데리아누스*로부터 유래하였다. 카디넨, 카디놀 및 유데스몰 유형의 세스퀴테르펜은 이 키메라들에 의해 생성되었다. 몇몇 활성 키메라들은 1800년대 켄터키주에서 멸종된 식물인 *오르벡실룸 스티폴라툼*으로부터도 생성되었다. 2가지 구아이엔 및 감마-비사볼렌은 이 합성효소들에 의해 생성되었다. 200년 이상 전에 멸종된 식물인 *류카덴드론 그란디플로룸*으로부터 7개의 기능성 SQTS 키메라들을 구성하였다. 3개의 다른 식물들로부터 유래한 키메라들과 함께 이 키메라들을 사용하여 다양한 세스퀴테르펜 및 세스퀴테르페놀 구조를 생성하였다.

[0118] [표 3]

세스퀴테르펜 합성효소에 의해 생성된 세스퀴테르펜을 확인하는 데 이용된 6가지 방법

방법 #	설명	주석
1	인증된 표준물과 일치된 질량 스펙트럼 및 보유 시간	구조 및 입체화학에서의 높은 신뢰도
2	식물로부터 유래된 정유 내의 이전에 특징규명된 화합물과 일치된 질량 스펙트럼 및 보유 시간	구조 및 입체화학에서의 높은 신뢰도
3	낮은 역가로 인해 수득된 좋지 않은 질량 스펙트럼; 인증된 표준물 또는 정유 내의 성분과 일치된 보유 시간 및 키메라 생성물 프로파일.	구조 및 입체화학에서의 꽤 높은 신뢰도
4	NIST/내부 데이터베이스 내의 화합물과 일치된 강한 질량 스펙트럼	구조에서의 꽤 높은 신뢰도, 이성질체일 수 있음.
5	낮은 역가로 인해 수득된 좋지 않은 질량 스펙트럼; 방법 # 4 를 이용하여 확인된 테르펜과 일치된 보유 시간 및 키메라 생성물 프로파일	구조에서의 꽤 높은 신뢰도, 이성질체일 수 있음.
6	낮은 역가로 인해 수득된 좋지 않은 질량 스펙트럼; NIST/내부 데이터베이스와 가능한 가장 좋은(가장 가까운) 동일성	이용가능한 질량 스펙트럼 데이터에 근거한 보다 낮은 신뢰도

[0119]

[0120] [표 4]

히비스카델푸스 윌데리아누스 서열로부터 유래한 기능성 세스퀴테르펜 합성효소 키메라 및 이의 관련 생성물

키메라 명칭	% 희귀 서열	테르펜 확인	확인 방법 [1]	% 조성 [2]
HibWilSQTS117	49%	델타-카디넨	3	100%
HibWilSQTS118	50%	델타-카디넨	3	100%
HibWilSQTS120	46%	델타-카디넨	3	13%
		에피-쿠베놀	5	3%
		세스퀴테르페놀	6	2%
		타우-카디놀	2	82%
HibWilSQTS121	50%	델타-카디넨	2	99%
		알파-카디놀	3	1%
HibWilSQTS123	47%	델타-카디넨	2	99%
		알파-카디놀	3	1%
HibWilSQTS124	48%	델타-카디넨	2	98%
		알파-카디놀	3	2%
HibWilSQTS126	44%	델타-카디넨	2	97%
		알파-카디놀	3	3%
HibWilSQTS19	12%	감마-셀리넨	4	1%
		10-에피-감마-유데스몰	2	2%
		감마-유데스몰	2	49%
		알파/베타-유데스몰 [3]	4	22%
		주니퍼 캄포르	6	1%
		7-에피-알파-유데스몰	4	1%
		크립토메리디올 이성질체 1	4	1%
		크립토메리디올 이성질체 2	4	2%
		크립토메리디올 이성질체 3	4	21%
HibWilSQTS34	13%	세스퀴테르펜	6	6%
		10-에피-감마-유데스몰	3	15%
		감마-유데스몰	3	27%
		알파/베타-유데스몰 [3]	5	52%
HibWilSQTS52	12%	델타-카디넨	2	60%
		타우-카디놀	3	9%
		알파/베타-유데스몰 [3]	4	31%
HibWilSQTS54	13%	델타-카디넨	2	99%
		알파-카디놀	2	1%
HibWilSQTS55	12%	델타-카디넨	3	71%
		타우-카디놀	3	6%
		알파-카디놀	3	23%
HibWilSQTS63	12%	세스퀴테르펜	6	11%
		델타-카디넨	2	29%
		세스퀴테르페놀	6	15%

[0121]

		세스퀴테르페놀	6	5%
		타우-카디놀	3	10%
		알파-카디놀	3	30%
HibWilSQTS90	25%	세스퀴테르펜	6	40%
		알파/베타-유데스몰 [3]	5	60%

[1] 구조 확인 랭킹 핵심은 표 3 에 정의되어 있고, 이때 보다 낮은 숫자는 보다 높은 신뢰도를 표시한다. [2] 각각의 키메라로부터의 총 세스퀴테르펜의 조성은 통상의 이온 카운트(m/z 204.2)에 근거한 대략적인 추정치이었다. 대사물질의 비는 생성 균주에서 상이하였을 수 있고, 샘플이 제조되었을 때 다른 소수 대사물질들이 검출되었을 수 있다. **굵은 글자체**로 표시된 키메라에 대한 대표적인 GC/MS 크로마토그램은 도 9 에서 확인될 수 있다. [3] 이 실행 조건 하에서 공-용출되었다. 피크는 더 긴 실행 조건 하에서 부분적으로 해상되었다, 약 6/4 알파/베타-유데스몰.

[0122]

[0123] [표 5]

류카덴드론 그란디플로룸 서열로부터 유래한 기능성 세스퀴테르펜 합성효소 키메라 및 이의 관련 생성물

키메라 명칭	% 회귀 서열	테르펜 확인	확인 방법 [1]	% 조성 [2]
LeuGraSQTS335	14%	세스퀴테르펜	6	1%
		10-에피-감마-유데스몰	3	1%
		감마-유데스몰	3	49%
		알파/베타-유데스몰 [3]	5	23%
		크립토메리디올 이성질체 2	5	1%
		크립토메리디올 이성질체 3	5	25%
LeuGraSQTS345	12%	후물렌	3	100%
LeuGraSQTS365	11%	알파-구아이엔	3	20%
		델타-구아이엔	3	80%
LeuGraSQTS377	14%	델타-카디넨	3	98%
		알파-카디놀	3	2%
LeuGraSQTS379	12%	델타-카디넨	3	98%
		알파-카디놀	3	2%
LeuGraSQTS385	13%	진기베렌	4	55%
		베타-비사볼렌	2	19%
		베타-파르네센	1	6%
		베타-세스퀴펠란드렌	2	6%
		쿠베놀	5	5%
		알파-비사보롤	1	4%
		알파-쿠르쿠멘	5	3%
		트랜스-네롤리돌	1	2%
LeuGraSQTS393	10%	감마-비사볼렌	4	100%

[1] 구조 확인 랭킹 핵심은 표 3 에 정의되어 있고, 이때 보다 낮은 숫자는 보다 높은 신뢰도를 표시한다. [2] 각각의 키메라로부터의 총 세스퀴테르펜의 조성은 통상의 이온 카운트(m/z 204.2)에 근거한 대략적인 추정치이었다. 대사물질의 비는 생성 균주에서 상이하였을 수 있고, 샘플이 제조되었을 때 다른 소수 대사물질들이 검출되었을 수 있다. **굵은 글자체**로 표시된 키메라에 대한 대표적인 GC/MS 크로마토그램은 도 10 및 11 에서 확인될 수 있다. [3] 이 실행 조건 하에서 공-용출되었다. 피크는 더 긴 실행 조건 하에서 부분적으로 해상되었다, 약 6/4 알파/베타-유데스몰.

[0124]

[0125] [표 6]

매크로스타일리스 빌로사 서열로부터 유래한 기능성 세스퀴테르펜 합성효소 키메라 및 이의 관련 생성물

키메라 명칭	% 회귀서열	테르펜 확인	확인 방법 [1]	% 조성 [2]
MacVolSQTS1139	14%	알파-구아이엔	3	19%
		델타-구아이엔	3	81%
MacVolSQTS2198	62%	베타-카리오필렌	1	85%
		후물렌	1	15%
MacVolSQTS2202	69%	베타-카리오필렌	1	86%
		후물렌	1	14%
MacVolSQTS2222	69%	베타-카리오필렌	1	86%
		후물렌	1	14%
MacVolSQTS2251	65%	베타-카리오필렌	1	87%
		후물렌	1	13%
MacVolSQTS2274	38%	비공지된 세스퀴테르펜	6	16%
		트랜스-세스퀴사비넨 수화물	5	14%
		델타-엘레멘	6	34%
		비공지된 세스퀴테르펜	6	16%

[1] 구조 확인 랭킹 핵심은 표 3 에 정의되어 있고, 이때 보다 낮은 숫자는 보다 높은 신뢰도를 표시한다. [2] 각각의 키메라로부터의 총 세스퀴테르펜의 조성은 통상의 이온 카운트(m/z 204.2)에 근거한 대략적인 추정치이었다. 대사물질의 비는 생성 균주에서 상이하였을 수 있고, 샘플이 제조되었을 때 다른 소수 대사물질들이 검출되었을 수 있다. **굵은 글자체**로 표시된 키메라에 대한 대표적인 GC/MS 크로마토그램은 도 12 에서 확인될 수 있다.

[0126]

[0127] [표 7]

오르벡실룸 스티폴라툼 서열로부터 유래한 기능성 세스퀴테르펜 합성효소 키메라 및 이의 관련 생성물

키메라 명칭	% 희귀 서열	테르펜 확인	확인 방법 [1]	% 조성 [2]
OrbStiSQTS1368	10%	감마-비사볼렌	5	100%
OrbStiSQTS1414	42%	알파-구아이엔	3	21%
		델타-구아이엔	3	79%

[1] 구조 확인 랭킹 핵심은 표 3 에 정의되어 있고, 이때 보다 낮은 숫자는 보다 높은 신뢰도를 표시한다. [2] 각각의 키메라로부터의 총 세스퀴테르펜의 조성은 통상의 이온 카운트(m/z 204.2)에 근거한 대략적인 추정치이었다. 대사물질의 비는 생성 균주에서 상이하였을 수 있고, 샘플이 제조되었을 때 다른 소수 대사물질들이 검출되었을 수 있다.

[0128]

[0129] [표 8]

쇼레아 쿠스피다타 서열로부터 유래한 기능성 세스퀴테르펜 합성효소 키메라 및 이의 관련 생성물

키메라 명칭	% 희귀 서열	테르펜 확인	확인 방법 [1]	% 조성 [2]
ShoCusSQTS154	38%	델타-카디넨	3	41%
		세스퀴테르펜	6	41%
		알파-카디놀	3	18%
ShoCusSQTS155	35%	델타-카디넨	3	41%
		세스퀴테르펜	6	41%
		알파-카디놀	3	18%
ShoCusSQTS156	36%	알파-카디놀	2	34%
		델타-카디넨	2	25%
		베타-카리오필렌	1	10%
		타우-카디놀	2	10%
		세스퀴테르펜	6	10%
		세스퀴테르펜	6	7%
		후물렌	1	4%
ShoCusSQTS157	38%	알파-카디놀	3	59%
		세스퀴테르펜	6	25%
		타우-카디놀	3	16%
ShoCusSQTS160	36%	알파-카디놀	3	33%
		세스퀴테르펜	6	32%
		델타-카디넨	3	5%
ShoCusSQTS161	37%	델타-카디넨	3	36%
		알파-카디놀	3	34%
		세스퀴테르펜	6	12%
		타우-카디놀	3	10%
		베타-카리오필렌	3	5%
		세스퀴테르펜	6	3%

[1] 구조 확인 랭킹 핵심은 표 3 에 정의되어 있고, 이때 보다 낮은 숫자는 보다 높은 신뢰도를 표시한다. [2] 각각의 키메라로부터의 총 세스퀴테르펜의 조성은 통상의 이온 카운트(m/z 204.2)에 근거한 대략적인 추정치이었다. 대사물질의 비는 생성 균주에서 상이하였을 수 있고, 샘플이 제조되었을 때 다른 소수 대사물질들이 검출되었을 수 있다. **굵은 글자체**로 표시된 키메라에 대한 대표적인 GC/MS 크로마토그램은 도 13 에서 확인될 수 있다.

[0130]

[0131] [표 9]

웬들란디아 구스티폴리아 서열로부터 유래한 기능성 세스퀴테르펜 합성효소 키메라 및 이의 관련 생성물

키메라 명칭	% 희귀 서열	테르펜 확인	확인 방법 [1]	% 조성 [2]
WenAngSQTS1007	81%	시스-유데슴-6-엔-11-올	4	100%
WenAngSQTS1086	80%	다우센	5	5%
		이소다우센	5	6%
		세스퀴테르펜	6	4%
		시스-유데슴-6-엔-11-올	4	85%
WenAngSQTS267	11%	감마-유데스몰	3	66%
		알파/베타-유데스몰 [3]	5	15%
		크립토메리디올 이성질체 3	5	19%
WenAngSQTS302	17%	세스퀴테르펜	6	2%
		트랜스-베르가모텐	4	5%
		알파-진기베렌	4	56%
		세스퀴사비넨 수화물	4	20%
		베타-세스퀴펠란드렌	2	7%
		트랜스-네롤리돌	1	2%
		세스퀴테르페놀	6	4%
		세스퀴테르페놀	6	4%
WenAngSQTS738	46%	세스퀴테르펜	6	6%
		세스퀴테르펜	6	7%
		델타-카디넨	2	36%
		확인되지 않은 세스퀴테르페놀	4	27%
		타우-카디놀	3	15%
		알파-카디놀	3	9%
WenAngSQTS760	43%	세스퀴테르펜	6	9%
		세스퀴테르펜	6	4%
		세스퀴테르펜	6	6%
		델타-카디넨	2	41%
		세스퀴테르페놀	6	22%
		타우-카디놀	3	11%
		알파/베타-유데스몰 [3]	5	7%
WenAngSQTS780	41%	세스퀴테르펜	6	9%
		세스퀴테르펜	6	3%
		세스퀴테르펜	6	6%
		델타-카디넨	2	40%
		세스퀴테르페놀	6	24%
		타우-카디놀	3	11%
		알파/베타-유데스몰 [3]	5	7%

[0132]

WenAngSQTS793	75%	다우센	5	3%
		베타-파르네센	1	2%
		8-이소프로페닐-1,5-디메틸-1,5-사이클로데카디엔	4	5%
		세스퀴테르펜	6	3%
		시스-유데슴-6-엔-11-올	4	87%
WenAngSQTS805	42%	세스퀴테르펜	6	5%
		세스퀴테르펜	6	6%
		델타-카디넨	2	39%
		확인되지 않은 세스퀴테르페놀	4	27%
		타우-카디놀	3	15%
		알파-카디놀	3	8%
WenAngSQTS826	47%	델타-카디넨	3	42%
		세스퀴테르페놀	6	36%
		타우-카디놀	3	22%
WenAngSQTS829	74%	시스-유데슴-6-엔-11-올	5	100%
WenAngSQTS843	45%	델타-카디넨	3	53%
		세스퀴테르페놀	6	47%
WenAngSQTS848	84%	시스-유데슴-6-엔-11-올	5	100%
WenAngSQTS849	75%	다우센	4	3%
		베타-파르네센	1	1%
		이소다우센	4	8%
		세스퀴테르펜	6	2%
		시스-유데슴-6-엔-11-올	4	86%
WenAngSQTS864	81%	다우센	5	2%
		8-이소프로페닐-1,5-디메틸-1,5-사이클로데카디엔	4	5%
		세스퀴테르펜	6	3%
		시스-유데슴-6-엔-11-올	4	90%
WenAngSQTS925	80%	세스퀴테르펜	6	3%
		세스퀴테르펜	6	8%
		세스퀴테르펜	6	3%
		시스-유데슴-6-엔-11-올	5	86%
WenAngSQTS960	81%	델타-카디넨	2	99%
		알파-카디놀	3	1%

[1]구조 확인 랭킹 핵심은 표 3 에 정의되어 있고, 이때 보다 낮은 숫자는 보다 높은 신뢰도를 표시한다. [2]각각의 키메라로부터의 총 세스퀴테르펜의 조성은 통상의 이온 카운트(m/z 204.2)에 근거한 대략적인 추정치이었다. 대사물질의 비는 생성 균주에서 상이하였을 수 있고, 샘플이 제조되었을 때 다른 소수 대사물질들이 검출되었을 수 있다. **굵은 글자체**로 표시된 키메라에 대한 대표적인 GC/MS 크로마토그램은 첨부된 도 14 및 도 15 에서 확인될 수 있다. [3]이 실행 조건 하에서 공-용출되었다. 피크는 더 긴 실행 조건 하에서 부분적으로 해상되었다, 약 6/4 알파/베타-유데스몰.

[0133]

[0134] [표 10]

세스퀴테르펜 키메라의 아미노산(AA) 및 핵산 서열

키메라 명칭	희귀 DNA 공급원	현존 스카폴드 Uniprot #	% 희귀 DNA	키메라 AA 서열(첫 번째로 코딩된 아미노산 M 후 시작됨)	키메라 핵산 서열
HibWilSQTS117	*히비스카델푸스 윌데리아누스*	Q9SAN0	49%	ASQASQVLASPHPAISSENRPKADFHPGIWGDMFIICPDTDIDAATELQYEELKAQVRKMIMEPVDDSNQKLPFIDAVQRLGVSYHFEKEIEDELENIYRDTNNNDADTDLYTTALRFRLLREHGFDISCDAFNKLKDEEGNFKASLTSDVPGLLELYEASYLRVHGEDILDEAISFATAQLTLALPTLHHPLSEQVGHALKQSIRRGLPRVEARNFISIYQDLESHNKALLQFAKIDFNMLQLLHRKELSEICRWWKDLDFTRKLPFARDRVVEGYFWIMGVYFEPQYSLGRKMLTKVIAMASIVDDTYDSFATYDELIPYTDAIERWDIKCMNQLPNYMQISYKALLDVYEEMEQLLADKGRQYRVEYAKKAMIRLVQAYLLEAKWTHLNYKPTFEEFRDNALPTSGYAMLAITAFVGMGEVITPETFEWAASDPKIIKASTIICRFMDDIAEHKFNHRREDDCSAIECYMEQYKVTAQEAYDEFNKHIESSWKDVNEEFLKPTEMPTPVLCRSLNLARVMDVLYREGDGYTHVGKAAKGGITSLLIDPIQI(서열번호 1)	atggccagtcaggcttcacaagttttagcatctccccacccagctatatcctctgaaaaccggccaaaggctgatttccatcctggtatctggggcgacatgtttattatctgtccagatacggacattgatgccgctacagagctgcaatatgaagaattgaaagcgcaagtccgcaagatgatcatggaaccagtagacgattctaatcaaaagctaccattcattgacgctgttcaaaggctcggagtgagctaccactttgaaaaagaaattgaagacgaacttgaaaacatctaccgtgataccaataacaacgacgcagacactgatctatacactaccgccttgagattcagattattgagagagcatggttttgatatttcctgcgatgctttcaacaagttgaaagacgaagaaggtaatttcaaggcttcgttgacttctgacgttcctggtttgttagaactctatgaggcttcctacttgagagtccacggtgaagatatcctagatgaagccatatctttcgctactgctcagttaaccttggctttgccaactttgcatcacccgctttcagagcaagttggtcacgcattgaagcaaagtatcagaagaggcctgccaagagttgaagccagaaactttatctctatttaccaagatttagaatcccacaataaggctttgttgcaattcgccaaaattgactttaacatgttacaattgctacataggaaggagctcagcgaaatttgtagatggtggaaagatcttgattttaccagaaagttacctttcgctcgtgaccgtgtcgtcgaaggttatttctggattatgggagtttacttcgaaccacaatatagcttgggtagaaagatgttgaccaaggttattgctatggcttctatcgtcgatgatacatacgattccttcgctacttacgacgaattgataccatatactgacgccatcgaaagatgggacatcaagtgtatgaatcagctgccaaactatatgcaaatttcgtacaaagcgttattggatgtatacgaggaaatggaacaattgcttgcagataaaggtcgacagtacagagtggaatacgctaagaaagctatgattcggttggtgcaagcatatttgttagaagcgaagtggacccatttaaactacaagccaactttcgaagaatttagagacaatgctttgccgacatctgggtatgccatgctagctataaccgcgttcgttggtatgggtgaagttatcacgccagaaaccttgaatgggctgcttctgacccaaagattattaaggcctccactatcatctgccgctttatggatgatatcgctgagcataagttcaaccacagaagggaggatgactgttccgctat

[0135]

					tgaatgttacatggagcaatacaaagtcacagctc aagaagcatacgacgaatttaacaagcacataga atcgtcttggaaggacgttaatgaagagttcttga aaccaactgaaatgcctactccggtactgtgtaga agtttgaacctagccagagtcatggatgttttgtac agagaaggtgacggttatactcatgttggaaaag ccgctaagggtggtataacatcacttcttatcgatc ccattcaaatctaa(서열번호 67)
HibWil SQTS1 18	*허비스카 델푸스 윌데리아 누스*	Q9SAN0	50%	ASQASQVLASPHPAISS ENRPKADFHPGIWGDM FIICPDTDIDAATELQYE ELKAQVRKMIMEPVDD SNQKLPFIDAVQRLGVS YHFEKEIEDELENIYRD TNNNDADTDLYTTALR FRLLREHGFDISCEAFN KLKDEEGNFKASLTSD VRGLLELYQASYMRIH GEDILDEAISFTTAQLTL ALPTLDPPLSEQVGHAL KQSIRRGLPRVEARNFI SIYQDLESHNKALLQFA KIDFNMLQLLHRKELSE ICRWWKDLDFTRKLPF ARDRVVEGYFWIMGV YFEPQYSLGRKMLTKVI AMASIVDDTYDSFATY DELIPYTDAIERWDIKC MNQLPNYMQISYKALL DVYEEMEQLLADKGR QYRVEYAKKAMIRLVQ AYLLEAKWTHLNYKPT FEEFRDNALPTSGYAM LAITAFVGMGEVITPET FEWAASDPKIIKASTIIC RFMDDIAEHKFNHRRE DDCSAIECYMKQYGAT AQEAYDEFNKHIESSW KDVNEEFLKPTEMPTP VLCRSLNLARVMDVLY REGDGYTHVGKAAKG GITSLLIDPIQI(서열번호 2)	atggccagtcaggcttcacaagttttagcatctcc ccacccagctatatcctctgaaaaccggccaaag gctgatttccatcctggtatctggggcgacatgttt attatctgtccagatacggacattgatgccgctac agagctgcaatatgaagaattgaaagcgcaagtc cgcaagatgatcatggaaccagtagacgattcta atcaaaagctaccattcattgacgctgttcaaagg ctcggagtgagctaccactttgaaaaagaaattga agacgaacttgaaaacatctaccgtgataccaata acaacgacgcagacactgatctatacactaccgc cttgagattcagattattgagagagcatggttttgat atttcctgcgaagctttcaacaagttgaaagacga agagggtaatttcaaggcttcgttgacttctgatgtt agaggtttgttagaactctatcaggcttcctacatg agaatccacggtgaagatattcttgatgaagccat atctttcaccactgctcaattaaccttggctttgcct actttggatcccccattgtcagagcaagtcggtca tgccctaaagcagagtataagaagaggcctacc aagagttgaagccagaaactttatctctatttacca agacttggaatcccacaataaggctttattgcaatt cgctaaaattgactttaacatgttacaattgctacat aggaaggagctcagcgaaatctgtcgttggtgga aagatcttgattttactagaaagttgccttcgcacg ggaccgtgtcgttgaaggttatttctggattatggg agtttacttcgaaccacaatatagcttgggtagaa agatgttgaccaaggttattgctatggcttctatcgt cgatgatacatacgattccttcgctacatacgacg aattgatcccatatactgacgccattgaaagatgg gacatcaagtgtatgaatcaactgccaaactatat gcaaatttcgtacaaagcattattggatgtatacga ggaaatggaacaattgcttgcggataaaggtcgg cagtacagagtggaatacgctaagaaagctatga ttcgattggtacaagcatatttattagaagcgaagt ggactcacttgaactacaagccaaccttcgaaga atttagagacaatgctttaccgacatctgggtatgc tatgcttgctataaccgcgttcgttggtatgggtga agtcatcacgccagaaacttttgaatgggccgctt ctgacccgaagattatcaaggcttccactatcatct gccgctttatggatgatatcgctgagcataagttca accacagaagggaggatgactgttccgctattga atgttacatgaagcaatacggtgcaaccgcccaa gaggcatacgacgaatttaacaaacacatagaat cgtcttggaaggacgttaatgaagagttcttgaaa

[0136]

					ccaactgaaatgcctactccagtgctgtgtagaag tttgaaccttgctagagtcatggatgttttgtacaga gaaggtgacggttatactcatgtcgggaaagccg ctaagggtggtataacctcattgctaattgatccca ttcaaatctaa(서열번호 68)
HibWil SQTS1 20	*히비스카 델푸스 윌데리아 누스*	Q9SAN0	46%	ASQASQVLASPHPAISS ENRPKADFHPGIWGDM FIICPDTDIDAATELQYE ELKAQVRKMIMEPVDD SNQKLPFIDAVQRLGVS YHFEKEIEDELENIYRD TNNNDADTDLYTTALR FRLLREHGFDISCDAFN KLKDEEGNFKASLTSD VPGLLELYEASYLRVH GEDILDEAISFATAQLT LALPTLHHPLSEQVGH ALKQSIRRGLPRVEARN FISIYQDLESHNKALLQ FAKIDFNMLQLLHRKE LSEICRWWKDLDFTRK LPFARDRVVEGYFWIM GVVFEPQYSLGRKMLT KVIAMASIVDDTYDSFA TYDELIPYTDAIERWDI KCMNQLPNYMQISYKA LLDVYEEMEQLLADKG RQYRVEYAKKAMIRLV QAYLLEAKWTHLNYKP TFEEFRDNALPTSGYA MLAITAFVGMGEVITPE TFEWAASDPKIIKASTII CRFMDDIAEHKFNHRR EDDCSAIECYMKQYGA TAQEAYDEFNKHIESS WKDVNEEFLKPTEMPT PVLCRSLNLARVMDVL YREGDGYTHVGKAAK GGITSLLIDPIQI(서열번 호 3)	atggccagtcaggcttcacaagttttagcatctcc ccacccagctatatcctctgaaaaccggccaaag gctgatttccatcctggtatctggggcgacatgttt attatctgtccagatacggacattgatgccgctac agagctgcaatatgaagaattgaaagcgcaagtc cgcaagatgatcatggaaccagtagacgattcta atcaaaagctaccattcattgacgctgttcaaagg ctcggagtgagctaccactttgaaaaagaaattga agacgaacttgaaaacatctaccgtgataccaata acaacgacgcagacactgatctatacactaccgc cttgagattcagattattgagagagcatggttttgat atttcctgcgatgctttcaacaagttgaaagacga agaaggtaatttcaaggcttcgttgacttctgacgt tcctggtttgttagaactctatgaggcttcctacttg agagtccacggtgaagatatcctagatgaagcca tatctttcgctactgctcagttaaccttggctttgcc aactttgcatcacccgctttcagagcaagttggtc acgcattgaagcaaagtatcagaagaggcctgc caagagttgaagccagaaactttatctctatttacc aagatttagaatcccacaataaggctttgttgcaat tcgccaaaattgactttaacatgttacaattgctaca taggaaggagctcagcgaaatttgtagatggtgg aaagatcttgattttaccagaaagttacctttcgctc gtgaccgtgtcgtcgaaggttatttctggattatgg gagtttacttcgaaccacaatatagcttgggtaga aagatgttgaccaaggttattgctatggcttctatc gtcgatgatacatacgattccttcgctacttacgac gaattgataccatatactgacgccatcgaaagatg ggacatcaagtgtatgaatcagctgccaaactata tgcaaatttcgtacaaagcgttattggatgtatacg aggaaatggaacaattgcttgcagataaaggtcg acagtacagagtggaatacgctaagaaagctatg attcggttggtgcaagcatatttgttagaagcgaa gtggacccatttaaactacaagccaactttcgaag aatttagagacaatgctttgccgacatctgggtatg ccatgctagctataaccgcgttcgttggtatgggt gaagttatcacgccagaaaccctttgaatgggctg cttctgacccaaagattattaaggcctccactatca tctgccgctttatggatgatatcgctgagcataagt tcaaccacagaagggaggatgactgttccgctat tgaatgttacatgaagcaatacggtgcaacagctc aagaggcatacgacgaatttaacaaacacataga atcgtcttggaaggacgtcaatgaagagttcttga aaccaactgaaatgcctactccggtactgtgtaga agtttgaacctagccagagtcatggatgttttgtac agagaaggtgacggttatactcatgttgggaaag

[0137]

					ccgctaagggtggtataacatcacttcttatcgatc ccattcaaatctaa(서열번호 69)
HibWil SQTS1 21	*히비스카 델푸스 윌데리아 누스*	Q9SAN0	50%	ASQASQVLASPHPAISS ENRPKADFHPGIWGDM FIICPDTDIDAATELQYE ELKAQVRKMIMEPVDD SNQKLPFIDAVQRLGVS YHFEKEIEDELENIYRD TNNNDADTDLYTTALR FRLLREHGFDISCEAFN KLKDEEGNFKASLTSD VRGLLELYQASYMRIH GEDILDEAISFTTAQLTL ALPTLDPPLSEQVGHAL KQSIRRGLPRVEARNFI SIYQDLESHNKSLLEFA KIDFNLLQLLHRKELSEI CRWWKDLDFTRKLPFA RDRVVEGYFWIMGVYF EPQYSLGRKMLTKVIA MASIVDDTYDSFATYD ELIPYTDAIERWDIKCM NQLPNYMQISYKALLD VYEEMEQLLADKGRQ YRVEYAKKAMIRLVQA YLLEAKWTHLNYKPTF EEFRDNALPTSGYAML AITAFVGMGEVITPETF EWAASDPKIIKASTIICR FMDDIAEHKFNHRRED DCSAIECYMEQYKVTA QEAYDEFNKHIESSWK DVNEEFLKPTEMPTPVL CRSLNLARVMDVLYRE GDGYTHVGKAAKGGIT SLLIDPIQI(서열번호 4)	atggcctcacaggcttcccaagttttagcatctcct cacccagctatatcttccgaaaaccgtccaaagg ctgatttccatccaggtatctggggcgacatgttta ttatctgtccagatacagacattgatgccgctacc gagttgcaatatgaagaattgaaagcccaagtca gaaagatgatcatggaaccagttgacgattctaat caaaagttgcctttcattgacgctgtccaaagattg ggtgtttcataccactttgaaaaagaaattgaaga cgaattagaaaacatctacagagatactaataaca acgacgcagacactgatttgtacaccactgccttg agattcagattattgcgtgagcatggttttgatattt cttgcgaagctttcaacaagttgaaagacgaaga gggtaatttcaaggcttccttaacctctgatgtcag aggtttgttggaattgtatcaggcttcctacatgag aatccacggtgaagatattttggatgaagctatatc tttcacaactgctcaattaactttagctttaccaactt tggatcctccattgtctgagcaagttggtcatgcct tgaagcagtcaatacgtagaggtttgccaagagtt gaagccagaaactttatctctatttaccaagacttg gaatcccacaataagtctttattagaatttgctaaaa ttgatttcaacttattgcaattgttacacagaaagga gttgtccgaaatctgtagatggtggaaagacttgg attttaccagaaagttacctttcgctagagatcgtgt cgttgaaggttatttctggatcatgggtgtctacttc gaaccacaatactccttgggtagaaagatgttgac caaagttattgctatggcctctattgttgacgatact tatgactcatttgcaacctacgacgaattgatacca tatacagacgctattgaaagatgggatatcaagtg tatgaaccaattgccaaattatatgcaaatatcttac aaggctttgttagacgtttacgaggaaatggaaca attgttggctgataagggtagacaatatagagtcg agtacgcaaaaaaagccatgatcagattggttca ggcctacttattagaggctaagtggacccatttga actacaagcctacttttgaagagttcagagacaat gctttaccaacctccggttatgccatgttggctatc actgcattcgttggtatgggtgaagtcattacacca gaaacttttgaatgggctgcctctgatccaaagatt attaaggcttctactatcatctgccgtttcatggatg atattgctgaacacaaattcaaccacagaagaga ggacgattgttccgctattgaatgttacatggaaca atacaaggttacagcccaagaagcatacgacga atttaacaagcatatcgaatcatcttggaaggacg ttaatgaagaatttttaaagcctaccgaaatgccaa caccagtcttgtgtagatctttgaacttggccagag ttatggatgtcttgtaccgtgaaggtgatggttata ctcatgtcggtaaggctgctaaaggtggtatcacc tccttgttgatcgaccctattcaaatttaa(서열 번호 70)

[0138]

[0139]

HibWilSQTS123	*히비스카델푸스윌데리아누스*	Q9SAN0	47%	ASQASQVLASPHPAISSENRPKADFHPGIWGDMFIICPDTDIDAATELQYEELKAQVRKMIMEPVDDSNQKLPFIDAVQRLGVSYHFEKEIEDELENIYRDTNNNDADTDLYTTALRFRLLREHGFDISCDAFNKLKDEEGNFKASLTSDVPGLLELYEASYLRVHGEDILDEAISFATAQLTLALPTLHHPLSEQVGHALKQSIRRGLPRVEARNFISIYQDLESHNKSLLEFAKIDFNLLQLLHRKELSEICRWWKDLDFTRKLPFARDRVVEGYFWIMGVYFEPQYSLGRKMLTKVIAMASIVDDTYDSFATYDELIPYTDAIERWDIKCMNQLPNYMQISYKALLDVYEEMEQLLADKGRQYRVEYAKKAMIRLVQAYLLEAKWTHLNYKPTFEEFRDNALPTSGYAMLAITAFVGMGEVITPETFEWAASDPKIIKASTIICRFMDDIAEHKFNHRREDDCSAIECYMEQYKVTAQEAYDEFNKHIESSWKDVNEEFLKPTEMPTPVLCRSLNLARVMDVLYREGDGYTHVGKAAKGGITSLLIDPIQI(서열번호 5)	atggcctcacaggcttcccaagttttagcatctcctcacccagctatatcttccgaaaaccgtccaaaggctgatttccatccaggtatctggggcgacatgtttattatctgtccagatacagacattgatgccgctaccgagttgcaatatgaagaattgaaagcccaagtcagaaagatgatcatggaaccagttgacgattctaatcaaaagttgcctttcattgacgctgtccaaagattgggtgtttcataccactttgaaaaagaaattgaagacgaattagaaaacatctacagagatactaataacaacgacgcagacactgatttgtacaccactgccttgagattcagattattgcgtgagcatggttttgatatttcttgcgatgctttcaacaagttgaaagacgaagaaggtaatttcaaggcttccttaacctctgacgtccaggtttgttggaattgtatgaggcttcctacttaagagttcacggtgaagatatcttggatgaagctatatcttttcgccactgctcagttaaccttggctttaccaacttgcatcacccattgtctgagcaagttggtcacgcattgaagcaatcaatcagaagaggtttgccaagagttgaagctagaaactttatctctatttaccaagatttagaatcccacaataagtctttattagaatttgccaaaattgatttcaacttgttgcaattgttacaccgtaaggagttgtccgaaatatgtagatggtggaaagacttagattttacaagaaagttacctttcgctagagatagagtcgttgaaggttatttctggattatgggtgtctacttcgaaccacaatactccttgggtagaaagatgttgaccaaagttattgctatggcttctatcgttgacgatacttatgactcatttgccacttacgacgaattgatccctatatacagacgctattgaacgttgggatatcaagtgtatgaaccagttgccaaattatatgcaaatatcttacaaggctttgttagacgtttacgaggaaatggaacaattgttggctgataagggtagacaatatagagtcgagtacgccaaaaaagcaatgattagattggttcaggcctacttattagaggctaagtggacccatttgaactacaagcctacatttgaagagttcagagacaatgctttaccaacttccggttatgccatgttggctataaccgcattcgttggtatgggtgaagtcattaccccagaaacttttgaatgggccgcttctgatccaaagattatcaaggcttctactatcatctgccgtttcatggatgatattgccgaacataaattcaaccacagaagagaggacgattgttccgctattgaatgttacatggaacaatacaaggttacagcccaagaagcttacgacgaatttaacaagcacatcgaatcatcttggaaggacgtcaatgaagaatttttgaagcctaccgaaatgccaactccagtcttgtgtagatctttgaacttggcaagagttatggatgtcttgtacagagaaggtgatggttatactcatgtcggtaaggctgctaaaggtggtatcacctccttgttgatcgaccctattcaaatttaa(서열번호 71)
HibWilSQTS124	*히비스카델푸스윌데리아*	Q9SAN0	48%	ASQASQVLASPHPAISSENRPKADFHPGIWGDMFIICPDTDIDAATELQYE	atggcctcacaggcttcccaagttttagcatctcctcacccagctatatcttccgaaaaccgtccaaaggctgatttccatccaggtatctggggcgacatgttta

	누스			ELKAQVRKMIMEPVDD SNQKLPFIDAVQRLGVS YHFEKEIEDELENIYRD TNNNDADTDLYTTALR FRLLREHGFDISCEAFN KLKDEEGNFKASLTSD VRGLLELYQASYMRIH GEDILDEAISFTTAQLTL ALPTLDPPLSEQVGHAL KQSIRRGLPRVEARNFI SIYQDLESHNKSLLEFA KIDFNLLQLLHRKELSEI CRWWKDLDFTRKLPFA RDRVVEGYFWIMGVYF EPQYSLGRKMLTKVIA MASIVDDTYDSFATYD ELIPYTDAIERWDIKCM NQLPNYMQISYKALLD VYEEMEQLLADKGRQ YRVEYAKKAMIRLVQA YLLEAKWTHLNYKPTF EEFRDNALPTSGYAML AITAFVGMGEVITPETF EWAASDPKIIKASTIICR FMDDIAEHKFNHRRED DCSAIECYMKQYGATA QEAYDEFNKHIESSWK DVNEEFLKPTEMPTPVL CRSLNLARVMDVLYRE GDGYTHVGKAAKGGIT SLLIDPIQI(서열번호 6)	ttatctgtccagatacagacattgatgccgctacc gagttgcaatatgaagaattgaaagcccaagtca gaaagatgatcatggaaccagttgacgattctaat caaaagttgcctttcattgacgctgtccaaagattg ggtgtttcataccactttgaaaaagaaattgaaga cgaattagaaaacatctacagagatactaataaca acgacgcagacactgatttgtacaccactgccttg agattcagattattgcgtgagcatggttttgatattt cttgcgaagctttcaacaagttgaaagacgaaga gggtaatttcaaggcttccttaacctctgatgtcag aggtttgttggaattgtatcaggcttcctacatgag aatccacggtgaagatattttggatgaagctatatc tttcacaactgctcaattaactttagctttaccaactt tggatcctccattgtctgagcaagttggtcatgcct tgaagcagtcaatacgtagaggtttgccaagagtt gaagccagaaactttatctctatttaccaagacttg gaatcccacaataagtctttattagaatttgctaaaa ttgatttcaacttattgcaattgttacacagaaagga gttgtccgaaatctgtagatggtggaaagacttgg attttaccagaaagttacctttcgctagagatcgtgt cgttgaaggttatttctggatcatgggtgtctacttc gaaccacaatactccttgggtagaaagatgttgac caaagttattgctatggcctctattgttgacgatact tatgactcatttgcaacctacgacgaattgatacca tatacagacgctattgaaagatgggatatcaagtg tatgaaccaattgccaaattatatgcaaatatcttac aaggctttgttagacgtttacgaggaaatggaaca attgttggctgataagggtagacaatatagagtcg agtacgcaaaaaaagccatgatcagattggttca ggcctacttattagaggctaagtggacccatttga actacaagcctacttttgaagagttcagagacaat gctttaccaacctccggttatgccatgttggctatc actgcattcgttggtatgggtgaagtcattacacca gaaacttttgaatgggctgcctctgatccaaagatt attaaggcttctactatcatctgccgtttcatggatg atattgctgaacacaaattcaaccacagaagaga ggacgattgttccgctattgaatgttacatgaaaca atacggtgctacagcccaagaagcatacgacga atttaacaagcatatcgaatcatcttggaaggacg ttaatgaagaatttttaaagcctaccgaaatgccaa caccagtcttgtgtagatctttgaacttggcaagag ttatggatgtcttgtaccgtgaaggtgatggttata ctcatgtcggtaaggctgctaaaggtggcatcac ctccttgttgatcgaccctattcaaatttaa(서열 번호 72)
HibWil SQTS1 26	*허비스카 델푸스 윌데리아 누스*	Q9SAN0	44%	ASQASQVLASPHPAISS ENRPKADFHPGIWGDM FIICPDTDIDAATELQYE ELKAQVRKMIMEPVDD SNQKLPFIDAVQRLGVS YHFEKEIEDELENIYRD	atggcctcacaggcttcccaagttttagcatctcct cacccagctatatcttccgaaaaccgtccaaagg ctgatttccatccaggtatctggggcgacatgttta ttatctgtccagatacagacattgatgccgctacc gagttgcaatatgaagaattgaaagcccaagtca gaaagatgatcatggaaccagttgacgattctaat

[0140]

				TNNNDADTDLYTTALR FRLLREHGFDISCDAFN KLKDEEGNFKASLTSD VPGLLELYEASYLRVH GEDILDEAISFATAQLT LALPTLHHPLSEQVGH ALKQSIRRGLPRVEARN FISIYQDLESHNKSLLEF AKIDFNLLQLLHRKELS EICRWWKDLDFTRKLP FARDRVVEGYFWIMGV YFEPQYSLGRKMLTKVI AMASIVDDTYDSFATY DELIPYTDAIERWDIKC MNQLPNYMQISYKALL DVYEEMEQLLADKGR QYRVEYAKKAMIRLVQ AYLLEAKWTHLNYKPT FEEFRDNALPTSGYAM LAITAFVGMGEVITPET FEWAASDPKIIKASTIIC RFMDDIAEHKFNHRRE DDCSAIECYMKQYGAT AQEAYDEFNKHIESSW KDVNEEFLKPTEMPTP VLCRSLNLARVMDVLY REGDGYTHVGKAAKG GITSLLIDPIQI(서열번호 7)	caaaagttgcctttcattgacgctgtccaaagattg ggtgtttcataccactttgaaaaagaaattgaaga cgaattagaaaacatctacagagatactaataaca acgacgcagacactgatttgtacaccactgccttg agattcagattattgcgtgagcatggttttgatattt cttgcgatgctttcaacaagttgaaagacgaagaa ggtaatttcaaggcttccttaacctctgacgtccca ggtttgttggaattgtatgaggcttcctacttaaga gttcacggtgaagatatcttggatgaagctatatct ttcgccactgctcagttaaccttggctttaccaactt tgcatcacccattgtctgagcaagttggtcacgca ttgaagcaatcaatcagaagaggtttgccaagag ttgaagctagaaactttatctctatttaccaagattta gaatcccacaataagtctttattagaatttgccaaa attgatttcaacttgttgcaattgttacaccgtaagg agttgtccgaaatatgtagatggtggaaagactta gattttacaagaaagttacctttcgctagagataga gtcgttgaaggttatttctggattatgggtgtctactt cgaaccacaatactccttgggtagaaagatgttga ccaaagttattgctatggcttctatcgttgacgatac ttatgactcatttgccacttacgacgaattgatccct tatacagacgctattgaacgttgggatatcaagtgt atgaaccagttgccaaattatatgcaaatatcttac aaggctttgttagacgtttacgaggaaatggaaca attgttggctgataagggtagacaatatagagtcg agtacgccaaaaaagcaatgattagattggttcag gcctacttattagaggctaagtggacccatttgaa ctacaagcctacatttgaagagttcagagacaatg ctttaccaacttccggttatgccatgttggctataac cgcattcgttggtatgggtgaagtcattaccccag aaacttttgaatgggccgcttctgatccaaagatta tcaaggcttctactatcatctgccgtttcatggatga tattgccgaacataaattcaaccacagaagagag gacgattgttccgctattgaatgttacatgaaacaa tacggtgctacagcccaagaagcatacgacgaa tttaacaagcacatcgaatcatcttggaaggacgt taatgaagaatttttgaagcctaccgaaatgccaa ctccagtcttgtgtagatctttgaacttggccagag ttatggatgtcttgtacagagaaggtgatggttata ctcatgtcggtaaggctgctaaaggtggcatcac ctccttgttgatcgaccctattcaaatttaa(서열 번호 73)
HibWilSQTS19	*히비스카델푸스 윌데리아누스*	A0A067FTE8	12%	SIQVPQISSQNAKSQVM RRTANFHPSVWGDRFA NYTAEDKMNHARDLK ELKALKEEVGRKLLAT AGPIQLNLIDAIQRLGV GYHFERELEQALQHLY NEKYSDDDTEDDLYRIS LRFRLLRQHGYNVSCD KFNMFKDDKGNFKESL	atgtccatacaggttccccaaatttcttcgcaaaat gcaaagtcacaagtaatgcgtagaaccgccaact ttcatccatctgtgtggggagacagattcgctaact acacggctgaggataaaatgaaccacgctcgcg acttgaaggaacttaaagcgttaaaggaagaagt tggtagaaagctgttggccacagctggcccaatt caactcaatctaatcgatgctatccaaagattgggt gtcggttatcacttcgaacgagaattggaacaag ctttgcaacatttatacaacgagaagtatagcgat

[0141]

				ASDALGMLSLYEAAHL GVHGEDILDEAIAFTTT HLKSVATHLSNPLKAQ VRHALRQPLHRGLPRL EHRRYISIYQDDASHYK ALLTLAKLDFNLVQSL HKKELCEISRWWKDLD FARKLPFARDRMVECY FWILGVYFEPNYSLARR ILTKVIAMTSIIDDIYDV YGTPEELKLFTEVIERW DESSMDQLPEYMQTFF GALLDLYNEIEKEIANE GWSYRVQYAKEAMKI LVEGYYDESKWFHENY IPKMEEYMRVALVTSG YTMLTTVSFLGMDNIV TKETFDWVFSRPKIIRA SEIIGRFMDDIKSHKFEQ ERGHCASAVECYMREH GVSEEEACSELKKQVD NAWKDINHEMIFSETSK AVPMSVLTRVLNLTRVI DVVYKEGDGYTHVGN EMKQNVAALLIDQVPI(서열번호 8)	gacgacactgaagatgatttgtacaggatttctctg agatttagattgttaagacagcacggttacaatgtc tcctgcgacaaattcaacatgtttaaggatgacaa aggtaacttcaaggaaagtttggcttctgatgccctt gggtatgctctccttatacgaagcggctcatttgg gcgttcacggtgaagatatcttagacgaagctatt gcatttaccactactcatctaaagtccgtcgctact cacttatctaatcctctaaaggcccaagttcgtcat gccttgagacaaccgcttcacagaggtttgccaa gattggaacacagaaggtatatcagcatttaccag gatgacgcttctcattacaaagctttgttgaccctg cgaagttggatttcaatctagttcaatcattgcaca aaaaggagctatgtgagatctccagatggtggaa ggatttagacttcgctcgtaagttgccttttgctaga gatagaatggtcgaatgttatttctggatcttgggt gtgtatttcgaaccaaactactcactggcccggag aatattgaccaaagttattgctatgacttctattattg atgacatctatgacgtttacgggacaccagaaga attgaagttgttcactgaagtaatcgaacgttggg acgaatcgtcaatggaccaactaccagaatacat gcaaacgtttttcggtgctcttttagatttatacaatg agatagaaaaggaaattgccaacgaaggttggtc ttacagagtccaatatgcaaaagaagctatgaag attttagttgagggttactacgatgaatctaagtggt tccatgaaaactacataccaaagatggaggaata tatgcgggtagcattagttaccagcggatacaca atgttgactaccgtcagttttctggggatggacaa cattgttactaaggagacatttgattgggttttctcc agacctaaaatcataagagcatcagaaattatcg gtagattcatggacgatattaaatctcacaaattcg aacaggaaagaggtcactgtgcgtccgctgtcg aatgttatatgagggaacatggcgtgtctgaaga ggaagcttgcagtgagctcaagaagcaagtcga taacgcctggaaggacatcaaccacgaaatgatt ttctccgaaacttctaaggctgttcctatgagcgtg ctaaccagagttttgaacttgacgagagttattgat gtcgtctacaaggaaggtgatggttatactcatgt gggtaatgaaatgaaacaaaacgttgctgctctttt gatcgaccaagtcccaatttaa(서열번호 74)
HibWilSQTS34	*히비스카델푸스 윌데리아누스*	B1B1U4	13%	EKQSLTFDGDEEAKIDR KSSKYHPSIWGDYFIQN SSLTHAKESTQRMIKRV EELKVQVKSMFKDTSD LLQLMNLINSIQMLGLD YHFENEIDEALRLIYEV DDKSYGLYETSLRFQLL RQHGYHVDGEEAFNM LKDEEGNFKASLTSDVP GLLELYQASYMRIHGE DILDEAISFTTAQLTLAL PTLDPPLSAQVSLFLELP	atggaaaagcagtccttgacatttgatggcgacg aggaagcaaaaatagatcgtaagtcgtcaaagta ccatcctagtatttggggtgactatttcatccaaaat tccagcttaacccacgccaaagaatctactcaaa ggatgatcaagagagttgaagaactaaaggtaca agtcaaatctatgttcaaggacacttctgatttgttg caactgatgaacttaattaactctattcaaatgctag gacttgactaccactttgaaaatgaaatcgatgag gctctccgcttgatctatgaagttgacgataagtca tacggtctgtacgaaacgagcttgagattccagtt gttgagacaacatggttaccacgtggatggtgaa

[0142]

				LCRRNKILLARKYILIY QEDAMRNNVILELAKL NFNLLQSLYQEELKKISI WWNDLAFAKSLSFTRD RVVEGYYWVLTIYFEP QHSRARVICSKVFAFLS IMDDIYDNYGILEECTL LTEAIKRWNPQAIDGLP EYLKDYYLKLLKTFEEF EDELELNEKYRMLYLQ DEVKALAISYLQEAKW GIERHVPSLDEHLHNSL ISSGSSTVICASFVGMG EVATKEVFDWLSSFPK VVEACCVIGRLLNDIRS HELEQGRDHTASTVES YMKEHDTNVDVACEK LREIVEKAWKDLNNES LNPTKVPRLMIERIVNL SKSNEEIYKYNDTYTNS DTTMKDNISLVLVESC DYFNK(서열번호 9)	gaagctttcaacatgcttaaagacgaagagggta actttaaggcgtccttgacctctgatgttccaggttt attggaattatatcaagctagctacatgagaataca tggtgaagatattttggatgaagccattagtttcact accgctcaattgactttagctcttcccaccttagac ccgccattgtcggcacaagtctctttgttcttggag ctaccattatgcagaagaaacaagattttgcttgcc agaaaatacatcttgatatatcaagaagatgctatg cgtaataatgttattctcgagttggctaagcttaact ttaacttattgcaatccttgtaccaagaagaactga agaaaatctctatctggtggaatgacttagcttttg caaagtctttatctttcactagagatagagtcgttga aggttattactgggtcctaaccatctacttcgaacc acagcactcccgagctagggtcatttgttcaaaag tttttgccttttttgtccattatggatgacatttatgaca actatggaatccttgaagaatgtacattattaacag aagctattaagagatggaacccacaagccatcga cgggttgcctgaatacctaaaagactattacttga agttgttgaagactttcgaggaatttgaagatgagt tggaattgaatgagaagtacagaatgctgtatttg caagatgaagttaaagctctggctatctcatactta caagaggccaagtggggtattgaaagacacgta ccatcgttagatgagcatcttcacaattctttgataa gttccggctcttcgactgtgatttgtgctagcttcgt tggtatgggtgaagttgccacgaaggaagtcttc gattggttgtcctctttcccaaaggttgtcgaagctt gttgtgtcatcggtaggctcttgaacgatattcgttc ccatgaattagagcagggcagagaccacacgg cttccactgttgaatcttacatgaaggaacacgac accaatgtggacgttgcctgcgaaaagttgagag aaatcgtcgaaaaggcgtggaaagatctgaaca acgaatctctaaaccctactaaggttccaagattg atgatagaaagaatagtaaacttgtcaaagtccaa cgaagaaatttacaaatacaacgacacctacact aattctgatactacaatgaaggacaatattagtcta gtattggttgagtcctgtgattatttcaacaaataa(서열번호 75)
HibWilSQTS52	*히비스카델푸스윌데리아누스*	Q39760	12%	ASQVSQMPSSSPLSSNK DEMRPKADFQPSIWGD LFLNCPDKNIDAETEKR HQQLKEEVRKMIVAPM ANSTQKLAFIDSVQRLG VSYHFTKEIEDELENIY HNNNDAENDLYTTSLR FRLLREHGFNVSCDVF NKFKDEQGNFKSSVTS DVRGLLELYQASYLRV HGEDILDEAISFTTNHLS LAVASLDYPLSEEVSHA LKQSIRRGLPRVEARHY LSVYQDIESHNKVLLEF AKIDFNMVQLLHRKEL	atggccagtcaggtttcacaaatgccttcctcttct ccactatccagcaacaaagatgagatgagacca aaggctgactttcaaccctcgatatggggcgatttt gttcctgaattgcccagacaagaacattgatgctg aaaccgaaaagcgtcatcaacaattgaaagaag aagtcagaaagatgatcgtggcaccaatggctaa ttctacacaaaagttggctttcattgactctgttcag aggcttggagtatcctaccactttactaaagaaatt gaggatgaattagaaaacatctatcacaacaataa cgacgcagaaaacgatttgtacacgacttcccta agattcagattattgagagaacatggtttcaatgtc tcttgtgacgtttttaacaagtttaaggatgagcaa ggtaatttcaagtcaagtgttacctctgacgtccgc ggtctcttggaattataccaagcgtcgtatttgaga

[0143]

				SEISRWWKDLDFQRKL PYARDRVVEGYFWISG VYFEPQYSLGRKMLTK VIAMASIVDDTYDSYA TYEELIPYTKAIERWDI KCIDELPEYMKPSYKAL LDVYEEMEQLVAKHG RQYRVEYAKNAMIRLA QSYLVEARWTLQNYKP SFEEFKANALPTCGYA MLAITSFVGMGDIVTPE TFKWAANDPKIIQASTII CRFMDDVAEHKFEQER GHCASAVECYMREHG VSEEEACSELKKQVDN AWKDINHEMIFSETSKA VPMSVLTRVLNLTRVM DVLYREGDGYTYVGK AAKGGITSLLIEPVAL(서열번호 10)	gttcacggtgaagatatcttggacgaagctatttc gttcacaactaatcatctctctttggccgttgcttcct tagattaccctctgtctgaagaggtctctcacgcttt gaagcaaagcataagacgtggtcttccaagagta gaagccagacactatttgagcgtttaccaagatat cgaatctcataacaaagtcttgttagaatttgctaa gattgacttcaacatggttcaattgctacataggaa agagctaagtgaaatttcaagatggtggaaagat ctcgattttcaaagaaagttaccttatgcacgcgac cgtgtagtcgaaggttacttctggatctccggggtt tacttcgaaccacaatacagcttgggtagaaagat gttgactaaggttattgctatggcttctatcgttgat gatacctatgactcctacgccacctacgaggaatt gatcccatatactaaggccattgaaagatgggac atcaagtgtatagacgaactgccagaatatatgaa gcctagttacaaagctttattggatgtctatgagga aatggaacaattggtcgccaaacacggtcgaca gtacagagtggaatacgctaagaatgctatgattc gattggcgcaatcctacttggttgaagcgagatg gactcttcaaaactacaagccatctttcgaagaatt taaggccaatgctttaccgacatgtggatatgctat gctagctataaccagcttcgttggtatgggtgatat tgtcacgccagaaacttttaaatgggctgcaaatg acccgaagattatccaggcttctactatcatctgcc gatttatggatgatgtagctgagcataagttcgaa caagaaaggggcactgtgcttccgctgtcgagt gttacatgagagaacacggtgtgtcagaagaag aggcatgttctgaattgaaaaagcaagtcgacaa cgcctggaaggacattaaccatgaaatgatttttc ggaaacctccaaagctgtcccaatgtcggttctca ctagagttcttaacttgactagagttatggacgtatt gtacagagaaggtgatggttatacatatgttggta aggctgcaaagggcggtatcacctctttattgatt gaaccagttgccttgtaa(서열번호 76)
HibWil SQTS5 4	*히비스카 델푸스 윌데리아 누스*	Q39761	13%	ASQVSQMPSSSPLSSNK DEMRPKADFQPSIWGD LFLNCPDKNIDAETEKR HQQLKEEVRKMIVAPM ANSTQKLAFIDSVQRLG VSYHFTKEIEDELENIY HNNNDAENDLYTTSIRF RLLREHGYHVDGEEAF NMLKDEEGNFKASLTS DVPGLLELYQASYMRI HGEDILDEAISFTTAQL TLALPTLDPPLSEEVSH ALKQSIRRGLPRVEARH YLSVYQDIESHNKALLE FAKIDFNMLQFLHRKEL SEICRWWKDLDFQRKL PYARDRVVEGYFWISG VYFEPQYSLGRKMLTK	atggccagtcaggtttcacaaatgccttcctcttct ccactatccagcaacaaagatgagatgagacca aaggctgactttcaaccctcgatatggggcgatttt gttcctgaattgcccagacaagaacattgatgctg aaaccgaaaagcgtcatcaacaattgaaagaag aagtcagaaagatgatcgtggcaccaatggctaa ttctacacaaaagttggctttcattgactctgttcag aggcttggagtatcctaccactttactaaagaaatt gaggatgaattagaaaacatctatcacaacaataa cgacgcagaaaacgatttgtacacgacttccata agattcagattattgagagaacatggttaccacgt cgatggtgaggaagccttcaacatgctcaaggac gaagaaggtaattttaaggcttctttgacctcagac gttcctggtttgttagaactatatcaagcctcataca tgcgaatccatggtgaagatattttggacgaagcg atctcttttactactgctcaattaaccttggctttgcc aaccctggatccaccgctctctgaagaggtcagt

[0144]

				VIAMASIVDDTYDSYA TYEELIPYTNAIERWDI KCIDEIPEYMKPSYKAL LDVYEEMVQLVAEHG RQYRVEYAKNAMIRLA QSYLVEAKWTLQNYKP SFEEFKANALPTCGYA MLAITSFVGMGDIVTPE TFKWAASDPKIIQASTII CRFMDDVAEHKFKHRR EDDCSAIECYMEEYGV TAQEAYDVFNKHVESA WKDLNQEFLKPTEMPT EVLNRSLNLARVMDVL YREGDGYTYVGKAAK GGITSLLIEPIAL(서열번호 11)	cacgcgctaaagcaaagtattagaagaggtttac cacgtgtagaagctagacattatctgtccgtttacc aagacatcgaatctcacaataaagctctattggaa tttgccaagattgatttcaacatgttgcagttcctcc acagaaaggaactttcagaaaatatgtcgttggtgg aaagatttggacttccaacgcaagttaccatatgct agagatcgcgttgtcgagggttacttctggatcag cggagtttactttgagccacaatacagtttgggtc ggaagatgttaactaaagttattgctatggcttctat tgtcgatgacacatatgactcctacgccacctacg aagaattaatcccttatactaacgccatcgaaaga tgggacattaagtgtatcgatgaaattccggaata catgaaaccatcttacaaagctttgcttgacgtcta cgaagaaatggtacaattggttgctgagcatggta ggcaatacagagttgaatatgcaaagaatgccat gattagattggctcaatcttacttggtggaagcaaa gtggacgttgcaaaattacaaacctagctttgagg aatttaaggcgaacgctctgcccacctgtgggtat gccatgctggcaattacttccttcgttggtatgggc gacattgtcactcctgaaacattcaaatgggctgc atccgatccaaagatcattcaagcttcgacgataa tctgtcgattcatggatgatgtcgctgagcacaag ttcaagcacaggagagaagatgactgttctgcca tagaatgttacatggaagaatacggtgttaccgcc caggaggcttacgatgtcttcaacaagcacgttg aatccgcgtggaaagatttgaaccaagaatttctc aagccaactgaaatgccaacagaggtgttgaac agatcacttaacctcgctcgtgttatggacgtattg tatagagaaggtgatggttatacttacgttggtaag gctgctaagggcggtatcacctctttattgatcgaa ccaatcgctttgtaa(서열번호 77)
HibWilSQTS55	*히비스카델푸스윌데리아누스*	Q43714	12%	ASQASQVLASPHPAISS ENRPKADFHPGIWGDM FIICPDTDIDAATELQYE ELKAQVRKMIMEPVDD SNQKLPFIDAVQRLGVS YHFEKEIEDELENIYRD TNNNDADTDLYTTALR FRLLREHGFDISCDAFN KFKDEAGNFKASLTSD VQGLLELYEASYMRVH GEDILDEAISFTTAQLTL ALPTLHHPLSEQVGHA LKQSIRRGLPRVEARNF ISIYQDLESHNKSLLQF AKIDFNLLQLLHRKELS EICRWWKDLDFTRKLP FARDRVVEGYFWIMGV YFEPQYSLGRKMLTKVI AMASIVDDTYDSYATY DELIPYTNAIERWDIKC MNQLPNYMKISYKALL	atggccagtcaggcttcacaagttttagcatctcc ccacccagctatatcctctgaaaaccggccaaag gctgatttccatcctggtatctggggcgacatgttt attatctgtccagatacggacattgatgccgctac agagctgcaatatgaagaattgaaagcgcaagtc cgcaagatgatcatggaaccagtagacgattcta atcaaaagctaccattcattgacgctgttcaaagg ctcggagtgagctaccactttgaaaaagaaattga agacgaacttgaaaacatctaccgtgataccaata acaacgacgcagacactgatctatacactaccgc cttgagattcagattattgagagagcatggttttgat atttcctgcgatgctttcaacaagttcaaagacgaa gctggtaatttcaaggcttcgttgacttctgacgttc aaggtttgttggaattgtatgaggcctcctacatga gagtccacggtgaagatatcctagatgaagctat atcttttaccactgctcagttaaccttggctttaccta ctttgcatcacccgttgtcagagcaagttggtcac gcactcaagcagagtatcagaagaggcctgcca agagttgaagccagaaactttatctctatttaccaa gatttggaatcccacaataagtccttgttacaattc

[0145]

				NVYEEMEQLLANQGR QYRVEYAKKAMIRLVQ AYLLEAKWTHQNYKPT FEEFRDNALPTSGYAM LAITAFVGMGEVITPET FKWAASDPKIIKASTIIC RFMDDIAEHKFEQERG HCASAVECYMREHGVS EEEACSELKKQVDNAW KDINHEMIFSETSKAVP MSVLTRVLNLTRVMDV LYREGDGYTHVGKAA KGGITSLLIDPIQI(서열 번호 12)	gctaaaattgactttaacctttacaattgctccata ggaaggaactcagcgaaatttgtagatggtggaa agatcttgatttcactagaaagttgccttttgcacgt gaccgtgtcgtcgaaggttatttctggattatggga gtttacttcgaaccacaatatagcttgggtagaaa gatgttgaccaaggttattgctatggcttctatcgtc gatgatacatacgattcttacgctacatatgacgaa ttgataccatatactaacgccatcgaaagatggga catcaagtgtatgaatcaactgccaaactacatga agattagttacaaagcattattgaatgtatatgagg agatggaacaattgcttgcgaatcaaggtcgaca gtacagagtggaatacgctaagaaagctatgatt cggttggtgcaagcctacttattagaagcgaagtg gactcatcaaaactacaagccaaccttcgaagaa tttagagacaatgctttgccgacatcagggtatgct atgctagctataaccgcgttcgttggtatgggtga agttatcacgccagaaacttttaaatgggccgctt ctgacccaaagattattaaggcttccactatcatct gccgctttatggatgatatcgctgagcataagttc gagcaagaaaggggcactgtgcttccgctgtc gaatgttacatgagagaacacggtgtctcagaag aagaggcctgttctgaattgaaaaagcaggtcga caacgcctggaaggatattaaccatgagatgattt ttagtgaaacatccaaagctgtcccaatgagtgtt ctaaccagagttttgaaccttactagagttatggac gtattgtacagagaaggtgatggttatacgcatgt cggtaaggctgcaaagggtggtatcacctctttgt tgattgaccccattcaaatctaa(서열번호 78)
HibWilSQTS63	*히비스카델푸스윌데리아누스*	Q9FQ26	12%	AASFANKCRPLANFHP TVWGYHFLYYNPEITN QEKIEVDEYKETIRKML VEAPEGSEQKLVLIDA MQRLGVAYHFHNEIET SIQNIFDAPKQNNDDNL HIVSLRFRLVRQQGHY MSSDVFKQFTNQDGKF KETLTNDVQGLLSLYE ASHLRVRNEEILEEALT FTTTHLESIVSNLSNKN NSLKVEVSEALSQPIRM TLPRIGARKYISIYENND AHNHLLLKFAKLDFNM LQKFHQRELSDLTRWW KDLDFANKIPYARDRL VECYFWILGVYFEPKYS RARKMMTKVLKMTSII DDTFDAYANFDELVPF NDAIQRWDANAIDSIPP YMRPIYQALLDIYGEM DQVLSKEGKLDRVYYA KYEMKKLVRAYFKESQ WLNDDNHIPKYEEHME	atggccgcatcatttgctaacaaatgtagacctttta gctaatttccacccaactgtttggggttaccatttct tgtattacaacccagagataaccaatcaggaaaa gatcgaagtcgatgaatacaaggaaacaattcgt aagatgttggttgaagcccctgaagggtccgagc aaaaattggtcttaatcgacgctatgcaaagattg ggtgttgcatatcactttcataacgaaattgaaacc tctattcaaaatatcttcgatgctccaaagcaaaac aacgacgataacttgcacattgtctctttaagattc agattggtccgtcaacagggtcattacatgtcctct gacgtttttaagcaattcactaaccaagatggtaaa ttcaaggaaaccttgactaatgatgtccaaggtttg ttgtcattatatgaagcttctcacttgagagttagaa atgaagaaatattagaggaagctttgacttttacca caactcatttggaatccatcgtttctaacttatcaaa caaaaataactctttaaaggttgaagtttctgaagc tttgtcccaaccaatcagaatgactttgccaagaat tggtgccagaaagtacatttccatatacgaaaaca atgacgcccacaaccatttgttgttaaagttcgcta agttggattttaatatgttacaaaagttccaccaaa gagaattgtccgacttgaccagatggtggaaaga cttggactttgctaacaagatcccatatgctagag

[0146]

				NAIVTVGYMMGATNC LVGMEEFISKETFEWL MSEPVIVRASSLIGRAM DDIVGHEVEQERGHCA SAVECYMREHGVSEEE ACSELKKQVDNAWKDI NHEMIFSETSKAVPMSV LTRVLNLTRVIDTLYQE EDEYTNAKGKLKNMIH SILIESVKI(서열번호 13)	atcgtttagtcgagtgctatttttggattttgggtgttt acttcgaacctaaatactctcgtgctagaaagatg atgaccaaggtcttgaaaatgacatctattattgat gatacttttgatgcttacgccaatttcgacgaattg gttccattcaatgacgccatccaaagatgggacg ctaacgcaatcgattctattccaccatacatgcgtc caatctaccaggccttgttagatatatatggtgaaa tggaccaagttttatccaaagagggtaagttggat agagtctactatgctaagtatgagatgaaaaagtt ggtcagagcctactttaaggaatctcaatggttaa acgacgataatcatatacctaagtatgaagaacac atggaaaacgctattgttactgtcggttacatgatg ggtgctacaaactgtttggttggtatggaggaattt atctcaaaagaaaccttcgaatggttgatgtcaga accagttattgttagagcatcttccttgataggtag agcaatggatgatatcgtcggtcacgaggttgaa caagaacgtggtcattgtgcttcagcagtcgaatg ttacatgagagagcatggtgtttctgaagaagaag cttgctccgaattaaagaagcaagttgacaacgct tggaaggacattaaccacgagatgatcttctctga aacttctaaagctgtcccaatgtctgtcttaaccag agttttaaacttgacaagagttattgatactttgtac caggaagaagatgaatacaccaacgctaagggt aaattaaaaaatatgatccactccatcttgattgagt cagtcaagatctaa(서열번호 79)
HibWilSQTS90	*허비스카 델푸스 윌데리아누스*	B1B1U4	25%	EKQSLTFDGDEEAKIDR KSSKYHPSIWGDYFIQN SSLTHAKESTQRMIKRV EELKVQVKSMFKDTSD LLQLMNLINSIQMLGLD YHFENEIDEALRLIYEV DDKSYGLYETSLRFQLL RQHGYHVDGEEAFNM LKDEEGNFKASLTSDVP GLLELYQASYMRIHGE DILDEAISFTTAQLTLAL PTLDPPLSAQVSLFLELP LCRRNKILLARKYILIY QEDAMRNNVILELAKL NFNLLQSLYQEELKKISI WWNDLAFAKSLSFTRD RVVEGYYWVLTIYFEP QHSRARVICSKVFAFLS IMDDIYDNYGILEECTL LTEAIKRWNPQAIDGLP EYLKDYYLKLLKTFEEF EDELELNEKYRMLYLQ DEVKALAISYLQEAKW GIERHVPSLDEHLHNSL ISSGSSTVICASFVGMG EVATKEVFDWLSSFPK VVEACCVIGRLLNDIRS HEFEQERGHCASAVEC	atggaaaagcagtctttgacatttgatggtgacga ggaagcaaaaatagatcgtaagtcatccaagtac catccttctatttggggcgactatttcatccaaaatt cctctttaacccacgccaaagaatctactcaaaga atgatcaagagagttgaagaattgaaggtccaag ttaaatcaatgttcaaggacacttccgatttattgca attgatgaacttaattaactctattcaaatgttgggtt tggactaccactttgaaaatgaaatcgatgaggct ttgagattgatctatgaagtcgacgataagtcctac ggtttgtacgaaacatcattaagattccagttgttaa gacaacatggttaccacgttgatggtgaagaagc tttcaacatgttgaaggatgaggaaggtaactttaa agcttctttaacctccgacgttccaggtttgttaga gttgtatcaagcctcttacatgcgtattcatggtga agatatattggatgaagctatttcattcactaccgct caattaactttggctttgccaactttagacccaccat tgtccgcacaagtctctttgttcttggagttgccatt atgcagaagaaacaagattttgttggccagaaaat acatcttgatatatcaagaagatgctatgcgtaata atgttatttttggagttagccaagttgaactttaactta ttgcaatctttataccaagaagaattgaagaaaatc tctatctggtggaatgacttagcttttgctaagtcttt atctttcaccagagatagagtcgttgaaggttatta ctgggtcttgactatctacttcgaacctcagcactc cagagccagagttatttgttccaaagtttttgctttt tgtctattatggatgacatttatgacaactatggtat

[0147]

				YMREHGVSEEEACSEL KKQVDNAWKDINHEMI FSETSKAVPMSVLTRVL NLTRGNEEIYKYNDTY TNSDTTMKDNISLVLVE SCDYFNK(서열번호 14)	cttggaagaatgtacattattaaccgaagctattaa gagatggaacccacaagcaatcgacggtttgcc agaatacttgaaagactattacttgaagttgttaaa gactttcgaggaatttgaagatgaattagaattgaa tgagaagtacagaatgttgtatttgcaagatgaag ttaaagctttggctatctcctacttacaagaggcca agtggggtattgaaagacacgtcccttcattagat gagcatttgcacaattctttgatatcctctggttcttc cactgtcatttgtgcttcattcgttggtatgggtgaa gttgctaccaaggaagtcttcgattggttgtcctctt tcccaaaggttgtcgaagcctgttgtgttatcggta gattgttgaacgatattcgttcccatgaatttgagc aggaaagaggtcactgcgcttccgctgttgaatgt tacatgagagaacacggtgtctctgaagaagaag cctgctcagaattgaagaagcaagttgacaacgc atggaaagatataaaccatgaaatgatattctctga aacatctaaggccgttcctatgtcagtcttgacca gagttttgaacttgacccgtggtaatgaagaaatct acaagtacaacgatacttatactaattcagacacc accatgaaagacaacatctccttggtcttggttga atcttgtgactatttcaacaagtaa(서열번호 80)
LeuGr aSQTS 335	*류카덴드론 그란디플로룸*	A0A067F TE8	14%	SIQVPQISSQNAKSQVM RRTANFHPSVWGDRFA NYTAEDKMNHARDLK ELKALKEEVGRKLLAT AGPIQLNLIDAIQRLGV GYHFERELEQALQHLY NEKYSDDDTEDDLYRIS LRFRLLRQHGYNVSCD AFNRFKDTKGSFKEDLI KDVNSMLCLYEATHLR VHGEDILDEALGFTTSQ LKSILPKLKPLLASQVM HALKQPLHRGLPRLEH RRYISIYQDDASHYKAL LTLAKLDFNLVQSLHK KELCEISRWWKDLDFA RKLPFARDRMVECYFW ILGVYFEPNYSLARRILT KVIAMTSIIDDIYDVYG TPEELKLFTEVIERWDE SSMDQLPEYMQTFFGA LLDLYNEIEKEIANEGW SYRVQYAKEAMKILVE GYYDESKWFHENYIPK MEEYMRVALVTSGYT MLTTVSFLGMDNIVTK ETFDWVFSRPKIIRASEI IGRFMDDIKSHKFEQER GHAASAVECYMKQHG LSEQEVCEELYRQVSN AWKDINEECLNPTAVP	atgtccatacaggttccccaaatttcttcgcaaaat gcaaagtcacaagtaatgcgtagaaccgccaact ttcatccatctgtgtggggagacagattcgctaact acacggctgaggataaaatgaaccacgctcgcg acttgaaggaacttaaagcgttaaaggaagaagt tggtagaaagctgttggccacagctggcccaatt caactcaatctaatcgatgctatccaaagattgggt gtcggttatcacttcgaacgagaattggaacaag ctttgcaacatttatacaacgagaagtatagcgat gacgacactgaagatgatttgtacaggatttctctg agatttagattgttaagacagcacggttacaatgtc tcctgcgacgccttcaacagatttaaagataccaa gggtagtttcaaggaagacttgatcaaagatgtta actctatgctctgtttatacgaagcaactcatttgcg ggttcacggtgaagatattttggacgaagctttgg gatttacaacttcccaactaaagtccatcttaccta agttaaaaccattgctggcttctcaagtcatgcatg ccttgaagcaaccgctacaccgtggtttgccaag actcgaacacagaaggtatattagcatttaccagg atgacgcttctcattacaaagccttgttgactcttgc gaagttggatttcaatctagttcaatcattacacaa aaaggagctctgtgagatctccagatggtggaag gatttagacttcgctcgtaagttgccttttgctagag atagaatggtcgaatgttatttctggatcttgggtgt gtatttcgaaccaaactactcactggctagaagaa tattgaccaaagttattgctatgacctctattatcgat gacatttatgacgtttacggcactccagaagaatt gaagctattcactgaagtaatcgaacgttgggac gaatcgtcaatggaccaactgccagaatacatgc

[0148]

				MPLLMRALNLARVIDV VYKEGDGYTHVGNEM KQNVAALLIDQVPI(서열번호 15)	aaacgtttttcggtgctttgttagatttatacaatgag atagaaaaggaaattgcaaacgaaggttggtctt acagagtccagtatgcgaaagaagctatgaagat tttggttgagggttactacgatgaatctaagtggtt ccatgaaaattacatacccaagatggaggaatat atgcgggtagccttagttaccagcgggtacacaa tgttgactaccgtcagttttctggggatggacaac atcgttactaaggagacatttgattgggttttctcca gacctaagataatccgagccagtgaaattattggt agattcatggacgatatcaaatctcataagtttgaa caagagagaggtcacgctgcaagcgctgtcgaa tgttatatgaagcaacacggtctctcagaacaaga agtctgtgaagaactttacagacaagtctccaacg cttggaaggacatcaatgaggaatgcttgaatcc aaccgctgttccaatgccattgttgatgagagcac taaacttggcacgcgtaatcgacgtagtttataaa gaaggtgacggttacactcacgttggtaacgaaa tgaagcaaaacgtggctgctctacttattgatcaa gtaccaatctaa(서열번호 81)
LeuGr aSQTS 345	*류카덴드론 그란디플로룸*	A0A0A0Q UT9	12%	SAAQVSPAPVPAHNAA ASKEEVRRSAGYHPSF WGEFFLTHTSEYAKKD DKIQKQHEELKQEVKG MLVDATTEPTKKLELID AILRLGVGYHFEDEIQA ELERIHRLGDLDCDLYN TCIWFRVLRGQGFTVS AEEFNKFKNSDGNFKE DLINDVSGMLCLYEAT HLRVHGEDILDEALEFT TTRLKSILPDLEPPLATQ VMHALELPYHKGMQR LEARQYIPIYEADMTKN ISLLHFAKLDFNLLQAL HQSEIREITRWWKDLDF KTRLPYARDRLVECYF WILGVQYEPQYSMSRL FLTKVISLASVFDDTYD IYGTFEELKLLTDAIER WEIEATDSLPSYMQILY RALLDVFDEYKDKLIN VQGKDYCLYYGKEAM KGLIRSYHTEAVSFHTG YVQNFEEYLDNSAVSS GYPMLTVEALIGMGHP YATKEALDWALKVPR VIKASSDICRLVDDLRT YKVEEERGDAPSGVHC YMRDYNVSEEEACSKI EEMIDLAWKAINEEMQ KPGHLPLPILLPALNFTR MMEVLYQNIDGYTNSG GRTKDRITSLLVHPITI(	atgtccgcagcgcaagtcagtcctgctccagttcc agcccacaatgctgctgcttctaaggaagaggtg cgtagatcggccggatatcatccatcattctgggg tgaatttttccttactcacacaagcgaatacgctaa aaaggacgataagattcagaaacaacatgaaga attgaagcaagaggttaagggcatgctagtagat gctacgaccgaacccactaaaaagttagaattga tagacgccatcctgagattgggtgtcggttaccac tttgaagatgagattcaagctgaattggaaaggat ccacagactcggtgacttagattgcgacttgtata acacctgtatttggttcagagttcttagaggtcaag gttttactgtctctgctgaagaatttaacaagttcaa aaattccgacggaaacttcaaggaagatttgatca atgacgtttctggtatgttgtgtttatacgaagccac ccatttgcgggttcacggtgaggatattttggatga agcgctcgaatttactaccacacgtttaaagtctat cttaccagacttggaaccgccattggctactcaag taatgcacgcactagaactaccttaccataagggt atgcagagattggaagcccgacaatacattccaa tctatgaagccgatatgactaaaaacatcagcttgt tgcatttcgctaagcttgatttcaacctgttacaggc tctccaccaatccgaaatcagagagataacccgc tggtggaaagatcttgactttaaaactagattgcca tatgctagagatcgcttagtcgaatgttacttctgg attctaggcgttcaatacgagccacaatacagtat gtctcggttgtttttaaccaaggttatttcattggctt ctgtcttcgatgacacatatgacatttacggtacctt cgaagaattaaagttgttgactgacgccatagaaa gatgggagatcgaagcaacagattccttgccgtc ttacatgcaaattttatatcgcgctttgctggacgtc ttcgatgaatacaaggataaattgattaacgttcaa gggaaggactattgtttgtattacggtaaagaagc

[0149]

				서열번호 16)	gatgaagggtttgattcgtagctaccacactgaag ctgtgtcgtttcataccggctatgttcagaatttcga ggaatacttagacaactccgcagtttcctctggtta cccaatgctgacggttgaagctttgattggtatgg gacacccttacgctactaaggaagctttagattgg gcattgaaggtgccaagagttatcaaggctagttc agacatctgtagattagtcgatgacttaaggacgt acaaggtcgaggaggaaagaggtgatgctccct cgggggtccattgctacatgagagactataatgtc tcagaagaagaagcatgttctaagatcgaagaaa tgatcgatctggcctggaaagctataaacgaaga aatgcaaaagccaggtcatctaccactaccaatct tgttgcctgccttgaacttcactagaatgatggag gtcctttaccaaaatattgatggttatacaaattccg gtggtagaaccaaggacagaatcacctctttgttg gttcacccaattactatttaa(서열번호 82)
LeuGr aSQTS 365	*류카덴드론 그란디플로룸*	D0VMR6	11%	SSAKLGSASEDVNRRD ANYHPTVWGDFFLTHS SNFLENNDSILEKHEEL KQEVRNLLVVETSDLPS KIQLTDEIIRLGVGYHFE TEIKAQLEKLHDHQLH LNFDLLTTSVWFRLLR GHGFSISSDIFNKFKNSD GNFKEDLINDVSGMLC LYEATHLRVHGEDILDE ALEFTTTRLKSILPDLEP PLNECVRDALHIPYHRN VQRLAARQYIPQYDAE PTKIESLSLFAKIDFNML QALHQRELREASRWW KEFDFPSKLPYARDRIA EGYYWMMGAHFEPKF SLSRKFLNRIIGITSLIDD TYDVYGTLEEVTLFTE AVERWDIEAVKDIPKY MQVIYTGMLGIFEDFK DNLINARGKDYCIDYAI EVFKEIVRSYQREAEYF HTGYVPSYDEYMENSII SGGYKMFIILMLIGRGE FELKETLDWASTIPEMV EASSLIARYIDDLQTYK AEEERGETVSAVRCYM REFGVSEEQACKKMRE MIEIEWKRLNKTTLEAD EISSSVVIPSLNFTRVLE VMYDKGDGYSDSQGV TKDRIAALLRHAIEI(서 열번호 17)	atgtcctcagcaaaattgggttctgcttctgaagat gtcaaccgtagagacgctaattaccatccaaccg tttggggagatttctttttaacacactcctctaacttc ttggagaacaatgactcaatattggaaaagcacg aagaattgaagcaagaggttagaaacttattggtc gttgaaacttctgacttgccttccaagattcagttga ctgatgaaattatcagattaggtgtcggttatcatttt gagaccgaaatcaaagcccaattagaaaagttgc acgatcatcaattgcacttgaacttcgacttgttga ccacatctgtttggttcagattattgagaggtcacg gtttttccatttcttccgacatcttcaataagttcaaa aattcagatggtaactttaaggaagatttaatcaac gacgtttctggtatgttgtgcttgtacgaagctactc atttgcgtgtccacggtgaagatattttagacgaa gccttggaatttactactaccagattgaagtctattt tgccagatttagaaccaccattaaatgaatgtgtca gagacgctttgcatattccttatcacagaaacgttc aacgtttggctgcaagacaatacataccacagta cgatgccgaaccaacaaaaatcgagtctttgtcat tattcgctaagattgatttcaacatgttgcaagcttt gcatcaaagagaattgagagaggcttccagatg gtggaaagaatttgacttcccttctaagttaccatat gccagagatcgtatcgctgaaggttactactggat gatgggtgcccactttgaaccaaagttctcattgtc tcgtaagttcttaaacagaatcattggtatcacttctt taattgatgacacctatgatgtttacggtactttgga ggaagttactttgtttaccgaagctgttgaaagatg ggacattgaagctgtcaaggacattccaaaatac atgcaagtcatctatacaggtatgttaggtatatttg aagatttcaaagacaacttgataaatgctagaggt aaggattactgtatcgactatgcaatcgaggttttc aaagaaatcgttagatcctaccaaagagaagctg aatatttccacaccggttacgttccatcctacgatg aatacatggaaaactctattatatctggtggttaca agatgttcattatcttaatgttaatcggtagaggag

[0150]

					aatttgagttgaaggaaactttggactgggcttcc actattcctgaaatggtcgaggcatcttccttgatc gctcgttatattgacgacttgcaaacctataaagct gaagaagagagaggagaaaccgtctccgcagt cagatgttacatgcgtgaatttggtgtttcagaaga acaagcctgtaagaagatgagagagatgatcga aattgaatggaagagattgaataaaacaactttag aagctgacgaaatttcttcatctgtcgttattccatc attgaacttcaccagagttttggaggtcatgtacga taagggtgatggttactctgattcccaaggtgttac taaagaccgtatcgccgctttattgagacacgcca tcgaaatctaa(서열번호 83)
LeuGr aSQTS 377	*류카덴드론 그란디플로룸*	Q39760	14%	ASQVSQMPSSSPLSSNK DEMRPKADFQPSIWGD LFLNCPDKNIDAETEKR HQQLKEEVRKMIVAPM ANSTQKLAFIDSVQRLG VSYHFTKEIEDELENIY HNNNDAENDLYTTSLR FRLLREHGFNVSCDAF NRFKDTKGSFKEDLIKD VNSMLCLYEATHLRVH GEDILDEALGFTTSQLK SILPKLKPLLASQVMHA LKQPLRRGLPRVEARH YLSVYQDIESHNKVLLE FAKIDFNMVQLLHRKE LSEISRWWKDLDFQRK LPYARDRVVEGYFWIS GVYFEPQYSLGRKMLT KVIAMASIVDDTYDSY ATYEELIPYTKAIERWD IKCIDELPEYMKPSYKA LLDVYEEMEQLVAKHG RQYRVEYAKNAMIRLA QSYLVEARWTLQNYKP SFEEFKANALPTCGYA MLAITSFVGMGDIVTPE TFKWAANDPKIIQASTII CRFMDDVAEHKFKHRR EDDCSAIECYMEEYGV TAQEAYDVFNKHVESA WKDVNKEFLKPTEMPT EVLNRSLNLARVMDVL YREGDGYTYVGKAAK GGITSLLIEPVAL(서열번호 18)	atggccagtcaggtttcacaaatgccttcctcttct ccactatccagcaacaaagatgagatgagacca aaggctgactttcaaccctcgatatggggcgattt gttcctgaattgcccagacaagaacattgatgctg aaaccgaaaagcgtcatcaacaattgaaagaag aagtcagaaagatgatcgtggcaccaatggctaa ttctacacaaaagttggctttcattgactctgttcag aggcttggagtatcctaccactttactaaagaaatt gaggatgaattagaaaacatctatcacaacaataa cgacgcagaaaacgatttgtacacgacttcccta agattcagattattgagagaacatggtttcaatgtc tcttgtgacgcctttaacagatttaaggataccaaa ggttcattcaaggaagacttgatcaaggatgttaat tccatgttgtgtttatacgaagcgactcaccttcga gttcatggtgaggatattttggacgaagctttgggt ttcacaacctctcaactcaaatcaatcttacctaagt taaagccattgctggcttcgcaagtcatgcacgct ttgaagcaaccgctaagacgtggtttgccaagag ttgaagccagacactatttgagcgtttaccaagat attgaatctcataacaaagtcttgttggaatttgcta agatcgacttcaacatggttcaacttctccatagga aggagctcagtgaaattagtagatggtggaaaga tttagacttccaacgtaaattgccatacgctagaga tcgcgttgtcgaaggttatttttggattagtggggta tacttcgaaccgcaatattccctgggtagaaagat gttaactaaggttattgccatggcttctatcgtcga cgatacctacgattcttacgcaacttatgaggaatt aatcccatacaccaaagctatagaaagatgggat ataaagtgtatagacgaattgcctgagtatatgaa gccatcatacaaggctttgttggacgtgtacgaag aaatggaacagttagttgccaaacacggtcggca atacagagttgaatatgctaagaatgctatgatcc ggctagcccaatcttatctggtcgaggctagatgg actctacaaaactacaagccttccttcgaagaattt aaggctaacgcattgccaacttgtggttacgctat gttggcgatcacttctttcgttggtatgggcgacat tgttaccccagaaacatttaagtgggccgcgaac gatccaaagattattcaagcttcaacgataatctgc cggtttatggatgacgtcgccgaacacaagttca

[0151]

					aacataggagggaagacgattgttctgctatcga gtgttatatggaagaatacggagtaactgcccag gaggcctacgacgtcttcaataagcacgtggaat cagcttggaaggatgttaataaggaatttttgaag cccaccgagatgcctacggaagtgctgaacaga tctttgaacctcgcaagagttatggatgtcttgtac agagaaggtgatggttatacttatgtgggtaaggc tgctaaaggtgggattacctccctattgatcgaac cagtcgctttataa(서열번호 84)
LeuGr aSQTS 379	*류카덴드론 그란디플로룸*	Q39761	12%	ASQVSQMPSSSPLSSNK DEMRPKADFQPSIWGD LFLNCPDKNIDAETEKR HQQLKEEVRKMIVAPM ANSTQKLAFIDSVQRLG VSYHFTKEIEDELENIY HNNNDAENDLYTTSIRF RLLREHGYNVSCDIFNK FKNSDGNFKEDLINDVS GMLCLYEATHLRVHGE DILDEALEFTTTRLKSIL PDLEPPLATQVMHALK QSIRRGLPRVEARHYLS VYQDIESHNKALLEFA KIDFNMLQFLHRKELSE ICRWWKDLDFQRKLPY ARDRVVEGYFWISGVY FEPQYSLGRKMLTKVIA MASIVDDTYDSYATYE ELIPYTNAIERWDIKCID EIPEYMKPSYKALLDV YEEMVQLVAEHGRQY RVEYAKNAMIRLAQSY LVEAKWTLQNYKPSFE EFKANALPTCGYAMLA ITSFVGMGDIVTPETFK WAASDPKIIQASTIICRF MDDVAEHKFKHRRED DCSAIECYMEEYGVTA QEAYDVFNKHVESAW KDLNQEFLKPTEMPTE VLNRSLNLARVMDVLY REGDGYTYVGKAAKG GITSLLIEPIAL(서열번호 19)	atggccagtcaggtttcacaaatgccttcctcttct ccactatccagcaacaaagatgagatgagacca aaggctgactttcaaccctcgatatggggcgattt gttcctgaattgcccagacaagaacattgatgctg aaaccgaaaagcgtcatcaacaattgaaagaag aagtcagaaagatgatcgtggcaccaatggctaa ttctacacaaaagttggctttcattgactctgttcag aggcttggagtatcctaccactttactaaagaaatt gaggatgaattagaaaacatctatcacaacaataa cgacgcagaaaacgatttgtacacgacttccata agattcagattattgagagaacatggttacaatgtc tcttgtgacatctttaacaagttcaagaatagcgat ggtaacttcaaggaagacttgattaatgatgtttca ggtatgctctgtttatatgaagcgacccacttgcga gttcatggtgaggatatcttagacgaagctttgga atttacaactactcgcctaaaatctattttgcctgac ttagaaccacccctggccacccaagtcatgcacg ctttgaagcaaagcatcagacgtggtcttccaaga gttgaagccagacactacttgagtgtttatcaagat attgaatctcataacaaagctttgttggaatttgcta agattgatttcaacatgttacaattcctacatagga aggagctatcggaaatctgtagatggtggaaaga tctcgattttcaaagaaagttaccttacgcacggg accgtgtcgtcgaaggttatttctggatttccgggg tttacttcgaaccacaatacagtttgggtagaaag atgttgactaaggttattgctatggcttctatcgtcg atgacacctacgattcttacgccacctatgaggaa ttgataccatatactaacgccatcgaaagatggga catcaagtgtatagacgagatcccagaatacatg aagccttcgtataaagctttattggatgtatacgag gaaatggtgcaattggttgccgaacacggtagac agtacagagtggaatacgctaagaatgctatgatt cgccttgcgcaatcctacttggttgaagcgaaatg gactctccaaaactacaagccatctttcgaagaat ttaaggccaatgctttaccgacatgcggatatgct atgctagctatcaccagcttcgttggtatgggtgat attgtcacgccagaaacttttaaatgggctgcatct gacccaaagattattcaggcttccactatcatctgt aggttcatggatgatgttgctgaacataagtttaag cacagaagagaagacgactgttcagctattgaat gttacatggaagaatacggcgtcaccgcgcaag aagcctacgacgtattcaacaaacacgtcgagtc

[0152]

					ggcatggaaggatctgaaccaagaatttctaaaa cccactgagatgccaacagaagttctcaacagaa gtttgaacttggctagagtaatggacgttttgtata gagagggtgatggttatacttatgttggtaaagcc gctaagggtggcattacctcattgcttatcgagcc aatcgctttgtaa(서열번호 85)
LeuGr aSQTS 385	*류카텐드론 그란디플로룸*	Q5SBP4	13%	ESRRSANYQASIWETNF TNSPLLSKLQNELSVAH LEELKLEVKQLIWSTKD PLFLLKFIDSIQRLGVAY HFEEEIKESLHLVYLEE RNGDHQHYKEKGLHFT ALRFRILRQDGYHVPQ DVFSSFMNKAGDFEES LSKDTKGLVSLYEASY LSMEGETILDMAKDFSS HHLHKMVEDATDKRV ANQIIHSLEMPLHRRVQ KLEAIWFIQFYECGSDA NPTLVELAKLDFNMVQ ATYQEELKRLSRWYEE TGLQEKLSFARHRLAE AFLWSMGIIPEGHFGYG RMHLMKIGAYITLLDDI YDVYGTLEELQVLTEII ERWDINLLDQLPEYMQ IFFLYMFNSTNELAYEIL RDQGINVISNLKGLWV ELSQCYFKEATWFHNG YTPTTEEYLNVACISAS GPVILFSGYFTTTNPINK HELQSLERHAHSLSMIL RLADDLGTSSDEMKRG DVPKAIQCFMNDTGCC EEEARQHVKRLIDAEW KKMNKDILMEKPFKNF CPTAMNLGRISMSFYE HGDGYGGPHSDTKKK MVSLFVQPMNITI(서열 번호 20)	atggaaagtaggcgttcagcaaattatcaggcttc catatgggagacaaactttactaactctccacttttta tctaagttgcaaaatgaactgtcggtcgcccatct cgaagaattgaaactagaggtgaagcaattaatct ggagcacgaaggatcccttattccttttgaaattca ttgactccattcaaagattgggcgttgcttaccactt tgaagaagaaatcaaggaatctttgcacctggtct acctggaagagcgaaacggtgatcatcaacact ataaggaaaaaggattgcatttcaccgctttgaga ttcagaatattgagacaggacggttaccacgtacc acaagatgtttttttcttcattcatgaataaggctggt gactttgaagaaagtttatccaaagacactaaggg tttggtctctttgtacgaagcctcctacctctctatg gaaggtgaaaccattttggatatggccaaggattt ctcctctcaccatttacacaagatggttgaagatgc tactgacaaaagagttgctaaccaaatcattcata gcttggagatgcctttgcatagaagagttcaaaag ctagaggctatctggttcatccaattttatgaatgc ggttccgacgccaacccgaccttggtcgaattgg cgaaattagattttaatatggtgcaagctacttacc aagaagaattaaagcgtctatctaggtggtacga ggaaaccggtctccaagaaaagttgtctttcgctc gtcacagattggctgaagctttcttgtggtctatgg gcattattcctgaaggtcatttcggatatggcagaa tgcaccttatgaagatcggtgcatacattaccttatt ggatgatatttatgacgtttatggtactttggaagaa ttgcaagtattgacagaaatcatcgaaagatggg atattaacctttggaccagttgccagaatacatgc aaatattcttcctctacatgtttaactctacaaatgaa ctagcttacgaaatcttaagagaccaaggtattaat gtcatatccaaccttaaaggtctttgggtcgaactg tcacaatgttatttcaaagaagccacgtggttccac aacggttataccccaaccactgaggaatacctaa acgttgcttgtatttcagcgtccggtccagttatctt gttttcgggatactttactactacaaatccaatcaac aagcatgaattgcaatctttagaaagacacgctca ctccttaagtatgatcttaagactagcggatgacct aggtacttcttcggatgagatgaagcggggtgat gttcctaaggctattcaatgtttcatgaacgacacg gggtgttgcgaagaagaagccagacagcacgtt aagagattgattgacgcagaatggaagaagatg aataaggatatcttgatggagaagccatttaaaaa cttctgtccaactgcaatgaatttaggccgtatcag tatgtctttctacgagcacggtgacggttacggcg gtccacattctgataccaaaaagaagatggtctcg

[0153]

					ttgtttgttcaacccatgaatattaccatttaa(서열번호 86)
LeuGraSQTS393	*류카덴드론 그란디플로룸*	Q9T0J9	10%	ESQTTFKYESLAFTKLSHCQWTDYFLSVPIDESELDVITREIDILKPEVMELLSSQGDDETSKRKVLLIQLLLSLGLAFHFENEIKNILEHAFRKIDDITGDEKDLSTISIMFRVFRTYGHNLPSSIFNKFKNSDGNFKEDLINDVSGMLCLYEATHLRVHGEDILDEALEFTTTRLKSILPGGTCRPHILRLIRNTLYLPQRWNMEAVIAREYISFYEQEEDHDKMLLRLAKLNFKLLQLHYIKELKSFIKWWMELGLTSKWPSQFRERIVEAWLAGLMMYFEPQFSGGRVIAAKFNYLLTILDDACDHYFSIHELTRLVACVERWSPDGIDTLEDISRSVFKLMLDVFDDIGKGVRSEGSSYHLKEMLEELNTLVRANLDLVKWARGIQVPSFEEHVEVGGIALTSYATLMYSFVGMGETAGKEAYEWVRSRPRLIKSLAAKGRLMDDITDFDSDMSNGFAANAINYYMKQFVVTKEEAILECQRMIVDINKTINEELLKTTSVPGRVLKQALNFGRLLELLYTKSDDIYNCSEGKLKEYIVTLLIDPIRL(서열번호 21)	atggaatcacagactacattcaaatatgagtcttagcatttaccaagttgtcccattgccaatggactgattacttcttgtctgttccaatagacgaatccgaattggacgtcatcaccagagaaattgatattttaaagcctgaggttatggaattgttatcttcacaaggtgatgacgaaacatctaagcgtaaagtcttgttgatccaattgttgttatctttgggattagcctttcacttcgaaaacgagattaagaatatcttggaacacgctttcagaaagattgatgacatcactggtgacgaaaaggatttgtccaccatttccataatgtttagagttttcagaacttacggtcataacttgccatcctctatctttaataaattcaaaaactcagatggtaatttcaaggaagacttgataaacgatgtttctggtatgttgtgtttatacgaagctactcacttgagagtccatggtgaagacattttagatgaagctttagagtttaccactacccgtttgaagtctatcttgccaggtggtacttgtagacctcacattttaagattgattagaaacactttatatttgccacaaagatggaacatggaagccgtcatcgctcgtgaatacatatcctttacgaacaagaggaagaccacgataagatgttattgagattggctaagttgaatttcaaattgttacagttgcattatattaaggaattgaagtcattcatcaaatggtggatggaattgggtttaacatctaaatggccatctcaatttagagagcgtatcgttgaagcctggttagctggtttgatgatgtactttgaaccacaattctccggtggtagagttattgcagctaagttcaactatttattgaccattttggatgatgcttgtgatcactacttctcaattcatgaattgaccagattggtcgcttgtgttgaaagatggtctccagacggtatcgatacattggaggacatctcccgttctgtctttaagttaatgttggatgttttttgacgatatcggtaagggtgttagatccgaaggttcttcctatcacttgaaagaaatgttggaagaatttaaatactttagttagagcaaatttggacttggttaaatgggccagaggtatccaagtcccatctttcgaagagcatgttgaggttggtggtattgctttaacatcctacgccactttgatgtactctttcgtcggaatgggtgaaaccgctggtaaggaagcctacgaatgggttcgttccagacctcgtttgataaagtctttggcagctaaaggtagattgatggacgacattactgattttgattcagatatgtctaacggtttcgctgctaacgcaattaactattacatgaagcaattcgtcgttaccaaggaagaagccatcttagaatgccagagaatgatcgtcgacatcaacaagaccattaatgaagagttgttaaaaactacatctgttcctggtagagtcttgaagcaagctttgaacttcggtagattattggaattgttgtacactaaatctgacgacatctataattgttccgaaggtaagttaaaggaatacattgttacttttgttgatcgatccaataagattgtaa(서열번호 87)
MacVo	*매크로스*	D0VMR6	14%	SSAKLGSASEDVNRRD	atgtcctcagcaaaattgggttctgcttctgaagat

[0154]

[0155]

lSQTS 1139	*타일리스 빌로사*			ANYHPTVWGDFFLTHS SNFLENNDSILEKHEGL EQKIRTMLISPTDTISKK LSLIDAVQRLGVAYHFE KEIEDEIEKLSCKEYND GNDLQTVALRFRLLRQ QGYFVSCDVFKRFKNT KGEFETEDARTLWCLY EATHLRVDGEDILEEAI QFSRKKLEALLPELSFP LNECVRDALHIPYHRN VQRLAARQYIPQYDAE PTKIESLSLFAKIDFNML QALHQRELREASRWW KEFDFPSKLPYARDRIA EGYYWMMGAHFEPKF SLSRKFLNRIIGITSLIDD TYDVYGTLEEVTLFTE AVERWDIEAVKDIPKY MQVIYTGMLGIFEDFK DNLINARGKDYCIDYAI EVFKEIVRSYQREAEYF HTGYVPSYDEYMENSII SGGYKMFIILMLIGRGE FELKETLDWASTIPEMV EASSLIARYIDDLQTYK AEEERGETVSAVRCYM REFGVSEEQACKKMRE MIEIEWKRLNKTTLEAD EISSSVVIPSLNFTRVLE VMYDKGDGYSDSQGV TKDRIAALLRHAIEI(서열번호 22)	gtcaaccgtagagacgctaattaccatccaaccg tttggggagatttctttttaacacactcctctaacttc ttggagaacaatgactcaatattggaaaagcacg aaggtttggaacaaaagattagaactatgttaatct ctcctaccgatactatctccaagaaattatctttgat tgacgccgttcagagattgggtgtcgcttatcatttt gagaaggaaattgaagatgaaatcgaaaagttat catgtaaagagtacaacgacggtaatgacttgca aaccgtcgccttgagattcagattattgagacaac aaggttatttcgtttcctgcgatgtttttaagcgtttc aagaacactaagggtgaatttgagactgaagatg ctagaacattgtggtgtttatacgaagctactcactt gagagttgacggtgaagatattttggaagaagct atccaattctctcgtaagaaattagaagcattgttg ccagaattatcctttccattgaatgaatgtgttagag atgccttgcatatcccataccacagaaacgtccag agattggctgcacgtcaatatataccacaatacga cgctgagcctaccaagattgaatccttatctttgttc gctaagattgactttaatatgttgcaggccttgcac caaagagaattgagagaagcttccagatggtgg aaggagttcgattttccatctaaattgccttatgccc gtgatagaatcgctgaaggttactactggatgatg ggtgctcatttcgaaccaaaattttctttgtctcgta agttcttaaacagaatcattggtataacctccttaat tgatgatacttatgacgtctacggtactttagaaga agttaccttgttcaccgaagccgttgaaagatggg atattgaggctgtcaaagacatcccaaagtacatg caagttatatacacaggtatgttaggtattttcgaa gatttcaaagacaatttgattaacgccagaggtaa ggattattgcatcgattacgctatcgaagttttcaa ggagattgtcagatcttaccaaagagaagcagaa tactttcacactggttacgttccatcttatgacgaat acatggaaaactcaattatctcaggtggttacaaa atgtttataatcttgatgttaatcggtagaggtgagt tcgaattgaaagaaaccttagattgggcttcaact attccagaaatggtcgaagcttcttccttgatagct agatacatcgacgatttgcaaacatacaaggccg aagaagaacgtggtgaaacagtttcagcagtcag atgttacatgagagagtttggtgtttctgaggaaca agcttgtaagaagatgagagaaatgattgagatc gaatggaagagattgaacaagactaccttggaag ctgacgaaatttcttcttccgttgttattccatctttga actttactagagtcttggaagtcatgtatgacaagg gagacggttattctgattcccaaggtgttaccaag gatcgtattgctgctttgttaagacacgccattgag atataa(서열번호 88)
MacVo lSQTS 2198	*매크로스 타일리스 빌로사*	A0A067D 5M4	62%	RDLKSVLSSKESTKAD VNRRSSNYHPSIWGDH FINVSSNEKYTNTEVEK RFETLKAEIEKLLVSNN TAWKTLEEIVAIVNQLQ	atgcgtgacttgaaatccgtcttatcttcaaaggaa tctacaaaggcagatgttaatagaagatcctctaa ctatcacccttccatctggggtgatcatttcattaac gtttcttcaaatgagaagtacactaacactgaagtc gaaaaaagatttgaaaccttgaaggccgaaatag

				RLGLAYHFENQIKEAL QSIYDSHVNGNCDVNY DHNNDLYIVALRFRLL RQHGYKVSADIFKKFR DEKGEFKAMLTNDAK GLLCLYEASYLRVQGE NILEEACEFSRKHLKSL LSHLSTSLAEQVKHSLE IPLHRGMPRLEARHYISI YEEDNSSRNELILELAK LDFNLLQALHRRELGEI SRWWKDIDFATKLPFA RDRLVECYFWILGVYF EPKYSITRKFMTKVIAI ASVIDDIYDVYGTLEEL KLFTHAIERWETVAAN ELPKYMQVCYFALLDV FKEMEDKLVNKGLLYS MPCAKEAVKGLVRAYF VEAEWFNANYMPTFEE YMENSTMSSGYPMLAV EALIGIEDATISKEAFD WAISVPKIIRSCALIARL VDDIHTYKVEQERGDA PSSVECYMQQYDVSEE EACNRIKGMVEIEWMN INEEIQDPNHPPLQWLL PSLNLARMMVVLYQN GDNYTNSSGKTKDRIA SLLVDPLPM(서열번호 23)	aaaagttgttagtttctaacaacaccgcttggaag accttggaggaaattgtcgctatcgttaatcagttg caaagattagggttggcttaccacttcgaaaacca aatcaaagaagccttgcaatccatttatgactctca tgtcaacggtaattgcgacgttaattacgatcaca acaacgatttgtacatagtcgctttaagatttcgttt gttgagacaacacggttataaagtctctgctgaca ttttcaagaagtttagagatgaaaagggtgaattta aggctatgttaacaaatgacgccaaaggtttgttgt gtttatacgaagcatcctatttgagagttcaaggtg aaaatatcttagaagaggcttgtgaattttctcgtaa gcatttgaagtcattattgtctcacttgtccacctcat tggctgagcaagttaagcactctttggaaatccca ttacatagaggtatgccaagattggaagctagac attacatttctatttacgaggaagataactcctctcg taatgaattgatattagagttggcaaagttggactt caacttgttgcaggccttacacagaagagaattg ggtgaaatttctcgttggtggaaagatattgatttc gctactaaattgccattcgccagagacagattagt tgaatgttacttctggatcttgggtgtttattttgaac ctaaatactccatcactagaaagttcatgactaag gttatcgctattgcttccgtcatcgatgatatatacg acgtttatggtaccttggaggaattgaagttgttca ctcatgctattgaaagatgggaaactgtcgctgcc aacgaattaccaaagtacatgcaagtttgttacttt gctttgttagacgtctttaaggaaatggaagataaa ttagtcaataaaggtttgttatactccatgccatgtg caaaggaggctgttaaaggtttggttagagcttac ttcgttgaggctgaatggttcaacgctaactatatg ccaaccttcgaagaatatatggaaaactcaactat gtcctctggttatccaatgttggctgtcgaagctttg atcggtattgaagacgcaactatttcaaaggaagc cttcgattgggcaatatctgttcctaaaattatccgt tcatgcgcattgatcgccagattggtcgatgacatt cacacctacaaggtcgaacaagagagaggtgat gccccatcttccgtcgaatgttacatgcaacaata cgacgtttctgaggaagaagcctgtaatagaatta agggtatggttgaaattgaatggatgaatataaac gaggaaatccaggatccaaaccacccaccttac aatggttgttgccatctttgaacttagctcgtatgat ggtcgttttgtaccaaaatggtgacaactatacaa actcctccggtaaaaccaaggatagaattgcttcc ttgttggtcgacccttgccaatgtaa(서열번호 89)
MacVolSQTS2202	*매크로스타일리스빌로사*	A0A067D5M4	69%	RDLKSVLSSKESTKAD VNRRSSNYHPSIWGDH FINVSSNEKYTNTEVEK RFETLKAEIEKLLVSNN TAWKTLEEIVAIVNQLQ RLGLAYHFENQIKEAL QSIYDSHVNGNCDVNY	atgcgtgacttgaaatccgtcttatcttcaaaggaa tctacaaaggcagatgttaatagaagatcctctaa ctatcacccttccatctggggtgatcatttcattaac gtttcttcaaatgagaagtacactaacactgaagtc gaaaaaagatttgaaaccttgaaggccgaaatag aaaagttgttagtttctaacaacaccgcttggaag accttggaggaaattgtcgctatcgttaatcagttg

[0156]

				DHNNDLYIVALRFRLL RQHGYKVSADIFKKFK DEKGEFKDMIRNDARG LLCLYEASHLRVKGEDI LEEATEFSRKHLKSLLP QLSTSLAEQVKHSLEIP LHRGMPRLEARHYISIY EENNSSRNELLLELAKL DFNLLQALHRRELGDIS RWWKDIDFATKLPFAR DRLVECYFWILGVYFEP KYSITRKFMTKVIAIAS VIDDIYDVYGTLEELKL FTHAIERWETVAANELP KYMQVCYFALLDVFKE MEDKLVNKGLLYSMPC AKEAVKGLVRAYFVEA EWFNANYMPTFEEYME NSTMSSGYPMLAVEAL IGIEDATISKEAFDWAIS VPKIIRSCALIARLVDDI HTYKVEQERGDAPSSV QCYVQQYGVSEEEACN KIKGMVEIEWMNINEEI QDPNHPPLQWLLPSLN LARMMVVLYQNGDNY TNSSGKTKDRIASLLVD PLPM(서열번호 24)	caaagattagggttggcttaccacttcgaaaacca aatcaaagaagccttgcaatccatttatgactctca tgtcaacggtaattgcgacgttaattacgatcaca acaacgatttgtacatagtcgctttaagatttcgttt gttgagacaacacggttataaagtctctgctgaca ttttcaagaagtttaaagatgaaaagggtgaattta aggatatgatcagaaatgacgccagaggtttattg tgtttatacgaagcatcccatttgagagttaagggt gaagatattttagaagaggctactgaattttctcgt aagcacttgaagtcattgttaccacaattgtccaca tcattggctgagcaagttaagcactctttggaaatc ccattacatagaggtatgccaagattggaagcta gacattacatttctatttatgaggaaaacaactcctc tcgtaatgaattgttgttagagttggcaaagttgga cttcaacttgttgcaggctttacacagaagagaatt gggtgatatttctcgttggtggaaagacatcgattt cgccactaaattgccattcgccagagacagatta gttgaatgttacttctggatcttgggtgtttattttga acctaaatactccattactagaaaattcatgaccaa ggttatcgctatagcttctgtcatcgatgatatatac gacgtttacggtaccttggaagaattgaagttgttc actcatgctattgagcgttgggaaactgtcgctgc taatgaattaccaaagtatatgcaagtttgttacttt gctttgttagacgtctttaaggaaatggaagataaa ttagtcaataaaggtttgttatactccatgccatgtg caaaggaggctgttaagggtttggttagagccta cttcgttgaggctgaatggttcaacgctaactatat gccaaccttcgaagaatatatggaaaactcaacta tgtcctctggttatcctatgttggctgtcgaagcttt gatcggtattgaagacgcaactatttcaaaggaa gccttcgattgggcaatatccgttccaaaaattatc agatcttgtgcattgatcgccagattggtcgatga cattcacacctacaaggtcgaacaagagagagg tgatgccccatcttctgtccaatgctacgttcaaca atacggtgtctccgaagaagaagcctgtaataaa attaagggtatggttgagattgaatggatgaatata aacgaagaaatccaggatccaaaccacccaccctt tacaatggttgttgccatctttgaacttagctcgtat gatggttgttttgtaccaaaatggtgacaactacac aaactcctccggtaaaaccaaggatagaattgctt ccttgttggtcgacccttgccaatgtaa(서열 번호 90)
MacVolSQTS2222	*매크로스타일리스빌로사*	A0A067D5M4	69%	RDLKSVLSSKESTKAD VNRRSSNYHPSIWGDH FINVSSNEKYTNTEVEK RFETLKAEIEKLLVSNN TAWKTLEEIVAIVNQLQ RLGLAYHFENQIKEAL QSIYDSHVNGNCDVNY DHNNDLYIVALRFRLL RQHGYKVSADIFKKFK	atgcgtgacttgaaatccgtcttatcttcaaaggaa tctacaaaggcagatgttaatagaagatcctctaa ctatcacccttccatctggggtgatcatttcattaac gtttcttcaaatgagaagtacactaacactgaagtc gaaaaaagatttgaaaccttgaaggccgaaatag aaaagttgttagtttctaacaacaccgcttggaag accttggaggaaattgtcgctatcgttaatcagttg caaagattagggttggcttaccacttcgaaaacca aatcaaagaagccttgcaatccatttatgactctca

[0157]

[0158]

				DEKGEFKDMIRNDARG LLCLYEASHLRVKGEDI LEEATEFSRKHLKSLLP QLSTSLAEQVKHSLEIP LHRGMPRLEARHYISIY EENNSSRNELLLELAKL DFNLLQALHRRELGDIS RWWKDIDFATKLPFAR DRLVECYFWILGVYFEP KYSITRKFMTKVIAIAS VIDDIYDVYGTLEELKL FTHAIERWETVAANELP KYMQVCYFALLDVFKE MEDKLVNKGLLYSMPC AKEAVKGLVKAYFVEA KWFHAKYVPTFEEYME NSTMSSGYPMLAVEAL VGLEDMAITKRALDWA ISVPKIIRSCALIARLDD DVHTYKVEQERGDAPS SVQCYMQQYDVSEEEA CNRIKGMVETAWMEIN GEIQDTNHLPLQWLLPS LNLARMMVVLYQNGD NYTNSSGKTKDRIASLL VDPLPM(서열번호 25)	tgtcaacggtaattgcgacgttaattacgatcaca acaacgatttgtacatagtcgctttaagatttcgttt gttgagacaacacggttataaagtctctgctgaca ttttcaagaagtttaaagatgaaaagggtgaattta aggatatgatcagaaatgacgccagaggtttattg tgtttatacgaagcatcccatttgagagttaagggt gaagatattttagaagaggctactgaattttctcgt aagcacttgaagtcattgttaccacaattgtccaca tcattggctgagcaagttaagcactctttggaaatc ccattacatagaggtatgccaagattggaagcta gacattacatttctatttatgaggaaaacaactcctc tcgtaatgaattgttgttagagttggcaaagttgga cttcaacttgttgcaggctttacacagaagagaatt gggtgatatttctcgttggtggaaagacatcgattt cgccactaaattgccattcgccagagacagatta gttgaatgttacttctggatcttgggtgtttattttga acctaaatactccattactagaaaattcatgaccaa ggttatcgctatagcttctgtcatcgatgatatatac gacgtttacggtaccttggaagaattgaagttgttc actcatgctattgagcgttgggaaactgtcgctgc taatgaattaccaaagtatatgcaagtttgttacttt gctttgttagacgtctttaaggaaatggaagataaa ttagtcaataaaggtttgttatactccatgccatgtg caaaggaggctgttaagggtttggttaaggccta cttcgttgaggctaagtggttccacgctaagtatgt cccaaccttcgaagaatatatggaaaactcaacta tgtcctctggttatcctatgttggctgttgaagctttg gttggtttagaagacatggccattacaaagagag ctttggattgggcaatatccgttccaaaaattatca gatcatgtgcattgatcgccagattggacgatgac gttcacacttacaaggtcgaacaagagagaggtg atgccccatcttctgtccaatgctacatgcaacaat acgacgtctccgaagaagaagcatgtaatcgtatt aagggtatggttgaaactgcttggatggaaatcaa cggtgagatccaggataccaaccacttgccatta caatggttgttgccatctttgaacttagctagaatg atggtcgttttgtaccaaaatggtgacaactacac caactcctccggtaaaaccaaggatagaattgcc tctttgttggtcgacccttgcctatgtaa(서열 번호 91)
MacVolSQTS2251	*매크로스타일리스빌로사*	A0A067D5M4	65%	RDLKSVLSSKESTKAD VNRRSSNYHPSIWGDH FINVSSNEKYTNTEVEK RFETLKAEIEKLLVSNN TAWKTLEEIVAIVNQLQ RLGLAYHFENQIKEAL QSIYDSHVNGNCDVNY DHNNDLYIVALRFRLL RQHGYKVSADIFKKFK DEKGEFKDMIRNDARG LLCLYEASHLRVKGEDI LEEATEFSRKHLKSLLP	atgcgtgacttgaaatccgtcttatcttcaaaggaa tctacaaaggcagatgttaatagaagatcctctaa ctatcacccttccatctggggtgatcatttcattaac gtttcttcaaatgagaagtacactaacactgaagtc gaaaaaagatttgaaaccttgaaggccgaaatag aaaagttgttagtttctaacaacaccgcttggaag accttggaggaaattgtcgctatcgttaatcagttg caaagattagggttggcttaccacttcgaaaacca aatcaaagaagccttgcaatccatttatgactctca tgtcaacggtaattgcgacgttaattacgatcaca acaacgatttgtacatagtcgctttaagatttcgttt

[0159]

				QLSTSLAEQVKHSLEIP LHRGMPRLEARHYISIY EENNSSRNELLLELAKL DFNLLQALHRRELGDIS RWWKDIDFATKLPFAR DRLVECYFWILGVYFEP KYSITRKFMTKVIAIAS VIDDIYDVYGTLEELKL FTHAIERWETVAANELP KYMQVCYFALLDVFKE MEDKLVNKGLLYSMPC AKEAVKGLVKAYFVEA KWFHAKYVPTFEEYME NSTMSSGYPMLAVEAL VGLEDMAITKRALDWA ISVPKIIRSCALIARLDD DVHTYKVEQERGDAPS SVECYMQQYDVSEEEA CNRIKGMVEIEWMNIN EEIQDPNHPPLQWLLPS LNLARMMVVLYQNGD NYTNSSGKTKDRIASLL VDPLPM(서열번호 26)	gttgagacaacacggttataaagtctctgctgaca ttttcaagaagtttaaagatgaaaagggtgaattta aggatatgatcagaaatgacgccagaggtttattg tgtttatacgaagcatcccatttgagagttaagggt gaagatattttagaagaggctactgaattttctcgt aagcacttgaagtcattgttaccacaattgtccaca tcattggctgagcaagttaagcactctttggaaatc ccattacatagaggtatgccaagattggaagcta gacattacatttctatttatgaggaaaacaactcctc tcgtaatgaattgttgttagagttggcaaagttgga cttcaacttgttgcaggctttacacagaagagaatt gggtgatatttctcgttggtggaaagacatcgattt cgccactaaattgccattcgccagagacagatta gttgaatgttacttctggatcttgggtgtttattttga acctaaatactccattactagaaaattcatgaccaa ggttatcgctatagcttctgtcatcgatgatatatac gacgtttacggtaccttggaagaattgaagttgttc actcatgctattgagcgttgggaaactgtcgctgc taatgaattaccaaagtatatgcaagtttgttacttt gctttgttagacgtctttaaggaaatggaagataaa ttagtcaataaaggtttgttatactccatgccatgtg caaaggaggctgttaagggtttggttaaggccta cttcgttgaggctaagtggttccacgctaagtatgt cccaaccttcgaagaatatatggaaaactcaacta tgtcctctggttatcctatgttggctgttgaagctttg gttggtttagaagacatggccattacaaagagag ctttggattgggcaatatccgttccaaaaattatca gatcatgtgcattgatcgccagattggacgatgac gttcacacttacaaggtcgaacaagagagaggtg atgccccatcttctgtcgaatgctacatgcaacaat acgacgtctccgaagaagaagcatgtaatcgtatt aagggtatggttgagattgaatggatgaacataaa cgaagaaatccaggatccaaaccacccaccttta caatggttgttgccatctttgaacttagctagaatg atggtcgttttgtaccaaaatggtgacaactacac caactcctccggtaaaaccaaggatagaattgctt ctttgttggtcgacccttgccaatgtaa(서열 번호 92)
MacVolSQTS2274	*매크로스타일리스빌로사*	A0A097ZIE0	38%	SFAVSASPAKFIQNVEK DSTRRSANFHPSIWGDH FLQYTCDSQEPDDDGS VKHQQLKEEIRKMLTA ETKLSQKLDLIDAIQRL GVAYHFESEIDEILGRV HQAYQESDLCVNENDG LYYISLQFRLLRENGYR ISADVFNKFRDIDGNFK PSLARNVRGMLSLYEA THLRVHGENILDEAHA FATSHLESIATHQISSPL AEQVKHALFQPIHKGV QRLEARNYMPFYQEEA	atgtccttcgcagtttcagcctctcctgctaaatttat acagaatgtcgagaaggattctaccagacgttct gctaacttccacccatccatctggggtgaccatttt ttgcaatacacttgcgactcacaagaaccagatg atgacgggtctgttaagcatcaacaattaaaggaa gaaattagaaaaatgttgacagctgaaactaagtt gtcccagaagttagatttgattgacgccatccaaa gattgggtgtcgcttatcacttcgaatctgaaatcg atgagattttaggtagagttcaccaagcttaccaa gaatcagacttgtgtgtcaacgaaaatgacggttt gtattacatttctttgcaattcagattattgcgtgaaa acggttacagaatatctgccgatgtctttaacaaat tcagagatatcgatggtaattttaagccatccttgg

[0160]

				SHNEALLTFAKLDFNK LQKLHQKELSEITRWW KELDFAHNLPFTIRDRI AECYFWAVAVYFEPQY SLGRRMLAKVFPMTSII DDIYDVYGKFEELELFT SAIERWDISAIDELPEY MKLCYRALLDVYSEAE KDLASQGKLYHLHYAK EAMKNQVKNYFFEAK WCHQNYIPSVDEYMTV ASVTSGYPMLSTTSFVG MGDIVTKESFEWSLTNP RVIRASSVAARLMNDM VSHKFEQSREHVASSIE CYMKQYGATEEETCNE LRKQVSNAWKDINEEC LCPTAVPMPLIVRILNL TRFLDVVYRFEDGYTH SGVVLKDFVASLLINPV SI(서열번호 27)	ctagaaacgttagaggtatgttatccttgtatgaag ccacccatttgcgtgttcacggtgaaaacattttgg acgaagctcacgctttcgcaacttctcatttagaat ctattgccacccaccaaatctcttcccattggctg agcaggtcaagcatgctttgttccaaccaattcac aaaggtgttcaaagattagaagcaagaaattacat gcctttctatcaagaagaagcttcccacaacgag gctttgttaacatttgctaagttggactttaacaagtt gcaaaagttgcatcagaaagaattgtctgaaatca ctcgttggtggaaggaattagatttcgctcacaatt tgccatttactattagagatagaatcgcagaatgtt acttctgggctgttgcagtttacttcgagccacaat attccttaggtagacgtatgttggccaaagtttttcc tatgacctctataattgacgatatctacgacgtcta cggtaaattcgaagaattagaattgttcacctcag ctatcgaaagatgggatatctctgctatcgatgagt taccagagtatatgaagttgtgttacagagccttgt tagatgtctactctgaagccgaaaaggacttagca tcccaaggtaagttgtatcacttgcattacgccaaa gaagctatgaagaatcaggttaagaactacttttc gaggctaagtggtgccatcaaaactatattccatc tgttgatgaatacatgaccgttgcttccgtcacttca ggttacccaatgttgtccactacttcttttgtcggtat gggtgatattgttacaaaggaatccttcgaatggt ctttgaccaatcctagagttatcagagcttcctctgt tgctgctagattaatgaatgacatggtctcacaca agttcgaacaatctcgtgaacacgtcgcttcttcaa tagaatgttacatgaaacaatacggtgcaactgag gaagaaacctgtaacgagttgagaaaacaagttt ctaacgcttggaaggatattaacgaagaatgtttat gtccaacagccgtcccaatgcctttgatagtcaga attttaaatttgactagattcttggacgttgtttatcgt ttgaagacggttacacccattccggtgtcgtcttg aaggactttgttgcctctttgttgattaacccagtttc catctaa(서열번호 93)
OrbSti SQTS1 368	*오르벡실 룸 스티폴라 룸*	Q9T0J9	10%	ESQTTFKYESLAFTKLS HCQWTDYFLSVPIDESE LDVITREIDILKPEVMEL LSSQGDDETSKRKVLLI QLLLSLGLAFHFENEIK NILEHAFRKIDDITGDE KDLSTISIMFRVFRTYG HNLPAEVFERFKDQHG NFKASLSSDVEGMLSL YEASFLDYEGEDILDEA KAFTSFHLRGALAGGT CRPHILRLIRNTLYLPQR WNMEAVIAREYISFYE QEEDHDKMLLRLAKLN FKLLQLHYIKELKSFIK WWMELGLTSKWPSQF RERIVEAWLAGLMMYF	atggaatcacagactacattcaaatatgagtcttta gcatttaccaagttgtcccattgccaatggactgat tacttcttgtctgttccaatagacgaatccgaattgg acgtcatcaccagagaaaattgatatttttaaagcctg aggttatggaattgttatcttcacaaggtgatgacg aaacatctaagcgtaaagtcttgttgatccaattgtt gttatctttgggattagcctttcacttcgaaaacga gattaagaatatcttggaacacgctttcagaaaga ttgatgacatcactggtgacgaaaaggatttgtcc accatttccataatgtttagagttttcagaacttacg gtcataacttgccagctgaagtctttgaaagattca aagaccaacacggtaatttcaaagcttctttgtcat ccgatgttgaaggtatgttgtctttatacgaagcct ctttcttggactatgaaggtgaagatattttagatga agctaaggcctttacttcttttcatttgcgtggtgctt tggctggtggtacctgtagacctcacatcttaagat

				EPQFSGGRVIAAKFNYL LTILDDACDHYFSIHEL TRLVACVERWSPDGID TLEDISRSVFKLMLDVF DDIGKGVRSEGSSYHL KEMLEELNTLVRANLD LVKWARGIQVPSFEEH VEVGGIALTSYATLMY SFVGMGETAGKEAYE WVRSRPRLIKSLAAKG RLMDDITDFDSDMSNG FAANAINYYMKQFVVT KEEAILECQRMIVDINK TINEELLKTTSVPGRVL KQALNFGRLLELLYTK SDDIYNCSEGKLKEYIV TLLIDPIRL(서열번호 28)	tgatcagaaacactttatacttgccacaaagatgg aacatggaggccgtcatagctcgtgaatatatctc cttttacgaacaagaggaagaccacgataagatg ttattgagattagctaagttgaatttcaagttgttaca gttgcattacattaaggaattgaaatcattcatcaa gtggtggatggaattgggtttaacatctaaatggc catctcaatttagagagcgtattgttgaagcttggtt agctggtttgatgatgtacttcgaaccacaattctc cggtggtagagttattgcagccaagtttaactattt gttaaccattttggatgatgcttgtgatcactatttct caatccatgaattgactagattggtcgcttgtgttg aaagatggtctccagacggtatcgataccttgga ggacatctcccgttctgtctttaagttaatgttggat gtttttgacgatattggtaaaggtgttagatccgaa ggttcttcctaccacttgaaagaaatgttggaaga attaaatacctttagttagagcaaacttggacttggtt aaatgggccagaggtatccaagtcccatctttcga agagcatgttgaggttggtggtattgctttaacatc ctacgcaactttgatgtactctttcgtcggaatggg tgaaactgctggtaaggaagcatacgaatgggtt cgttcaagacctcgtttgataaagtctttggccgct aagggtagattgatggacgacatcactgattttga ttccgatatgtctaacggtttcgctgctaacgcaatt aactattacatgaagcagttcgtcgttacaaagga agaagccatcttagaatgccaaagaatgattgtcg acatcaataagaccatcaatgaagagttgttaaaa actacctctgttccaggtagagtcttgaaacaagc tttgaacttcggtagattattggaattgttgtatacta agtccgacgacatttacaactgttctgaaggtaaa ttaaaggaatacatagttactttgttgattgatccaa taagattgtaa(서열번호 94)
OrbSti SQTS1 414	*오르벡실룸 스티폴라룸*	A0A067F TE8	43%	SIQVPQISSQNAKSQVM RRTANFHPSVWGDRFA NYTAEDKMNHARDLK ELKALKEEVGRKLLAT AGPIVKLELVDDVKRL GIGYRFEKEIVEALHRC FISSERFTHRNLHQTAL SFRLLRECGYDVTCDK FNKFTNKEGKFNSKLG ENIKGMIDLYEASQLGI AGEYILAEAGEFSGLVL KEKVACINNNPLKAQV RHALRQPLHRGLPRLE HRRYISIYQDDASHYKA LLTLAKLDFNLVQSLH KKELCEISRWWKDLDF ARKLPFARDRMVECYF WILGVYFEPQYSVPRRT TTKVIGLCSVIDDMYD AYGTIDELELFTNAIER LDTSTMDQLPEYMQTF	atgtccatacaggttccccaaatttcttcgcaaaat gcaaagtcacaagtaatgcgtagaaccgccaact ttcatccatctgtgtggggagacagattcgctaact acacggctgaggataaaatgaaccacgctcgcg acttgaaggaacttaaagcgttaaaggaagaagt tggtagaaagctgttggccacagctggcccaatt gttaagctagagttggtcgatgatgtcaaaagact cgggatcggttatagattcgaaaaggaaatcgttg aagctttacaccgttgctttattagttccgaaagatt cactcataggaatttgcaccaaaccgccttgagct tcagattgttacgggaatgtggttacgacgtcactt gtgataagtttaataagttcactaacaaagagggt aagtttaactcaaagttgggtgaaaatatcaaggg tatgatagacttgtatgaagctagccaacttggtat tgctggtgaatacatcttggctgaagcaggtgaat tttcgggcttagttctaaaagaaaaggttgcttgtat taacaataacccattgaaagcgcaggtcagacat gccctaagacaacctctgcacagaggtctcccaa gattagaacacaggagatacatctctatttaccaa gatgacgcttctcactataaggctttgttgaccctg

[0161]

[0162]

				FGALLDLYNEIEKEIAN EGWSYRVQYAKEAMK ILVEGYYDESRWLKCN HAPTMEEYMKVRGVSS GYPLLITISFIGMEDTTE EILTWATSEPMIIRASVI VCRLMDDIKSHKFEQE RGHAASAVECYMKQH GLSEQEVCEELYRQVS NAWKDINEECLNPTAV PMPLLMRALNLARVID VVYKEGDGYTHVGNE MKQNVAALLIDQVPI(서열번호 29)	gccaagttggatttcaacttggttcaatccctccat aagaaagagctttgcgaaatttccagatggtgga aagatcttgacttcgctcggaagttacctttgcac gtgaccgtatggtcgaatgttatttctggatcttgg gagtttacttcgaaccacaatacagtgtaccaaga agaactaccactaaggttattggtttgttctgtca tcgatgatatgtacgatgcttacggtacaattgacg aattagagctttttactaacgccatcgaaagatttgg acacctctactatggatcagctaccagaatatatg caaacttttctttggtgctttattggatttgtataacga gatcgaaaaagaaatcgcaaatgaaggttggtcc taccgagtgcaatacgctaaggaagctatgaaaa ttttggtggaaggatactatgatgaaagcagatgg ttgaagtgtaaccacgccccaaccatggaagaat acatgaaggtccgtggtgttagttctggttaccctc tcttgataaccatatctttcataggtatggaggaca ctactgaagagatcttaacatgggctacatctgaa cctatgattatcagagccagtgtcattgtttgtagat tgatggacgacattaaatcccataagtttgagcaa gagaggggcatgctgcgagcgctgtagaatgc tatatgaagcaacacggtctatcagaacaagaag tttgtgaagaacttacagacaggtctctaatgcat ggaaggacatcaatgaagaatgtttgaacccgac cgctgttccaatgccattgttaatgagagcgctga acttggctcgcgtcattgacgtagtttataaagaag gtgacggctacacccacgttggtaatgaaatgaa gcaaaacgtagctgctctcctaatcgatcaagtac caatctaa(서열번호 95)
ShoCusSQTS154	*쇼레아 쿠스피다타*	ShoBecSQTS1	38%	ALQDSEVPSSILNATAG NRPTASYHPTLWGEKF LVVSTQSTSGSMKNEPT TQGEYDELKQQVTKML TDATTNDPSKKLHLID MVQRLGIAYHFEIEIEN ALEKINLGDANYFEYD LYTIALGFRLLRQQGIK VSSEIFKKFMDEKGKFK EDVVNDVLGMLNLYE AAHLRLRGEDILDEAL AFTTSHLESMATKVSPL LAEQIAHALNCPIQKGL PRIEARHYISLYSRETHF ASSNAALLRFAKIDFN MVQALHQKEISGITKW WKNLDFSTKLPYARDR IVECYFWIMGAYFEPK YSLARTFLTKVIAMTSI LDDTYDNYGTNKELEL LTKCIERWDIDVIDQLP EYMKLVYQALLNVYSE MEAKVAKEGRSYAIDY AKESMKKTMKAYLDE AKWRQEDYVPPIEEYM	atggctttgcaggattcagaagtcccttcttccatat taaacgccactgctggtaatcgtccaaccgcatct taccatccaacattgtggggagagaaattcttagtt gtttccactcaatctacctctggttccatgaagaac gaaccaactacacaaggtgaatatgacgaattga agcaacaagtcaccaagatgttgactgatgctac cactaacgacccatccaaaaagttgcacttgatcg atatggttcaaagattaggtattgcctaccactttga gattgaaatcgaaaatgctttggaaaagattaactt aggtgacgctaactacttcgaatatgacttgtaca ccatcgctttgggttttagattgttgagacaacagg gtattaaagtctcatctgaaatcttcaagaagtttat ggatgagaaaggtaagttcaaagaagacgttgtt aatgatgtcttaggtatgttgaacttatacgaagca gcccatttgagattaagaggtgaagatatcttgga cgaggctttagccttcactacctcccacttggaatc tatggctacaaaggtttctcctttgttggctgaaca aatagcccatgctttaaattgcccaattcaaaagg gtttaccaagaattgaagccagacactatatctcat tgtactcccgtgaaactcactttgcttcttctaacgc tgcattgttgagattcgctaaaattgacttcaacatg gttcaagctttgcaccagaaggagatctctggtatt acaaagtggtggaaaaatttggatttctcaactaa

[0163]

				QVARISSAYPMLITNSF VGMGEVATKEAFDWIS NDPKILKASTTICRLMD DITSHEFEQTRDHVASG VECYMKQYGVSREETV KLFREDVANAWKDINE GFMKPAIFPMPILTVVL NFARVMDFLYKDGDN YTNSHMLKDYITSLLV NPLLI(서열번호 30)	gttgccatacgctagagacagaatcgtcgaatgtt atttttggatcatgggtgcttactttgaacctaagtat tccttggctagaacttttttgaccaaggttatagcaa tgacctctatattagatgatacatacgataactacg gtactaataaggaattggagttgttaactaaatgta ttgaacgttgggacatcgacgttattgatcaattac cagaatatatgaagttggtctaccaagcattgttga acgtttactcagaaatggaagccaaagtcgctaa ggagggtcgttcttacgccattgactatgctaagg aatccatgaaaaagaccatgaaggcatacttgga tgaagctaaatggagacaagaagactacgttcct ccaatagaagaatatatgcaagtcgctagaatttc ctctgcctacccaatgttaatcactaattccttcgtt ggtatgggtgaagttgctaccaaagaggcattcg attggatttccaatgacccaaagattttgaaggctt ctactactatatgtagattgatggatgatatcacttc tcatgaatttgaacaaacaagagaccatgttgcct ctggtgtcgaatgttatatgaaacaatacggtgttt cacgtgaagaaaccgttaagttattcagagagga tgtcgctaacgcttggaaagacattaacgagggtt tcatgaagcctgctatattcccaatgccaatcttga ctgttgttttgaactttgccagagtcatggatttctta tacaaggatggtgacaactatactaattctcatatg ttgaaggattacattacatcattgttggtcaatccat tattaatctaa(서열번호 96)
ShoCu sSQTS 155	*쇼레아 쿠스피다타*	ShoBecSQ TS1	35%	ALQDSEVPSSILNATAG NRPTASYHPTLWGEKF LVVSTQSTSGSMKNEPT TQGEYDELKQQVTKML TDATTNDPSKKLHLID MVQRLGIAYHFEIEIEN ALEKINLGDANYFEYD LYTIALGFRLLRQQGIK VSSEIFKKFMDEKGKFK EDVVNDVLGMLNLYE AAHLRLRGEDILDEAL AFTTSHLESMATKVSPL LAEQIAHALNCPIQKGL PRIEARHYISLYSRETHF ASSNAALLRFAKIDFN MVQALHQKEISGITKW WKNLDFSTKLPYARDR IVECYFWIMGAYFEPK YSLARTFLTKVIAMTSI LDDTYDNYGTNKELEL LTKCIERWDIDVIDQLP EYMKLVYQALLNVYSE MEAKVAKEGRSYAIDY AKESMKKTMKAYLDE AKWRQEDYVPTIEEYM QVALISSAYPMLITNSF VGMGEVATKEAFDWIS NNPKMLKASTIICRLMD	atggcattgcaggattctgaagtcccttcctcaata ttaaacgccaccgctggtaatagaccaactgcttc ttatcacccaacattgtggggagagaagttcttgg ttgtttccactcaatctacctcaggttctatgaaaaa cgaaccaaccactcaaggtgaatacgacgaatta aagcaacaagtcacaaagatgttgactgatgcca ctactaatgacccatccaaaaagttgcatttaatcg atatggttcaacgtttgggtattgcttaccactttga aattgagatcgaaaacgctttggaaaaaataaact taggtgacgctaattatttcgaatacgatttgtacac cattgctttaggttttagattgttgagacaacaaggt atcaaggtctcttctgagattttcaagaaatttatgg acgaaaagggtaagttcaaagaagatgttgtcaa cgatgttttgggtatgttgaacttgtacgaagcagc tcatttaagattaagaggtgaagacatcttggacg aagccttggccttcacaacctcccacttagagtca atggctactaaggtctctccttttgttggctgaacaa attgcccatgctttgaactgcccaatccaaaaggg tttaccacgtattgaagcaagacactatatttctttat actccagagaaactcacttcgcttcctctaatgctg ctttgttgagatttgctaagatcgatttcaatatggtt caagccttgcatcagaaggaaatatcaggtataa ccaaatggtggaagaacttggacttttccactaaa ttaccatatgctagagatcgtattgttgaatgttactt ctggatcatgggtgcttactttgaaccaaagtattc tttagcaagaacattcttgaccaaagtcattgcaat

				DITSHEFEQTRDHVASG VECYMKQYGVSREETV KLFREDVANAWKDINE GFMKPAIFPMPILTVVL NFARVMDFLYKDGDN YTNSHMLKDYITSLLV NPLLI(서열번호 31)	gacctctatcttagacgatacttacgacaactacg gtactaacaaggaattggagttgttgactaagtgt atcgaaagatgggatattgatgttatcgaccagtta cctgagtatatgaagttggtttatcaagctttgttaa atgtttactctgaaatggaagctaaggtcgccaaa gaaggtcgttcctacgccattgactacgcaaaag aatctatgaagaaaaccatgaaagcctacttgga cgaggctaagtggagacaagaagattacgtccct accattgaagaatatatgcaagttgcattaatatca tccgcttatccaatgttgattacaaactcattcgtcg gtatgggtgaggtcgctactaaggaagcttttgac tggatctccaataacccaaagatgttgaaggcttc tactattatatgtagattgatggatgatatcacttcc catgaatttgaacagaccagagaccacgttgcct ctggtgttgaatgttacatgaaacaatacggtgtct ccagagaagaaaccgttaagttgttcagagaaga tgttgctaacgcttggaaggacatcaatgaaggtt tcatgaagccagcaatcttcccaatgcctatcttga ctgttgtcttgaattttgccagagttatggacttttgt acaaggatggtgataactatactaactctcatatgt taaaagactacattacctcattattggttaatccatt attgatttaa(서열번호 97)
ShoCu sSQTS 156	*쇼레아 쿠스피다 타*	ShoBecSQ TS1	36%	ALQDSEVPSSILNATAG NRPTASYHPTLWGEKF LVVSTQSTSGSMKNEPT TQGEYDELKQQVTKML TDATTNDPSKKLHLID MVQRLGIAYHFEIEIEN ALEKINLGDANYFEYD LYTIALGFRLLRQQGIK VSSEIFKKFMDEKGKFK EDVVNDVLGMLNLYE AAHLRLRGEDILDEAL AFTTSHLESMATKVSPL LAEQIAHALNCPIQKGL PRIEARHYISLYSRETHF ASSNAALLRFAKIDFN MVQALHQKEISGITKW WKNLDFSTKLPYARDR IVECYFWIMGAYFEPK YSLARTFLTKVIAMTSI LDDTYDNYGTNKELEL LTKCIERWDIDVIDQLP EYMKLVYQALLNVYSE MEAKVAKEGRSYAIDY AKESMKKTMKAYLDE AKWRQEDYVPPIEEYM QVARISSGYPMLITNSL VGMGEVATKEAFDLIS NDPKMLKASTTICRLM DDITSHEFEQTRDHVAS GVECYMKQYGVSREET VKLFREDVANAWKDIN	atggctttacaggactccgaggttccttcatctatat tgaacgccaccgctggtaatcgtccaactgcatct tatcatccaacattgtggggtgaaaaattcttggtc gtttctactcaatccacctctgggtccatgaagaac gaaccaactacccaaggtgaatacgatgaattaa agcaacaagtcacaaagatgttgactgatgctac cactaatgacccatctaaaaagttgcacttgattga catggttcaaagattaggtatcgcctaccactttga aattgagatcgaaaacgctttggaaaagattaact taggtgatgctaattatttcgaatacgatttgtacac tatagccttgggttttagattattgagacaacaggg tatcaaggtttcatctgaaatcttcaaaaagttcatg gacgagaaaggtaagtttaaggaagacgtcgtta acgatgtcttgggtatgttaaacttgtatgaagctg cccatttgagattgcgtggtgaagacattttagatg aggctttggcttttaccacatcccacttagaatcaa tggcaactaaggtttcacctttgttggctgaacaaa tcgcccacgctttaaattgcccaattcaaaaaggtt tgccaagaatagaagccagacattacatttctttgt actccagagaaacccacttcgcttcttctaacgca gcattgttgcgtttcgctaagatcgactttaatatgg ttcaagcattgcatcagaaagagatttccggtatta ctaagtggtggaagaatttagatttctctacaaaatt gccatatgctagagatagaatcgtcgaatgttactt ctggattatgggtgcttattttgaaccaaagtactct ttggccagaaccttttaaccaaagtcattgctatg acttctatcttagatgacacatacgacaattacggt actaacaaggaattggaattgttaaccaagtgtatt gaaagatgggatatagatgttatcgatcaattgcct

[0164]

[0165]

				EGFMKPAIFPMPILTVV LNFARVMDFLYKDGD NYTNSHMLKDYITSLL VNPLLI(서열번호 32)	gaatacatgaagttagtttatcaagctttgttgaac gtctactccgaaatggaggctaaggtcgctaagg aaggtcgttcctatgccatcgattacgctaaggaa tccatgaaaaagactatgaaagcctatttggacga agctaagtggagacaagaggactacgttccacct atcgaagagtacatgcaagttgcaagaatttcttc cggttatccaatgttaattaccaactccttggttggt atgggtgaagtcgccactaaagaagccttcgattt gatttctaacgacccaaaaatgttgaaggcttcca ccactatatgtagattgatggacgatatcacttctc acgaatttgaacaaactagagatcacgtcgcttca ggtgttgaatgttatatgaagcaatacggtgtttctc gtgaggaaaccgttaagttattcagagaagacgt cgctaacgcatggaaggacattaatgagggtttc atgaagccagcaatctttccaatgccaatcttgact gtcgtcttaaacttcgctagagttatggacttttgta caaagatggtgataattacacaaactctcatatgtt aaaggattacatcacttcattgttggtcaacccttg ttgatttaa(서열번호 98)
ShoCusSQTS157	*쇼레아 쿠스피다타*	ShoBecSQTS1	38%	ALQDSEVPSSILNATAG NRPTASYHPTLWGEKF LVVSTQSTSGSMKNEPT TQGEYDELKQQVTKML TDATTNDPSKKLHLID MVQRLGIAYHFEIEIEN ALEKINLGDANYFEYD LYTIALGFRLLRQQGIK VSSEIFKKFMDEKGKFK EDVVNDVLGMLNLYE AAHLRLRGEDILDEAL AFTTSHLESMATKVSPL LAEQIAHALNCPIQKGL PRIEARHYISLYSRETHF ASSNAALLRFAKIDFN MVQALHQKEISGITKW WKNLDFSTKLPYARDR IVECYFWIMGAYFEPK YSLARTFLTKVIAMTSI LDDTYDNYGTNKELEL LTKCIERWDIDVIDQLP EYMKLVYQALLNVYSE MEAKVAKEGRSYAIDY AKESMKKTMKAYLDE AKWRQEDYVPPMDEY MQVALISCGYPMLITNS FVGMGEVATKEAFDWI SNDPKILKASTTICRLM DDITSHEFEQTRDHVAS GVECYMKQYGVSREET VKLFREDVANAWKDIN EGFMKPAIFPMPILTVV LNFARVMDFLYKDGD NYTNSHMLKDYITSLL	atggccttacaggactccgaagttccatcatctatt ttgaacgctactgctggtaatagacctacagcatc ttaccatccaaccttgtggggagagaagtttttggt cgtttccactcaatctacctccggttctatgaaaaa cgaaccaactacacaaggtgaatatgatgaatta aagcaacaagtcaccaagatgttgactgatgcta ctaccaacgacccatctaaaaagttgcacttaata gatatggttcaacgtttgggtatcgcctaccacttc gagattgaaatcgaaaatgctttagaaaaaattaa cttgggtgacgctaactacttcgaatatgatttgta cactatcgcattaggttttagattgttgagacaaca gggtattaaggtctcctcagaaattttcaagaagtt catggatgaaaaaggtaagtttaaggaggacgtt gtcaatgacgttttaggtatgttgaacttgtatgaag ctgctcatttacgtttgagaggtgaagatatcttgg acgaagccttggctttcactacatcacacttggaat ctatggctaccaaggtttccccattgttggccgag caaatagcacatgccttaaattgtcctattcaaaaa ggtttgccaagaatcgaagctagacactacatctc tttatactctcgtgaaactcactttgcttcctctaacg ctgccttgttgagattcgctaagattgattttaatatg gttcaagccttgcaccagaaagaaatctctggtat caccaagtggtggaagaatttggacttctccacca agttgccatatgctagagacagaattgtcgaatgc tacttctggataatgggtgcatattttgaacctaagt actctttagctagaacttttttgactaaagttattgct atgacatcaattttggatgatacttacgataactac ggtactaacaaagaattagaattattgaccaagtg tatcgagagatgggacattgacgtcattgaccaat taccagaatacatgaagttggtttatcaagctttgtt gaacgtctactccgagatggaagcaaaggttgcc aaggaaggtcgttcttatgctatagattatgctaaa

				VNPLLI(서열번호 33)	gaatctatgaaaaagacaatgaaggcatacttgg acgaagctaagtggagacaagaggattatgttcc tccaatggatgaatacatgcaagttgctttgatatc ctgtggttacccaatgttgatcaccaactctttcgtt ggtatgggtgaagtcgctaccaaagaagcctttg attggatctctaatgacccaaagattttgaaagcat ctaccactatctgtagattaatggatgacattacct cccatgagttcgaacagacaagagatcacgttgc ttcaggtgtcgaatgttatatgaagcaatacggtgt ttctcgtgaagaaactgttaaattattcagagagga tgttgctaacgcttggaaagacattaatgaaggttt catgaagcctgctattttcccaatgccaattttgac cgtcgtcttgaatttcgctagagtcatggatttttat acaaggacggtgataactacacaaactcacatat gttgaaagattacatcacttcattattagttaatccat tgttgatataa(서열번호 99)
ShoCu sSQTS 160	*쇼레아 쿠스피다 타*	ShoBecSQ TS1	36%	ALQDSEVPSSILNATAG NRPTASYHPTLWGEKF LVVSTQSTSGSMKNEPT TQGEYDELKQQVTKML TDATTNDPSKKLHLID MVQRLGIAYHFEIEIEN ALEKINLGDANYFEYD LYTIALGFRLLRQQGIK VSSEIFKKFMDEKGKFK EDVVNDVLGMLNLYE AAHLRLRGEDILDEAL AFTTSHLESMATKVSPL LAEQIAHALNCPIQKGL PRIEARHYISLYSRETHF ASSNAALLRFAKIDFN MVQALHQKEISGITKW WKNLDFATMLPYARD RIVECYFWIMGVYFEPK YSLARTFLTKVIAMTSI LDDTYDNYGTNKELEL LTKCIERWDIDVIDQLP EYMKLVYQALLNVYSE MEAKVAKEGRSYAIDY AKESMKKTMKAYLDE AKWRQEDYVPTIEEYM QVALISSAYPMLITNSF VGMGEVATKEAFDWIS NNPKMLKASTIICRLMD DITSHEFEQTRDHVASG VECYMKQYGVSREETV KLFREDVANAWKDINE GFMKPAIFPMPILTVVL NFARVMDFLYKDGDN YTNSHMLKDYITSLLV NPLLI(서열번호 34)	atggcattacaggattcagaggtcccatcctctatt ttgaacgctactgccggtaatcgtcctaccgcttct taccacccaacattgtggggtgaaaagtttttagtt gtttccactcaatctacctccggctctatgaaaaac gaaccaaccactcaaggtgaatatgacgaattga agcaacaagtcactaagatgttgacagatgctact accaatgacccatctaaaaagttgcatttgatagat atggttcaaagattgggtattgcctaccacttcgaa atcgaaatcgaaaacgctttagaaaagattaattta ggtgacgctaactatttcgaatacgatttatacaca atcgctttgggttttagattgttgagacagcaaggt atcaaggtctcttcagagattttcaaaaagttcatg gatgagaaaggtaagtttaaggaagacgttgtca acgacgttttgggtatgttgaatttatatgaagcag cccatttgagattgcgtggtgaagatatattggac gaggctttagctttcactacctcccacttggaatct atggcaaccaaagtttccccattgttagctgaaca aattgcccacgctttgaactgtcctatccaaaagg gtttgccaagaattgaagccagacattacatatctt tgtattcaagagaaactcacttcgcttcttccaatg ctgctttattaagatttgctaagatcgattttaacatg gtccaagctttgcatcaaaaagagatctctggtatt acaaagtggtggaagaacttggacttcgctactat gttaccatacgccagagatcgtattgttgaatgcta cttctggatcatgggtgtttatttttgaaccaaagtac tccttagctagaaccttcttgaccaaagttattgca atgacttctatttttagacgatacatacgacaactac ggtactaataaggaattggaattgttgactaaatgt attgaaagatgggacatcgatgtcattgatcaattg cctgagtatatgaagttggtttatcaggcattattga acgtctactcagaaatggaagctaaggttgccaa agagggtagatcctacgctattgattacgccaaa gaatctatgaagaagaccatgaaggcctatttgg acgaagctaagtggagacaagaagactacgtcc ctaccatcgaagaatatatgcaagtcgctttaatat

[0166]

					cttcagcctacccaatgttaataactaattcatttgt cggtatgggtgaggttgccactaaggaagcttttg attggatctctaacaacccaaaaatgttaaaggctt ccactattatttgtagattgatggatgacatcacctc ccacgaatttgaacagacccgtgaccacgttgcc tctggtgttgaatgttatatgaagcaatacggtgttt cacgtgaggaaaccgtcaagttgttcagagaaga tgttgctaatgcttggaaagacatcaatgagggttt catgaagccagcaatcttcccaatgccaattttga ctgtcgttttgaacttcgcaagagttatggatttctta tataaggacggcgacaattacactaactctcatat gttgaaagactacatcacttctttgttggtcaaccc attgttaatataa(서열번호 100)
ShoCusSQTS161	*쇼레아쿠스피다타*	ShoBecSQTS1	37%	ALQDSEVPSSILNATAGNRPTASYHPTLWGEKFLVVSTQSTSGSMKNEPTTQGEYDELKQQVTKMLTDATTNDPSKKLHLIDMVQRLGIAYHFEIEIENALEKINLGDANYFEYDLYTIALGFRLLRQQGIKVSSEIFKKFMDEKGKFKEDVVNDVLGMLNLYEAAHLRLRGEDILDEALAFTTSHLESMATKVSPLLAEQIAHALNCPIQKGLPRIEARHYISLYSRETHFASSNAALLRFAKIDFNMVQALHQKEISGITKWWKNLDFATMLPYARDRIVECYFWIMGVYFEPKYSLARTFLTKVIAMTSILDDTYDNYGTNKELELLTKCIERWDIDVIDQLPEYMKLVYQALLNVYSEMEAKVAKEGRSYAIDYAKESMKKTMKAYLDEAKWRQEDYVPPIEEYMQVARISSGYPMLITNSLVGMGEVATKEAFDLISNDPKMLKASTTICRLMDDITSHEFEQTRDHVASGVECYMKQYGVSREETVKLFREDVANAWKDINEGFMKPAIFPMPILTVVLNFARVMDFLYKDGDNYTNSHMLKDYITSLLVNPLLI(서열번호 35)	atggctttgcaagactctgaagtcccttcctcaattttaaacgcaaccgctggtaatagaccaacagcctcttaccatccaactttgtggggtgagaaatttttggttgtttccactcagtctacctcaggttctatgaagaacgaaccaactacccaaggtgaatatgatgaattgaagcaacaagtcactaagatgttaacagatgctactaccaatgacccatccaaaaagttgcacttgatagatatggttcaacgtttgggtatcgcctaccacttcgaaatcgagattgaaaacgctttagagaaaatcaactgggcgacgctaattacttcgaatatgatttatacaccattgccttaggttttagattgttgagacaacaaggtattaaggtttcttccgaaattttcaagaagtttatggatgaaaaaggtaagttcaaggaagacgtcgttaacgacgttttaggtatgttgaacttgtatgaagctgcccatttaagattgcgtggtgaagatatcttggatgaagctttagcattcacaacctctcacttggaatctatggctactaaagtctctccattgttagctgagcagatcgcccacgctttgaattgccctatccaaaagggttgccaagaatagaagcaagacattacatttccttgtactcaagagaaacacacttcgcttcctctaacgctgctttgttaagatttgctaaaattgactttaatatggttcaagccttacatcaaaaggagatttctggtatcaccaagtggtggaagaacttggacttcgcaactatgttgccatacgcaagagaccgtattgttgaatgttatttctggatcatgggtgtctacttcgaacctaagtactcattggctagaacttttttaactaaagtcatagccatgacctccattttggatgacacctacgataactatggtactaacaaggaattagagttgttaacaaagtgtatagaaagatgggacattgatgtcatcgatcaattgcctgaatacatgaagttggtttaccaggctttgttaaatgtctactcagaaatggaagctaaggttgctaaagaaggtcgttcttatgcaattgattacgcaaaggagtctatgaagaaaactatgaaagcttatttggacgaagctaaatggagacaagaagactatgttccaccaatcgaagaatatatgcaagtcgctagaatctcttccggttacccaatgttgattactaactcattagtcggtatgggtgaggttgccactaaggaagctttcgacttgatttctaatgatccaaagatgttaaaagcct

[0167]

					ccactacaatctgtagattgatggacgacattactt ctcatgaatttgaacagacacgtgatcacgttgcc tctggtgtcgagtgctatatgaagcaatacggtgtt tccagagaagaaaccgtcaagttgtttagagaag acgttgctaacgcttggaaggatatcaatgaagg cttcatgaaaccagcaatctttccaatgccaattttg accgttgttttgaacttcgctagagtcatggacttct tgtataaggatggcgacaactacactaattcacat atgttgaaagattacataacttcattattagttaacc ctttattgatctaa(서열번호 101)
WenA ngSQT S1007	*웬들란디아 안구스티폴리아*	A0A068U HT0	81%	ASAQASLPSNNRQETV RPLADFPENIWADRIAP FTLDKQEYEMCQREIE MLKAEVASMLLATGKT MMQRFDFIDKIERLGVS HHFDIEIENQLQEFFNV YTNLGEYSAYDLSSAA LQFRLFRQHGFNISCGIF DQFIDAKGKFKESLCN DIRGLLSLYEAAHVRTH GDKILEEALAFTTTHMT SGGPHLDSSLAKQVKY ALEQPLHKGILRYEAW RYISIYEEDESNNKLLL RLAKLDYHLLQMSYKQ ELCEITRWGKGLESVSN FPYARDRFVECYFWAV GTLYEPQYSLARMTFA KVAALITMIDDIYDAYG TLDELQILTDSAERWD GSGVDQLSDYIRASYN TLLKFNKEVGEDLAKK QRTYAFDKYIEDWKQY MRTNFSQSRWFFTKEL PSFADYINNGAITIGAY LVASAAFLYMDSAKED VINWMSTNPKLVVAYS THSRLINDFGGHKFEKE RGSSTAIECYMKDHNV SEEEAANKFREMMEDA WKVMNEECLRPTTIPR DGLKMLLNIARVGETV YKHRIDGFTQPHAIEEH IRAMLVDFMSI(서열번호 36)	atggcctcagcacaagcttccttaccttctaataac agacaggaaacagtccgtccattggctgacttcc cagagaacatctgggctgatagaattgccccattt accttggataagcaagaatacgaaatgtgtcaaa gagaaatagagatgttaaaagctgaagttgcttct atgttgttggcaactggtaagactatgatgcaaag attcgacttcattgataagatcgaaagattggggg tctcccaccattttgacattgaaatcgaaaatcaatt gcaagagtttttcaacgtttataccaacttaggtga atactctgcctatgatttgtcatctgctgccttgcag ttccgtttatttagacaacacggtttcaatatttcctg cggtattttcgaccaatttatcgacgctaaaggtaa gttcaaggaatctttatgtaacgatatcagaggttt gttgtctttgtacgaagctgctcatgttagaactca cggtgataaaattttggaagaagctttagctttcac cactactcacatgacctccggtggtccacatttag attcttcattggccaagcaagttaaatacgcattgg aacagccattgcataagggtatattgagatatgaa gcttggagatacatatctatctacgaagaggacg aatccaacaataagttattattgcgtttggctaagtt ggactatcacttgttacaaatgtcatacaagcaag agttgtgtgaaattacaagatggggtaaaggtttg gaatctgtctccaactttccttatgcccgtgacaga ttcgttgaatgttacttttgggctgtcggtactttgta cgaaccacaatactcattggctagaatgaccttcg ctaaggttgctgctttaattactatgatcgatgatatt tatgatgcctacggtaccttggacgaattgcaaat attaactgactctgccgaaagatgggatggttccg gtgtcgatcagttgtctgactatattagagcttccta taatacattattgaaatttaataaggaggttggtga agatttggcaaaaaagcaacgtacctacgctttcg acaagtacatcgaagattggaaacaatacatgag aaccaacttctctcaatcaagatggtttttcactaag gagttgccatctttcgctgattacattaacaacggt gccatcacaatcggtgcatatttggttgcctctgct gctttcttatatatggactccgcaaaagaagatgtt atcaactggatgtccacaaaccctaagttggtcgt tgcttactccactcactctcgtttaattaatgactttg gtggtcacaagttcgaaaaggagagaggttcctc tactgctattgaatgctacatgaaggaccataatgt ctccgaagaagaagccgcaaacaagtttagaga

[0168]

					aatgatggaggacgcttggaaggttatgaatgaa gaatgtttaagaccaactaccatccctagagacg ggttgaagatgttgttaaacatagccagagtcggt gaaactgtttacaagcatagaatcgatggttttacc caaccacatgctattgaagaacacataagagcca tgttggtcgatttcatgtctatttaa(서열번호 102)
WenA ngSQT S1086	*웬들란디아 안구스티폴리아*	A0A068U HT0	80%	ASAQASLPSNNRQETV RPLADFPENIWADRIAP FTLDKQEYEMCQREIE MLKAEVASMLLATGKT MMQRFDFIDKIERLGVS HHFDIEIENQLQEFFNV YTNLGEYSAYDLSSAA LQFRLFRQHGFNISCGIF DQFIDAKGKFKESLCN DIRGLLSLYEAAHVRTH GDKILEEALAFTTTHMT SGGPHLDSSLAKQVKY ALEQPLHKGILRYEAW RYISIYEEDESNNKLLL RLAKLDYHLLQMSYKQ ELCEITRWGKGLESVSN FPYARDRFVECYFWAV GTLYEPQYSLARMTFA KVAALITMIDDIYDAYG TLDELQILTDSAERWD GSGVDQLSDYIRASYN TLLKFNKEVGEDLAKK QRTYAFDKYIEDWKQY MRTNFSQSRWFFTKEL PSFADYINNGAITIGAY LVASAAFLYMDSAKED VINWMSTNPKLVVAYS THSRLINDFGGHKFDKE RGTGTAIECYMKDHNIS EEEAAKKFREMIENTW KVMNEECLRPIPIPRDT LKMLLNIARVGETVYK HRIDGFTQPHAIEEHIRA MLVDFMSI(서열번호 37)	atggcctcagcacaagcttccttaccttctaataac agacaggaaacagtccgtccattggctgacttcc cagagaacatctgggctgatagaattgccccattt accttggataagcaagaatacgaaatgtgtcaaa gagaaatagagatgttaaaagctgaagttgcttct atgttgttggcaactggtaagactatgatgcaaag attcgacttcattgataagatcgaaagattggggg tctcccaccattttgacattgaaatcgaaaatcaatt gcaagagtttttcaacgtttataccaacttaggtga atactctgcctatgatttgtcatctgctgccttgcag ttccgtttatttagacaacacggtttcaatatttcctg cggtattttcgaccaatttatcgacgctaaaggtaa gttcaaggaatctttatgtaacgatatcagaggttt gttgtctttgtacgaagctgctcatgttagaactca cggtgataaaatttggaagaagctttagctttcac cactactcacatgacctccggtggtccacatttag attcttcattggccaagcaagttaaatacgcattgg aacagccattgcataagggtatattgagatatgaa gcttggagatacatatctatctacgaagaggacg aatccaacaataagttattattgcgtttggctaagtt ggactatcacttgttacaaatgtcatacaagcaag agttgtgtgaaattacaagatggggtaaaggtttg gaatctgtctccaacttccttatgcccgtgacaga ttcgttgaatgttacttttgggctgtcggtactttgta cgaaccacaatactcattggctagaatgaccttcg ctaaggttgctgctttaattactatgatcgatgatatt tatgatgcctacggtaccttggacgaattgcaaat attaactgactctgccgaaagatgggatggttccg gtgtcgatcagttgtctgactatattagagcttccta taatacattattgaaatttaataaggaggttggtga agatttggcaaaaaagcaacgtacctacgctttcg acaagtacatcgaagattggaaacaatacatgag aaccaacttctctcaatcaagatggtttttcactaag gagttgccatctttcgctgattacattaacaacggt gccatcacaatcggtgcatatttggttgcctctgct gctttcttatatatggactccgcaaaagaagatgtt atcaactggatgtccacaaaccctaagttggtcgt tgcttactccactcactctcgtttaattaatgactttg gtggtcacaagttcgacaaggagagaggtaccg gtactgctattgaatgctacatgaaggaccataat atatccgaagaagaagccgcaaagaagtttaga gaaatgatcgagaacacctggaaggtcatgaatg aagaatgtttaagaccaattccaatccctagagac acattgaagatgttgttaaacatcgccagagttggt

[0169]

					gaaactgtctacaagcatagaatcgatggttttact caaccacatgctattgaagaacacataagagctat gttggttgatttcatgtctatttaa(서열번호 103)
WenA ngSQT S267	*웬들란디아 안구스티폴리아*	G5CV47	11%	SLLEGNVNHENGIFRPE ANFSPSMWGNIFRDSSK DNQISEEVVEEIEALKE VVKHMIISTTSNAIEQK LELVDNLERLGLAYHF EGQINRLLSSAYNANHE DEGNHKRNKEDLYAA ALEFRIFRQHGFNVSSD CFNQFKDTKGKFKKTL LIDVKGMLSLYEAAHV REHGDDILEEALIFATF HLERITPNSLDSTLEKQ VGHALMQSLHRGIPRA EAHFNISIYEECGSSNEK LLRLAKLDYNLVQVLH KEELSELTKWWKDLDF ASKLSYVRDRMVECFF WTVGVYFEPQYSRARV MLAKCIAMISVIDDTYD SYGTLDELIIFTEVVDR WDISEVDRLPNYMKPI YISLLYLFNEYEREINEQ DRFNGVNYVKEAMKEI VRSYYIEAEWFIEGKIPS FEEYLNNALVTGTYYL LAPASLLGMESTSKRTF DWMMKKPKILVASAII GRVIDDIATYKIEKEKG QLVTGIECYMQENNLS VEKASAQLSEIAESAW KDLNKECIKTTTSNIPN EILMRVVNLTRLIDVVY KNNQDGYSNPKNNVKS VIEALLVNPINM(서열번호 38)	atgtccttgttagaaggtaacgttaatcacgagaa cggaatatttagaccagaagctaatttctcaccttc tatgtggggtaacattttccgtgattcttccaaaga caaccaaatctctgaagaagtcgttgaagaaatc gaggcattgaaggaagtcgttaagcatatgattat ttctacaacctccaacgccatcgaacagaaattag agttggtcgataatttggaaagattgggtttggctt accacttcgaaggtcaaatcaacagattattatcat ctgcctataatgctaaccatgaagacgaaggtaa ccacaagagaaataaggaggacttgtacgcagc tgctttggaatttagaattttcagacaacatggtttta acgtttcctctgattgctttaatcaattcaaagatact aagggtaagttcaaaaagactttgttgattgatgtc aagggtatgttgtccttgtatgaagctgcccacgtt cgtgaacatggtgacgacatcttagaagaagcttt gatctttgctaccttccacttagaaagaattactcca aattctttggattccacattggaaaaacaagttggt cacgcattgatgcaatcattacacagaggtattcc aagagccgaagctcattttaacatatctatttacga agagtgtggttcttctaatgaaaagttgttaagattg gctaagttggactacaacttagtccaagtcttgca caaggaggaattatcagaattgaccaaatggtgg aaagatttagacttcgcttctaagttgtcctacgttc gtgatagaatggttgaatgtttttctggactgtcgg tgtttatttcgaaccacagtactccagagccagag ttatgttagctaagtgtattgctatgatctctgttatc gacgatacttacgattcctatggtaccttggacga gttaattatattcactgaagtcgttgatagatgggat atatccgaggtcgaccgtttgcctaactatatgaa accaatctacatttctttgttatacttgtttaacgaata tgaaagagaaattaacgaacaagaccgtttcaat ggtgttaactacgttaaggaagctatgaaggaaat cgtcagatcttattacatcgaggccgaatggttcat agaaggtaaaatcccatctttcgaagagtacttga acaatgcattggttacaggtacctattacttattggc cccagcatctttgttgggtatggaatccacctcaa agagaacttttgattggatgatgaagaagccaaa aattttggtcgcttctgctatcattggtagagttattg atgatattgctacttacaagatagaaaaggaaaag ggacagttagtcactggtattgaatgctacatgca agagaacaacttatcagttgaaaaggcctccgct caattgtctgaaatcgccgagtccgcttggaaag acttgaataaagaatgtatcaaaactaccacctcc aacattcctaacgaaatattgatgagagttgtcaac ttgacaagattaattgacgttgtctacaagaataat caagatggttattctaaccctaagaacaatgttaag tcagtcatcgaagctttgttggttaatccaatcaata

[0170]

					tgtaa(서열번호 104)
WenA ngSQT S302	*웬들란디아 안구스티폴리아*	Q5SBP4	17%	ESRRSANYQASIWDDN FIQSLASPYAGEKYVSQ ANELKEQVKMMLDEE DMKLLDCLELVDNLER LGLAYHFEGQINRLLSS AYNANHEDEGNHKRN KEDLYAAALEFRIFRQH GFNVPQDVFSSFMNKA GDFEESLSKDTKGLVSL YEASYLSMEGETILDM AKDFSSHHLHKMVEDA TDKRVANQIIHSLEMPL HRRVQKLEAIWFIQFYE CGSDANPTLVELAKLD FNMVQATYQEELKRLS RWYEETGLQEKLSFAR HRLAEAFLWSMGIIPEG HFGYGRMHLMKIGAYI TLLDDIYDVYGTLEELQ VLTEIIERWDINLLDQLP EYMQIFFLYMFNSTNEL AYEILRDQGINVISNLK GLWVELSQCYFKEATW FHNGYTPTTEEYLNVA CISASGPVILFSGYFTTT NPINKHELQSLERHAHS LSMILRLADDLGTSSDE MKRGDVPKAIQCFMND TGCCEEEARQHVKRLI DAEWKKMNKDILMEK PFKNFCPTAMNLGRISM SFYEHGDGYGGPHSDT KKKMVSLFVQPMNITI(서열번호 39)	atggaaagtaggcgttcagcaaattatcaggcttc catatgggatgacaactttattcaatctcttgcctct ccttacgctggagagaagtacgtctcgcaagcta acgaattgaaagaacaagtgaagatgatgttaga cgaagaggatatgaaactgttagattgcttggaat tggttgacaacttggaaagactaggcttggcttat cacttcgagggtcaaatcaatagactcttgagcag tgcctacaacgctaaccatgaagatgaaggtaat cacaagagaaataaggaagacttatacgcggcg gctttggagttcagaatttttagacaacatggtttca acgttccacaggacgtcttctcttcctttatgaataa ggccggtgattttgaagaatccctttctaaggatac aaaaggtttggtttcattgtatgaagcttcttacctat caatggaaggtgaaaccatcttagacatggctaa ggatttctcctctcaccatttacacaaaatggtcga agatgctactgataagcgagttgctaaccaaatca ttcacagccttgaaatgccattgcacagaagggta caaaaactcgaagcaatatggttcattcaattctac gaatgtggttctgacgccaaccccactttggtaga attggctaagttagacttcaacatggttcaagctac gtatcaagaagaactaaagagattgtcgagatgg tacgaagagaccggactgcaagaaaagttatctttt tgcacgtcatcgtttggccgaagctttttgtggtct atgggtatcattccagaaggccatttcggttacgg tagaatgcacttgatgaagatcggtgcctatattac tttattggatgatatttatgatgtctacggtaccttgg aagagttgcaagttctaactgaaatcatcgaacgt tgggacattaatttgttggaccagctgcctgagta catgcaaatcttcttttttatacatgttcaattccacaa acgaattagcttatgagatacttagagatcaagga attaatgttatctctaacctcaaagggttgtgggtc gaattgtcccagtgttatttttaaggaagcaacctgg tttcataacggttacactccaactacagaggaata cttgaacgttgcttgtattagtgcatctggtccagtg atccttttctccggttatttcaccacgactaacccga ttaataagcatgaattacaaagtttagaaagacac gctcattcactaagcatgattctgagattggctgac gaccttgggacctcatctgatgaaatgaaacggg gcgatgtgccaaaggccatccagtgctttatgaat gacactggttgttgtgaagaagaggcaagacaa cacgtcaaaagactcatagacgctgaatggaag aagatgaacaaggacatcttgatggaaaaaccct ttaagaacttctgtccaactgctatgaatttaggtag gataagcatgtccttttacgagcacggtgatggtt acggtggtccacactctgataccaaaaaaaagat ggttagcttgttcgttcaacctatgaacattaccatc taa(서열번호 105)
WenA ngSQT	*웬들란디아*	A0A068VE40	46%	ASTEIAVPLNNQHESVR QLADFPENIWADRVAS	atggcctcaacagaaatcgcagttcctttgaataa ccagcacgagtccgtccgtcaattagctgacttcc

[0171]

S738	*안구스티폴리아*			FTLDKQGHDMCAKEIEMLKEEVMSMLLEEKPMMEKFNLIDNIERLGISYHFGDKIEDQLQEYYDACTNFEKHAECDLSIAALQFRLFRQHGFNISCGIFDGFLDANGKFKESLCNDIKGLLSLYEAAHVRTHGDKILEEALFFTTTHLTREIPNVGSTLAKQVKYALEQPLHKGIPRYEAWRYISIYEEDESSNKLLLRLAKLDYHLSQMLNKQDLCEIIRWGKELDIISKVPYARDRIVECYFWAVATYYEPQYSLARMTLTKATVFAGMIDDTYDAYGTLDELKIFTEAVERWDSSGIDQLSDYMKAAYTLVLNFNKEVGEDLAKKQRTYAFDKYIEEWKQYARTSFTQSKWFLTNELPSFSDYLSNGMVTSTYYLLSAAAFLDMDSASEDVINWMSTNPKLFVALTTHARLANDVGSHKFEKERGSGTAIECYMKDYHVSEEEAMKKFEEMCDDAWKVMNEECLRSTTIPREILKVILNLARTCEVVYKHRGDGFTDQRRIEAHINAMLMDSVSI(서열번호 40)	cagaaaacatttgggctgatagagttgcttctttta ccttggataagcaaggtcatgacatgtgtgctaaa gaaatagaaatgttaaaggaagaagtcatgtctat gttgttggaggaaaagccaatgatggaaaaattc aacttgatcgataatattgaaagattaggcatctcc taccacttcggtgacaagattgaagatcaattaca agaatattacgacgcctgcactaactttgagaagc atgctgaatgtgatttgtcaatagctgccttgcaatt cagattgtttagacaacacggtttcaatatttcttgt ggtatctttgacggtttcttggatgcaaacggtaaa ttcaaggaatctttatgtaatgacattaagggtttgtt gtccttatacgaagccgctcatgttagaactcacg gtgataaaatttggaggaagctttgttttttaccact actcatttgacccgtgaaatcccaaacgttggttct actttggctaagcaggtcaaatatgctttagagca accattgcacaagggtatcccaagatacgaagcc tggagatatatttcaatttacgaagaagacgaatct tccaacaagttgttattacgtttggcaaagttggatt accatttgtcccaaatgttgaacaaacaggacttgt gcgagatcattagatggggtaaggaattagacatt atttctaaggttccttatgctagagatagaatcgtc gaatgttacttctgggctgttgccacatattacgaa ccacaatactccttggctagaatgacattgaccaa agctactgtttttgctggtatgatcgatgatacctat gacgcttacggtactttagatgagttgaagatattc actgaagcagtcgaacgttgggactcttccggtat tgaccaattgtcagattacatgaaagcagcttaca ccttagtcttaaattttaacaaggaagttggtgaag atttagccaagaaacaaagaacttacgccttcgac aagtacatcgaagaatggaagcaatatgctagaa cctctttcacccaatctaagtggttcttgaccaatg agttgccatccttttctgattatttgtctaacggtatg gttacttcaacatactacttattgtctgccgctgcctt cttggacatggattccgcttctgaagacgtcataa attggatgtctaccaaccctaaattgttcgtcgcttt gacaactcacgctagattggccaacgacgttggt tctcataaatttgaaaaggaaagaggttcaggtac cgcaatagaatgttatatgaaggattaccacgtttc tgaggaagaagctatgaagaaattcgaggaaat gtgtgacgatgcttggaaggtcatgaacgaagaa tgcttgcgttccactacaatcccaagagagattttg aaggttattttgaacttggcaagaacttgtgaagtc gtttacaagcatcgtggtgatggcttcaccgatca aagaagaattgaagctcacatcaacgccatgtta atggactccgtttccatctaa(서열번호 106)
WenA ngSQT S760	*웬들란디아 안구스티폴리아*	A0A068VE40	43%	ASTEIAVPLNNQHESVRQLADFPENIWADRVASFTLDKQGHDMCAKEIEMLKEEVMSMLLEEKPMMEKFNLIDNIERLGIS	atggcctcaacagaaatcgcagttcctttgaataa ccagcacgagtccgtccgtcaattagctgacttcc cagaaaacatttgggctgatagagttgcttctttta ccttggataagcaaggtcatgacatgtgtgctaaa gaaatagaaatgttaaaggaagaagtcatgtctat

[0172]

				YHFGDKIEDQLQEYYD ACTNFEKHAECDLSIAA LQFRLFRQHGFNISCGIF DGFLDANGKFKESLCN DIKGLLSLYEAAHVRT HGDKILEEALFFTTTHL TREIPNVGSTLAKQVKH ALEQPLHRGIPRYEAYC FISIYEEDESNNKLLLRL AKLDYHLLQMSYKREL SEIIRWGKELDIISKVPY ARDRIVECYFWAVATY YEPQYSLARMTLTKAT VFAGMIDDTYDAYGTL DELKIFTEAVERWDSSG IDQLSDYMKAAYTLVL NFNKEVGEDLAKKQRT YAFDKYIEEWKQYART SFTQSKWFLTNELPSFS DYLSNGMVTSTYYLLS AATFLGMDGASEDVIN WMSTNPKLFVALTTHA RLANDVGSHKFEKERG SGTAIECYMKDYHVSE EEAMKKFEEMCDDAW KVMNEECLRSTTIPREI LKVILNLARTCEVVYK HRGDGFTDQRRIEAHIN AMLMDSVSI(서열번호 41)	gttgttggaggaaaagccaatgatggaaaaattc aacttgatcgataatattgaaagattaggcatctcc taccacttcggtgacaagattgaagatcaattaca agaatattacgacgcctgcactaactttgagaagc atgctgaatgtgatttgtcaatagctgccttgcaatt cagattgtttagacaacacggtttcaatatttcttgt ggtatctttgacggtttcttggatgcaaacggtaaa ttcaaggaatctttatgtaatgacattaagggtttgtt gtccttatacgaagccgctcatgttagaactcacg gtgataaaatttggaggaagctttgttttttaccact actcatttgacccgtgaaatcccaaacgttggttct actttggctaagcaggtcaaacacgctttagagca accattgcacagaggtatcccaagatatgaagcc tactgcttcatttcaatttatgaagaagacgaatcta acaacaagttgttattacgtttggcaaagttggatt accatttgttgcaaatgtcctacaaaagagaattgt ccgagatcattagatggggtaaggaattagacatt atttctaaggttccttatgctagagatagaatcgtc gaatgttacttttgggctgttgccacatattacgag ccacaatactccttggctagaatgacattgaccaa agctactgttttcgctggtatgatcgatgatacctat gacgcttacggtactttagacgaattgaagatattc actgaagcagtcgaacgttgggattcttccggtat tgaccaattgtcagattacatgaaagcagcttaca ccttagtcttaaattttaacaaggaagttggtgagg atttagccaagaaacaaagaacttacgccttcgac aagtacatcgaagaatggaagcaatatgctagaa cctctttcacccaatctaagtggttcttgaccaatg aattgccatcctttttctgattatttgtctaacggtatg gttacttcaacatactacttattgtctgccgctacatt cttgggtatggacggtgcttctgaagacgtcataa attggatgtctactaaccctaaattgttcgtcgctttt gacaacccatgctagattggccaacgacgttggt tctcacaagtttgaaaaggaaagaggctccggta ctgcaatagaatgttatatgaaagattaccacgttt ctgaggaggaagctatgaagaaattcgaagaaat gtgtgacgatgcctggaaggtcatgaacgaaga atgcttgcgttctactaccatcccaagagagatttt gaaggttattttgaacttggccagaacctgtgaag tcgtttacaagcatcgtggtgatggtttcactgatc agagaagaattgaagctcacatcaacgctatgtta atggactccgtttccatctaa(서열번호 107)
WenA ngSQT S780	*웬들란디아 안구스티폴리아*	A0A068V E40	41%	ASTEIAVPLNNQHESVR QLADFPENIWADRVAS FTLDKQGHDMCAKEIE MLKEEVMSMLLEEKP MMEKFNLIDNIERLGIS YHFGDKIEDQLQEYYD ACTNFEKHAECDLSIAA LQFRLFRQHGFNISCGIF	atggcctcaacagaaatcgcagttcctttgaataa ccagcacgagtccgtccgtcaattagctgacttcc cagaaaacatttgggctgatagagttgcttctttta ccttggataagcaaggtcatgacatgtgtgctaaa gaaatagaaatgttaaaggaagaagtcatgtctat gttgttggaggaaaagccaatgatggaaaaattc aacttgatcgataatattgaaagattaggcatctcc taccacttcggtgacaagattgaagatcaattaca

[0173]

				DGFLDANGKFKESLCN DIKGLLSLYEAAHVRT HGDKILEEALFFTTTHL TREIPNVGSTLAKQVKH ALEQPLHRGIPRYEAYC FISMYEEDESSNKLLLR LAKLDYHLSQMLNKQ DLCEIIRWGKELDIISKV PYARDRIVECYFWAVA TYYEPQYSLARMTLTK ATVFAGMIDDTYDAYG TLDELKIFTEAVERWDS SGIDQLSDYMKAAYTL VLNFNKEVGEDLAKKQ RTYAFDKYIEEWKQYA RTSFTQSKWFLTNELPS FSDYLSNGMVTSTYYL LSAATFLGMDGASEDV INWMSTNPKLFVALTT HARLANDVGSHKFEKE RGSGTAIECYMKDYHV SEEEAMKKFEEMCDDA WKVMNEECLRSTTIPR EILKVILNLARTCEVVY KHRGDGFTDQRRIEAHI NAMLMDSVSI(서열번호 42)	agaatattacgacgcctgcactaactttgagaagc atgctgaatgtgatttgtcaatagctgccttgcaatt cagattgtttagacaacacggtttcaatatttcttgt ggtatctttgacggtttcttggatgcaaacggtaaa ttcaaggaatctttatgtaatgacattaagggtttgtt gtccttatacgaagccgctcatgttagaactcacg gtgataaaattttggaggaagctttgttttttaccact actcatttgacccgtgaaatcccaaacgttggttct actttggctaagcaggtcaaacacgctttagagca accattgcacagaggtatcccaagatatgaagcc tactgcttcatttcaatgtatgaagaagacgaatctt ccaacaagttgttattacgtttggcaaagttggatt accatttgtcccaaatgttgaacaaacaggacttgt gtgagatcattagatggggtaaggaattagacatt atttctaaggttccttatgctagagatagaattgtcg aatgttacttttgggctgttgccacatactacgaac cacaatattccttggctagaatgacattgaccaaa gctactgttttcgctggtatgatcgatgatacctatg acgcttacggtactttagatgagttgaagatattca ctgaagcagtcgaacgttgggactcttccggtatt gaccaattgtcagattacatgaaagcagcttacac cttagtcttaaattttaacaaggaagttggtgaaga tttagccaagaaacaaagaacttacgccttcgaca agtacatcgaagaatggaagcaatatgctagaac ctctttcacccaatctaagtggttcttgaccaatga gttgccatccttttctgattatttgtctaacggtatgg ttacttcaacatactacttattgtctgccgctacattc ttgggtatggacggtgcttctgaagatgtcataaat tggatgtctactaaccctaaattgttcgtcgctttga caacccatgctagattggccaacgacgttggttct cacaagtttgaaaaggaaagaggctccggtactg caatagaatgctatatgaaagattaccacgtttctg aggaagaagctatgaagaaattcgaggaaatgt gtgacgatgcctggaaggtcatgaacgaagaat gtttgcgttctactaccatcccaagagagattttga aggttattttgaacttggccagaacctgtgaagtc gtttacaagcatcgtggtgatggtttcactgaccaa agaagaatcgaagctcacattaacgctatgttaat ggactccgtttccatctaa(서열번호 108)
WenA ngSQT S793	*웬들란디아 안구스티폴리아*	A0A068U HT0	75%	ASAQASLPSNNRQETV RPLADFPENIWADRIAP FTLDKQEYEMCQREIE MLKAEVASMLLATGKT MMQRFDFIDKIERLGVS HHFDIEIENQLQEFFNV YTNLGEYSAYDLSSAA LQFRLFRQHGFNISCGIF DQFIDAKGKFKESLCN DIRGLLSLYEAAHVRTH GDKILEEALAFTTTHMT SGGPHLDSSLAKQVKY ALEQPLHKGILRYEAW	atggcctcagcacaagcttccttaccttctaataac agacaggaaacagtccgtccattggctgacttcc cagagaacatctgggctgatagaattgccccatttt accttggataagcaagaatacgaaatgtgtcaaa gagaaatagagatgttaaaagctgaagttgcttct atgttgttggcaactggtaagactatgatgcaaag attcgacttcattgataagatcgaaagattggggg tctcccaccattttgacattgaaatcgaaaatcaatt gcaagagtttttcaacgtttataccaacttaggtga atactctgcctatgatttgtcatctgctgccttgcag ttccgtttatttagacaacacggtttcaatatttcctg cggtattttcgaccaatttatcgacgctaaaggtaa

[0174]

				RYISIYEEDESNNKLLL RLAKLDYHLLQMSYKQ ELCEITRWGKGLESVSN FPYARDRFVECYFWAV GTLYEPQYSLARMTFA KVAALITMIDDIYDAYG TLDELQILTDSAERWD GSGVDQLSDYIRASYN TLLKFNKEVGEDLAKK QRTYAFDKYIEDWKQY MRTSFTQSKWFLTNEL PSFADYISNGAITIGAYL IASAGFLDMDSALEDVI NWMSTNPKLMVAYST HSRLINDYGGHKFDKE RGSVTALDCYMKDYSV SEEEAAKKFREMCEDN WKVMNEECLRPTTIPR DGLKMLLNIARVGETV YKHRIDGFTQPHAIEEH IRAMLVDFMSI(서열번호 43)	gttcaaggaatctttatgtaacgatatcagaggttt gttgtctttgtacgaagctgctcatgttagaactca cggtgataaaattttggaagaagctttagctttcac cactactcacatgacctccggtggtccacatttag attcttcattggccaagcaagttaaatacgcattgg aacagccattgcataagggtatattgagatatgaa gcttggagatacatatctatctacgaagaggacg aatccaacaataagttattattgcgtttggctaagtt ggactatcacttgttacaaatgtcatacaagcaag agttgtgtgaaattacaagatggggtaaaggtttg gaatctgtctccaacttttccttatgcccgtgacaga ttcgttgaatgttacttttgggctgtcggtactttgta cgaaccacaatactcattggctagaatgaccttcg ctaaggttgctgctttaattactatgatcgatgatatt tatgatgcctacggtaccttggacgaattgcaaat attaactgactctgccgaaagatgggatggttccg gtgtcgatcagttgtctgactatattagagcttccta taatacattattgaaatttaataaggaggttggtga agatttggcaaaaaagcaacgtacctacgctttcg acaagtacatcgaagattggaaacaatacatgag aacctctttcactcaatcaaagtggtttttgactaac gagttgccatctttcgctgattacatttccaacggt gccatcacaatcggtgcatatttaattgcctctgcc ggtttttttggatatggattccgccttggaagacgtt attaactggatgtctaccaacccaaaattaatggtc gcttattccacccactcaagattgatcaatgattac ggtggtcacaagttcgacaaggaaagagggtca gttactgctttggattgctacatgaaggattactcc gtctctgaggaagaagctgcaaagaagttcaga gaaatgtgtgaagacaactggaaggttatgaatg aagaatgtttgagacctactacaattccaagagat ggtttgaagatgttgttaaacattgctagagtcggt gaaactgtttacaaacatagaatcgacggttttact caacctcatgcaatcgaggagcacattagagcca tgttagttgacttcatgtctatttaa(서열번호 109)
WenA ngSQT S805	*웬들란디아 안구스티폴리아*	A0A068V E40	42%	ASTEIAVPLNNQHESVR QLADFPENIWADRVAS FTLDKQGHDMCAKEIE MLKEEVMSMLLEEKP MMEKFNLIDNIERLGIS YHFGDKIEDQLQEYYD ACTNFEKHAECDLSIAA LQFRLFRQHGFNISCGIF DGFLDANGKFKESLCN DIKGLLSLYEAAHVRT HGDKILEEALFFTTTHL TREIPNVGSTLAKQVKY ALEQPLHKGIPRYEAW RYISIYEEDESNNKLLL RLAKLDYHLLQMSYKR ELSEIIRWGKELDIISKV	atggcctcaacagaaatcgcagttcctttgaataa ccagcacgagtccgtccgtcaattagctgacttcc cagaaaacatttgggctgatagagttgcttctttta ccttggataagcaaggtcatgacatgtgtgctaaa gaaatagaaatgttaaaggaagaagtcatgtctat gttgttggaggaaaagccaatgatggaaaaattc aacttgatcgataatattgaaagattaggcatctcc taccacttcggtgacaagattgaagatcaattaca agaatattacgacgcctgcactaactttgagaagc atgctgaatgtgatttgtcaatagctgccttgcaatt cagattgtttagacaacacggtttcaatatttcttgt ggtatctttgacggtttcttggatgcaaacggtaaa ttcaaggaatctttatgtaatgacattaagggtttgtt gtccttatacgaagccgctcatgttagaactcacg gtgataaaattttggaggaagctttgtttttaccact

[0175]

				PYARDRIVECYFWAVA TYYEPQYSLARMTLTK ATVFAGMIDDTYDAYG TLDELKIFTEAVERWDS SGIDQLSDYMKAAYTL VLNFNKEVGEDLAKKQ RTYAFDKYIEEWKQYA RTSFTQSKWFLTNELPS FSDYLSNGMVTSTYYL LSAATFLGMDGASEDV INWMSTNPKLFVALTT HARLANDVGSHKFEKE RGSSTAIECYMKDYHV SEEEAMEKFEEMCDDA WKVMNEECLRSTTIPR EILKVILNLARTCEVVY KHRGDGFTDQRRIEAHI NAMLMDSVSI(서열번호 44)	actcatttgacccgtgaaatcccaaacgttggttct actttggctaagcaggtcaaatatgctttagagca accattgcacaagggtatcccaagatacgaagcc tggagatatatttcaatttacgaagaagacgaatct aacaacaagttgttattacgtttggcaaagttggat taccatttgttgcaaaatgtcctacaaaagagaattg tccgagatcattagatggggtaaggaattagacat tatttctaaggttccttatgctagagatagaatcgtc gaatgttatttctgggctgttgccacatactacgag ccacaatactccttggctagaatgacattgaccaa agctactgtttttgctggtatgatcgatgatacctat gacgcttacggtactttagacgaatttgaagatattc actgaagcagtcgaacgttgggattcttccggtat tgaccaattgtcagattacatgaaagcagcttaca ccttagtcttaaattttaacaaggaagttggtgagg atttagccaagaaacaaagaacttacgccttcgac aagtacatcgaagaatggaagcaatatgctagaa cctctttcacccaatctaagtggttcttgaccaatg aattgccatccttttctgattatttgtctaacggtatg gttacttcaacatactacttattgtctgccgctacatt cttgggtatggacggtgcttctgaagacgtcataa attggatgtctactaaccctaaattgttcgtcgcttt gacaacccacgctagattggccaacgacgttggt tctcataaatttgaaaaggaaagaggctcctccac tgcaatagaatgctatatgaaggattaccacgtttc tgaggaggaagctatggaaaaattcgaagaaat gtgtgacgatgcctggaaggtcatgaacgaaga atgcttgcgttccactaccatcccaagagagatttt gaaggttattttgaacttggccagaacctgtgaag tcgtttacaagcatcgtggtgatggtttcactgatc agagaagaattgaagctcacatcaacgctatgtta atggactcagtttccatctaa(서열번호 110)
WenA ngSQT S826	*웬들란디아 안구스티폴리아*	A0A068V E40	47%	ASTEIAVPLNNQHESVR QLADFPENIWADRVAS FTLDKQGHDMCAKEIE MLKEEVMSMLLEEKP MMEKFNLIDNIERLGIS YHFGDKIEDQLQEYYD ACTNFEKHAECDLSIAA LQFRLFRQHGFNISCGIF DGFLDANGKFKESLCN DIKGLLSLYEAAHVRT HGDKILEEALFFTTTHL TREIPNVGSTLAKQVKY ALEQPLHKGIPRYEAW RYISIYEEDESNNKLLL RLAKLDYHLLQMSYKR ELSEIIRWGKELDIISKV PYARDRIVECYFWAVA TYYEPQYSLARMTLTK ATVFAGMIDDTYDAYG	atggcctcaacagaaatcgcagttcctttgaataa ccagcacgagtccgtccgtcaattagctgacttcc cagaaaacatttgggctgatagagttgcttctttta ccttggataagcaaggtcatgacatgtgtgctaaa gaaatagaaatgttaaaggaagaagtcatgtctat gttgttggaggaaaagccaatgatggaaaaattc aacttgatcgataatattgaaagattaggcatctcc taccacttcggtgacaagattgaagatcaattaca agaatattacgacgcctgcactaactttgagaagc atgctgaatgtgatttgtcaatagctgccttgcaatt cagattgtttagacaacacggtttcaatatttcttgt ggtatctttgacggtttcttggatgcaaacggtaaa ttcaaggaatctttatgtaatgacattaagggtttgtt gtccttatacgaagccgctcatgttagaactcacg gtgataaaatttggaggaagctttgttttttaccact actcatttgacccgtgaaatcccaaacgttggttct actttggctaagcaggtcaaatatgctttagagca accattgcacaagggtatcccaagatacgaagcc

[0176]

				TLDELKIFTEAVERWDS SGIDQLSDYMKAAYTL VLNFNKEVGEDLAKKQ RTYAFDKYIEEWKQYA RTSFTQSKWFLTNELPS FADYLSNGMVTSTYYL LSAAALLDMDSALEDV INWMSTNPKFFVALTT HARLTNDVGSHKFEKE RGSGTAIECYMKDYHV SEEEAMKKFEEMCDDA WKVMNEECLRSTTIPR EILKVILNLARTCEVVY KHRGDGFTDQRRIEAHI NAMLMDSVSI(서열번호 45)	tggagatatatttcaatttacgaagaagacgaatct aacaacaagttgttattacgtttggcaaagttggat taccatttgttgcaaatgtcctacaaaagagaattg tccgagatcattagatggggtaaggaattagacat tatttctaaggttccttatgctagagatagaatcgtc gaatgttatttctgggctgttgccacatactacgag ccacaatactccttggctagaatgacattgaccaa agctactgtttttgctggtatgatcgatgatacctat gacgcttacggtactttagacgaattgaagatattc actgaagcagtcgaacgttgggattcttccggtat tgaccaattgtcagattacatgaaagcagcttaca ccttagtcttaaattttaacaaggaagttggtgagg atttagccaagaaacaaagaacttacgccttcgac aagtacatcgaagaatggaagcaatatgctagaaa cctctttcacccaatctaagtggttcttgaccaatg aattgccatcctttgcagattatttgtctaacggtat ggttacttcaacatactacttattgtctgctgctgcc ttgttggacatggactccgctttagaagatgtcata aattggatgtctaccaaccctaaattcttcgtcgctt tgacaactcacgctagattgaccaacgacgttggt tctcataaatttgaaaaggaaagaggttccggtac tgcaatagaatgctatatgaaggattaccacgtttc tgaggaggaagctatgaagaaattcgaagaaat gtgtgacgatgcctggaaggtcatgaacgaaga atgcttgcgttctactacaatcccaagagagatttt gaaggttattttgaacttggccagaacctgtgaag tcgtttacaagcatcgtggtgatggcttcactgacc agagaagaattgaagctcacatcaacgccatgtt aatggactccgtttccatctaa(서열번호 111)
WenA ngSQT S829	*웬들란디아 안구스티폴리아*	A0A068U HT0	74%	ASAQASLPSNNRQETV RPLADFPENIWADRIAP FTLDKQEYEMCQREIE MLKAEVASMLLATGKT MMQRFDFIDKIERLGVS HHFDIEIENQLQEFFNV YTNLGEYSAYDLSSAA LQFRLFRQHGFNISCGIF DQFIDAKGKFKESLCN DIRGLLSLYEAAHVRTH GDKILEEALAFTTTHMT SGGPHLDSSLAKQVKY ALEQPLHKGILRYEAW RYISIYEEDESNNKLLL RLAKLDYHLLQMSYKQ ELCEITRWGKGLESVSN FPYARDRFVECYFWAV GTLYEPQYSLARMTFA KVAALITMIDDIYDAYG TLDELQILTDSAERWD GSGVDQLSDYIRASYN TLLKFNKEVGEDLAKK QRTYAFDKYIEDWKQY	atggccagtgcgcaagcatcattaccttccaataa cagacaggaaacagtccgtcccctagctgacttc ccagagaacatctgggctgataggattgctccatt taccctggataagcaagaatacgaaatgtgtcaa agagaaatagagatgttgaaagctgaagtggcct ctatgttgcttgccactggaaagactatgatgcaa cgattcgacttcattgataagatcgaaagattggg cgtatcgcaccattttgacattgaaatcgaaaatca actccaagagtttttcaacgtttataccaacttgggt gaatacagcgcgtatgatctgtcatctgctgcattg cagttcagattatttagacaacacggtttcaatattt cctgcggtattttcgaccaatttatcgacgctaaag gtaagttcaaggaatctttatgtaacgatatccggg gtttgttgtctctctacgaagctgctcatgttagaac gcacggtgataaaatttttggaagaagcattggctt ttactactacccatatgacttccggtggtccacacc tagactctagcttggctaagcaagtcaagtacgc gcttgagcaaccattacacaagggattttgagat acgaagcttggcgttatatatccatctacgaagaa gacgaatctaataacaaacttctgttaagattggct aaactcgattatcatttgcttcaaatgtcctacaagc

[0177]

				MRTSFTQSKWFLTNEL PSFADYISNGAITIGAYL IASAGFLDMDSALEDVI NWMSTNPKLMVAYST HSRLINDYGGHKFDKE RGTGTAIECYMKDHNIS EEEAAKKFREMIENTW KVMNEECLRPIPIPRDT LKMLLNIARVGETVYK HRIDGFTQPHAIEEHIRA MLVDFMSI(서열번호 46)	aggaattatgtgaaatcacgagatggggcaagg gtttagagtcagtttctaatttcccttacgctagaga tcgttttgttgaatgttatttctgggccgtaggaaca ttgtacgaaccgcaatacagtctagccagaatga cctttgctaaagttgctgccttgattactatgattga cgatatctacgatgcctatggtaccttggacgagtt acaaatattgaccgattctgctgaaagatgggatg gttcgggagtcgaccaattgtctgactatatacgc gctagttataacactttgttgaagttcaacaaggaa gtcggtgaggatttagccaaaaagcaaagaacgt acgcatttgacaaatacatcgaagattggaagca atacatgagaacttctttcacccagtccaagtggtt cctgaccaacgaactcccttccttcgctgactaca tttccaatggggctattacaattggtgcttacttgat cgccagcgcgggttttttggatatggattctgccct agaagacgttattaactggatgtctactaacccaa aattgatggtggcttattcaactcacagcagactta tcaatgattatggtggtcacaagttcgacaaggaa agagggacgggtacagctattgaatgctacatga aggatcataacatctctgaggaagaagctgcaaa gaagttcagagaaatgatcgagaacacttggaag gttatgaatgaagaatgtctacggccaattccaatt ccaagagatactctcaagatgctattgaacattgct agggtcggtgaaactgtttacaaacacagaatcg acggttttacccaaccacatgcaatcgaggaaca catcagggccatgttggtcgacttcatgtcaatttta a(서열번호 112)
WenA ngSQT S843	*웬들란디아 안구스티폴리아*	A0A068V E40	45%	ASTEIAVPLNNQHESVR QLADFPENIWADRVAS FTLDKQGHDMCAKEIE MLKEEVMSMLLEEKP MMEKFNLIDNIERLGIS YHFGDKIEDQLQEYYD ACTNFEKHAECDLSIAA LQFRLFRQHGFNISCGIF DGFLDANGKFKESLCN DIKGLLSLYEAAHVRT HGDKILEEALFFTTTHL TREIPNVGSTLAKQVKH ALEQPLHRGIPRYEAYC FISIYEEDESNNKLLLRL AKLDYHLLQMSYKREL SEIIRWGKELDIISKVPY ARDRIVECYFWAVATY YEPQYSLARMTLTKAT VFAGMIDDTYDAYGTL DELKIFTEAVERWDSSG IDQLSDYMKAAYTLVL NFNKEVGEDLAKKQRT YAFDKYIEEWKQYART SFTQSKWFLTNELPSFS DYLSNGMVTSTYYLLS AAAFLDMDSASEDVIN	atggcctcaacagaaatcgcagttcctttgaataa ccagcacgagtccgtccgtcaattagctgacttcc cagaaaacatttgggctgatagagttgcttctttta ccttggataagcaaggtcatgacatgtgtgctaaa gaaatagaaatgttaaaggaagaagtcatgtctat gttgttggaggaaaagccaatgatggaaaaattc aacttgatcgataatattgaaagattaggcatctcc taccacttcggtgacaagattgaagatcaattaca agaatattacgacgcctgcactaactttgagaagc atgctgaatgtgatttgtcaatagctgccttgcaatt cagattgtttagacaacacggtttcaatatttcttgt ggtatctttgacggtttcttggatgcaaacggtaaa ttcaaggaatctttatgtaatgacattaagggtttgtt gtccttatacgaagccgctcatgttagaactcacg gtgataaaatttggaggaagctttgtttttttaccact actcatttgacccgtgaaatcccaaacgttggttct actttggctaagcaggtcaaacacgctttagagca accattgcacagaggtatcccaagatatgaagcc tactgcttcatttcaatttatgaagaagacgaatcta acaacaagttgttattacgtttggcaaagttggatt accatttgttgcaaatgtcctacaaaagagaattgt ccgagatcattagatggggtaaggaattagacatt atttctaaggttccttatgctagagatagaatcgtc gaatgttacttttgggctgttgccacatattacgag

[0178]

				WMSTNPKLFVALTTHARLANDVGSHKFEKERGSGTAIECYMKDYNVSEEEALKKFEEMCEDTWKVMNEECLRSTTIPREILKVILNLARTCEVVYKHRGDGFTDQRRIEAHINAMLMDSVSI(서열번호 47)	ccacaatactccttggctagaatgacattgaccaaagctactgttttcgctggtatgatcgatgatacctatgacgcttacggtactttagacgaattgaagatattcactgaagcagtcgaacgttgggattcttccggtattgaccaattgtcagattacatgaaagcagcttacaccttagtcttaaattttaacaaggaagttggtgaggatttagccaagaaacaaagaacttacgccttcgacaagtacatcgaagaatggaagcaatatgctagaacctctttcacccaatctaagtggttcttgaccaatgaattgccatccttttctgattatttgtctaacggtatggttacttcaacatactacttattgtctgccgctgccttcttggacatggactccgcttctgaagatgtcataaattggatgtctaccaaccctaaattgttcgtcgctttgacaactcatgctagattggccaacgacgttggttctcacaagtttgaaaaggaaagaggttcaggtaccgcaatagaatgttatatgaaagattacaacgtttctgaggaggaagctttgaagaaattcgaagaaatgtgtgaagatacttggaaggtcatgaacgaagaatgcttgcgttccactacaatcccaagagagattttgaaggttattttgaacttggccagaacctgtgaagtcgtttacaagcatcgtggtgacggcttcactgatcagagaagaattgaagctcacatcaatgctatgttaatggactccgtttccatctaa(서열번호 113)
WenAngSQTS848	*웬들란디아 안구스티폴리아*	A0A068UHT0	84%	ASAQASLPSNNRQETVRPLADFPENIWADRIAPFTLDKQEYEMCQREIEMLKAEVASMLLATGKTMMQRFDFIDKIERLGVSHHFDIEIENQLQEFFNVYTNLGEYSAYDLSSAALQFRLFRQHGFNISCGIFDQFIDAKGKFKESLCNDIRGLLSLYEAAHVRTHGDKILEEALAFTTTHMTSGGPHLDSSLAKQVKYALEQPLHKGILRYEAWRYISIYEEDESNNKLLLRLAKLDYHLLQMSYKQELCEITRWGKGLESVSNFPYARDRFVECYFWAVGTLYEPQYSLARMTFAKVAALITMIDDIYDAYGTLDELQILTDSAERWDGSGVDQLSDYIRASYNTLLKFNKEVGEDLAKKQRTYAFDKYIEDWKQYMRTNFSQSRWFFTKELPSFADYINNGAITIGAYLVASAAFLYMDSAKEDVINWMSTNPKLVVAYSTHSRLINDFGGHKFDKERGSGTALECYMKDYNVSEEEAANKFREMMEDattaactgactctgccgaaagatgggatggttccg	

[0179]

				AWKVMNEDCLRPTSIP RDVSKVLLNVARAGEI VYKHRIDGFTEPHIIKD HIRATLVDFMAIN(서열 번호 48)	gtgtcgatcagttgtctgactatattagagcttccta taatacattattgaaatttaataaggaggttggtga agatttggcaaaaaagcaacgtacctacgctttcg acaagtacatcgaagattggaaacaatacatgag aaccaacttctctcaatcaagatggtttttcactaag gagttgccatctttcgctgattacattaacaacggt gccatcacaatcggtgcatatttggttgcctctgct gctttcttatatatggactccgcaaaagaagatgtt atcaactggatgtccacaaaccctaagttggtcgt tgcttactccactcactctcgtttaattaatgactttg gtggtcacaagttcgacaaggagagaggttccg gtactgctttggaatgctacatgaaggactacaat gtctctgaagaagaagccgcaaacaagtttagag aaatgatggaggacgcttggaaggttatgaatga agactgtttaagaccaacttccatccctagagatgt ctccaaggttttgttaaacgtcgccagagctggtg aaattgtttacaagcatagaatcgatggttttaccg aaccacatatcattaaagatcacataagagccac cttggttgatttcatggctattaattaa(서열번 호 114)
WenA ngSQT S849	*웬들란디아 안구스티폴리아*	A0A068U HT0	75%	ASAQASLPSNNRQETV RPLADFPENIWADRIAP FTLDKQEYEMCQREIE MLKAEVASMLLATGKT MMQRFDFIDKIERLGVS HHFDIEIENQLQEFFNV YTNLGEYSAYDLSSAA LQFRLFRQHGFNISCGIF DQFIDAKGKFKESLCN DIRGLLSLYEAAHVRTH GDKILEEALAFTTTHMT SGGPHLDSSLAKQVKY ALEQPLHKGILRYEAW RYISIYEEDESNNKLLL RLAKLDYHLLQMSYKQ ELCEITRWGKGLESVSN FPYARDRFVECYFWAV GTLYEPQYSLARMTFA KVAALITMIDDIYDAYG TLDELQILTDSAERWD GSGVDQLSDYIRASYN TLLKFNKEVGEDLAKK QRTYAFDKYIEDWKQY MRTSFTQSKWFLTNEL PSFADYISNGAITIGAYL IASAGFLDMDSALEDVI NWMSTNPKLMVAYST HSRLINDYGGHKFDKE RGSVTALDCYMKDYSV SEEEAAKKFREMIENT WKVMNEECLRPIPIPRD TLKMLLNIARVGETVY KHRIDGFTEPHIIKDHIR	atggccagtgcgcaagcatcattaccttccaataa cagacaggaaacagtccgtcccctagctgacttc ccagagaacatctgggctgataggattgctccatt taccctggataagcaagaatacgaaatgtgtcaa agagaaatagagatgttgaaagctgaagtggcct ctatgttgcttgccactggaaagactatgatgcaa cgattcgacttcattgataagatcgaaagattggg cgtatcgcaccatttgacattgaaatcgaaaatca actccaagagtttttcaacgtttataccaacttgggt gaatacagcgcgtatgatctgtcatctgctgcattg cagttcagattatttagacaacacggtttcaatattt cctgcggtattttcgaccaatttatcgacgctaaag gtaagttcaaggaatctttatgtaacgatatccggg gtttgttgtctctctacgaagctgctcatgttagaac gcacggtgataaaatttggaagaagcattggctt ttactactacccatatgacttccggtggtccacacc tagactctagcttggctaagcaagtcaagtacgc gcttgagcaaccattacacaagggattttgagat acgaagcttggcgttatatatccatctacgaagaa gacgaatctaataacaaacttctgttaagattggct aaactcgattatcatttgcttcaaatgtcctacaagc aggaattatgtgaaatcacgagatggggcaagg gtttagagtcagtttctaatttcccttacgctagaga tcgttttgttgaatgttatttctgggccgtaggaaca ttgtacgaaccgcaatacagtctagccagaatga cctttgctaaagttgctgccttgattactatgattga cgatatctacgatgcctatggtaccttggacgagtt acaaatattgaccgattctgctgaaagatgggatg gttcgggagtcgaccaattgtctgactatatacgc gctagttataacactttgttgaagttcaacaaggaa gtcggtgaggatttagccaaaaagcaaagaacgt

[0180]

				AMLVDFMAIN(서열번호 49)	acgcatttgacaaatacatcgaagattggaagca atacatgagaacttctttcacccagtccaagtggtt cctgaccaacgaactcccttccttcgctgactaca tttccaatggggctattacaattggtgcttacttgat cgccagcgcgcgggtttttggatatggattctgccct agaagacgttattaactggatgtctactaacccaa aattgatggtggcttattcaactcacagcagactta tcaatgattatggtggtcacaagttcgacaaggaa agagggagcgttacagctttggattgctacatgaa ggattacagtgtctctgaggaagaagctgcaaag aagttcagagaaatgatcgaaaacacctggaag gttatgaatgaagaatgtctgcggccaattccaatt ccaagagatactctaaagatgctattgaacattgct agggtaggtgaaactgtttacaaacatagaatcg acggttttactgaaccacatataattaaggaccac atcagggcaatgttggtcgacttcatggctattaac taa(서열번호 115)
WenA ngSQT S864	*웬들란디아 안구스티폴리아*	A0A068U HT0	81%	ASAQASLPSNNRQETV RPLADFPENIWADRIAP FTLDKQEYEMCQREIE MLKAEVASMLLATGKT MMQRFDFIDKIERLGVS HHFDIEIENQLQEFFNV YTNLGEYSAYDLSSAA LQFRLFRQHGFNISCGIF DQFIDAKGKFKESLCN DIRGLLSLYEAAHVRTH GDKILEEALAFTTTHMT SGGPHLDSSLAKQVKY ALEQPLHKGILRYEAW RYISIYEEDESNNKLLL RLAKLDYHLLQMSYKQ ELCEITRWGKGLESVSN FPYARDRFVECYFWAV GTLYEPQYSLARMTFA KVAALITMIDDIYDAYG TLDELQILTDSAERWD GSGVDQLSDYIRASYN TLLKFNKEVGEDLAKK QRTYAFDKYIEDWKQY MRTNFSQSRWFFTKEL PSFADYINNGAITIGAY LVASAAFLYMDSAKED VINWMSTNPKLVVAYS THSRLINDFGGHKFDKE RGSVTALDCYMKDYSV SEEEAAKKFREMCEDN WKVMNEECLRPTTIPR DGLKMLLNIARVGETV YKHRIDGFTQPHAIEEH IRAMLVDFMSI(서열번호 50)	atggcctcagcacaagcttccttaccttctaataac agacaggaaacagtccgtccattggctgacttcc cagagaacatctgggctgatagaattgccccatttt accttggataagcaagaatacgaaatgtgtcaaa gagaaatagagatgttaaaagctgaagttgcttct atgttgttggcaactggtaagactatgatgcaaag attcgacttcattgataagatcgaaagattgggggg tctcccaccattttgacattgaaatcgaaaatcaatt gcaagagtttttcaacgtttataccaacttaggtga atactctgcctatgatttgtcatctgctgccttgcag ttccgtttatttagacaacacggtttcaatatttcctg cggtattttcgaccaatttatcgacgctaaaggtaa gttcaaggaatctttatgtaacgatatcagaggttt gttgtctttgtacgaagctgctcatgttagaactca cggtgataaaatttggaagaagctttagctttcac cactactcacatgacctccggtggtccacatttag attcttcattggccaagcaagttaaatacgcattgg aacagccattgcataagggtatattgagatatgaa gcttggagatacatatctatctacgaagaggacg aatccaacaataagttattattgcgtttggctaagtt ggactatcacttgttacaaatgtcatacaagcaag agttgtgtgaaattacaagatggggtaaaggtttg gaatctgtctccaactttccttatgcccgtgacaga ttcgttgaatgttacttttgggctgtcggtactttgta cgaaccacaatactcattggctagaatgaccttcg ctaaggttgctgctttaattactatgatcgatgatatt tatgatgcctacggtaccttggacgaattgcaaat attaactgactctgccgaaagatgggatggttccg gtgtcgatcagttgtctgactatattagagcttccta taatacattattgaaatttaataaggaggttggtga agatttggcaaaaaagcaacgtacctacgctttcg acaagtacatcgaagattggaaacaatacatgag aaccaacttctctcaatcaagatggtttttcactaag gagttgccatctttcgctgattacattaacaacggt

[0181]

					gccatcacaatcggtgcatatttggtttgcctctgct gctttcttatatatggactccgcaaaagaagatgtt atcaactggatgtccacaaaccctaagttggtcgt tgcttactccactcactctcgtttaattaatgactttg gtggtcacaagttcgacaaggagagaggttccgt tactgctttggactgctacatgaaggactactctgt ctccgaagaagaagccgcaaagaagtttagaga aatgtgtgaagacaattggaaggtcatgaatgaa gagtgtttaagaccaactaccatccctagagatgg gttgaagatgttgttaaacatagccagagttggtg aaactgtctacaagcatagaattgatggttttaccc aaccacatgctatcgaagaacacatcagagctat gttggttgatttcatgtctatttaa(서열번호 116)
WenA ngSQT S925	*웬들란디아 안구스티폴리아*	A0A068U HT0	80%	ASAQASLPSNNRQETV RPLADFPENIWADRIAP FTLDKQEYEMCQREIE MLKAEVASMLLATGKT MMQRFDFIDKIERLGVS HHFDIEIENQLQEFFNV YTNLGEYSAYDLSSAA LQFRLFRQHGFNISCGIF DQFIDAKGKFKESLCN DIRGLLSLYEAAHVRTH GDKILEEALAFTTTHMT SGGPHLDSSLAKQVKY ALEQPLHKGILRYEAW RYISIYEEDESNNKLLL RLAKLDYHLLQMSYKQ ELCEITRWGKGLESVSN FPYARDRFVECYFWAV GTLYEPQYSLARMTFA KVAALITMIDDIYDAYG TLDELQILTDSAERWD GSGVDQLSDYIRASYN TLLKFNKEVGEDLAKK QRTYAFDKYIEDWKQY MRTNFSQSRWFFTKEL PSFADYINNGAITIGAY LVASAAFLYMDSAKED VINWMSTNPKLVVAYS THSRLINDFGGHKFDKE RGSVTALDCYMKDYSV SEEEAAKKFREMIENT WKVMNEECLRPIPIPRD TLKMLLNIARVGETVY KHRIDGFTEPHIIKDHIR AMLVDFMAIN(서열번호 51)	atggcctcagcacaagcttccttaccttctaataac agacaggaaacagtccgtccattggctgacttcc cagagaacatctgggctgatagaattgccccattt accttggataagcaagaatacgaaatgtgtcaaa gagaaatagagatgttaaaagctgaagttgcttct atgttgttggcaactggtaagactatgatgcaaag attcgacttcattgataagatcgaaagattggggg tctcccaccattttgacattgaaatcgaaaatcaatt gcaagagtttttcaacgtttataccaacttaggtga atactctgcctatgatttgtcatctgctgccttgcag ttccgtttatttagacaacacggtttcaatatttcctg cggtattttcgaccaatttatcgacgctaaaggtaa gttcaaggaatctttatgtaacgatatcagaggttt gttgtctttgtacgaagctgctcatgttagaactca cggtgataaaatttttggaagaagctttagctttcac cactactcacatgacctccggtggtccacatttag attcttcattggccaagcaagttaaatacgcattgg aacagccattgcataagggtatattgagatatgaa gcttggagatacatatctatctacgaagaggacg aatccaacaataagttattattgcgtttggctaagtt ggactatcacttgttacaaatgtcatacaagcaag agttgtgtgaaattacaagatggggtaaaggtttg gaatctgtctccaactttccttatgcccgtgacaga ttcgttgaatgttacttttgggctgtcggtactttgta cgaaccacaatactcattggctagaatgaccttcg ctaaggttgctgctttaattactatgatcgatgatatt tatgatgcctacggtaccttggacgaattgcaaat attaactgactctgccgaaagatgggatggttccg gtgtcgatcagttgtctgactatattagagcttccta taatacattattgaaatttaataaggaggttggtga agatttggcaaaaaagcaacgtacctacgctttcg acaagtacatcgaagattggaaacaatacatgag aaccaacttctctcaatcaagatggtttttcactaag gagttgccatctttcgctgattacattaacaacggt gccatcacaatcggtgcatatttggttgcctctgct gctttcttatatatggactccgcaaaagaagatgtt atcaactggatgtccacaaaccctaagttggtcgt

[0182]

[0183]

					tgcttactccactcactctcgtttaattaatgactttg gtggtcacaagttcgacaaggagagaggttccgt tactgctttggactgctacatgaaggactactctgt ctccgaagaagaagccgcaaagaagtttagaga aatgatcgaaaacacctggaaggtcatgaatgaa gagtgtttaagaccaattccaatccctagagacac attgaagatgttgttaaacatagccagagttggtg aaactgtctacaagcatagaattgatggttttactg aaccacatatcatcaaagatcacatcagagctatg ttggttgatttcatggctattaattaa(서열번호 117)
WenA ngSQT S960	*웬들란디아 안구스티폴리아*	A0A068V I46	81%	YEREIEMLKAEVESML LATGKTMMQRFDFIDK IERLGVSHHFDIEIENQL QEFFNVYTNFGEYSAY DLSSAALQFKQWCDHN RSLSCSITRGLLSLYEA AHVRTHGDKILEEALH LTSGESHLDSTLAKQV KCALEQPLHKGIPRYEA WRYISIYEEDESHNKLL LRLAKLDYHFLQISYRQ DLCEIIRWDSSGVDQLS DYIRAVGEELAKKQRT YAFGTFLGMDGASEDV INWMSTIPKLMFACSTH ARLINDFGGHKFDKER GTGTALECYMKDYNVS EEEAANKFREMMEDA WKVMNEECLRPTTIPR EILKMLLNIVRVGETTN KHRIDGFTQPHAIEEHIR AMLVDFMSV(서열번호 52)	atgtatgagagagaaatcgaaatgttaaaggctg aagtcgaatctatgttgttggccaccggtaaaaca atgatgcagcgtttcgattttatagacaagattgaa agattgggcgtttcccaccatttcgatattgaaatc gagaaccaattacaagaatttttcaatgtttacacta acttcggtgaatactcagcttacgacttgtcttccg cagccttgcaatttaagcaatggtgtgaccacaat agatcattatcttgctctattactagaggtttgttatc cttgtatgaggctgctcatgtcagaacccacggtg ataagatcttggaagaagctttacacttgacttctg gtgaatcccatttggactccaccttggctaaacaa gttaaatgtgcattagaacaaccattgcacaaggg tatacctcgttacgaagcctggagatatatttctatc tacgaagaggatgaatcacataacaagttgttgtt gagattagctaaattggattatcacttcttacagatt tcttacagacaagatttgtgtgaaatcattcgttgg gactcatctggtgtcgaccaattatctgattacatc agagcagttggtgaggaattggctaagaagcaa agaacatacgctttcggtacttttttaggtatggatg gtgcctctgaagatgttattaactggatgtccacta tcccaaagttgatgttcgcttgctctacacatgcca gattgattaatgactttggtggtcataaattcgataa ggaaagaggtactggtaccgctttagagtgttata tgaaagactataacgtctccgaagaagaagccg ccaacaagtttagagaaatgatggaggacgcttg gaaagttatgaatgaagaatgtttgcgtccaacca ctattccaagagaaatattaaagatgttgttgaaca tcgtccgtgttggtgaaactactaataagcacaga atcgatggtttcacacagcctcacgctattgagga acacattagagctatgttggttgacttttatgtccgtc taa(서열번호 118)

[0184] [표 11]

희귀 식물로부터 유래한 서열 단편(들)의 비제한적 예

키메라 명칭	고대 DNA 공급원	단편	서열번호
HibWilSQTS117	히비스카델푸스 월데리아누스	LKDEEGNFKASLTSDVPGLLELYEASYLRVHGEDILDEAISFA	119
		NKALLQFAKIDFNMLQLLHRKELSEICRWWKDLDFTRKLP	120
		DRVVEGYFWIMGVYFEPQYSLGRKMLTKVIAMASIVDDTYDSFATYDELIPYTDAIER	121
		YMQISYKALLDVYEEMEQLLADKGRQYRVEY	122
		WTHLNYKPTFEEFRDNALPTSGYAMLAIT	123
		TFEWAASDPKIIKASTIICRFMDDIAE	124
		EDDCSAIECYMEQYKVTAQEAYDEFNKHIESSWKDVNEEFLK	125
HibWilSQTS118	히비스카델푸스 월데리아누스	EAFNKLKDEEGNFKASLTSDVRGLLELYQASYMRIHGEDILDEAISFTTAQLTLALPTLDPP	126
		NKALLQFAKIDFNMLQLLHRKELSEICRWWKDLDFTRKLP	127
		DRVVEGYFWIMGVYFEPQYSLGRKMLTKVIAMASIVDDTYDSFATYDELIPYTDAIER	128
		YMQISYKALLDVYEEMEQLLADKGRQYRVEY	129
		WTHLNYKPTFEEFRDNALPTSGYAMLAIT	130
		TFEWAASDPKIIKASTIICRFMDDIAE	131
		SAIECYMKQYGATAQEAYDEFNKHIESSWK	132
HibWilSQTS120	히비스카델푸스 월데리아누스	LKDEEGNFKASLTSDVPGLLELYEASYLRVHGEDILDEAISFA	133
		NKALLQFAKIDFNMLQLLHRKELSEICRWWKDLDFTRKLP	134
		DRVVEGYFWIMGVYFEPQYSLGRKMLTKVIAMASIVDDTYDSFATYDELIPYTDAIER	135
		YMQISYKALLDVYEEMEQLLADKGRQYRVEY	136
		WTHLNYKPTFEEFRDNALPTSGYAMLAIT	137
		TFEWAASDPKIIKASTIICRFMDDIAE	138
		SAIECYMKQYGATAQEAYDEFNKHIESSWK	139
HibWilSQTS121	히비스카델푸스 월데리아누스	EAFNKLKDEEGNFKASLTSDVRGLLELYQASYMRIHGEDILDEAISFTTAQLTLALPTLDPP	140
		LLEFAKIDFNLLQLLHRKELSEICRWWKD	141
		DRVVEGYFWIMGVYFEPQYSLGRKMLTKVIAMASIVDDTYDSFATYDELIPYTDAIER	142
		YMQISYKALLDVYEEMEQLLADKGRQYRVEY	143
		WTHLNYKPTFEEFRDNALPTSGYAMLAIT	144
		TFEWAASDPKIIKASTIICRFMDDIAE	145
		EDDCSAIECYMEQYKVTAQEAYDEFNKHIESSWKDVNEEFLK	146
HibWilSQTS123	히비스카델푸스 월데리아누스	LKDEEGNFKASLTSDVPGLLELYEASYLRVHGEDILDEAISFA	147
		LLEFAKIDFNLLQLLHRKELSEICRWWKD	148
		DRVVEGYFWIMGVYFEPQYSLGRKMLTKVIAMASIVDDTYDSFATYDELIPYTDAIER	149
		YMQISYKALLDVYEEMEQLLADKGRQYRVEY	150
		WTHLNYKPTFEEFRDNALPTSGYAMLAIT	151

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		TFEWAASDPKIIKASTIICRFMDDIAE	152
		EDDCSAIECYMEQYKVTAQEAYDEFNKHIESSWK DVNEEFLK	153
HibWilSQTS124	히비스카델푸스 윌데리아누스	EAFNKLKDEEGNFKASLTSDVRGLLELYQASYMR IHGEDILDEAISFTTAQLTLALPTLDPP	154
		LLEFAKIDFNLLQLLHRKELSEICRWWKD	155
		DRVVEGYFWIMGVYFEPQYSLGRKMLTKVIAMA SIVDDTYDSFATYDELIPYTDAIER	156
		YMQISYKALLDVYEEMEQLLADKGRQYRVEY	157
		WTHLNYKPTFEEFRDNALPTSGYAMLAIT	158
		TFEWAASDPKIIKASTIICRFMDDIAE	159
		SAIECYMKQYGATAQEAYDEFNKHIESSWK	160
HibWilSQTS126	히비스카델푸스 윌데리아누스	LKDEEGNFKASLTSDVPGLLELYEASYLRVHGEDI LDEAISFA	161
		LLEFAKIDFNLLQLLHRKELSEICRWWKD	162
		DRVVEGYFWIMGVYFEPQYSLGRKMLTKVIAMA SIVDDTYDSFATYDELIPYTDAIER	163
		YMQISYKALLDVYEEMEQLLADKGRQYRVEY	164
		WTHLNYKPTFEEFRDNALPTSGYAMLAIT	165
		TFEWAASDPKIIKASTIICRFMDDIAE	166
		SAIECYMKQYGATAQEAYDEFNKHIESSWK	167
HibWilSQTS19	히비스카델푸스 윌데리아누스	FEQERGHCASAVECYMREHGVSEEEACSELKKQV DNAWKDINHEMIFSETSKAVPMSVLTRVLNLTR	168
HibWilSQTS34	히비스카델푸스 윌데리아누스	GYHVDGEEAFNMLKDEEGNFKASLTSDVPGLLEL YQASYMRIHGEDILDEAISFTTAQLTLALPTLDPPL S	169
HibWilSQTS52	히비스카델푸스 윌데리아누스	FEQERGHCASAVECYMREHGVSEEEACSELKKQV DNAWKDINHEMIFSETSKAVPMSVLTRVLNLTR	170
HibWilSQTS54	히비스카델푸스 윌데리아누스	GYHVDGEEAFNMLKDEEGNFKASLTSDVPGLLEL YQASYMRIHGEDILDEAISFTTAQLTLALPTLDPPL SE	171
HibWilSQTS55	히비스카델푸스 윌데리아누스	FEQERGHCASAVECYMREHGVSEEEACSELKKQV DNAWKDINHEMIFSETSKAVPMSVLTRVLNLTR	172
HibWilSQTS63	히비스카델푸스 윌데리아누스	EQERGHCASAVECYMREHGVSEEEACSELKKQV DNAWKDINHEMIFSETSKAVPMSVLTRVLNLTR	173
HibWilSQTS90	히비스카델푸스 윌데리아누스	GYHVDGEEAFNMLKDEEGNFKASLTSDVPGLLEL YQASYMRIHGEDILDEAISFTTAQLTLALPTLDPPL S	174
		FEQERGHCASAVECYMREHGVSEEEACSELKKQV DNAWKDINHEMIFSETSKAVPMSVLTRVLNLTRG	175
LeuGraSQTS335	류카덴드론 그란디플로룸	DAFNRFKDTKGSFKEDLIKDVNSMLCLYEATHLR VHGEDILDEALGFTTSQLKSILPKLKPLLASQVMH ALKQPL	176
LeuGraSQTS345	류카덴드론 그란디플로룸	FNKFKNSDGNFKEDLINDVSGMLCLYEATHLRVH GEDILDEALEFTTTRLKSILPDLEPPLATQVMHA	177
LeuGraSQTS365	류카덴드론 그란디플로룸	IFNKFKNSDGNFKEDLINDVSGMLCLYEATHLRV HGEDILDEALEFTTTRLKSILPDLEPPL	178
LeuGraSQTS377	류카덴드론 그란디플로룸	DAFNRFKDTKGSFKEDLIKDVNSMLCLYEATHLR VHGEDILDEALGFTTSQLKSILPKLKPLLASQVMH ALKQPL	179
LeuGraSQTS379	류카덴드론 그란디플로룸	IFNKFKNSDGNFKEDLINDVSGMLCLYEATHLRV HGEDILDEALEFTTTRLKSILPDLEPPLATQVMHA	180
LeuGraSQTS385	류카덴드론	ETNFTNSPLLSKLQNELSVAHLEELKLEVKQLIWS	181

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	그란디플로룸	TKDPLFLLKFIDSIQRLGVAYHFEEEIKESLHLVYL E	
LeuGraSQTS393	류카덴드론 그란디플로룸	IFNKFKNSDGNFKEDLINDVSGMLCLYEATHLRV HGEDILDEALEFTTTRLKSILP	182
MacVolSQTS1139	매크로스타일리스 빌로사	EGLEQKIRTMLISPTDTISKKLSLIDAVQRLGVAYH FEKEIEDEIEKLSCKEYNDGNDLQTVALRFRLLRQ QGYFVSC	183
MacVolSQTS2198	매크로스타일리스 빌로사	LQRLGLAYHFENQIKEALQSI	184
		LSHLSTSLAEQVKHSLEIPLHRGMPRLEARHYISIY EEDNSS	185
		ELAKLDFNLLQALHRRELGEISRWWKDIDFATKL PFARDRLVECYFWILGVYFEPKYSITRKFMTKVIAI ASVIDDIYDVYGTLEELKLFTHAIERWETVAANEL PKYMQVCYFALLDVFKEMEDKLVNKGLLYSMPC AKEAVKGLVRAYFVEAEWFNANYMPTFEEYMEN STMSSGYPMLAVEALIGIEDATISKEAFDWAISVP KIIRSCALIARLVDDIH	186
		DAPSSVECYMQQYDVSEEEACNRIKGMVEIEW	187
		NLARMMVVLYQNGDNYTNSSGKTKDRIASLLV	188
MacVolSQTS2202	매크로스타일리스 빌로사	LQRLGLAYHFENQIKEALQSI	189
		KFKDEKGEFKDMIRNDARGLLCLYEASHLRVKGE DILEEATEFSRKHLKSLLPQLSTSLAEQVKHSLEIP LHRGMPRLEARHYISIYEENNSSRNELLLELAKLD FNLLQALHRRELGDISRWWKDIDFATKLPFARDR LVECYFWILGVYFEPKYSITRKFMTKVIAIASVIDD IYDVYGTLEELKLFTHAIERWETVAANELPKYMQ VCYFALLDVFKEMEDKLVNKGLLYSMPCAKEAV KGLVRAYFVEAEWFNANYMPTFEEYMENSTMSS GYPMLAVEALIGIEDATISKEAFDWAISVPKIIRSC ALIARLVDDIH	190
		KVEQERGDAPSSVQCYVQQ	191
		NLARMMVVLYQNGDNYTNSSGKTKDRIASLLV	192
MacVolSQTS2222	매크로스타일리스 빌로사	LQRLGLAYHFENQIKEALQSI	193
		KFKDEKGEFKDMIRNDARGLLCLYEASHLRVKGE DILEEATEFSRKHLKSLLPQLSTSLAEQVKHSLEIP LHRGMPRLEARHYISIYEENNSSRNELLLELAKLD FNLLQALHRRELGDISRWWKDIDFATKLPFARDR LVECYFWILGVYFEPKYSITRKFMTKVIAIASVIDD IYDVYGTLEELKLFTHAIERWETVAANELPKYMQ VCYFALLDVFKEMEDKLVNKGLLYSMPCAKEAV	194
		YVPTFEEYMENSTMSSGYPMLAVEALV	195
		DWAISVPKIIRSCALIA	196
		KVEQERGDAPSSVQCYMQQYDVSEEEACNRIKG MVETAWMEINGEIQDTNHL	197
		NLARMMVVLYQNGDNYTNSSGKTKDRIASLLV	198
MacVolSQTS2251	매크로스타일리스 빌로사	LQRLGLAYHFENQIKEALQSI	199
		KFKDEKGEFKDMIRNDARGLLCLYEASHLRVKGE DILEEATEFSRKHLKSLLPQLSTSLAEQVKHSLEIP LHRGMPRLEARHYISIYEENNSSRNELLLELAKLD FNLLQALHRRELGDISRWWKDIDFATKLPFARDR LVECYFWILGVYFEPKYSITRKFMTKVIAIASVIDD IYDVYGTLEELKLFTHAIERWETVAANELPKYMQ VCYFALLDVFKEMEDKLVNKGLLYSMPCAKEAV	200
		YVPTFEEYMENSTMSSGYPMLAVEALV	201
		DWAISVPKIIRSCALIA	202

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		DAPSSVECYMQQYDVSEEEACNRIKGMVEIEW	203
		NLARMMVVLYQNGDNYTNSSGKTKDRIASLLV	204
MacVolSQTS2274	매크로스타일리스 빌로사	KFIQNVEKDSTRRSANFHPSIWGDH	205
		DDGSVKHQQLKEEIRKMLTAETKLSQKLDLIDAIQRLGVAYHFESEIDEIL	206
		SLARNVRGMLSLYEATHLRVHGENILDEA	207
		LEARNYMPFYQEEASHNEALLTFAKLDFNKLQKLHQKELSEITR	208
		FEQSREHVASSIECYMKQYGATEEETCNELRKQVSNAWKDINEECLCPTAVPMPLIVRILNLT	209
OrbStiSQTS1368	오르벡실룸 스티폴라툼	AEVFERFKDQHGNFKASLSSDVEGMLSLYEASFLDYEGEDILDEAKAFTSFHLRGAL	210
OrbStiSQTS1414	오르벡실룸 스티폴라툼	VKLELVDDVKRLGIGYRFEKEIVEALHRCFISSERFTHRNLHQTALSFRLLRECGYDVT	211
		FNKFTNKEGKFNSKLGENIKGMIDLYEASQLGIAGEYILAEAGEFSGLVLKEKVACINN	212
		VYFEPQYSVPRRTTTKVIGLCSVIDDMYDAYGTIDELELFTNAIERLDTST	213
		RWLKCNHAPTMEEYMKVRGVSSGYPLLITISFIGMEDTTEEILTWATSEPMIIRASVIVCRLMDDI	214
ShoCusSQTS154	쇼레아 쿠스피다타	FMDEKGKFKEDVVNDVLGMLNLYEAAHLRLRGEDILDEALAFTTSHLE	215
		WWKNLDFSTKLPYARDRIVECYFWIMGAYFE	216
		SLARTFLTKVIAMTSILDDTYDNYG	217
		DYVPPIEEYMQVARISSAYPMLITNSFVGMGEVATKEAFDWISNDPKILKASTTICRLMDD	218
		EFEQTRDHVASGVECYMKQYGVSREETVK	219
ShoCusSQTS155	쇼레아 쿠스피다타	FMDEKGKFKEDVVNDVLGMLNLYEAAHLRLRGEDILDEALAFTTSHLE	220
		WWKNLDFSTKLPYARDRIVECYFWIMGAYFE	221
		SLARTFLTKVIAMTSILDDTYDNYG	222
		YMQVALISSAYPMLITNSFVGMGEVATKEAFDWISNNPKMLKASTII	223
		EFEQTRDHVASGVECYMKQYGVSREETVK	224
ShoCusSQTS156	쇼레아 쿠스피다타	FMDEKGKFKEDVVNDVLGMLNLYEAAHLRLRGEDILDEALAFTTSHLE	225
		WWKNLDFSTKLPYARDRIVECYFWIMGAYFE	226
		SLARTFLTKVIAMTSILDDTYDNYG	227
		DYVPPIEEYMQVARIS	228
		GYPMLITNSLVGMGEVATKEAFDLISNDPKMLKAST	229
		EFEQTRDHVASGVECYMKQYGVSREETVK	230
ShoCusSQTS157	쇼레아 쿠스피다타	FMDEKGKFKEDVVNDVLGMLNLYEAAHLRLRGEDILDEALAFTTSHLE	231
		WWKNLDFSTKLPYARDRIVECYFWIMGAYFE	232
		SLARTFLTKVIAMTSILDDTYDNYG	233
		VPPMDEYMQVALISCGYPMLITNSFVGMGEVATKEAFDWISNDPKILKASTTICRLMDD	234
		EFEQTRDHVASGVECYMKQYGVSREETVK	235
ShoCusSQTS160	쇼레아 쿠스피다타	FMDEKGKFKEDVVNDVLGMLNLYEAAHLRLRGEDILDEALAFTTSHLE	236
		WWKNLDFATMLPYARDRIVECYFWIMGVYFEPKYSLARTFLTKVIAMTSILDDTYDNYG	237
		YMQVALISSAYPMLITNSFVGMGEVATKEAFDWI	238

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		SNNPKMLKASTII	
		EFEQTRDHVASGVECYMKQYGVSREETVK	239
ShoCusSQTS161	쇼레아 쿠스피다타	FMDEKGKFKEDVVNDVLGMLNLYEAAHLRLRGE DILDEALAFTTSHLE	240
		WWKNLDFATMLPYARDRIVECYFWIMGVYFEPK YSLARTFLTKVIAMTSILDDTYDNYG	241
		DYVPPIEEYMQVARIS	242
		GYPMLITNSLVGMGEVATKEAFDLISNDPKMLKA ST	243
		EFEQTRDHVASGVECYMKQYGVSREETVK	244
WenAngSQTS1007	웬들란디아 안구스토폴리아	SNNRQETVRPLADFPENIWADRIAPFT	245
		EMCQREIEMLKAEVASMLLATGKTMMQRFDFID KIERLGVSHHFD	246
		IFDQFIDAKGKFKESLCNDIRGLLSLYEAAHVRTH GDKILEEALAFTTTHMTSGGPHLDSSLAKQVKYA LEQPLHKGILRYEAWRYISIYEEDESNNKLLLRLA KLDYHLLQMSYKQEL	247
		RWGKGLESVSNFPYARDRFVECYFWAVGTLYEP QYSLARMTFAKVAA	248
		RWDGSGVDQLSDYIRASYNTLLKFNKEVGEDLAK KQRTYAFDKYIEDWKQYMRTNFSQSRWFFTKELP SFADYINNGAITIGAYLVASAAFLYMDSAKEDVIN WMSTNPKLVVAYSTHSRLINDFGGHKFEKERGSS TAIECYMKDHNVSEEEAANKFREMMEDAWKVM NEECLRPTTI	249
		ETVYKHRIDGFTQPHAIEEHIRAMLVDFMSI	250
WenAngSQTS1086	웬들란디아 안구스토폴리아	SNNRQETVRPLADFPENIWADRIAPFT	251
		EMCQREIEMLKAEVASMLLATGKTMMQRFDFID KIERLGVSHHFD	252
		IFDQFIDAKGKFKESLCNDIRGLLSLYEAAHVRTH GDKILEEALAFTTTHMTSGGPHLDSSLAKQVKYA LEQPLHKGILRYEAWRYISIYEEDESNNKLLLRLA KLDYHLLQMSYKQEL	253
		RWGKGLESVSNFPYARDRFVECYFWAVGTLYEP QYSLARMTFAKVAA	254
		RWDGSGVDQLSDYIRASYNTLLKFNKEVGEDLAK KQRTYAFDKYIEDWKQYMRTNFSQSRWFFTKELP SFADYINNGAITIGAYLVASAAFLYMDSAKEDVIN WMSTNPKLVVAYSTHSRLINDFGGHK	255
		KERGTGTAIECYMKDHN	256
		EMIENTWKVMNEECLRPIPIPRDTLKML	257
		ETVYKHRIDGFTQPHAIEEHIRAMLVDFMSI	258
WenAngSQTS267	웬들란디아 안구스토폴리아	LELVDNLERLGLAYHFEGQINRLLSSAYNANHED EGNHKRNKEDLYAAALEFRIFRQHGFNV	259
WenAngSQTS302	웬들란디아 안구스토폴리아	YVSQANELKEQVKMMLDEEDMKLLDCLELVDNL ERLGLAYHFEGQINRLLSSAYNANHEDEGNHKRN KEDLYAAALEFRIFRQHGFNVPQ	260
WenAngSQTS738	웬들란디아 안구스토폴리아	NNQHESVRQLADFPENIWADRV	261
		QGHDMCAKEIEMLKEEVMSMLLE	262
		STLAKQVKYALEQPLHKGIPRYEAWRYISIYEED	263
		LAKLDYHLSQMLNKQDLCEI	264
		RDRIVECYFWAVATYYEPQYSLARMT	265
		EVGEDLAKKQRTYAFDKYIE	266
		YARTSFTQSKWFLTNELPSFSDYL	267

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		AAFLDMDSASEDVINWMSTNPKLFVALTTHARLA NDVGSHKFEKERGSGTAIECYMKDYHVSEEEAM KKFEEMCDDAWKVMNEE	268
WenAngSQTS760	웬들란디아 안구스토폴리아	NNQHESVRQLADFPENIWADRV	269
		QGHDMCAKEIEMLKEEVMSMLLE	270
		QVKHALEQPLHRGIPRYEAYCFISIYEEDESNNKLL LRLAKLDYHLLQMSYKRE	271
		RDRIVECYFWAVATYYEPQYSLARMT	272
		EVGEDLAKKQRTYAFDKYIE	273
		YARTSFTQSKWFLTNELPSFSDYL	274
		TFLGMDGASEDVINWMSTNPKLFVA	275
		KFEKERGSGTAIECYMKDYHVSEEEAMKKFEEMC DDAWKVMNEE	276
WenAngSQTS780	웬들란디아 안구스토폴리아	NNQHESVRQLADFPENIWADRV	277
		QGHDMCAKEIEMLKEEVMSMLLE	278
		QVKHALEQPLHRGIPRYEAYCF	279
		LAKLDYHLSQMLNKQDLCEI	280
		RDRIVECYFWAVATYYEPQYSLARMT	281
		EVGEDLAKKQRTYAFDKYIE	282
		YARTSFTQSKWFLTNELPSFSDYL	283
		TFLGMDGASEDVINWMSTNPKLFVA	284
		KFEKERGSGTAIECYMKDYHVSEEEAMKKFEEMC DDAWKVMNEE	285
WenAngSQTS793	웬들란디아 안구스토폴리아	SNNRQETVRPLADFPENIWADRIAPFT	286
		EMCQREIEMLKAEVASMLLATGKTMMQRFDFID KIERLGVSHHFD	287
		IFDQFIDAKGKFKESLCNDIRGLLSLYEAAHVRTH GDKILEEALAFTTTHMTSGGPHLDSSLAKQVKYA LEQPLHKGILRYEAWRYISIYEEDESNNKLLLRLA KLDYHLLQMSYKQEL	288
		RWGKGLESVSNFPYARDRFVECYFWAVGTLYEP QYSLARMTFAKVAA	289
		RWDGSGVDQLSDYIRASYNTLLKFNKEVGEDLAK KQRTYAFDKYIEDWKQYMRTSFTQSKWFLTNELP SFADY	290
		LDMDSALEDVINWMSTNPKLMVAY	291
		KFDKERGSVTALDCYMKDYSVSEEEAAKKFREM CEDNWKVMNEECLRPTTI	292
		ETVYKHRIDGFTQPHAIEEHIRAMLVDFMSI	293
WenAngSQTS805	웬들란디아 안구스토폴리아	NNQHESVRQLADFPENIWADRV	294
		QGHDMCAKEIEMLKEEVMSMLLE	295
		STLAKQVKYALEQPLHKGIPRYEAWRYISIYEEDE SNNKLLLRLAKLDYHLLQMSYKRE	296
		RDRIVECYFWAVATYYEPQYSLARMT	297
		EVGEDLAKKQRTYAFDKYIE	298
		YARTSFTQSKWFLTNELPSFSDYL	299
		TFLGMDGASEDVINWMSTNPKLFVA	300
		STAIECYMKDYHVSEEEAMEKFEEMCDDAWKVM NEE	301
WenAngSQTS826	웬들란디아 안구스토폴리아	NNQHESVRQLADFPENIWADRV	302
		QGHDMCAKEIEMLKEEVMSMLLE	303
		STLAKQVKYALEQPLHKGIPRYEAWRYISIYEEDE SNNKLLLRLAKLDYHLLQMSYKRE	304
		RDRIVECYFWAVATYYEPQYSLARMT	305

[0190]

		EVGEDLAKKQRTYAFDKYIE	306
		YARTSFTQSKWFLTNELPSFADYLS	307
		AALLDMDSALEDVINWMSTNPKFFVALTTHARLT NDVGSHKFEKERGSGTAIECYMKDYHVSEEEAM KKFEEMCDDAWKVMNEE	308
WenAngSQTS829	웬들란디아 안구스토폴리아	SNNRQETVRPLADFPENIWADRIAPFT	309
		EMCQREIEMLKAEVASMLLATGKTMMQRFDFID KIERLGVSHHFD	310
		IFDQFIDAKGKFKESLCNDIRGLLSLYEAAHVRTH GDKILEEALAFTTTHMTSGGPHLDSSLAKQVKYA LEQPLHKGILRYEAWRYISIYEEDESNNKLLLRLA KLDYHLLQMSYKQEL	311
		RWGKGLESVSNFPYARDRFVECYFWAVGTLYEP QYSLARMTFAKVAA	312
		RWDGSGVDQLSDYIRASYNTLLKFNKEVGEDLAK KQRTYAFDKYIEDWKQYMRTSFTQSKWFLTNELP SFADY	313
		LDMDSALEDVINWMSTNPKLMVAY	314
		KERGTGTAIECYMKDHN	315
		EMIENTWKVMNEECLRPIPIPRDTLKML	316
		ETVYKHRIDGFTQPHAIEEHIRAMLVDFMSI	317
WenAngSQTS843	웬들란디아 안구스토폴리아	NNQHESVRQLADFPENIWADRV	318
		QGHDMCAKEIEMLKEEVMSMLLE	319
		QVKHALEQPLHRGIPRYEAYCFISIYEEDESNNKLL LRLAKLDYHLLQMSYKRE	320
		RDRIVECYFWAVATYYEPQYSLARMT	321
		EVGEDLAKKQRTYAFDKYIE	322
		YARTSFTQSKWFLTNELPSFSDYL	323
		AAFLDMDSASEDVINWMSTNPKLFVALTTHARLA NDVGSHK	324
		RGSGTAIECYMKDYNVSEEEALKKFEEMCEDTW KVMNEE	325
WenAngSQTS848	웬들란디아 안구스토폴리아	SNNRQETVRPLADFPENIWADRIAPFT	326
		EMCQREIEMLKAEVASMLLATGKTMMQRFDFID KIERLGVSHHFD	327
		IFDQFIDAKGKFKESLCNDIRGLLSLYEAAHVRTH GDKILEEALAFTTTHMTSGGPHLDSSLAKQVKYA LEQPLHKGILRYEAWRYISIYEEDESNNKLLLRLA KLDYHLLQMSYKQEL	328
		RWDGSGVDQLSDYIRASYNTLLKFNKEVGEDLAK KQRTYAFDKYIEDWKQYMRTNFSQSRWFFTKELP SFADYINNGAITIGAYLVASAAFLYMDSAKEDVIN WMSTNPKLVVAYSTHSRLINDFGGHKFDKERGSG TALECYMKDYNVSEEEAANKFREMMEDAWKVM NEDCLRPTSIPRDVSKVLLNVARAGEIVYKHRIDG FTEPHIIKDHIRATLVDFMAIN	329
		RWGKGLESVSNFPYARDRFVECYFWAVGTLYEP QYSLARMTFAKVAA	330
WenAngSQTS849	웬들란디아 안구스토폴리아	SNNRQETVRPLADFPENIWADRIAPFT	331
		EMCQREIEMLKAEVASMLLATGKTMMQRFDFID KIERLGVSHHFD	332
		IFDQFIDAKGKFKESLCNDIRGLLSLYEAAHVRTH GDKILEEALAFTTTHMTSGGPHLDSSLAKQVKYA LEQPLHKGILRYEAWRYISIYEEDESNNKLLLRLA KLDYHLLQMSYKQEL	333

[0191]

		RWGKGLESVSNFPYARDRFVECYFWAVGTLYEP QYSLARMTFAKVAA	334
		RWDGSGVDQLSDYIRASYNTLLKFNKEVGEDLAK KQRTYAFDKYIEDWKQYMRTSFTQSKWFLTNELP SFADY	335
		LDMDSALEDVINWMSTNPKLMVAY	336
		KFDKERGSVTALDCYMKDYSVSEEEAAKKFREMI ENTWKVMNEECLRPIPIPRDTLKML	337
		EPHIIKDHIRAMLVDFMAI	338
WenAngSQTS864	웬들란디아 안구스토폴리아	SNNRQETVRPLADFPENIWADRIAPFT	339
		EMCQREIEMLKAEVASMLLATGKTMMQRFDFID KIERLGVSHHFD	340
		IFDQFIDAKGKFKESLCNDIRGLLSLYEAAHVRTH GDKILEEALAFTTTHMTSGGPHLDSSLAKQVKYA LEQPLHKGILRYEAWRYISIYEEDESNNKLLLRLA KLDYHLLQMSYKQEL	341
		RWGKGLESVSNFPYARDRFVECYFWAVGTLYEP QYSLARMTFAKVAA	342
		RWDGSGVDQLSDYIRASYNTLLKFNKEVGEDLAK KQRTYAFDKYIEDWKQYMRTNFSQSRWFFTKELP SFADYINNGAITIGAYLVASAAFLYMDSAKEDVIN WMSTNPKLVVAYSTHSRLINDFGGHKFDKERGSV TALDCYMKDYSVSEEEAAKKFREMCEDNWKVM NEECLRPTTI	343
		ETVYKHRIDGFTQPHAIEEHIRAMLVDFMSI	344
WenAngSQTS925	웬들란디아 안구스토폴리아	SNNRQETVRPLADFPENIWADRIAPFT	345
		EMCQREIEMLKAEVASMLLATGKTMMQRFDFID KIERLGVSHHFD	346
		IFDQFIDAKGKFKESLCNDIRGLLSLYEAAHVRTH GDKILEEALAFTTTHMTSGGPHLDSSLAKQVKYA LEQPLHKGILRYEAWRYISIYEEDESNNKLLLRLA KLDYHLLQMSYKQEL	347
		RWGKGLESVSNFPYARDRFVECYFWAVGTLYEP QYSLARMTFAKVAA	348
		RWDGSGVDQLSDYIRASYNTLLKFNKEVGEDLAK KQRTYAFDKYIEDWKQYMRTNFSQSRWFFTKELP SFADYINNGAITIGAYLVASAAFLYMDSAKEDVIN WMSTNPKLVVAYSTHSRLINDFGGHKFDKERGSV TALDCYMKDYSVSEEEAAKKFREMIENTWKVMN EECLRPIPIPRDTLKML	349
		EPHIIKDHIRAMLVDFMAI	350
WenAngSQTS960	웬들란디아 안구스토폴리아	EAFNKLKDEEGNFKASLTSDVRGLLELYQASYMR IHGEDILDEAISFTTAQLTLALPTLDPP	351
		NKALLQFAKIDFNMLQLLHRKELSEICRWWKDLD FTRKLP	352
		DRVVEGYFWIMGVYFEPQYSLGRKMLTKVIAMA SIVDDTYDSFATYDELIPYTDAIER	353
		YMQISYKALLDVYEEMEQLLADKGRQYRVEY	354
		WTHLNYKPTFEEFRDNALPTSGYAMLAIT	355
		TFEWAASDPKIIKASTIICRFMDDIAE	356
		EDDCSAIECYMEQYKVTAQEAYDEFNKHIESSWK DVNEEFLK	357

[0192]

[0193] **실시예 2. 테르펜 합성효소 키메라의 구축을 위한 재료 및 방법**

[0194] *포획-seq 및 키메라 스카폴딩을 위한 테르펜 합성효소*

[0195] 희귀 꽃 게놈으로부터의 서열 단편들(표 11)을, UniProt 및 GenBank를 포함하는 공급원으로부터의 "스카폴드" 세스퀴테르펜 합성효소(SQTS)와 조합함으로써 후보 SQTS를 디자인하였다.

[0196] 포획-seq(테르펜 합성효소의 표적화된 서열분석)를 위해, EMBL/Genbank 내에 뉴클레오타이드 서열을 가진 5,171개의 테르펜 합성효소(TPS)들의 서브세트를 UniProt로부터 컴파일링하였다. TPS 상동성 서열에 대해 꽃 DNA 샘플을 농축하기 위해 올리고뉴클레오타이드 칩을 생성한 후, 먼저 일루미나(Illumina) 서열분석을 수행하였다. 포획-seq 라이브러리도 더 높은 깊이에서 다시 한 번 서열분석하였다.

[0197] SQTS 키메라 재구축을 위해, 어노테이션된(annotated) 모노테르펜, 디테르펜 또는 트리테르펜 합성효소보다 어노테이션된 SQTS에 더 가까운 서열을 선택하였다. 1,521개의 잠정적 SQTS의 이 세트를, 하기 키메라 구축 파이프라인에서 blastn 및 tblastn을 위한 질의(query) 서열로서 (뉴클레오타이드 및 펩타이드 형태 둘 다로) 사용하였다.

[0198] *키메라 재구축*

[0199] 키메라 SQTS를 구축하기 위해 2종의 방법들을 이용하였다: 1) blastn-mapDamage 파이프라인, 및 2) tblastn 파이프라인.

[0200] *blastn-mapdamage 파이프라인*

[0201] 일반적으로, blastn-mapdamage 파이프라인은 희귀 꽃에서 원래의 효소 서열과 매우 가까울 가능성이 높은 키메라 테르펜 합성효소(예를 들면, 키메라 세스퀴테르펜 합성효소)를 생성하는 스카폴드와 높은 뉴클레오타이드 유사성을 가진 단편을 보존적으로 검출한다. 정형화된 희귀 DNA 손상의 인공물일 수 있는 돌연변이를 검출하기 위해, 밤-포맷팅된(bam-formatted) 일루미나 리드 정렬을 mapDamage 소프트웨어 내로 입력하였다.

[0202] 구체적으로, 하기 단계들을 이용하여, 각각의 꽃으로부터의 DNA 단편과 다양한 SQTS 스카폴드들의 정렬을 생성하였다:

[0203] 1. 게놈 포획-seq 실행으로부터의 일루미나 리드(fastq 파일)들을 조합하고 SPADES를 통해 더 긴 콘티그로 어셈블링하였다.

[0204] 2. SQTS 스카폴드의 1521-세트를, SPADES 콘티그에 대한 디폴트 파라미터를 사용한 blastn 검색에서 질의로서 사용하였다. 상대적으로 적은 스카폴드들이 히트(hit)를 가졌으므로, 다음 단계에서 리드 정렬을 위한 기준물로서 사용하기 위해 히트를 가진 모든 스카폴드들을 선택하였다.

[0205] 3. (bbduk를 이용하여) 서열분석 실행으로부터의 조합된 리드들을 품질-트리밍하고 (bbmerge를 이용하여) 쌍-병합하고 bwa mem을 이용하여 선택된 SQTS 기준 서열에 정렬시켰다. 결과를 bam으로 재포맷팅하고 분류하고 인덱싱하였다.

[0206] 4. mapDamage를 정렬된 리드에 대해 실행하였다. 이것은 DNA 손상과 유사한 SNP가 낮은 품질 점수를 배정받는 리드 정렬을 야기하였다.

[0207] 5. 리드 정렬을 다음과 같이 처리하였다: 25 미만의 품질을 가진 염기를 표시하였고(기준물로 바뀜); 정렬을 fasta로 재포맷팅하였고; 6 미만의 카운트를 가진 SNP를 표시하였고; 이중 리드를 제거하였고; 0.1 미만의 빈도를 가진 SNP를 표시하였고; 다른 리드의 정확한 하위서열인 리드를 제거하였고; 리드를 기준물의 프레임으로 번역하였고; 하위서열을 다시 제거하였다. 정렬을 표시하는 데 사용된 품질 및 SNP 빈도 역치를 품질 및 SNP 빈도의 분포를 관찰함으로써 실험적으로 측정하였다.

[0208] 6. (기준물-프레임 번역 후) 리드 정렬과 SPADE 콘티그 정렬을 조합하였고 Clustal Omega를 이용하여 재정렬시켰다. 이것은 일부 콘티그들이 리드가 걸쳐 있지 않은 스카폴드의 영역에 걸쳐 있기 때문에 수행되었다.

[0209] 상기 단계들로부터의 정렬을 다음과 같이 이용하여 SQTS 키메라를 구축하였다:

[0210] 1. 각각의 하위영역이 또 다른 하위영역으로부터의 단편과 중첩되고 이 단편과 상이한 임의의 단편(정렬된 리드)을 함유하지 않도록 정렬을 "독립적인 하위영역"으로 분할하였다(하위영역들 사이에 동일한 중첩은 허용되었다).

[0211] 2. 각각의 하위영역에서, "양립가능한 단편들"의 모든 가능한 조합들의 수를 세었다. 양립가능한 단편들은 동일하게 중첩되었거나(그러므로, 더 긴 단편으로 병합될 수 있거나) 전혀 중첩되지 않은(그리고, 예를 들면, 동일한 일배체형으로부터 유래한 것으로 추정된) 단편들로서 정의되었다. 단편 조합은 "최대-커버리지"이었고, 즉 가능한 많은 양립가능한 단편들이 함유되었다. 각각의 최대-커버리지 단편 조합은 정렬의 그 영역의 가능한 재구축인 것으로 간주되었고, (갭을 함유하였을 수 있는) 수퍼단편으로 병합되고 저장되었다.

[0212] 3. 맞춤형 반복 알고리즘을 이용하여 각각의 하위영역으로부터의 수퍼단편을 90% 또는 95% 동일성까지 다운샘플링하였고, 상이한 하위영역들로부터의 다운샘플링된 수퍼단편들의 모든 가능한 조합들을 조합하였다. 특정 역치보다 더 짧은 영역을 단일 서열까지 다운샘플링하였다. 수퍼단편들의 각각의 조합을 스카폴드로 병합하여 키메라 서열을 생성하였다. 각각의 경우에 1개 초과 내지 100개 미만의 키메라들이 구축될 수 있도록 다운샘플링 파라미터를 샘플 및 스카폴드에 따라 약간 변경시켰다.

[0213] 각각의 샘플에 대해 상기 파이프라인을 실행한 후, 총 1136개의 키메라들이 생성되었다. 상당한 비율의 키메라들이 순전히 정렬된 리드로부터 구축되었다.

[0214] 이 방법들을 이용하여 총 652개의 세스퀴테르펜 합성효소 키메라들을 생성하였다.

[0215] *tblastn 파이프라인*

[0216] 일반적으로, tblastn 파이프라인은 SQTS 스카폴드와 상동한 단편을 검출하는 민감성을 최대함으로써, 잠재적으로 사용가능한 서열들을 폭넓게 고려한다.

[0217] 구체적으로, 하기 단계들을 이용하여 각각의 꽃으로부터의 DNA 단편과 다양한 SQTS 스카폴드들의 정렬을 생성하였다:

[0218] 1. (전술된) SPADES 콘티그의 모든 프레임 번역을 검색하기 위해 SQTS 스카폴드의 1521-세트를 tblastn에 대한 단백질 질의로서 사용하였다.

[0219] 2. 휴리스틱(heuristic) 함수로 히트(정렬된 콘티그)를, 스카폴드에 대한 최소 40% 동일성 및 히트 동일성에 의존하는 최소 길이까지 여과하였다. 모든 샘플들 전체에 걸쳐 히트 길이 대 동일성의 도표를 검사함으로써 여과 기준을 선택하였다.

[0220] 3. 각각의 히트에 대한 동일한 잔기의 수로 스카폴드를 계층적으로 클러스터링함으로써 스카폴드의 다운샘플링을 수행하였다. 그의 모든 히트들 전체에 걸쳐 동일성의 가장 큰 수를 가진 각각의 클러스터 내의 스카폴드를, 키메라 재구축을 위해 보관하였다. 다운샘플링은 스카폴드의 수를 20배까지 감소시켰다. 10개 미만의 스카폴드가 히트를 가진 샘플의 경우에는 이 단계를 생략하였다.

[0221] 4. 일부 스카폴드들은 활성을 가진 것으로서 이미 확인되었고/되었거나 문헌에 공지되어 있었기 때문에 (또 다른 서열이 히트에 대한 더 큰 동일성을 가진 경우조차도) 클러스터 표시로서 항상 선택되었다. 이 바람직한 스카폴드들을 다운샘플링하지 않았고, 키메라 구축을 위해 tblastn 히트를 보관하였다.

[0222] 5. Clustal Omega를 이용하여 스카폴드를 히팅하는 모든 콘티그들의 정렬된 부분들을 스카폴드에 재정렬시켰다. 콘티그의 정렬되지 않은 부분들은 인트론을 대표할 가능성이 높기 때문에 버려졌다. 그 다음, 키메라 구축을 위해 이 정렬을 사용하였다.

[0223] 6. 하위영역에서의 다운샘플링 없이 전술된 조합적 양립가능한 단편 방법을 이용하여 정렬된 tblastn 히트로부터 키메라를 구축하였다. "최대-커버리지"(각각의 세트에서 가능한 많은 양립가능한 단편들) 키메라 및 "최소-커버리지"(각각의 세트에서 오직 하나의 양립가능한 단편) 키메라 둘 다를 생성하였다. 최소-커버리지 키메라는 무관한 서열들로부터의 단편들의 조합을 피할 수 있다.

[0224] tblastn 파이프라인은 10,114개의 "최대-커버리지" 키메라들 및 2,624개의 "최소-커버리지" 키메라들을 제공하였다. 일부 최대-커버리지 키메라들을 CD-HIT로 95% 동일성까지 다운샘플링하였다. 이것은 388개(모호한 아미노산을 가진 서열을 제거한 후 382개)의 서열들이라는 결과를 제공하였다. 일부 최대-커버리지 키메라들을 60%의 최소 희귀 DNA 함량까지 여과하고 90% 동일성까지 다운샘플링하였다. 이것은 1320개의 서열들이라는 결과를 제공하였다. 일부 최소-커버리지 키메라들을 10%의 최소 희귀 DNA 함량까지 여과하고 CD-HIT로 95% 동일성까지 다운샘플링하였다.

[0225] *코딩 및 합성 순서*

[0226] 각각의 효소를 2회 코돈 최적화하였다: 효모 발현 가중 코돈 표를 사용하여 한 번, 그리고 10% 미만의 빈도를 가진 코돈을 제거한 후 효모 발현 가중 코돈 표를 사용하여 한 번. 상이한 무작위 수를, 각각의 코딩을 위한 시드로서 사용하였다. 상이한 효소들을 코딩하는 것은 완전 독립적이었다 - 스카폴드로부터 키메라에 의해 유전된 잔기에서 코돈을 보존하기 위해 특정 절차를 이용하지 않았다.

[0227] 키메라 효소를 코딩하는 서열을, pGAL1에 의해 유도되고 tCYC1에 의해 종결되는 pESC-URA3 스크리닝 벡터 내로 클로닝하였다.

[0228] *현존 전사체에 의해 보조된 키메라 재구축*

[0229] 멸종된 꽃 종들 중 하나인 *쇼레아 쿠스피다타*의 경우, 현존 동족인 *쇼레아 베카리아나*(*Shorea beccariana*)에 대한 전사체 서열분석 데이터를 이용할 수 있었다. 이것은 관련 꽃으로부터의 SQTS 스카폴드를 사용하여 키메라를 구축하는 것을 가능하게 하였다. 이것을 2-단계 공정에서 수행하였다:

[0230] 1. *에스. 베카리아나*(Sb) 전사체 데이터를 어셈블링하고 SQTS 상동체에 대해 조사하였다. NCBI SRA 데이터베이스로부터의 데이터 세트 SRR687302로부터 데이터를 다운로딩하였다. 트리니티(Trinity)를 이용하여 어셈블리를 수행하였고, 트랜스디코더(Transdecoder)를 통해 ORF를 예측하였다. BLAST를 이용하여 1,500개의 큐레이션된 SQTS 서열들의 세트와 상동한 단편들을 확인하였다.

[0231] 2. 확인된 Sb SQTS 또는 SQTS 단편을, 키메라를 재구축하기 위한 tblastn 또는 blastn-mapDamage 파이프라인에서 스카폴드 서열로서 사용하였다. 스카폴드가 단편 그 자체인 경우, 이를 가장 가까운 Uniprot-출처의 SQTS 서

열로 병합하여 전체 길이 키메라를 생성하였다.

[0232] *스크리닝 균주 및 세스퀴테르펜 합성효소 형질전환*

[0233] 키메라 세스퀴테르펜 합성효소를 갈락토스 유도성 P(gal1) 프로모터의 제어 하에서 고카피 pESC-URA3 유래의 발현 벡터 내로 형질전환시켰다(본 목적을 위해 전체적으로 본원에 참고로 포함된 문헌(Sikorski *et al.*, A system of shuttle vectors and yeast host strains designed for efficient manipulation of DNA in Saccharomyces cerevisiae. *Genetics*. 1989 May;122(1):19-27)).

[0234] 이 벡터를, 4번 염색체 상의 자웅동체 스위칭 엔도뉴클레아제(YDL227C) 좌위(하기 표시된 서열번호 53 참조)에서 수렴 P(gal1) 프로모터의 제어 하에서 HMG-CoA 환원효소 1의 촉매작용 영역의 2개 카피의 통합을 통해 세스퀴테르펜 유동을 증가시키도록 변형된 일배체형 사카로마이세스 세레비지애 CEN.PK2 균주(MATa ura3-52 trp1-289 leu2-3_112 his3Δ1 MAL2-8C SUC2) 내로 형질전환시켰다(전체적으로 본원에 각각 참고로 포함된 문헌(Entian *et al.*, Yeast Genetic Strain and Plasmid Collections. *Methods in Microbiology*. 2007; (36): 629-666); 문헌(tHMG1, Donald *et al.*, Effects of overproduction of the catalytic domain of 3-hydroxy-3-methylglutaryl coenzyme A reductase on squalene synthesis in Saccharomyces cerevisiae. *Appl Environ Microbiol*. 1997 Sep;63(9):3341-4); 문헌(Ozaydin *et al.*, Carotenoid-based phenotypic screen of the yeast deletion collection reveals new genes with roles in isoprenoid production. Metab Eng. 2013 Jan;15:174-83) 참조). Erg9(파르네실-디포스페이트 파르네실 트랜스퍼라제) 프로모터를 하기 서열번호 54로 표시된 메티오닌 억제성 Met3 프로모터로 대체하고 메티오닌을 함유하는 배지에서 항온처리함으로써 이 세포에서 파르네실 피로포스페이트에 대한 경쟁을 감소시켰다(본 목적을 위해 전체적으로 본원에 각각 참고로 포함된 문헌(Ro *et al.*, Production of the antimalarial drug precursor artemisinic acid in engineered yeast. *Nature*. 2006 Apr 13;440(7086):940-3); 및 문헌(Asadollahi *et al.*, Production of plant sesquiterpenes in Saccharomyces cerevisiae: effect of ERG9 repression on sesquiterpene biosynthesis. *Biotechnol Bioeng*. 2008 Feb 15;99(3):666-77) 참조). 하향조절된 Erg9를 갖고 4번 염색체 상의 갈락토스 유도성 tHMG1의 2개 카피를 함유하는 이 균주는 t119889로서 명명되었다.

[0235] 본 목적을 위해 전체적으로 본원에 참고로 포함된 문헌(Gietz *et al.*, Yeast transformation by the LiAc/SS Carrier DNA/PEG method. *Methods Mol Biol*. 2006;313:107-20)에서 입증된 화학적 형질전환 기법을 이용하여 균주 t119889 내로의 키메라 세스퀴테르펜 벡터의 형질전환을 수행하였다.

[0236] *세스퀴테르펜 생성 및 추출*

[0237] 형질전환체 콜로니를 96 딥웰 플레이트 내의 300 ㎕ SC-ura 배지(2% 덱스트로스를 가진 완전 합성, 첨가된 우라실 없음) 내로 접종하였다. 상기 플레이트를 엑셀 사이언티픽 애로실(Excel Scientific AeroSeal) 막(BS-25)으로 덮고 진탕 항온처리기 내에서 30℃에서 48시간 동안 항온처리하였다. 30 ㎕의 배양물(1:15 희석)을, 탄소 공급원으로서 1.8% 갈락토스 및 0.2% 라피노스를 함유하는 420 ㎕의 SC-ura 유도 배지와 혼합하여, 대략 0.1 내지 0.2의 출발 600 nm 광학 밀도(OD_{600})를 제공하였다. 0.88% 도데칸 오버레이(4 ㎕)를 각각의 웰에 첨가하였고, 플레이트를 애로실 막으로 덮고 4일 동안 진탕 항온처리기 내에서 30℃에서 항온처리하였다. 상기 4일의 말기에 OD_{600}을 측정하기 위해 15 ㎕의 각각의 배양물을 회수하였다. 350 ㎕의 에틸 아세테이트(250 μM 트리데칸 내부)를 각각의 웰에 직접 첨가하고 혼합하였다(1:1 추출). 그 다음, 96 웰 플레이트를 원심분리하였고, 에틸 아세테이트 추출물을 GC-MS로 분석할 때까지 -80℃에서 유리 바이알 내에서 저장하였다.

[0238] *세스퀴테르펜 구조 확인*

[0239] 에틸 아세테이트 샘플(1.0 ㎕)을 아질런트(Agilent)/게르스텔(Gerstel) 7890B GC 시스템 내로 주입하였는데, 이때 GC 입구는 2:1의 분할 비로 250C로 설정되었다. 모세관 컬럼은 1.5 ㎖/분으로 설정된 담체 기체(헬륨) 유동을 가진 아질런트 DB-5MS(20 m X 0.18 mm X 0.18 ㎛)이었다. GC 오븐 온도를 100℃로 설정하고(0.10 분 동안 유지) 40℃/분의 속도로 155℃까지 상승시킨 후, 15℃/분의 속도로 190℃까지 상승시킨 후, 마지막으로 75℃/분의 속도로 280C까지 변화시켰다(5분 방법). 표적의 보다 더 포괄적인 분석을 위해, GC 오븐 온도를 100℃로 설정하고(2.0분 동안 유지), 10℃/분의 속도로 250℃까지 상승시키는(2.0분 동안 유지) 방법(20분 방법)을 이용하였다. 상기 두 방법들에 대한 MS 공급원 및 사중극자를 아질런트 5977B MSD(Etune) 상에서 각각 230℃ 및 180℃로 설정하였다. 질량 스캔 범위를 40 내지 250 mz로 설정하였는데, 이때 사용가능한 표준물 및 정유 이외에 스펙트럼 및 선형 보유 지수 계산을 NIST MS 데이터베이스(2008 버전)와 일치시켰다.

[0240] 추출된 이온 크로마토그램(204.2 mz 모 질량)에 존재하는 피크를 6가지 방식들 중 하나로 확인하였다(표 3 참조). 생성물의 검증을 위해 이 스크린에서 사용된 인증된 표준물은 베타-카리오필렌(Sigma-Aldrich 카탈로그 # W225207-SAMPLE-K), 베타-파르네센(Sigma-Aldrich 카탈로그 # 73492-1ML-F), 트랜스-네롤리돌(Sigma-Aldrich 카탈로그 # 18143-100MG-F), 및 알파-후물렌(Sigma-Aldrich 카탈로그 # 53675-1ML)이었다. 구조 확인을 보조하기 위해 사용된 세스퀴테르펜 농후 정유는 하기 식물로부터 유래하였다: 로덴드론(Rhodendron), 스위트 바실(Sweet Basil), 블랙 페퍼(Black Pepper), 시트로넬라(Citronella), 일랑(Ylang), 발삼 코파이바(Balsam copaiba) 및 파촐리(Patchouli)

4번 염색체 상의 ΔHO(YDL227C)::2xP(gal)-tHMG1 통합

AGGGTTCGCAAGTCCTGTTTCTATGCCTTTCTCTTAGTAATTCACGAAATAAACCT
ATGGTTTACGAAATGATCCACGAAAATCATGTTATTATTTACATCAACATATCGCG
AAAATTCATGTCATGTCCACATTAACATCATTGCAGAGCAACAATTCATTTTCATAG
AGAAATTTGCTACTATCACCCACTAGTACTACCATTGGTACCTACTACTTTGAATTG
TACTACCGCTGGGCGTTATTAGGTGTGAAACCACGAAAAGTTCACCATAACTTCGA
ATAAAGTCGCGGAAAAAAGTAAACAGCTATTGCTACTCAAATGAGGTTTGCAGAAG
CTTGTTGAAGCATGATGAAGCGTTCTAAACGCACTATTCATCATTAAATATTTAAA
GCTCATAAAATTGTATTCAATTCCTATTCTAAATGGCTTTTATTTCTATTACAACTA
TTAGCTCGATGCACGAGCGCAACGCTCACAACGCTCGTCCAACGCCGGCGGACCT*ACG*
GATTAGAGCCGCCGAGCGGGTGACAGCCCTCCGAAGGAAGACTCTCCTCCGTGCGTCCTCG
TCTTCACCGGTCGCGTTCCTGAAACGCAGATGTGCCTCGCGCCGCACTGCTCCGAACAATAA
AGATTCTACAATACTAGCTTTTATGGTTATGAAGAGGAAAAATTGGCAGTAACCTGGCCCCACA
AACCTTCAAATGAACGAATCAAATTAACAACCATAGGATGATAATGCGATTAGTTTTTTAGCCTT
ATTTCTGGGGTAATTAATCAGCGAAGCGATGATTTTTGATCTATTAACAGATATATAAATGCAAA
AACTGCATAACCACTTTAACTAATACTTTCAACATTTTCGGTTTGTATTACTTCTTATTCAAATGT
*AATAAAAGTATCAACAAAAAATTGTTAATATACCTCTATACTTTAACGTCAAGGAGAAAAAACT*A
TA**ATGGCTGCAGACCAATTGGTGAAGACTGAAGTCACCAAGAAGTCTTTTACTGCT**
CCTGTACAAAAGGCTTCTACACCAGTTTTAACCAATAAAACAGTCATTTCTGGATC
GAAAGTCAAAAGTTTATCATCTGCGCAATCGAGCTCATCAGGACCTTCATCATCTA
GTGAGGAAGATGATTCCCGCGATATTGAAAGCTTGGATAAGAAAATACGTCCTTTA
GAAGAATTAGAAGCATTATTAAGTAGTGGAAATACAAAACAATTGAAGAACAAAGA
GGTCGCTGCCTTGGTTATTCACGGTAAGTTACCTTTGTACGCTTTGGAGAAAAAAT
TAGGTGATACTACGAGAGCGGTTGCGGTACGTAGGAAGGCTCTTTCAATTTTGGC
AGAAGCTCCTGTATTAGCATCTGATCGTTTACCATATAAAAATTATGACTACGACC
GCGTATTTGGCGCTTGTTGTGAAAATGTTATAGGTTACATGCCTTTGCCCGTTGGT
GTTATAGGCCCCTTGGTTATCGATGGTACATCTTATCATATACCAATGGCAACTAC
AGAGGGTTGTTTGGTAGCTTCTGCCATGCGTGGCTGTAAGGCAATCAATGCTGGC
GGTGGTGCAACAACTGTTTTAACTAAGGATGGTATGACAAGAGGCCCAGTAGTCC
GTTTCCCAACTTTGAAAAGATCTGGTGCCTGTAAGATATGGTTAGACTCAGAAGAG
GGACAAAACGCAATTAAAAAAGCTTTTAACTCTACATCAAGATTTGCACGTCTGCA
ACATATTCAAACTTGTCTAGCAGGAGATTTACTCTTCATGAGATTTAGAACAACTA
CTGGTGACGCAATGGGTATGAATATGATTTCTAAGGGTGTCGAATACTCATTAAAG
CAAATGGTAGAAGAGTATGGCTGGGAAGATATGGAGGTTGTCTCCGTTTCTGGTA
ACTACTGTACCGACAAAAAACCAGCTGCCATCAACTGGATCGAAGGTCGTGGTAA
GAGTGTCGTCGCAGAAGCTACTATTCCTGGTGATGTTGTCAGAAAAGTGTTAAAAA
GTGATGTTTCCGCATTGGTTGAGTTGAACATTGCTAAGAATTTGGTTGGATCTGCA
ATGGCTGGGTCTGTTGGTGGATTTAACGCACATGCAGCTAATTTAGTGACAGCTGT
TTTCTTGGCATTAGGACAAGATCCTGCACAAAATGTCGAAAGTTCCAACTGTATAA
CATTGATGAAAGAAGTGGACGGTGATTTGAGAATTTCCGTATCCATGCCATCCATC
GAAGTAGGTACCATCGGTGGTGGTACTGTTCTAGAACCACAAGGTGCCATGTTGG
ACTTATTAGGTGTAAGAGGCCCACATGCTACCGCTCCTGGTACCAACGCACGTCAA
TTAGCAAGAATAGTTGCCTGTGCCGTCTTGGCAGGTGAATTATCCTTATGTGCTGC
CCTAGCAGCCGGCCATTTGGTTCAAAGTTATATGACCCACAACAGGAAACCTGCTG
AACCAACAAAACCTAACAATTTGGACGCCACTGATATAAATCGTTTGAAAGATGGG
TCCGTCACCTGCATTAAATCCTAAGCTAGCTA***AGATCCGCTCTAACCGAAAAGGAAGG***

[0241]

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[0242]

[0243] **대문자, 굵은 글자체:** HO 업스트림 상동성 서열(서열번호 56)

[0244] *대문자, 이탤릭체 및 밑줄:* P(gal1)(서열번호 57)

[0245] **대문자, 밑줄 및 굵은 글자체:** *tHMG1*(서열번호 58)

[0246] ***대문자, 굵은 글자체 및 이탤릭체:*** CYC1 터미네이터(서열번호 59)

[0247] ***소문자, 굵은 글자체 및 이탤릭체:*** CYC1 터미네이터, 역상보체(서열번호 60)

[0248] **소문자, 밑줄 및 굵은 글자체:** *tHMG1*, 역상보체(서열번호 61)

[0249] *소문자, 이탤릭체 및 밑줄*: P(gal1), 역상보체(서열번호 62)

[0250] **소문자, 굵은 글자체:** H0 다운스트림 상동성 서열(서열번호 63)

포함된 플랭킹 유전자를 가진 Erg9의 업스트림에서의 P(met3) 통합

ATGTCCGGTAAATGGAGACTAGTGCTGACTGGGATAGGCAATCCAGAGCCTCAGT
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CATTATATAGAAGACGAACATTGTACGATACTAAGATCGGATGGCCAGTACATGAA
TCTAAGTGGAGAACAGGTGTGCAAGGTCTGGGCCCGGTACGCCAAGTACCAAGCC
CGACACGTTGTTATTCATGACGAGTTAAGTGTGGCGTGTGGAAAAGTGCAGCTCA
GAGCCCCCAGCACCAGTATTAGAGGTCATAATGGGCTGCGAAGTCTACTGAAATG
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GGGTCCCGCTCTAGAGACCCTGCGAGCGTCTCCCGCTGGGTTCTGGGAGCTCTAA
CTCCGCAGGAACTACAAACCTTGCTTACACAGAGTGAACCTGCTGCCTGGCGTGCT
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GCAACCAAAATAAGAAGCTTCTTTTATTCATTGAAATGATGAATATAAACCTAACAAAA
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[0251]

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tgatgaattggttccaacccaacaagaagaagagtacaagttcaatatggttttatctatcatcttgtccgttcttcttgggtttattatatat
acactttacacagagcgtga (서열번호 54)

[0252]

[0253] **대문자, 굵은 글자체 및 밑줄: 업스트림 서열 PTH1(YHR189W)**(서열번호 64)

[0254] 대문자 및 밑줄: P(met3)(서열번호 65)

[0255] **소문자, 굵은 글자체 및 밑줄: Erg9(YHR190W)**(서열번호 66)

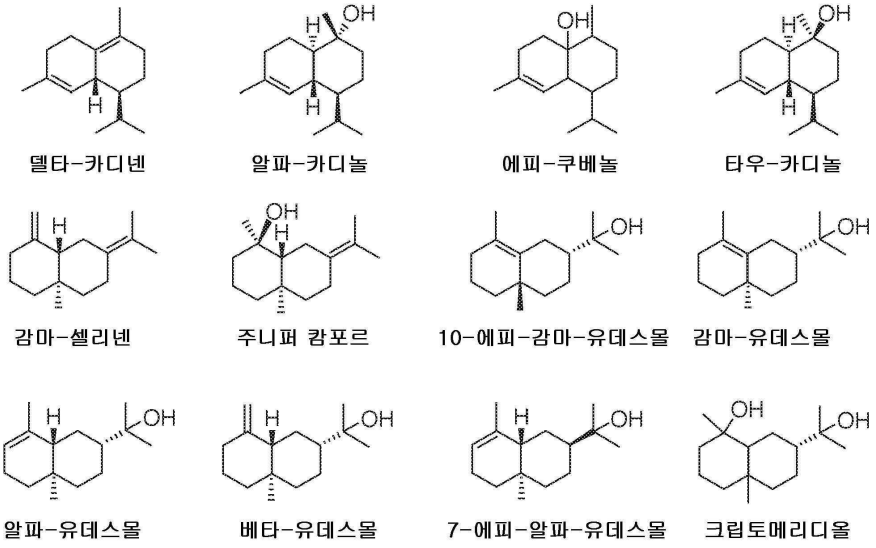
[0256] **균등물**

[0257] 당분야에서 숙련된 자라면, 통상적인 실험만을 이용하여 본원에 기재된 본 발명의 특정 실시양태들에 대한 많은 균등물을 인식하거나 확인할 수 있을 것이다. 이러한 균등물들은 하기 청구범위에 의해 포괄되도록 의도된다.

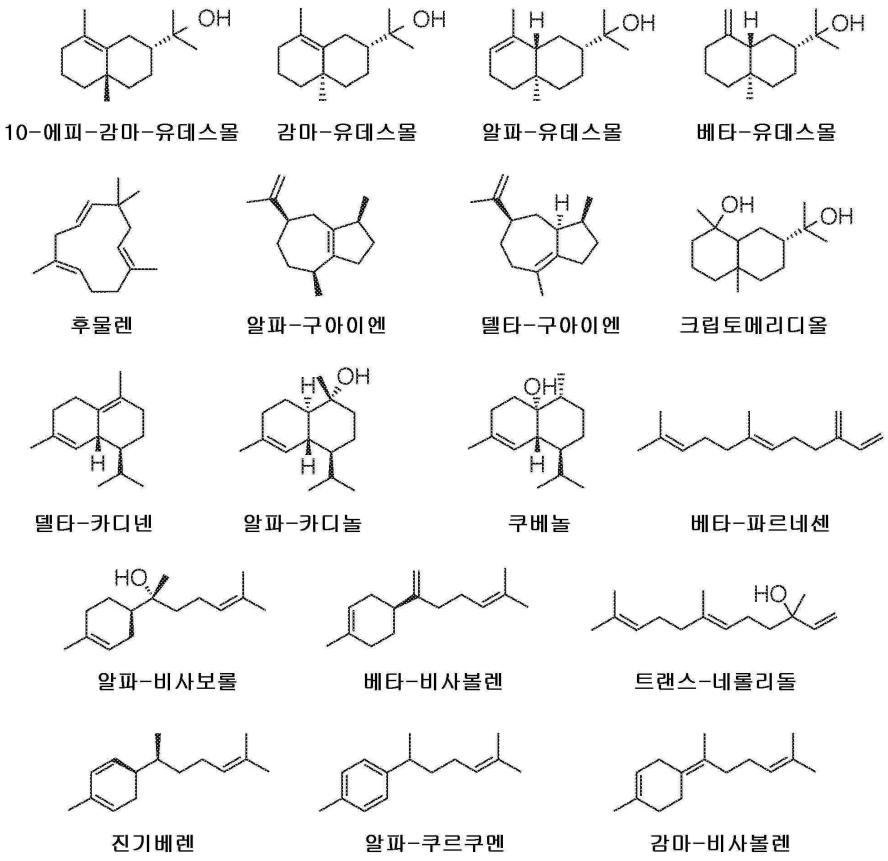
[0258] 본원에 개시된 특허 문헌들을 포함하는 모든 참고문헌들은, 특히 본원에서 참조된 개시내용을 위해, 전체적으로 참고로 포함된다.

도면

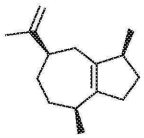
도면1


델타-카디넨
알파-카디놀
에피-쿠베놀
타우-카디놀
감마-셀리넨
주니퍼 캄포르
10-에피-감마-유데스몰
감마-유데스몰
알파-유데스몰
베타-유데스몰
7-에피-알파-유데스몰
크립토메리디올

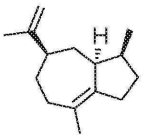
도면2


10-에피-감마-유데스몰
감마-유데스몰
알파-유데스몰
베타-유데스몰
후물렌
알파-구아이엔
델타-구아이엔
크립토메리디올
델타-카디넨
알파-카디놀
쿠베놀
베타-파르네센
알파-비사보롤
베타-비사볼렌
트랜스-네롤리돌
진기베렌
알파-쿠르쿠멘
감마-비사볼렌

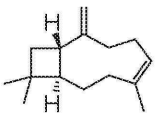
도면3



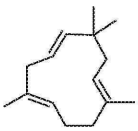
알파-구아이엔



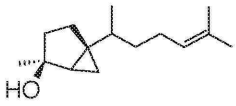
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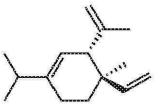
베타-카리오필렌



후물렌

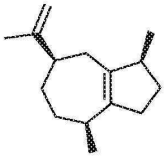


트랜스-세스퀴사비넨 수화물

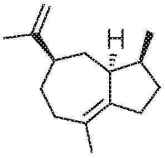


델타-엘레멘

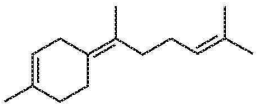
도면4



알파-구아이엔

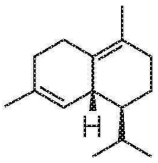


델타-구아이엔

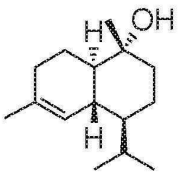


감마-비사볼렌

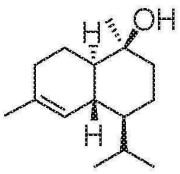
도면5



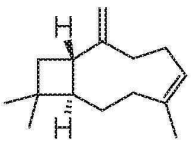
델타-카디넨



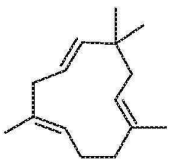
알파-카디놀



타우-카디놀

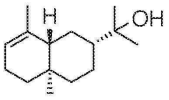


베타-카리오필렌

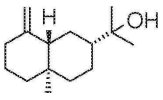


후물렌

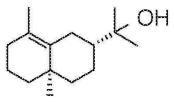
도면6



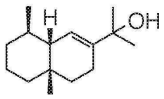
알파-유데스몰



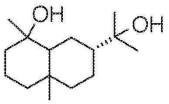
베타-유데스몰



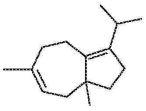
감마-유데스몰



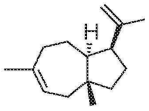
시스-유데슴-6-엔-11-올



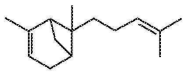
크립토메리디올



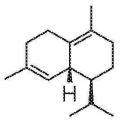
다우센



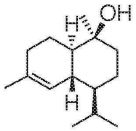
이소다우센



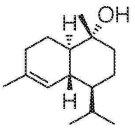
(알파)-트랜스-베르가모텐



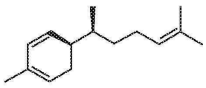
델타-카디넨



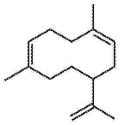
타우-카디놀



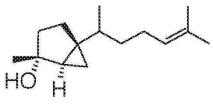
알파-카디놀



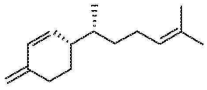
알파-진기베렌



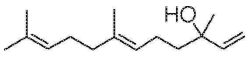
8-이소프로페닐-1,5-디메틸-1,5-사이클로데카디엔



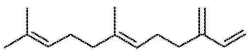
세스퀴사비넨 수화물



베타-세스퀴펠란드렌

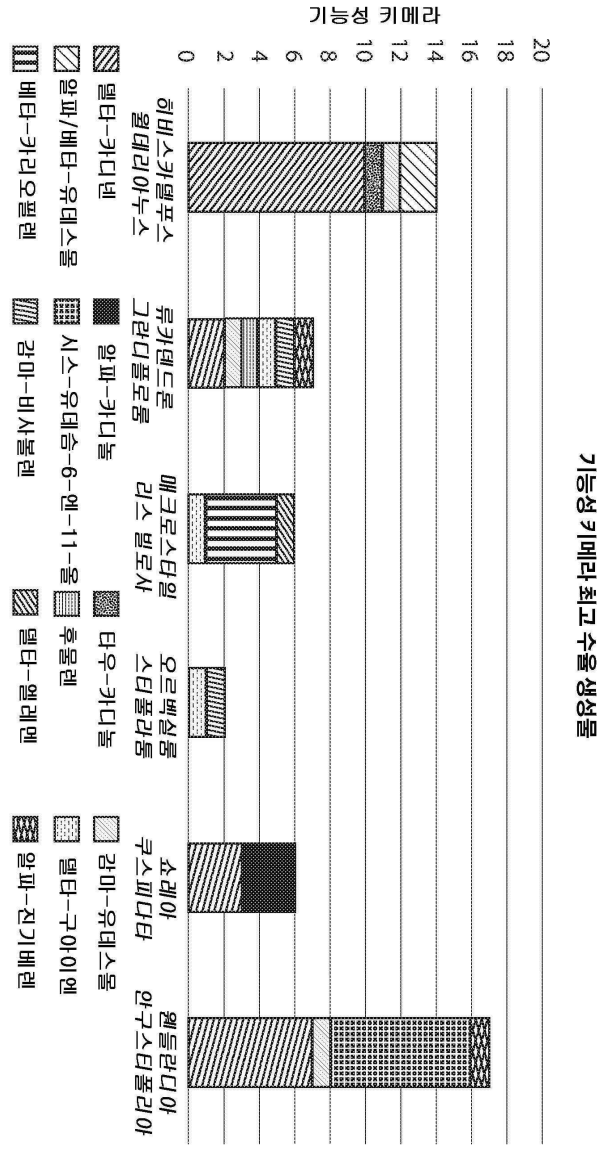


트랜스-네롤리돌

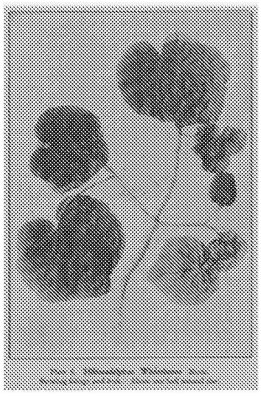


베타-파르네센

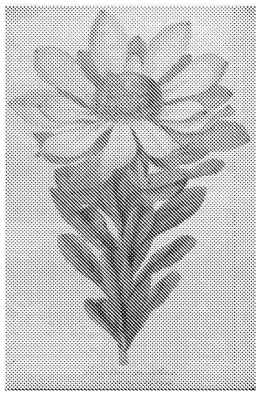
도면7


기능성 키메라 최고 수율 생성물
기능성 키메라
0
2
4
6
8
10
12
14
16
18
20
헤비스카델푸스 울데리아누스
퓨카덴드론 그란디플로룸
메크로스타일 라스 빌로사
오르벡실룸 스티폴라툼
쇼레아 쿠스피다타
웰틀라디아 안구스티폴리아
델타-카디넨
알파/베타-유데스몰
베타-카리오필렌
알파-카디놀
시스-유데슴-6-엔-11-올
감마-비사볼렌
타우-카디놀
델타-올레메
감마-유데스몰
델타-구아이엔
알파-진기베렌

도면8



8a



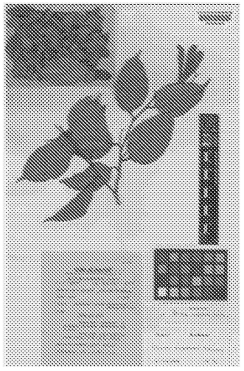
8b



8c



8d

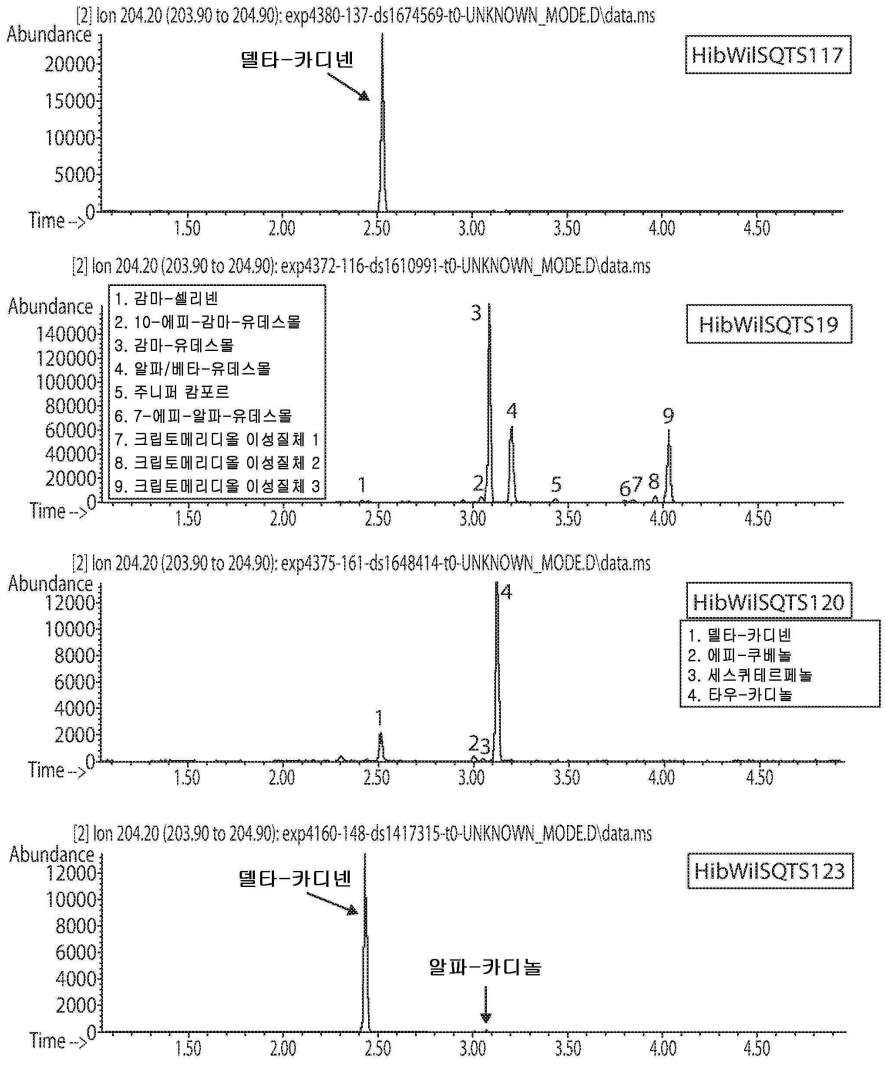


8e

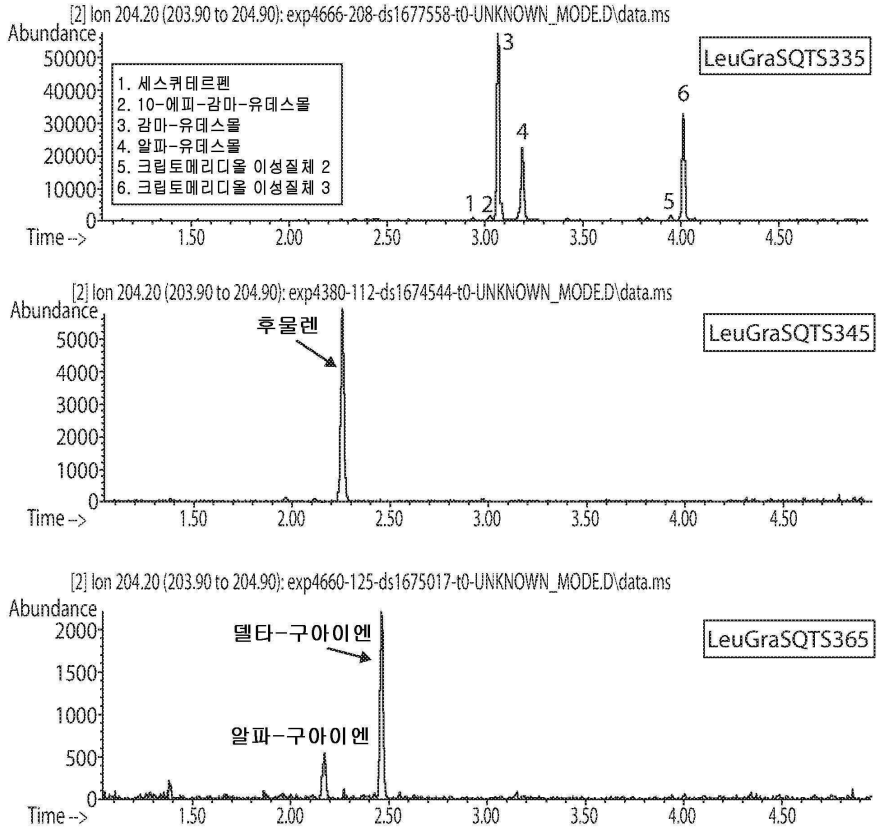


8f

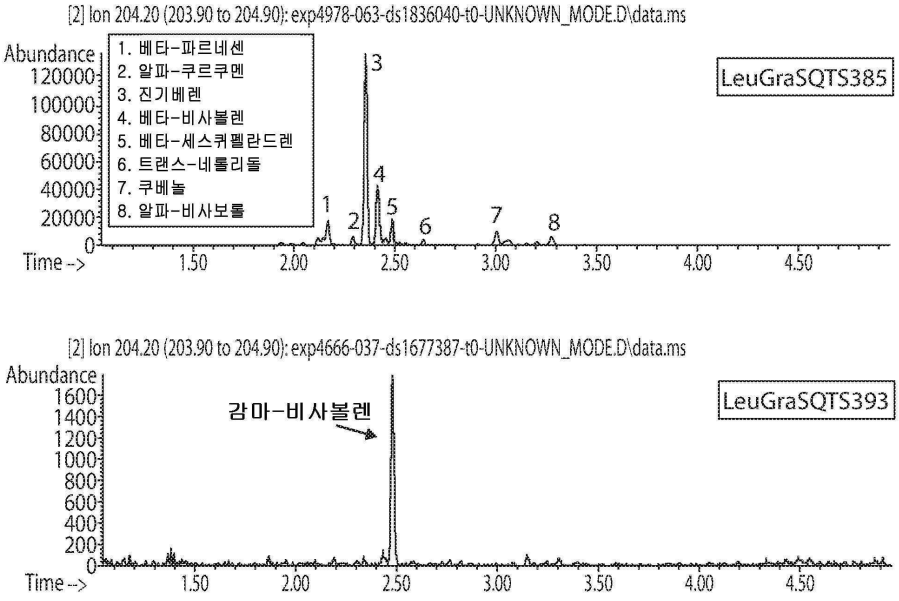
도면9


[2] Ion 204.20 (203.90 to 204.90): exp4380-137-ds1674569-t0-UNKNOWN_MODE.D\data.ms
Abundance
델타-카디넨
HibWilSQTS117
Time -->
[2] Ion 204.20 (203.90 to 204.90): exp4372-116-ds1610991-t0-UNKNOWN_MODE.D\data.ms
1. 감마-셀리넨
2. 10-에피-감마-유데스몰
3. 감마-유데스몰
4. 알파/베타-유데스몰
5. 주니퍼 캄포르
6. 7-에피-알파-유데스몰
7. 크립토메리디올 이성질체 1
8. 크립토메리디올 이성질체 2
9. 크립토메리디올 이성질체 3
HibWilSQTS19
[2] Ion 204.20 (203.90 to 204.90): exp4375-161-ds1648414-t0-UNKNOWN_MODE.D\data.ms
HibWilSQTS120
1. 델타-카디넨
2. 에피-쿠베놀
3. 세스퀴테르페놀
4. 타우-카디놀
[2] Ion 204.20 (203.90 to 204.90): exp4160-148-ds1417315-t0-UNKNOWN_MODE.D\data.ms
델타-카디넨
알파-카디놀
HibWilSQTS123

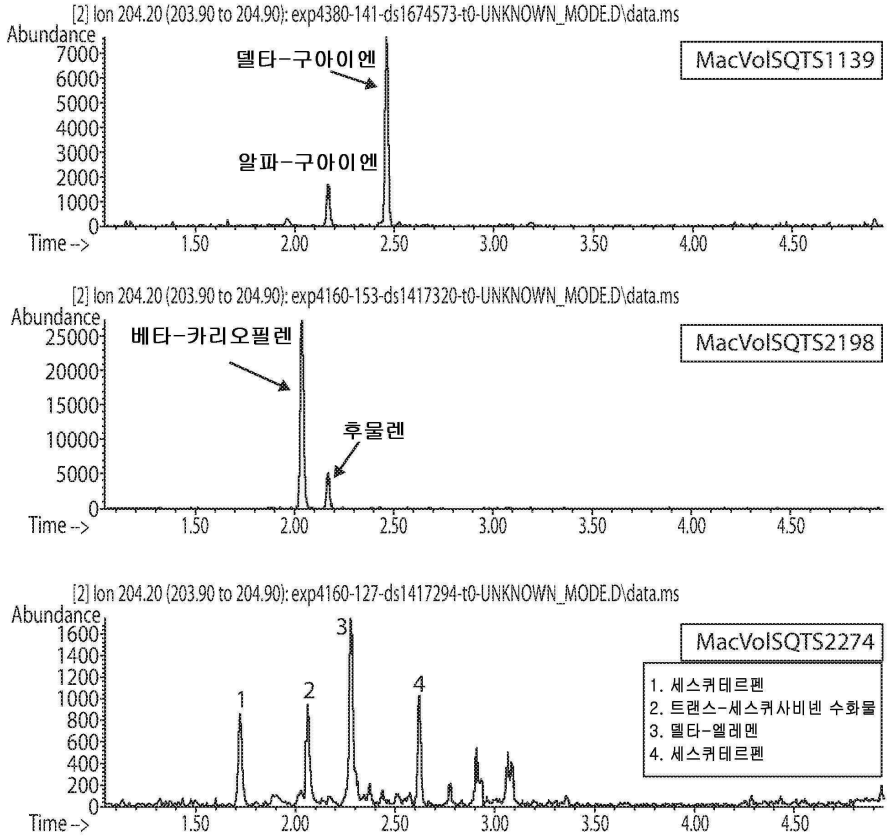
도면10


[2] Ion 204.20 (203.90 to 204.90): exp4666-208-ds1677558-t0-UNKNOWN_MODE.D\data.ms
Abundance
1. 세스퀴테르펜
2. 10-에피-감마-유데스몰
3. 감마-유데스몰
4. 알파-유데스몰
5. 크립토메리디올 이성질체 2
6. 크립토메리디올 이성질체 3
LeuGraSQTS335
Time -->
[2] Ion 204.20 (203.90 to 204.90): exp4380-112-ds1674544-t0-UNKNOWN_MODE.D\data.ms
Abundance
후물렌
LeuGraSQTS345
Time -->
[2] Ion 204.20 (203.90 to 204.90): exp4660-125-ds1675017-t0-UNKNOWN_MODE.D\data.ms
Abundance
델타-구아이엔
알파-구아이엔
LeuGraSQTS365
Time -->

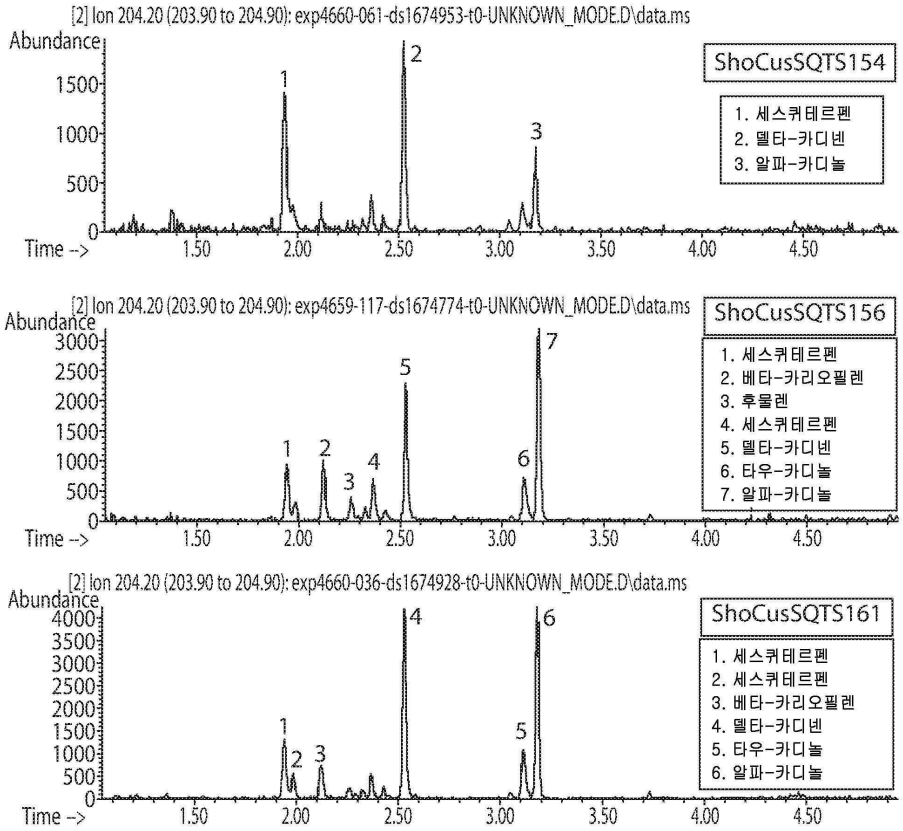
도면11


[2] Ion 204.20 (203.90 to 204.90): exp4978-063-ds1836040-t0-UNKNOWN_MODE.D\data.ms
Abundance
1. 베타-파르네센
2. 알파-쿠르쿠멘
3. 진기베렌
4. 베타-비사볼렌
5. 베타-세스퀴펠란드렌
6. 트랜스-네롤리돌
7. 쿠베놀
8. 알파-비사보롤
LeuGraSQTS385
Time -->
[2] Ion 204.20 (203.90 to 204.90): exp4666-037-ds1677387-t0-UNKNOWN_MODE.D\data.ms
Abundance
감마-비사볼렌
LeuGraSQTS393
Time -->

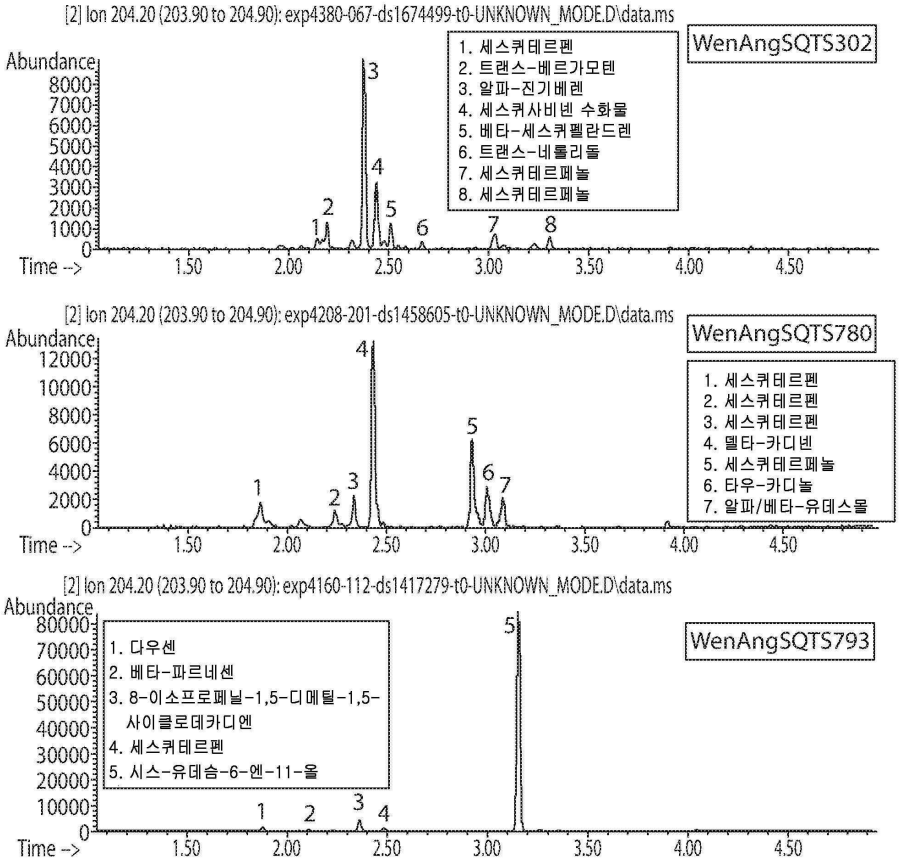
도면12


[2] Ion 204.20 (203.90 to 204.90): exp4380-141-ds1674573-t0-UNKNOWN_MODE.D\data.ms
Abundance
델타-구아이엔
알파-구아이엔
MacVolSQTS1139
Time -->
[2] Ion 204.20 (203.90 to 204.90): exp4160-153-ds1417320-t0-UNKNOWN_MODE.D\data.ms
Abundance
베타-카리오필렌
후물렌
MacVolSQTS2198
Time -->
[2] Ion 204.20 (203.90 to 204.90): exp4160-127-ds1417294-t0-UNKNOWN_MODE.D\data.ms
Abundance
MacVolSQTS2274
1. 세스퀴테르펜
2. 트랜스-세스퀴사비넨 수화물
3. 델타-엘레멘
4. 세스퀴테르펜
Time -->

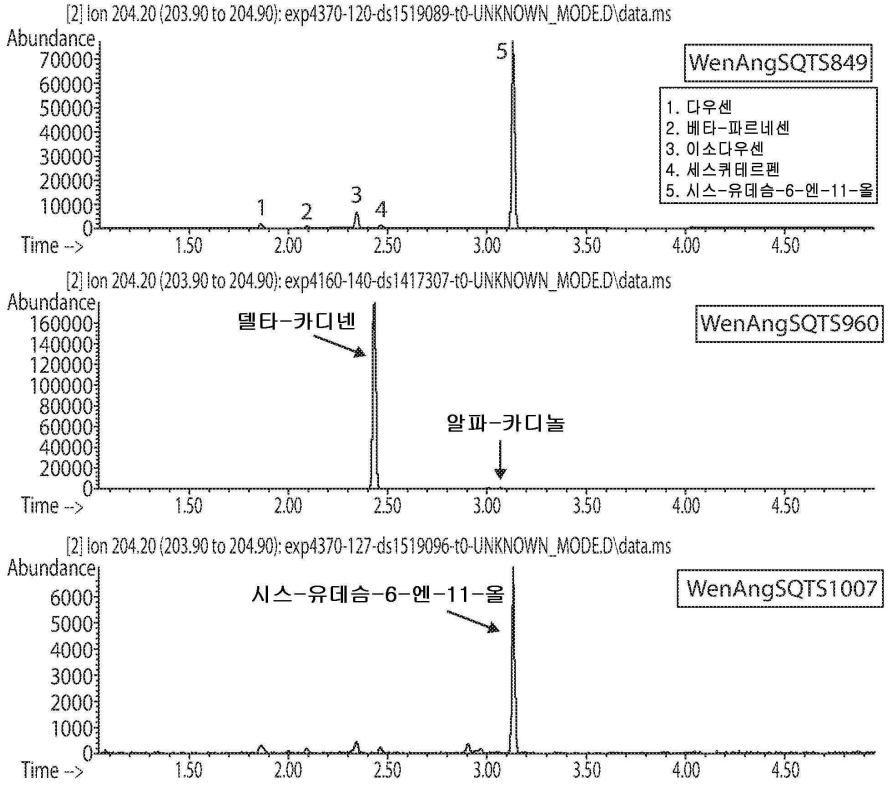
도면13


[2] Ion 204.20 (203.90 to 204.90): exp4660-061-ds1674953-t0-UNKNOWN_MODE.D\data.ms
Abundance
Time -->
ShoCusSQTS154
1. 세스퀴테르펜
2. 멜타-카디넨
3. 알파-카디놀
[2] Ion 204.20 (203.90 to 204.90): exp4659-117-ds1674774-t0-UNKNOWN_MODE.D\data.ms
Abundance
Time -->
ShoCusSQTS156
1. 세스퀴테르펜
2. 베타-카리오필렌
3. 후물렌
4. 세스퀴테르펜
5. 멜타-카디넨
6. 타우-카디놀
7. 알파-카디놀
[2] Ion 204.20 (203.90 to 204.90): exp4660-036-ds1674928-t0-UNKNOWN_MODE.D\data.ms
Abundance
Time -->
ShoCusSQTS161
1. 세스퀴테르펜
2. 세스퀴테르펜
3. 베타-카리오필렌
4. 멜타-카디넨
5. 타우-카디놀
6. 알파-카디놀

도면14


[2] Ion 204.20 (203.90 to 204.90): exp4380-067-ds1674499-t0-UNKNOWN_MODE.D\data.ms
WenAngSQTS302
1. 세스퀴테르펜
2. 트랜스-베르가모텐
3. 알파-진기베렌
4. 세스퀴사비넨 수화물
5. 베타-세스퀴펠란드렌
6. 트랜스-네롤리돌
7. 세스퀴테르페놀
8. 세스퀴테르페놀
[2] Ion 204.20 (203.90 to 204.90): exp4208-201-ds1458605-t0-UNKNOWN_MODE.D\data.ms
WenAngSQTS780
1. 세스퀴테르펜
2. 세스퀴테르펜
3. 세스퀴테르펜
4. 델타-카디넨
5. 세스퀴테르페놀
6. 타우-카디놀
7. 알파/베타-유데스몰
[2] Ion 204.20 (203.90 to 204.90): exp4160-112-ds1417279-t0-UNKNOWN_MODE.D\data.ms
WenAngSQTS793
1. 다우센
2. 베타-파르네센
3. 8-이소프로페닐-1,5-디메틸-1,5-사이클로데카디엔
4. 세스퀴테르펜
5. 시스-유데슴-6-엔-11-올
Abundance
Time -->

도면15


[2] Ion 204.20 (203.90 to 204.90): exp4370-120-ds1519089-t0-UNKNOWN_MODE.D\data.ms
WenAngSQTS849
1. 다우센
2. 베타-파르네센
3. 이소다우센
4. 세스퀴테르펜
5. 시스-유데슴-6-엔-11-올
[2] Ion 204.20 (203.90 to 204.90): exp4160-140-ds1417307-t0-UNKNOWN_MODE.D\data.ms
WenAngSQTS960
델타-카디넨
알파-카디놀
[2] Ion 204.20 (203.90 to 204.90): exp4370-127-ds1519096-t0-UNKNOWN_MODE.D\data.ms
WenAngSQTS1007
시스-유데슴-6-엔-11-올
Abundance
Time -->

서 열 목 록

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<130> G0919.70022WO00

<140> Not Yet Assigned

<141> Concurrently Herewith

<150> US 62/630,640

<151> 2018-02-14

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20 25 30

Met Phe Ile Ile Cys Pro Asp Thr Asp Ile Asp Ala Ala Thr Glu Leu
35 40 45

Gln Tyr Glu Glu Leu Lys Ala Gln Val Arg Lys Met Ile Met Glu Pro
50 55 60

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

Leu Gly Val Ser Tyr His Phe Glu Lys Glu Ile Glu Asp Glu Leu Glu

85 90 95

Asn Ile Tyr Arg Asp Thr Asn Asn Asn Asp Ala Asp Thr Asp Leu Tyr
100 105 110

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

115 120 125

Ser Cys Asp Ala Phe Asn Lys Leu Lys Asp Glu Glu Gly Asn Phe Lys

130 135 140

Ala Ser Leu Thr Ser Asp Val Pro Gly Leu Leu Glu Leu Tyr Glu Ala

145 150 155 160

Ser Tyr Leu Arg Val His Gly Glu Asp Ile Leu Asp Glu Ala Ile Ser

165 170 175

Phe Ala Thr Ala Gln Leu Thr Leu Ala Leu Pro Thr Leu His His Pro

180 185 190

Leu Ser Glu Gln Val Gly His Ala Leu Lys Gln Ser Ile Arg Arg Gly

195 200 205

Leu Pro Arg Val Glu Ala Arg Asn Phe Ile Ser Ile Tyr Gln Asp Leu

210 215 220

Glu Ser His Asn Lys Ala Leu Leu Gln Phe Ala Lys Ile Asp Phe Asn

225 230 235 240

Met Leu Gln Leu Leu His Arg Lys Glu Leu Ser Glu Ile Cys Arg Trp

245 250 255

Trp Lys Asp Leu Asp Phe Thr Arg Lys Leu Pro Phe Ala Arg Asp Arg

260 265 270

Val Val Glu Gly Tyr Phe Trp Ile Met Gly Val Tyr Phe Glu Pro Gln

275 280 285

Tyr Ser Leu Gly Arg Lys Met Leu Thr Lys Val Ile Ala Met Ala Ser

290 295 300

Ile Val Asp Asp Thr Tyr Asp Ser Phe Ala Thr Tyr Asp Glu Leu Ile

305 310 315 320

Pro Tyr Thr Asp Ala Ile Glu Arg Trp Asp Ile Lys Cys Met Asn Gln

325 330 335

Leu Pro Asn Tyr Met Gln Ile Ser Tyr Lys Ala Leu Leu Asp Val Tyr

340 345 350

Glu Glu Met Glu Gln Leu Leu Ala Asp Lys Gly Arg Gln Tyr Arg Val

355 360 365

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

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

465 470 475 480
Gln Glu Ala Tyr Asp Glu Phe Asn Lys His Ile Glu Ser Ser Trp Lys
485 490 495
Asp Val Asn Glu Glu Phe Leu Lys Pro Thr Glu Met Pro Thr Pro Val
500 505 510
Leu Cys Arg Ser Leu Asn Leu Ala Arg Val Met Asp Val Leu Tyr Arg
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Thr Ser Leu Leu Ile Asp Pro Ile Gln Ile
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20 25 30

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

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

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

Glu Ser His Asn Lys Ala Leu Leu Gln Phe Ala Lys Ile Asp Phe Asn
225 230 235 240
Met Leu Gln Leu Leu His Arg Lys Glu Leu Ser Glu Ile Cys Arg Trp
245 250 255
Trp Lys Asp Leu Asp Phe Thr Arg Lys Leu Pro Phe Ala Arg Asp Arg

260 265 270

Val Val Glu Gly Tyr Phe Trp Ile Met Gly Val Tyr Phe Glu Pro Gln

275 280 285

Tyr Ser Leu Gly Arg Lys Met Leu Thr Lys Val Ile Ala Met Ala Ser

290 295 300

Ile Val Asp Asp Thr Tyr Asp Ser Phe Ala Thr Tyr Asp Glu Leu Ile

305 310 315 320

Pro Tyr Thr Asp Ala Ile Glu Arg Trp Asp Ile Lys Cys Met Asn Gln

325 330 335

Leu Pro Asn Tyr Met Gln Ile Ser Tyr Lys Ala Leu Leu Asp Val Tyr

340 345 350

Glu Glu Met Glu Gln Leu Leu Ala Asp Lys Gly Arg Gln Tyr Arg Val

355 360 365

Glu Tyr Ala Lys Lys Ala Met Ile Arg Leu Val Gln Ala Tyr Leu Leu

370 375 380

Glu Ala Lys Trp Thr His Leu Asn Tyr Lys Pro Thr Phe Glu Glu Phe

385 390 395 400

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

405 410 415

Ala Phe Val Gly Met Gly Glu Val Ile Thr Pro Glu Thr Phe Glu Trp

420 425 430

Ala Ala Ser Asp Pro Lys Ile Ile Lys Ala Ser Thr Ile Ile Cys Arg

435 440 445

Phe Met Asp Asp Ile Ala Glu His Lys Phe Asn His Arg Arg Glu Asp

450 455 460

Asp Cys Ser Ala Ile Glu Cys Tyr Met Lys Gln Tyr Gly Ala Thr Ala

465 470 475 480

Gln Glu Ala Tyr Asp Glu Phe Asn Lys His Ile Glu Ser Ser Trp Lys

485 490 495

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

500 505 510

Leu Cys Arg Ser Leu Asn Leu Ala Arg Val Met Asp Val Leu Tyr Arg
515 520 525
Glu Gly Asp Gly Tyr Thr His Val Gly Lys Ala Ala Lys Gly Gly Ile
530 535 540

Thr Ser Leu Leu Ile Asp Pro Ile Gln Ile
545 550

<210> 3
<211> 554
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 3
Ala Ser Gln Ala Ser Gln Val Leu Ala Ser Pro His Pro Ala Ile Ser
1 5 10 15
Ser Glu Asn Arg Pro Lys Ala Asp Phe His Pro Gly Ile Trp Gly Asp
20 25 30
Met Phe Ile Ile Cys Pro Asp Thr Asp Ile Asp Ala Ala Thr Glu Leu

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

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

Ser Tyr Leu Arg Val His Gly Glu Asp Ile Leu Asp Glu Ala Ile Ser

165 170 175

Phe Ala Thr Ala Gln Leu Thr Leu Ala Leu Pro Thr Leu His His Pro

180 185 190

Leu Ser Glu Gln Val Gly His Ala Leu Lys Gln Ser Ile Arg Arg Gly

195 200 205

Leu Pro Arg Val Glu Ala Arg Asn Phe Ile Ser Ile Tyr Gln Asp Leu

210 215 220

Glu Ser His Asn Lys Ala Leu Leu Gln Phe Ala Lys Ile Asp Phe Asn

225 230 235 240

Met Leu Gln Leu Leu His Arg Lys Glu Leu Ser Glu Ile Cys Arg Trp

245 250 255

Trp Lys Asp Leu Asp Phe Thr Arg Lys Leu Pro Phe Ala Arg Asp Arg

260 265 270

Val Val Glu Gly Tyr Phe Trp Ile Met Gly Val Tyr Phe Glu Pro Gln

275 280 285

Tyr Ser Leu Gly Arg Lys Met Leu Thr Lys Val Ile Ala Met Ala Ser

290 295 300

Ile Val Asp Asp Thr Tyr Asp Ser Phe Ala Thr Tyr Asp Glu Leu Ile

305 310 315 320

Pro Tyr Thr Asp Ala Ile Glu Arg Trp Asp Ile Lys Cys Met Asn Gln

325 330 335

Leu Pro Asn Tyr Met Gln Ile Ser Tyr Lys Ala Leu Leu Asp Val Tyr

340 345 350

Glu Glu Met Glu Gln Leu Leu Ala Asp Lys Gly Arg Gln Tyr Arg Val

355 360 365

Glu Tyr Ala Lys Lys Ala Met Ile Arg Leu Val Gln Ala Tyr Leu Leu

370 375 380

Glu Ala Lys Trp Thr His Leu Asn Tyr Lys Pro Thr Phe Glu Glu Phe

385 390 395 400

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

405 410 415

Ala Phe Val Gly Met Gly Glu Val Ile Thr Pro Glu Thr Phe Glu Trp

420 425 430

Ala Ala Ser Asp Pro Lys Ile Ile Lys Ala Ser Thr Ile Ile Cys Arg

435 440 445

Phe Met Asp Asp Ile Ala Glu His Lys Phe Asn His Arg Arg Glu Asp

450 455 460

Asp Cys Ser Ala Ile Glu Cys Tyr Met Lys Gln Tyr Gly Ala Thr Ala

465 470 475 480

Gln Glu Ala Tyr Asp Glu Phe Asn Lys His Ile Glu Ser Ser Trp Lys

485 490 495

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

500 505 510

Leu Cys Arg Ser Leu Asn Leu Ala Arg Val Met Asp Val Leu Tyr Arg

515 520 525

Glu Gly Asp Gly Tyr Thr His Val Gly Lys Ala Ala Lys Gly Gly Ile

530 535 540

Thr Ser Leu Leu Ile Asp Pro Ile Gln Ile

545 550

<210> 4

<211> 554

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 4

Ala Ser Gln Ala Ser Gln Val Leu Ala Ser Pro His Pro Ala Ile Ser

1 5 10 15

Ser Glu Asn Arg Pro Lys Ala Asp Phe His Pro Gly Ile Trp Gly Asp

20 25 30

Met Phe Ile Ile Cys Pro Asp Thr Asp Ile Asp Ala Ala Thr Glu Leu

35 40 45

Gln Tyr Glu Glu Leu Lys Ala Gln Val Arg Lys Met Ile Met Glu Pro

50 55 60

Val Asp Asp Ser Asn Gln Lys Leu Pro Phe Ile Asp Ala Val Gln Arg

65 70 75 80

Leu Gly Val Ser Tyr His Phe Glu Lys Glu Ile Glu Asp Glu Leu Glu

85 90 95

Asn Ile Tyr Arg Asp Thr Asn Asn Asn Asp Ala Asp Thr Asp Leu Tyr

100 105 110

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

115 120 125

Ser Cys Glu Ala Phe Asn Lys Leu Lys Asp Glu Glu Gly Asn Phe Lys

130 135 140

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

145 150 155 160

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

165 170 175

Phe Thr Thr Ala Gln Leu Thr Leu Ala Leu Pro Thr Leu Asp Pro Pro

180 185 190

Leu Ser Glu Gln Val Gly His Ala Leu Lys Gln Ser Ile Arg Arg Gly

195 200 205

Leu Pro Arg Val Glu Ala Arg Asn Phe Ile Ser Ile Tyr Gln Asp Leu

210 215 220

Glu Ser His Asn Lys Ser Leu Leu Glu Phe Ala Lys Ile Asp Phe Asn

225 230 235 240

Leu Leu Gln Leu Leu His Arg Lys Glu Leu Ser Glu Ile Cys Arg Trp

245 250 255

Trp Lys Asp Leu Asp Phe Thr Arg Lys Leu Pro Phe Ala Arg Asp Arg

260 265 270

Val Val Glu Gly Tyr Phe Trp Ile Met Gly Val Tyr Phe Glu Pro Gln

275 280 285

Tyr Ser Leu Gly Arg Lys Met Leu Thr Lys Val Ile Ala Met Ala Ser

290 295 300

Ile Val Asp Asp Thr Tyr Asp Ser Phe Ala Thr Tyr Asp Glu Leu Ile

305 310 315 320

Pro Tyr Thr Asp Ala Ile Glu Arg Trp Asp Ile Lys Cys Met Asn Gln

325 330 335

Leu Pro Asn Tyr Met Gln Ile Ser Tyr Lys Ala Leu Leu Asp Val Tyr

340 345 350

Glu Glu Met Glu Gln Leu Leu Ala Asp Lys Gly Arg Gln Tyr Arg Val

355 360 365

Glu Tyr Ala Lys Lys Ala Met Ile Arg Leu Val Gln Ala Tyr Leu Leu

370 375 380

Glu Ala Lys Trp Thr His Leu Asn Tyr Lys Pro Thr Phe Glu Glu Phe

385 390 395 400

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

405 410 415

Ala Phe Val Gly Met Gly Glu Val Ile Thr Pro Glu Thr Phe Glu Trp

420 425 430

Ala Ala Ser Asp Pro Lys Ile Ile Lys Ala Ser Thr Ile Ile Cys Arg

435 440 445

Phe Met Asp Asp Ile Ala Glu His Lys Phe Asn His Arg Arg Glu Asp

450 455 460

Asp Cys Ser Ala Ile Glu Cys Tyr Met Glu Gln Tyr Lys Val Thr Ala

465 470 475 480

Gln Glu Ala Tyr Asp Glu Phe Asn Lys His Ile Glu Ser Ser Trp Lys

485 490 495

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

500 505 510

Leu Cys Arg Ser Leu Asn Leu Ala Arg Val Met Asp Val Leu Tyr Arg

515 520 525

Glu Gly Asp Gly Tyr Thr His Val Gly Lys Ala Ala Lys Gly Gly Ile

530 535 540

Thr Ser Leu Leu Ile Asp Pro Ile Gln Ile
545 550

<210> 5

<211> 554

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 5

Ala Ser Gln Ala Ser Gln Val Leu Ala Ser Pro His Pro Ala Ile Ser
1 5 10 15

Ser Glu Asn Arg Pro Lys Ala Asp Phe His Pro Gly Ile Trp Gly Asp
20 25 30

Met Phe Ile Ile Cys Pro Asp Thr Asp Ile Asp Ala Ala Thr Glu Leu
35 40 45

Gln Tyr Glu Glu Leu Lys Ala Gln Val Arg Lys Met Ile Met Glu Pro
50 55 60

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

Leu Gly Val Ser Tyr His Phe Glu Lys Glu Ile Glu Asp Glu Leu Glu
85 90 95

Asn Ile Tyr Arg Asp Thr Asn Asn Asn Asp Ala Asp Thr Asp Leu Tyr
100 105 110

Thr Thr Ala Leu Arg Phe Arg Leu Leu Arg Glu His Gly Phe Asp Ile
115 120 125

Ser Cys Asp Ala Phe Asn Lys Leu Lys Asp Glu Glu Gly Asn Phe Lys
130 135 140

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

Ser Tyr Leu Arg Val His Gly Glu Asp Ile Leu Asp Glu Ala Ile Ser
165 170 175

Phe Ala Thr Ala Gln Leu Thr Leu Ala Leu Pro Thr Leu His His Pro

180 185 190

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

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

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

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

Ala Ala Ser Asp Pro Lys Ile Ile Lys Ala Ser Thr Ile Ile Cys Arg
435 440 445

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

Leu Cys Arg Ser Leu Asn Leu Ala Arg Val Met Asp Val Leu Tyr Arg
515 520 525
Glu Gly Asp Gly Tyr Thr His Val Gly Lys Ala Ala Lys Gly Gly Ile
530 535 540
Thr Ser Leu Leu Ile Asp Pro Ile Gln Ile
545 550

<210> 6
<211> 554
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 6

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

65 70 75 80

Leu Gly Val Ser Tyr His Phe Glu Lys Glu Ile Glu Asp Glu Leu Glu

85 90 95

Asn Ile Tyr Arg Asp Thr Asn Asn Asn Asp Ala Asp Thr Asp Leu Tyr

100 105 110

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

115 120 125

Ser Cys Glu Ala Phe Asn Lys Leu Lys Asp Glu Glu Gly Asn Phe Lys

130 135 140

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

145 150 155 160

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

165 170 175

Phe Thr Thr Ala Gln Leu Thr Leu Ala Leu Pro Thr Leu Asp Pro Pro

180 185 190

Leu Ser Glu Gln Val Gly His Ala Leu Lys Gln Ser Ile Arg Arg Gly

195 200 205

Leu Pro Arg Val Glu Ala Arg Asn Phe Ile Ser Ile Tyr Gln Asp Leu

210 215 220

Glu Ser His Asn Lys Ser Leu Leu Glu Phe Ala Lys Ile Asp Phe Asn

225 230 235 240

Leu Leu Gln Leu Leu His Arg Lys Glu Leu Ser Glu Ile Cys Arg Trp

245 250 255

Trp Lys Asp Leu Asp Phe Thr Arg Lys Leu Pro Phe Ala Arg Asp Arg

260 265 270

Val Val Glu Gly Tyr Phe Trp Ile Met Gly Val Tyr Phe Glu Pro Gln

275 280 285

Tyr Ser Leu Gly Arg Lys Met Leu Thr Lys Val Ile Ala Met Ala Ser

290 295 300

Ile Val Asp Asp Thr Tyr Asp Ser Phe Ala Thr Tyr Asp Glu Leu Ile

305 310 315 320

Pro Tyr Thr Asp Ala Ile Glu Arg Trp Asp Ile Lys Cys Met Asn Gln

325 330 335

Leu Pro Asn Tyr Met Gln Ile Ser Tyr Lys Ala Leu Leu Asp Val Tyr

340 345 350

Glu Glu Met Glu Gln Leu Leu Ala Asp Lys Gly Arg Gln Tyr Arg Val

355 360 365

Glu Tyr Ala Lys Lys Ala Met Ile Arg Leu Val Gln Ala Tyr Leu Leu

370 375 380

Glu Ala Lys Trp Thr His Leu Asn Tyr Lys Pro Thr Phe Glu Glu Phe

385 390 395 400

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

405 410 415

Ala Phe Val Gly Met Gly Glu Val Ile Thr Pro Glu Thr Phe Glu Trp

420 425 430

Ala Ala Ser Asp Pro Lys Ile Ile Lys Ala Ser Thr Ile Ile Cys Arg

435 440 445

Phe Met Asp Asp Ile Ala Glu His Lys Phe Asn His Arg Arg Glu Asp

450 455 460

Asp Cys Ser Ala Ile Glu Cys Tyr Met Lys Gln Tyr Gly Ala Thr Ala

465 470 475 480

Gln Glu Ala Tyr Asp Glu Phe Asn Lys His Ile Glu Ser Ser Trp Lys

485 490 495

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

500 505 510

Leu Cys Arg Ser Leu Asn Leu Ala Arg Val Met Asp Val Leu Tyr Arg

515 520 525

Glu Gly Asp Gly Tyr Thr His Val Gly Lys Ala Ala Lys Gly Gly Ile

530 535 540

Thr Ser Leu Leu Ile Asp Pro Ile Gln Ile

545 550

<210> 7

<211> 554

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 7

Ala Ser Gln Ala Ser Gln Val Leu Ala Ser Pro His Pro Ala Ile Ser
1 5 10 15

Ser Glu Asn Arg Pro Lys Ala Asp Phe His Pro Gly Ile Trp Gly Asp
20 25 30

Met Phe Ile Ile Cys Pro Asp Thr Asp Ile Asp Ala Ala Thr Glu Leu
35 40 45

Gln Tyr Glu Glu Leu Lys Ala Gln Val Arg Lys Met Ile Met Glu Pro
50 55 60

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

Leu Gly Val Ser Tyr His Phe Glu Lys Glu Ile Glu Asp Glu Leu Glu
85 90 95

Asn Ile Tyr Arg Asp Thr Asn Asn Asn Asp Ala Asp Thr Asp Leu Tyr
100 105 110

Thr Thr Ala Leu Arg Phe Arg Leu Leu Arg Glu His Gly Phe Asp Ile
115 120 125

Ser Cys Asp Ala Phe Asn Lys Leu Lys Asp Glu Glu Gly Asn Phe Lys
130 135 140

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

Ser Tyr Leu Arg Val His Gly Glu Asp Ile Leu Asp Glu Ala Ile Ser
165 170 175

Phe Ala Thr Ala Gln Leu Thr Leu Ala Leu Pro Thr Leu His His Pro
180 185 190

Leu Ser Glu Gln Val Gly His Ala Leu Lys Gln Ser Ile Arg Arg Gly
195 200 205

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

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

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

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

450 455 460

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

Glu Gly Asp Gly Tyr Thr His Val Gly Lys Ala Ala Lys Gly Gly Ile
530 535 540
Thr Ser Leu Leu Ile Asp Pro Ile Gln Ile
545 550

<210> 8
<211> 556
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 8

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

Tyr Asn Glu Lys Tyr Ser Asp Asp Asp Thr Glu Asp Asp Leu Tyr Arg
100 105 110
Ile Ser Leu Arg Phe Arg Leu Leu Arg Gln His Gly Tyr Asn Val Ser
115 120 125
Cys Asp Lys Phe Asn Met Phe Lys Asp Asp Lys Gly Asn Phe Lys Glu
130 135 140
Ser Leu Ala Ser Asp Ala Leu Gly Met Leu Ser Leu Tyr Glu Ala Ala

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

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

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

340 345 350

Glu Ile Glu Lys Glu Ile Ala Asn Glu Gly Trp Ser Tyr Arg Val Gln

355 360 365

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

370 375 380

Ser Lys Trp Phe His Glu Asn Tyr Ile Pro Lys Met Glu Glu Tyr Met

385 390 395 400

Arg Val Ala Leu Val Thr Ser Gly Tyr Thr Met Leu Thr Thr Val Ser

405 410 415

Phe Leu Gly Met Asp Asn Ile Val Thr Lys Glu Thr Phe Asp Trp Val

420 425 430

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

435 440 445

Met Asp Asp Ile Lys Ser His Lys Phe Glu Gln Glu Arg Gly His Cys

450 455 460

Ala Ser Ala Val Glu Cys Tyr Met Arg Glu His Gly Val Ser Glu Glu

465 470 475 480

Glu Ala Cys Ser Glu Leu Lys Lys Gln Val Asp Asn Ala Trp Lys Asp

485 490 495

Ile Asn His Glu Met Ile Phe Ser Glu Thr Ser Lys Ala Val Pro Met

500 505 510

Ser Val Leu Thr Arg Val Leu Asn Leu Thr Arg Val Ile Asp Val Val

515 520 525

Tyr Lys Glu Gly Asp Gly Tyr Thr His Val Gly Asn Glu Met Lys Gln

530 535 540

Asn Val Ala Ala Leu Leu Ile Asp Gln Val Pro Ile

545 550 555

<210> 9

<211> 554

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 9

Glu Lys Gln Ser Leu Thr Phe Asp Gly Asp Glu Glu Ala Lys Ile Asp
1 5 10 15

Arg Lys Ser Ser Lys Tyr His Pro Ser Ile Trp Gly Asp Tyr Phe Ile
20 25 30

Gln Asn Ser Ser Leu Thr His Ala Lys Glu Ser Thr Gln Arg Met Ile
35 40 45

Lys Arg Val Glu Glu Leu Lys Val Gln Val Lys Ser Met Phe Lys Asp
50 55 60

Thr Ser Asp Leu Leu Gln Leu Met Asn Leu Ile Asn Ser Ile Gln Met
65 70 75 80

Leu Gly Leu Asp Tyr His Phe Glu Asn Glu Ile Asp Glu Ala Leu Arg
85 90 95

Leu Ile Tyr Glu Val Asp Asp Lys Ser Tyr Gly Leu Tyr Glu Thr Ser
100 105 110

Leu Arg Phe Gln Leu Leu Arg Gln His Gly Tyr His Val Asp Gly Glu
115 120 125

Glu Ala Phe Asn Met Leu Lys Asp Glu Glu Gly Asn Phe Lys Ala Ser
130 135 140

Leu Thr Ser Asp Val Pro Gly Leu Leu Glu Leu Tyr Gln Ala Ser Tyr
145 150 155 160

Met Arg Ile His Gly Glu Asp Ile Leu Asp Glu Ala Ile Ser Phe Thr
165 170 175

Thr Ala Gln Leu Thr Leu Ala Leu Pro Thr Leu Asp Pro Pro Leu Ser
180 185 190

Ala Gln Val Ser Leu Phe Leu Glu Leu Pro Leu Cys Arg Arg Asn Lys
195 200 205

Ile Leu Leu Ala Arg Lys Tyr Ile Leu Ile Tyr Gln Glu Asp Ala Met
210 215 220

Arg Asn Asn Val Ile Leu Glu Leu Ala Lys Leu Asn Phe Asn Leu Leu
225 230 235 240

Gln Ser Leu Tyr Gln Glu Glu Leu Lys Lys Ile Ser Ile Trp Trp Asn
245 250 255
Asp Leu Ala Phe Ala Lys Ser Leu Ser Phe Thr Arg Asp Arg Val Val
260 265 270
Glu Gly Tyr Tyr Trp Val Leu Thr Ile Tyr Phe Glu Pro Gln His Ser
275 280 285

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

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

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

Cys Glu Lys Leu Arg Glu Ile Val Glu Lys Ala Trp Lys Asp Leu Asn

485 490 495

Asn Glu Ser Leu Asn Pro Thr Lys Val Pro Arg Leu Met Ile Glu Arg

500 505 510

Ile Val Asn Leu Ser Lys Ser Asn Glu Glu Ile Tyr Lys Tyr Asn Asp

515 520 525

Thr Tyr Thr Asn Ser Asp Thr Thr Met Lys Asp Asn Ile Ser Leu Val

530 535 540

Leu Val Glu Ser Cys Asp Tyr Phe Asn Lys

545 550

<210> 10

<211> 556

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 10

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

1 5 10 15

Lys Asp Glu Met Arg Pro Lys Ala Asp Phe Gln Pro Ser Ile Trp Gly

20 25 30

Asp Leu Phe Leu Asn Cys Pro Asp Lys Asn Ile Asp Ala Glu Thr Glu

35 40 45

Lys Arg His Gln Gln Leu Lys Glu Glu Val Arg Lys Met Ile Val Ala

50 55 60

Pro Met Ala Asn Ser Thr Gln Lys Leu Ala Phe Ile Asp Ser Val Gln

65 70 75 80

Arg Leu Gly Val Ser Tyr His Phe Thr Lys Glu Ile Glu Asp Glu Leu

85 90 95

Glu Asn Ile Tyr His Asn Asn Asn Asp Ala Glu Asn Asp Leu Tyr Thr

100 105 110

Thr Ser Leu Arg Phe Arg Leu Leu Arg Glu His Gly Phe Asn Val Ser

115 120 125

Cys Asp Val Phe Asn Lys Phe Lys Asp Glu Gln Gly Asn Phe Lys Ser

130 135 140

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

145 150 155 160

Tyr Leu Arg Val His Gly Glu Asp Ile Leu Asp Glu Ala Ile Ser Phe

165 170 175

Thr Thr Asn His Leu Ser Leu Ala Val Ala Ser Leu Asp Tyr Pro Leu

180 185 190

Ser Glu Glu Val Ser His Ala Leu Lys Gln Ser Ile Arg Arg Gly Leu

195 200 205

Pro Arg Val Glu Ala Arg His Tyr Leu Ser Val Tyr Gln Asp Ile Glu

210 215 220

Ser His Asn Lys Val Leu Leu Glu Phe Ala Lys Ile Asp Phe Asn Met

225 230 235 240

Val Gln Leu Leu His Arg Lys Glu Leu Ser Glu Ile Ser Arg Trp Trp

245 250 255

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

260 265 270

Val Glu Gly Tyr Phe Trp Ile Ser Gly Val Tyr Phe Glu Pro Gln Tyr

275 280 285

Ser Leu Gly Arg Lys Met Leu Thr Lys Val Ile Ala Met Ala Ser Ile

290 295 300

Val Asp Asp Thr Tyr Asp Ser Tyr Ala Thr Tyr Glu Glu Leu Ile Pro

305 310 315 320

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

325 330 335

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

340 345 350

Glu Met Glu Gln Leu Val Ala Lys His Gly Arg Gln Tyr Arg Val Glu

355 360 365

Tyr Ala Lys Asn Ala Met Ile Arg Leu Ala Gln Ser Tyr Leu Val Glu

370 375 380

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

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

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

545 550 555
<210> 11
<211> 554
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 11
Ala Ser Gln Val Ser Gln Met Pro Ser Ser Ser Pro Leu Ser Ser Asn
1 5 10 15
Lys Asp Glu Met Arg Pro Lys Ala Asp Phe Gln Pro Ser Ile Trp Gly
20 25 30

Asp Leu Phe Leu Asn Cys Pro Asp Lys Asn Ile Asp Ala Glu Thr Glu
35 40 45

Lys Arg His Gln Gln Leu Lys Glu Glu Val Arg Lys Met Ile Val Ala
50 55 60
Pro Met Ala Asn Ser Thr Gln Lys Leu Ala Phe Ile Asp Ser Val Gln
65 70 75 80
Arg Leu Gly Val Ser Tyr His Phe Thr Lys Glu Ile Glu Asp Glu Leu
85 90 95
Glu Asn Ile Tyr His Asn Asn Asn Asp Ala Glu Asn Asp Leu Tyr Thr
100 105 110

Thr Ser Ile Arg Phe Arg Leu Leu Arg Glu His Gly Tyr His Val Asp
115 120 125
Gly Glu Glu Ala Phe Asn Met Leu Lys Asp Glu Glu Gly Asn Phe Lys
130 135 140
Ala Ser Leu Thr Ser Asp Val Pro Gly Leu Leu Glu Leu Tyr Gln Ala
145 150 155 160
Ser Tyr Met Arg Ile His Gly Glu Asp Ile Leu Asp Glu Ala Ile Ser
165 170 175

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

Met Leu Gln Phe Leu His Arg Lys Glu Leu Ser Glu Ile Cys Arg Trp
245 250 255
Trp Lys Asp Leu Asp Phe Gln Arg Lys Leu Pro Tyr Ala Arg Asp Arg
260 265 270
Val Val Glu Gly Tyr Phe Trp Ile Ser Gly Val Tyr Phe Glu Pro Gln

275 280 285

Tyr Ser Leu Gly Arg Lys Met Leu Thr Lys Val Ile Ala Met Ala Ser

290 295 300

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

305 310 315 320

Pro Tyr Thr Asn Ala Ile Glu Arg Trp Asp Ile Lys Cys Ile Asp Glu

325 330 335

Ile Pro Glu Tyr Met Lys Pro Ser Tyr Lys Ala Leu Leu Asp Val Tyr

340 345 350

Glu Glu Met Val Gln Leu Val Ala Glu His Gly Arg Gln Tyr Arg Val

355 360 365

Glu Tyr Ala Lys Asn Ala Met Ile Arg Leu Ala Gln Ser Tyr Leu Val

370 375 380

Glu Ala Lys Trp Thr Leu Gln Asn Tyr Lys Pro Ser Phe Glu Glu Phe

385 390 395 400

Lys Ala Asn Ala Leu Pro Thr Cys Gly Tyr Ala Met Leu Ala Ile Thr

405 410 415

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

420 425 430

Ala Ala Ser Asp Pro Lys Ile Ile Gln Ala Ser Thr Ile Ile Cys Arg

435 440 445

Phe Met Asp Asp Val Ala Glu His Lys Phe Lys His Arg Arg Glu Asp

450 455 460

Asp Cys Ser Ala Ile Glu Cys Tyr Met Glu Glu Tyr Gly Val Thr Ala

465 470 475 480

Gln Glu Ala Tyr Asp Val Phe Asn Lys His Val Glu Ser Ala Trp Lys

485 490 495

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

500 505 510

Leu Asn Arg Ser Leu Asn Leu Ala Arg Val Met Asp Val Leu Tyr Arg

515 520 525

Glu Gly Asp Gly Tyr Thr Tyr Val Gly Lys Ala Ala Lys Gly Gly Ile
530 535 540
Thr Ser Leu Leu Ile Glu Pro Ile Ala Leu
545 550
<210> 12
<211> 557
<212
> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 12
Ala Ser Gln Ala Ser Gln Val Leu Ala Ser Pro His Pro Ala Ile Ser
1 5 10 15
Ser Glu Asn Arg Pro Lys Ala Asp Phe His Pro Gly Ile Trp Gly Asp
20 25 30
Met Phe Ile Ile Cys Pro Asp Thr Asp Ile Asp Ala Ala Thr Glu Leu
35 40 45
Gln Tyr Glu Glu Leu Lys Ala Gln Val Arg Lys Met Ile Met Glu Pro
50 55 60
Val Asp Asp Ser Asn Gln Lys Leu Pro Phe Ile Asp Ala Val Gln Arg
65 70 75 80
Leu Gly Val Ser Tyr His Phe Glu Lys Glu Ile Glu Asp Glu Leu Glu
85 90 95
Asn Ile Tyr Arg Asp Thr Asn Asn Asn Asp Ala Asp Thr Asp Leu Tyr
100 105 110
Thr Thr Ala Leu Arg Phe Arg Leu Leu Arg Glu His Gly Phe Asp Ile
115 120 125
Ser Cys Asp Ala Phe Asn Lys Phe Lys Asp Glu Ala Gly Asn Phe Lys
130 135 140
Ala Ser Leu Thr Ser Asp Val Gln Gly Leu Leu Glu Leu Tyr Glu Ala
145 150 155 160
Ser Tyr Met Arg Val His Gly Glu Asp Ile Leu Asp Glu Ala Ile Ser
165 170 175

Phe Thr Thr Ala Gln Leu Thr Leu Ala Leu Pro Thr Leu His His Pro

180 185 190

Leu Ser Glu Gln Val Gly His Ala Leu Lys Gln Ser Ile Arg Arg Gly

195 200 205

Leu Pro Arg Val Glu Ala Arg Asn Phe Ile Ser Ile Tyr Gln Asp Leu

210 215 220

Glu Ser His Asn Lys Ser Leu Leu Gln Phe Ala Lys Ile Asp Phe Asn

225 230 235 240

Leu Leu Gln Leu Leu His Arg Lys Glu Leu Ser Glu Ile Cys Arg Trp

245 250 255

Trp Lys Asp Leu Asp Phe Thr Arg Lys Leu Pro Phe Ala Arg Asp Arg

260 265 270

Val Val Glu Gly Tyr Phe Trp Ile Met Gly Val Tyr Phe Glu Pro Gln

275 280 285

Tyr Ser Leu Gly Arg Lys Met Leu Thr Lys Val Ile Ala Met Ala Ser

290 295 300

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

305 310 315 320

Pro Tyr Thr Asn Ala Ile Glu Arg Trp Asp Ile Lys Cys Met Asn Gln

325 330 335

Leu Pro Asn Tyr Met Lys Ile Ser Tyr Lys Ala Leu Leu Asn Val Tyr

340 345 350

Glu Glu Met Glu Gln Leu Leu Ala Asn Gln Gly Arg Gln Tyr Arg Val

355 360 365

Glu Tyr Ala Lys Lys Ala Met Ile Arg Leu Val Gln Ala Tyr Leu Leu

370 375 380

Glu Ala Lys Trp Thr His Gln Asn Tyr Lys Pro Thr Phe Glu Glu Phe

385 390 395 400

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

405 410 415

Ala Phe Val Gly Met Gly Glu Val Ile Thr Pro Glu Thr Phe Lys Trp

420 425 430

Ala Ala Ser Asp Pro Lys Ile Ile Lys Ala Ser Thr Ile Ile Cys Arg

435 440 445

Phe Met Asp Asp Ile Ala Glu His Lys Phe Glu Gln Glu Arg Gly His

450 455 460

Cys Ala Ser Ala Val Glu Cys Tyr Met Arg Glu His Gly Val Ser Glu

465 470 475 480

Glu Glu Ala Cys Ser Glu Leu Lys Lys Gln Val Asp Asn Ala Trp Lys

485 490 495

Asp Ile Asn His Glu Met Ile Phe Ser Glu Thr Ser Lys Ala Val Pro

500 505 510

Met Ser Val Leu Thr Arg Val Leu Asn Leu Thr Arg Val Met Asp Val

515 520 525

Leu Tyr Arg Glu Gly Asp Gly Tyr Thr His Val Gly Lys Ala Ala Lys

530 535 540

Gly Gly Ile Thr Ser Leu Leu Ile Asp Pro Ile Gln Ile

545 550 555

<210> 13

<211> 548

<212> PRT

<213> Artificial Sequence

<220

><223> Synthetic polypeptide

<400> 13

Ala Ala Ser Phe Ala Asn Lys Cys Arg Pro Leu Ala Asn Phe His Pro

1 5 10 15

Thr Val Trp Gly Tyr His Phe Leu Tyr Tyr Asn Pro Glu Ile Thr Asn

20 25 30

Gln Glu Lys Ile Glu Val Asp Glu Tyr Lys Glu Thr Ile Arg Lys Met

35 40 45

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

50 55 60

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

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

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

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

305 310 315 320

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

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

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

Leu Thr Arg Val Ile Asp Thr Leu Tyr Gln Glu Glu Asp Glu Tyr Thr
515 520 525
Asn Ala Lys Gly Lys Leu Lys Asn Met Ile His Ser Ile Leu Ile Glu
530 535 540
Ser Val Lys Ile
545

<210> 14

<211> 557

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 14

Glu Lys Gln Ser Leu Thr Phe Asp Gly Asp Glu Glu Ala Lys Ile Asp
1 5 10 15

Arg Lys Ser Ser Lys Tyr His Pro Ser Ile Trp Gly Asp Tyr Phe Ile
20 25 30

Gln Asn Ser Ser Leu Thr His Ala Lys Glu Ser Thr Gln Arg Met Ile
35 40 45

Lys Arg Val Glu Glu Leu Lys Val Gln Val Lys Ser Met Phe Lys Asp
50 55 60

Thr Ser Asp Leu Leu Gln Leu Met Asn Leu Ile Asn Ser Ile Gln Met
65 70 75 80

Leu Gly Leu Asp Tyr His Phe Glu Asn Glu Ile Asp Glu Ala Leu Arg
85 90 95

Leu Ile Tyr Glu Val Asp Asp Lys Ser Tyr Gly Leu Tyr Glu Thr Ser
100 105 110

Leu Arg Phe Gln Leu Leu Arg Gln His Gly Tyr His Val Asp Gly Glu
115 120 125

Glu Ala Phe Asn Met Leu Lys Asp Glu Glu Gly Asn Phe Lys Ala Ser
130 135 140

Leu Thr Ser Asp Val Pro Gly Leu Leu Glu Leu Tyr Gln Ala Ser Tyr
145 150 155 160

Met Arg Ile His Gly Glu Asp Ile Leu Asp Glu Ala Ile Ser Phe Thr
165 170 175

Thr Ala Gln Leu Thr Leu Ala Leu Pro Thr Leu Asp Pro Pro Leu Ser
180 185 190

Ala Gln Val Ser Leu Phe Leu Glu Leu Pro Leu Cys Arg Arg Asn Lys

195 200 205

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

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

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

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

Asp Ile Arg Ser His Glu Phe Glu Gln Glu Arg Gly His Cys Ala Ser
450 455 460

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

Tyr Asn Asp Thr Tyr Thr Asn Ser Asp Thr Thr Met Lys Asp Asn Ile
530 535 540
Ser Leu Val Leu Val Glu Ser Cys Asp Tyr Phe Asn Lys
545 550 555

<210> 15
<211> 553
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 15

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

85 90 95

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

100 105 110

Ile Ser Leu Arg Phe Arg Leu Leu Arg Gln His Gly Tyr Asn Val Ser

115 120 125

Cys Asp Ala Phe Asn Arg Phe Lys Asp Thr Lys Gly Ser Phe Lys Glu

130 135 140

Asp Leu Ile Lys Asp Val Asn Ser Met Leu Cys Leu Tyr Glu Ala Thr

145 150 155 160

His Leu Arg Val His Gly Glu Asp Ile Leu Asp Glu Ala Leu Gly Phe

165 170 175

Thr Thr Ser Gln Leu Lys Ser Ile Leu Pro Lys Leu Lys Pro Leu Leu

180 185 190

Ala Ser Gln Val Met His Ala Leu Lys Gln Pro Leu His Arg Gly Leu

195 200 205

Pro Arg Leu Glu His Arg Arg Tyr Ile Ser Ile Tyr Gln Asp Asp Ala

210 215 220

Ser His Tyr Lys Ala Leu Leu Thr Leu Ala Lys Leu Asp Phe Asn Leu

225 230 235 240

Val Gln Ser Leu His Lys Lys Glu Leu Cys Glu Ile Ser Arg Trp Trp

245 250 255

Lys Asp Leu Asp Phe Ala Arg Lys Leu Pro Phe Ala Arg Asp Arg Met

260 265 270

Val Glu Cys Tyr Phe Trp Ile Leu Gly Val Tyr Phe Glu Pro Asn Tyr

275 280 285

Ser Leu Ala Arg Arg Ile Leu Thr Lys Val Ile Ala Met Thr Ser Ile

290 295 300

Ile Asp Asp Ile Tyr Asp Val Tyr Gly Thr Pro Glu Glu Leu Lys Leu

305 310 315 320

Phe Thr Glu Val Ile Glu Arg Trp Asp Glu Ser Ser Met Asp Gln Leu

325 330 335

Pro Glu Tyr Met Gln Thr Phe Phe Gly Ala Leu Leu Asp Leu Tyr Asn

340 345 350

Glu Ile Glu Lys Glu Ile Ala Asn Glu Gly Trp Ser Tyr Arg Val Gln

355 360 365

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

370 375 380

Ser Lys Trp Phe His Glu Asn Tyr Ile Pro Lys Met Glu Glu Tyr Met

385 390 395 400

Arg Val Ala Leu Val Thr Ser Gly Tyr Thr Met Leu Thr Thr Val Ser

405 410 415

Phe Leu Gly Met Asp Asn Ile Val Thr Lys Glu Thr Phe Asp Trp Val

420 425 430

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

435 440 445

Met Asp Asp Ile Lys Ser His Lys Phe Glu Gln Glu Arg Gly His Ala

450 455 460

Ala Ser Ala Val Glu Cys Tyr Met Lys Gln His Gly Leu Ser Glu Gln

465 470 475 480

Glu Val Cys Glu Glu Leu Tyr Arg Gln Val Ser Asn Ala Trp Lys Asp

485 490 495

Ile Asn Glu Glu Cys Leu Asn Pro Thr Ala Val Pro Met Pro Leu Leu

500 505 510

Met Arg Ala Leu Asn Leu Ala Arg Val Ile Asp Val Val Tyr Lys Glu

515 520 525

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

530 535 540

Ala Leu Leu Ile Asp Gln Val Pro Ile

545 550

<210> 16

<211> 558

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 16

Ser Ala Ala Gln Val Ser Pro Ala Pro Val Pro Ala His Asn Ala Ala
1 5 10 15

Ala Ser Lys Glu Glu Val Arg Arg Ser Ala Gly Tyr His Pro Ser Phe
20 25 30

Trp Gly Glu Phe Phe Leu Thr His Thr Ser Glu Tyr Ala Lys Lys Asp
35 40 45

Asp Lys Ile Gln Lys Gln His Glu Glu Leu Lys Gln Glu Val Lys Gly
50 55 60

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

Asp Ala Ile Leu Arg Leu Gly Val Gly Tyr His Phe Glu Asp Glu Ile
85 90 95

Gln Ala Glu Leu Glu Arg Ile His Arg Leu Gly Asp Leu Asp Cys Asp
100 105 110

Leu Tyr Asn Thr Cys Ile Trp Phe Arg Val Leu Arg Gly Gln Gly Phe
115 120 125

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

Phe Lys Glu Asp Leu Ile Asn Asp Val Ser Gly Met Leu Cys Leu Tyr
145 150 155 160

Glu Ala Thr His Leu Arg Val His Gly Glu Asp Ile Leu Asp Glu Ala
165 170 175

Leu Glu Phe Thr Thr Thr Arg Leu Lys Ser Ile Leu Pro Asp Leu Glu
180 185 190

Pro Pro Leu Ala Thr Gln Val Met His Ala Leu Glu Leu Pro Tyr His
195 200 205

Lys Gly Met Gln Arg Leu Glu Ala Arg Gln Tyr Ile Pro Ile Tyr Glu
210 215 220

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

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

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

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

465 470 475 480

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

Lys Asp Arg Ile Thr Ser Leu Leu Val His Pro Ile Thr Ile
545 550 555

<210> 17
<211> 549
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 17

Ser Ser Ala Lys Leu Gly Ser Ala Ser Glu Asp Val Asn Arg Arg Asp
1 5 10 15
Ala Asn Tyr His Pro Thr Val Trp Gly Asp Phe Phe Leu Thr His Ser
20 25 30
Ser Asn Phe Leu Glu Asn Asn Asp Ser Ile Leu Glu Lys His Glu Glu

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

100 105 110

Arg Leu Leu Arg Gly His Gly Phe Ser Ile Ser Ser Asp Ile Phe Asn
115 120 125
Lys Phe Lys Asn Ser Asp Gly Asn Phe Lys Glu Asp Leu Ile Asn Asp
130 135 140
Val Ser Gly Met Leu Cys Leu Tyr Glu Ala Thr His Leu Arg Val His
145 150 155 160
Gly Glu Asp Ile Leu Asp Glu Ala Leu Glu Phe Thr Thr Thr Arg Leu

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

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

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

355 360 365

Val Phe Lys Glu Ile Val Arg Ser Tyr Gln Arg Glu Ala Glu Tyr Phe

370 375 380

His Thr Gly Tyr Val Pro Ser Tyr Asp Glu Tyr Met Glu Asn Ser Ile

385 390 395 400

Ile Ser Gly Gly Tyr Lys Met Phe Ile Ile Leu Met Leu Ile Gly Arg

405 410 415

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

420 425 430

Glu Met Val Glu Ala Ser Ser Leu Ile Ala Arg Tyr Ile Asp Asp Leu

435 440 445

Gln Thr Tyr Lys Ala Glu Glu Glu Arg Gly Glu Thr Val Ser Ala Val

450 455 460

Arg Cys Tyr Met Arg Glu Phe Gly Val Ser Glu Glu Gln Ala Cys Lys

465 470 475 480

Lys Met Arg Glu Met Ile Glu Ile Glu Trp Lys Arg Leu Asn Lys Thr

485 490 495

Thr Leu Glu Ala Asp Glu Ile Ser Ser Ser Val Val Ile Pro Ser Leu

500 505 510

Asn Phe Thr Arg Val Leu Glu Val Met Tyr Asp Lys Gly Asp Gly Tyr

515 520 525

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

530 535 540

His Ala Ile Glu Ile

545

<210

> 18

<211> 553

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 18

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

1 5 10 15

Lys Asp Glu Met Arg Pro Lys Ala Asp Phe Gln Pro Ser Ile Trp Gly

20 25 30

Asp Leu Phe Leu Asn Cys Pro Asp Lys Asn Ile Asp Ala Glu Thr Glu

35 40 45

Lys Arg His Gln Gln Leu Lys Glu Glu Val Arg Lys Met Ile Val Ala

50 55 60

Pro Met Ala Asn Ser Thr Gln Lys Leu Ala Phe Ile Asp Ser Val Gln

65 70 75 80

Arg Leu Gly Val Ser Tyr His Phe Thr Lys Glu Ile Glu Asp Glu Leu

85 90 95

Glu Asn Ile Tyr His Asn Asn Asn Asp Ala Glu Asn Asp Leu Tyr Thr

100 105 110

Thr Ser Leu Arg Phe Arg Leu Leu Arg Glu His Gly Phe Asn Val Ser

115 120 125

Cys Asp Ala Phe Asn Arg Phe Lys Asp Thr Lys Gly Ser Phe Lys Glu

130 135 140

Asp Leu Ile Lys Asp Val Asn Ser Met Leu Cys Leu Tyr Glu Ala Thr

145 150 155 160

His Leu Arg Val His Gly Glu Asp Ile Leu Asp Glu Ala Leu Gly Phe

165 170 175

Thr Thr Ser Gln Leu Lys Ser Ile Leu Pro Lys Leu Lys Pro Leu Leu

180 185 190

Ala Ser Gln Val Met His Ala Leu Lys Gln Pro Leu Arg Arg Gly Leu

195 200 205

Pro Arg Val Glu Ala Arg His Tyr Leu Ser Val Tyr Gln Asp Ile Glu

210 215 220

Ser His Asn Lys Val Leu Leu Glu Phe Ala Lys Ile Asp Phe Asn Met

225 230 235 240

Val Gln Leu Leu His Arg Lys Glu Leu Ser Glu Ile Ser Arg Trp Trp

245 250 255

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

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

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

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

500 505 510

Asn Arg Ser Leu Asn Leu Ala Arg Val Met Asp Val Leu Tyr Arg Glu

515 520 525

Gly Asp Gly Tyr Thr Tyr Val Gly Lys Ala Ala Lys Gly Gly Ile Thr

530 535 540

Ser Leu Leu Ile Glu Pro Val Ala Leu

545 550

<210> 19

<211> 553

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 19

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

1 5 10 15

Lys Asp Glu Met Arg Pro Lys Ala Asp Phe Gln Pro Ser Ile Trp Gly

20 25 30

Asp Leu Phe Leu Asn Cys Pro Asp Lys Asn Ile Asp Ala Glu Thr Glu

35 40 45

Lys Arg His Gln Gln Leu Lys Glu Glu Val Arg Lys Met Ile Val Ala

50 55 60

Pro Met Ala Asn Ser Thr Gln Lys Leu Ala Phe Ile Asp Ser Val Gln

65 70 75 80

Arg Leu Gly Val Ser Tyr His Phe Thr Lys Glu Ile Glu Asp Glu Leu

85 90 95

Glu Asn Ile Tyr His Asn Asn Asn Asp Ala Glu Asn Asp Leu Tyr Thr

100 105 110

Thr Ser Ile Arg Phe Arg Leu Leu Arg Glu His Gly Tyr Asn Val Ser

115 120 125

Cys Asp Ile Phe Asn Lys Phe Lys Asn Ser Asp Gly Asn Phe Lys Glu

130 135 140

Asp Leu Ile Asn Asp Val Ser Gly Met Leu Cys Leu Tyr Glu Ala Thr

145 150 155 160

His Leu Arg Val His Gly Glu Asp Ile Leu Asp Glu Ala Leu Glu Phe

165 170 175

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

180 185 190

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

195 200 205

Pro Arg Val Glu Ala Arg His Tyr Leu Ser Val Tyr Gln Asp Ile Glu

210 215 220

Ser His Asn Lys Ala Leu Leu Glu Phe Ala Lys Ile Asp Phe Asn Met

225 230 235 240

Leu Gln Phe Leu His Arg Lys Glu Leu Ser Glu Ile Cys Arg Trp Trp

245 250 255

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

260 265 270

Val Glu Gly Tyr Phe Trp Ile Ser Gly Val Tyr Phe Glu Pro Gln Tyr

275 280 285

Ser Leu Gly Arg Lys Met Leu Thr Lys Val Ile Ala Met Ala Ser Ile

290 295 300

Val Asp Asp Thr Tyr Asp Ser Tyr Ala Thr Tyr Glu Glu Leu Ile Pro

305 310 315 320

Tyr Thr Asn Ala Ile Glu Arg Trp Asp Ile Lys Cys Ile Asp Glu Ile

325 330 335

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

340 345 350

Glu Met Val Gln Leu Val Ala Glu His Gly Arg Gln Tyr Arg Val Glu

355 360 365

Tyr Ala Lys Asn Ala Met Ile Arg Leu Ala Gln Ser Tyr Leu Val Glu

370 375 380

Ala Lys Trp Thr Leu Gln Asn Tyr Lys Pro Ser Phe Glu Glu Phe Lys

385 390 395 400

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

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

Asn Arg Ser Leu Asn Leu Ala Arg Val Met Asp Val Leu Tyr Arg Glu
515 520 525
Gly Asp Gly Tyr Thr Tyr Val Gly Lys Ala Ala Lys Gly Gly Ile Thr
530 535 540
Ser Leu Leu Ile Glu Pro Ile Ala Leu
545 550

<210> 20
<211> 541
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 20
Glu Ser Arg Arg Ser Ala Asn Tyr Gln Ala Ser Ile Trp Glu Thr Asn

1 5 10 15
Phe Thr Asn Ser Pro Leu Leu Ser Lys Leu Gln Asn Glu Leu Ser Val
20 25 30
Ala His Leu Glu Glu Leu Lys Leu Glu Val Lys Gln Leu Ile Trp Ser
35 40 45

Thr Lys Asp Pro Leu Phe Leu Leu Lys Phe Ile Asp Ser Ile Gln Arg

50 55 60

Leu Gly Val Ala Tyr His Phe Glu Glu Glu Ile Lys Glu Ser Leu His

65 70 75 80

Leu Val Tyr Leu Glu Glu Arg Asn Gly Asp His Gln His Tyr Lys Glu

85 90 95

Lys Gly Leu His Phe Thr Ala Leu Arg Phe Arg Ile Leu Arg Gln Asp

100 105 110

Gly Tyr His Val Pro Gln Asp Val Phe Ser Ser Phe Met Asn Lys Ala

115 120 125

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

130 135 140

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

145 150 155 160

Met Ala Lys Asp Phe Ser Ser His His Leu His Lys Met Val Glu Asp

165 170 175

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

180 185 190

Pro Leu His Arg Arg Val Gln Lys Leu Glu Ala Ile Trp Phe Ile Gln

195 200 205

Phe Tyr Glu Cys Gly Ser Asp Ala Asn Pro Thr Leu Val Glu Leu Ala

210 215 220

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

225 230 235 240

Arg Leu Ser Arg Trp Tyr Glu Glu Thr Gly Leu Gln Glu Lys Leu Ser

245 250 255

Phe Ala Arg His Arg Leu Ala Glu Ala Phe Leu Trp Ser Met Gly Ile

260 265 270

Ile Pro Glu Gly His Phe Gly Tyr Gly Arg Met His Leu Met Lys Ile

275 280 285

Gly Ala Tyr Ile Thr Leu Leu Asp Asp Ile Tyr Asp Val Tyr Gly Thr

290 295 300

Leu Glu Glu Leu Gln Val Leu Thr Glu Ile Ile Glu Arg Trp Asp Ile

305 310 315 320

Asn Leu Leu Asp Gln Leu Pro Glu Tyr Met Gln Ile Phe Phe Leu Tyr

325 330 335

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

340 345 350

Gly Ile Asn Val Ile Ser Asn Leu Lys Gly Leu Trp Val Glu Leu Ser

355 360 365

Gln Cys Tyr Phe Lys Glu Ala Thr Trp Phe His Asn Gly Tyr Thr Pro

370 375 380

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

385 390 395 400

Val Ile Leu Phe Ser Gly Tyr Phe Thr Thr Thr Asn Pro Ile Asn Lys

405 410 415

His Glu Leu Gln Ser Leu Glu Arg His Ala His Ser Leu Ser Met Ile

420 425 430

Leu Arg Leu Ala Asp Asp Leu Gly Thr Ser Ser Asp Glu Met Lys Arg

435 440 445

Gly Asp Val Pro Lys Ala Ile Gln Cys Phe Met Asn Asp Thr Gly Cys

450 455 460

Cys Glu Glu Glu Ala Arg Gln His Val Lys Arg Leu Ile Asp Ala Glu

465 470 475 480

Trp Lys Lys Met Asn Lys Asp Ile Leu Met Glu Lys Pro Phe Lys Asn

485 490 495

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

500 505 510

Glu His Gly Asp Gly Tyr Gly Gly Pro His Ser Asp Thr Lys Lys Lys

515 520 525

Met Val Ser Leu Phe Val Gln Pro Met Asn Ile Thr Ile

530 535 540

<210> 21

<211> 553

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 21

Glu Ser Gln Thr Thr Phe Lys Tyr Glu Ser Leu Ala Phe Thr Lys Leu
1 5 10 15

Ser His Cys Gln Trp Thr Asp Tyr Phe Leu Ser Val Pro Ile Asp Glu
20 25 30

Ser Glu Leu Asp Val Ile Thr Arg Glu Ile Asp Ile Leu Lys Pro Glu
35 40 45

Val Met Glu Leu Leu Ser Ser Gln Gly Asp Asp Glu Thr Ser Lys Arg
50 55 60

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

Phe Glu Asn Glu Ile Lys Asn Ile Leu Glu His Ala Phe Arg Lys Ile
85 90 95

Asp Asp Ile Thr Gly Asp Glu Lys Asp Leu Ser Thr Ile Ser Ile Met
100 105 110

Phe Arg Val Phe Arg Thr Tyr Gly His Asn Leu Pro Ser Ser Ile Phe
115 120 125

Asn Lys Phe Lys Asn Ser Asp Gly Asn Phe Lys Glu Asp Leu Ile Asn
130 135 140

Asp Val Ser Gly Met Leu Cys Leu Tyr Glu Ala Thr His Leu Arg Val
145 150 155 160

His Gly Glu Asp Ile Leu Asp Glu Ala Leu Glu Phe Thr Thr Thr Arg
165 170 175

Leu Lys Ser Ile Leu Pro Gly Gly Thr Cys Arg Pro His Ile Leu Arg
180 185 190

Leu Ile Arg Asn Thr Leu Tyr Leu Pro Gln Arg Trp Asn Met Glu Ala
195 200 205

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

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

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

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

Val Gly Met Gly Glu Thr Ala Gly Lys Glu Ala Tyr Glu Trp Val Arg
420 425 430
Ser Arg Pro Arg Leu Ile Lys Ser Leu Ala Ala Lys Gly Arg Leu Met
435 440 445
Asp Asp Ile Thr Asp Phe Asp Ser Asp Met Ser Asn Gly Phe Ala Ala

450 455 460

Asn Ala Ile Asn Tyr Tyr Met Lys Gln Phe Val Val Thr Lys Glu Glu
465 470 475 480

Ala Ile Leu Glu Cys Gln Arg Met Ile Val Asp Ile Asn Lys Thr Ile
485 490 495

Asn Glu Glu Leu Leu Lys Thr Thr Ser Val Pro Gly Arg Val Leu Lys
500 505 510

Gln Ala Leu Asn Phe Gly Arg Leu Leu Glu Leu Leu Tyr Thr Lys Ser
515 520 525

Asp Asp Ile Tyr Asn Cys Ser Glu Gly Lys Leu Lys Glu Tyr Ile Val
530 535 540

Thr Leu Leu Ile Asp Pro Ile Arg Leu
545 550

<210> 22

<211> 546

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 22

Ser Ser Ala Lys Leu Gly Ser Ala Ser Glu Asp Val Asn Arg Arg Asp
1 5 10 15

Ala Asn Tyr His Pro Thr Val Trp Gly Asp Phe Phe Leu Thr His Ser
20 25 30

Ser Asn Phe Leu Glu Asn Asn Asp Ser Ile Leu Glu Lys His Glu Gly

35 40 45

Leu Glu Gln Lys Ile Arg Thr Met Leu Ile Ser Pro Thr Asp Thr Ile
50 55 60

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

Tyr His Phe Glu Lys Glu Ile Glu Asp Glu Ile Glu Lys Leu Ser Cys
85 90 95

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

100 105 110

Arg Leu Leu Arg Gln Gln Gly Tyr Phe Val Ser Cys Asp Val Phe Lys

115 120 125

Arg Phe Lys Asn Thr Lys Gly Glu Phe Glu Thr Glu Asp Ala Arg Thr

130 135 140

Leu Trp Cys Leu Tyr Glu Ala Thr His Leu Arg Val Asp Gly Glu Asp

145 150 155 160

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

165 170 175

Leu Pro Glu Leu Ser Phe Pro Leu Asn Glu Cys Val Arg Asp Ala Leu

180 185 190

His Ile Pro Tyr His Arg Asn Val Gln Arg Leu Ala Ala Arg Gln Tyr

195 200 205

Ile Pro Gln Tyr Asp Ala Glu Pro Thr Lys Ile Glu Ser Leu Ser Leu

210 215 220

Phe Ala Lys Ile Asp Phe Asn Met Leu Gln Ala Leu His Gln Arg Glu

225 230 235 240

Leu Arg Glu Ala Ser Arg Trp Trp Lys Glu Phe Asp Phe Pro Ser Lys

245 250 255

Leu Pro Tyr Ala Arg Asp Arg Ile Ala Glu Gly Tyr Tyr Trp Met Met

260 265 270

Gly Ala His Phe Glu Pro Lys Phe Ser Leu Ser Arg Lys Phe Leu Asn

275 280 285

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

290 295 300

Gly Thr Leu Glu Glu Val Thr Leu Phe Thr Glu Ala Val Glu Arg Trp

305 310 315 320

Asp Ile Glu Ala Val Lys Asp Ile Pro Lys Tyr Met Gln Val Ile Tyr

325 330 335

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

340 345 350

Ala Arg Gly Lys Asp Tyr Cys Ile Asp Tyr Ala Ile Glu Val Phe Lys

355 360 365

Glu Ile Val Arg Ser Tyr Gln Arg Glu Ala Glu Tyr Phe His Thr Gly

370 375 380

Tyr Val Pro Ser Tyr Asp Glu Tyr Met Glu Asn Ser Ile Ile Ser Gly

385 390 395 400

Gly Tyr Lys Met Phe Ile Ile Leu Met Leu Ile Gly Arg Gly Glu Phe

405 410 415

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

420 425 430

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

435 440 445

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

450 455 460

Met Arg Glu Phe Gly Val Ser Glu Glu Gln Ala Cys Lys Lys Met Arg

465 470 475 480

Glu Met Ile Glu Ile Glu Trp Lys Arg Leu Asn Lys Thr Thr Leu Glu

485 490 495

Ala Asp Glu Ile Ser Ser Ser Val Val Ile Pro Ser Leu Asn Phe Thr

500 505 510

Arg Val Leu Glu Val Met Tyr Asp Lys Gly Asp Gly Tyr Ser Asp Ser

515 520 525

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

530 535 540

Glu Ile

545

<210> 23

<211> 566

<

212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 23

Arg Asp Leu Lys Ser Val Leu Ser Ser Lys Glu Ser Thr Lys Ala Asp
1 5 10 15

Val Asn Arg Arg Ser Ser Asn Tyr His Pro Ser Ile Trp Gly Asp His
20 25 30

Phe Ile Asn Val Ser Ser Asn Glu Lys Tyr Thr Asn Thr Glu Val Glu
35 40 45

Lys Arg Phe Glu Thr Leu Lys Ala Glu Ile Glu Lys Leu Leu Val Ser
50 55 60

Asn Asn Thr Ala Trp Lys Thr Leu Glu Glu Ile Val Ala Ile Val Asn
65 70 75 80

Gln Leu Gln Arg Leu Gly Leu Ala Tyr His Phe Glu Asn Gln Ile Lys
85 90 95

Glu Ala Leu Gln Ser Ile Tyr Asp Ser His Val Asn Gly Asn Cys Asp
100 105 110

Val Asn Tyr Asp His Asn Asn Asp Leu Tyr Ile Val Ala Leu Arg Phe
115 120 125

Arg Leu Leu Arg Gln His Gly Tyr Lys Val Ser Ala Asp Ile Phe Lys
130 135 140

Lys Phe Arg Asp Glu Lys Gly Glu Phe Lys Ala Met Leu Thr Asn Asp
145 150 155 160

Ala Lys Gly Leu Leu Cys Leu Tyr Glu Ala Ser Tyr Leu Arg Val Gln
165 170 175

Gly Glu Asn Ile Leu Glu Glu Ala Cys Glu Phe Ser Arg Lys His Leu
180 185 190

Lys Ser Leu Leu Ser His Leu Ser Thr Ser Leu Ala Glu Gln Val Lys
195 200 205

His Ser Leu Glu Ile Pro Leu His Arg Gly Met Pro Arg Leu Glu Ala
210 215 220

Arg His Tyr Ile Ser Ile Tyr Glu Glu Asp Asn Ser Ser Arg Asn Glu
225 230 235 240

Leu Ile Leu Glu Leu Ala Lys Leu Asp Phe Asn Leu Leu Gln Ala Leu

245 250 255

His Arg Arg Glu Leu Gly Glu Ile Ser Arg Trp Trp Lys Asp Ile Asp

260 265 270

Phe Ala Thr Lys Leu Pro Phe Ala Arg Asp Arg Leu Val Glu Cys Tyr

275 280 285

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

290 295 300

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

305 310 315 320

Tyr Asp Val Tyr Gly Thr Leu Glu Glu Leu Lys Leu Phe Thr His Ala

325 330 335

Ile Glu Arg Trp Glu Thr Val Ala Ala Asn Glu Leu Pro Lys Tyr Met

340 345 350

Gln Val Cys Tyr Phe Ala Leu Leu Asp Val Phe Lys Glu Met Glu Asp

355 360 365

Lys Leu Val Asn Lys Gly Leu Leu Tyr Ser Met Pro Cys Ala Lys Glu

370 375 380

Ala Val Lys Gly Leu Val Arg Ala Tyr Phe Val Glu Ala Glu Trp Phe

385 390 395 400

Asn Ala Asn Tyr Met Pro Thr Phe Glu Glu Tyr Met Glu Asn Ser Thr

405 410 415

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

420 425 430

Glu Asp Ala Thr Ile Ser Lys Glu Ala Phe Asp Trp Ala Ile Ser Val

435 440 445

Pro Lys Ile Ile Arg Ser Cys Ala Leu Ile Ala Arg Leu Val Asp Asp

450 455 460

Ile His Thr Tyr Lys Val Glu Gln Glu Arg Gly Asp Ala Pro Ser Ser

465 470 475 480

Val Glu Cys Tyr Met Gln Gln Tyr Asp Val Ser Glu Glu Glu Ala Cys

485 490 495

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

500 505 510

Glu Ile Gln Asp Pro Asn His Pro Pro Leu Gln Trp Leu Leu Pro Ser

515 520 525

Leu Asn Leu Ala Arg Met Met Val Val Leu Tyr Gln Asn Gly Asp Asn

530 535 540

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

545 550 555 560

Val Asp Pro Leu Pro Met

565

<210> 24

<211> 566

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 24

Arg Asp Leu Lys Ser Val Leu Ser Ser Lys Glu Ser Thr Lys Ala Asp

1 5 10 15

Val Asn Arg Arg Ser Ser Asn Tyr His Pro Ser Ile Trp Gly Asp His

20 25 30

Phe Ile Asn Val Ser Ser Asn Glu Lys Tyr Thr Asn Thr Glu Val Glu

35 40 45

Lys Arg Phe Glu Thr Leu Lys Ala Glu Ile Glu Lys Leu Leu Val Ser

50 55 60

Asn Asn Thr Ala Trp Lys Thr Leu Glu Glu Ile Val Ala Ile Val Asn

65 70 75 80

Gln Leu Gln Arg Leu Gly Leu Ala Tyr His Phe Glu Asn Gln Ile Lys

85 90 95

Glu Ala Leu Gln Ser Ile Tyr Asp Ser His Val Asn Gly Asn Cys Asp

100 105 110

Val Asn Tyr Asp His Asn Asn Asp Leu Tyr Ile Val Ala Leu Arg Phe
115 120 125

Arg Leu Leu Arg Gln His Gly Tyr Lys Val Ser Ala Asp Ile Phe Lys
130 135 140

Lys Phe Lys Asp Glu Lys Gly Glu Phe Lys Asp Met Ile Arg Asn Asp
145 150 155 160

Ala Arg Gly Leu Leu Cys Leu Tyr Glu Ala Ser His Leu Arg Val Lys
165 170 175

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

Lys Ser Leu Leu Pro Gln Leu Ser Thr Ser Leu Ala Glu Gln Val Lys
195 200 205

His Ser Leu Glu Ile Pro Leu His Arg Gly Met Pro Arg Leu Glu Ala
210 215 220

Arg His Tyr Ile Ser Ile Tyr Glu Glu Asn Asn Ser Ser Arg Asn Glu
225 230 235 240

Leu Leu Leu Glu Leu Ala Lys Leu Asp Phe Asn Leu Leu Gln Ala Leu
245 250 255

His Arg Arg Glu Leu Gly Asp Ile Ser Arg Trp Trp Lys Asp Ile Asp
260 265 270

Phe Ala Thr Lys Leu Pro Phe Ala Arg Asp Arg Leu Val Glu Cys Tyr
275 280 285

Phe Trp Ile Leu Gly Val Tyr Phe Glu Pro Lys Tyr Ser Ile Thr Arg
290 295 300

Lys Phe Met Thr Lys Val Ile Ala Ile Ala Ser Val Ile Asp Asp Ile
305 310 315 320

Tyr Asp Val Tyr Gly Thr Leu Glu Glu Leu Lys Leu Phe Thr His Ala
325 330 335

Ile Glu Arg Trp Glu Thr Val Ala Ala Asn Glu Leu Pro Lys Tyr Met
340 345 350

Gln Val Cys Tyr Phe Ala Leu Leu Asp Val Phe Lys Glu Met Glu Asp

355 360 365

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

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

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

Val Asp Pro Leu Pro Met
565

<210> 25
<211> 566
<212> PRT
<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 25

Arg Asp Leu Lys Ser Val Leu Ser Ser Lys Glu Ser Thr Lys Ala Asp
1 5 10 15

Val Asn Arg Arg Ser Ser Asn Tyr His Pro Ser Ile Trp Gly Asp His
20 25 30

Phe Ile Asn Val Ser Ser Asn Glu Lys Tyr Thr Asn Thr Glu Val Glu
35 40 45

Lys Arg Phe Glu Thr Leu Lys Ala Glu Ile Glu Lys Leu Leu Val Ser
50 55 60

Asn Asn Thr Ala Trp Lys Thr Leu Glu Glu Ile Val Ala Ile Val Asn
65 70 75 80

Gln Leu Gln Arg Leu Gly Leu Ala Tyr His Phe Glu Asn Gln Ile Lys
85 90 95

Glu Ala Leu Gln Ser Ile Tyr Asp Ser His Val Asn Gly Asn Cys Asp
100 105 110

Val Asn Tyr Asp His Asn Asn Asp Leu Tyr Ile Val Ala Leu Arg Phe
115 120 125

Arg Leu Leu Arg Gln His Gly Tyr Lys Val Ser Ala Asp Ile Phe Lys
130 135 140

Lys Phe Lys Asp Glu Lys Gly Glu Phe Lys Asp Met Ile Arg Asn Asp
145 150 155 160

Ala Arg Gly Leu Leu Cys Leu Tyr Glu Ala Ser His Leu Arg Val Lys
165 170 175

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

Lys Ser Leu Leu Pro Gln Leu Ser Thr Ser Leu Ala Glu Gln Val Lys
195 200 205

His Ser Leu Glu Ile Pro Leu His Arg Gly Met Pro Arg Leu Glu Ala
210 215 220

Arg His Tyr Ile Ser Ile Tyr Glu Glu Asn Asn Ser Ser Arg Asn Glu

225 230 235 240

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

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

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

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

Val Gln Cys Tyr Met Gln Gln Tyr Asp Val Ser Glu Glu Glu Ala Cys
485 490 495

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

Val Asp Pro Leu Pro Met
565

<210> 26
<211> 566
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 26
Arg Asp Leu Lys Ser Val Leu Ser Ser Lys Glu Ser Thr Lys Ala Asp
1 5 10 15
Val Asn Arg Arg Ser Ser Asn Tyr His Pro Ser Ile Trp Gly Asp His
20 25 30
Phe Ile Asn Val Ser Ser Asn Glu Lys Tyr Thr Asn Thr Glu Val Glu
35 40 45

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

100 105 110

Val Asn Tyr Asp His Asn Asn Asp Leu Tyr Ile Val Ala Leu Arg Phe
115 120 125
Arg Leu Leu Arg Gln His Gly Tyr Lys Val Ser Ala Asp Ile Phe Lys
130 135 140
Lys Phe Lys Asp Glu Lys Gly Glu Phe Lys Asp Met Ile Arg Asn Asp
145 150 155 160
Ala Arg Gly Leu Leu Cys Leu Tyr Glu Ala Ser His Leu Arg Val Lys
165 170 175

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

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

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

Gln Val Cys Tyr Phe Ala Leu Leu Asp Val Phe Lys Glu Met Glu Asp
355 360 365

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

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

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

Val Asp Pro Leu Pro Met
565

<210> 27
<211> 562
<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 27

Ser Phe Ala Val Ser Ala Ser Pro Ala Lys Phe Ile Gln Asn Val Glu
1 5 10 15

Lys Asp Ser Thr Arg Arg Ser Ala Asn Phe His Pro Ser Ile Trp Gly
20 25 30

Asp His Phe Leu Gln Tyr Thr Cys Asp Ser Gln Glu Pro Asp Asp Asp
35 40 45

Gly Ser Val Lys His Gln Gln Leu Lys Glu Glu Ile Arg Lys Met Leu
50 55 60

Thr Ala Glu Thr Lys Leu Ser Gln Lys Leu Asp Leu Ile Asp Ala Ile
65 70 75 80

Gln Arg Leu Gly Val Ala Tyr His Phe Glu Ser Glu Ile Asp Glu Ile
85 90 95

Leu Gly Arg Val His Gln Ala Tyr Gln Glu Ser Asp Leu Cys Val Asn
100 105 110

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

Glu Asn Gly Tyr Arg Ile Ser Ala Asp Val Phe Asn Lys Phe Arg Asp
130 135 140

Ile Asp Gly Asn Phe Lys Pro Ser Leu Ala Arg Asn Val Arg Gly Met
145 150 155 160

Leu Ser Leu Tyr Glu Ala Thr His Leu Arg Val His Gly Glu Asn Ile
165 170 175

Leu Asp Glu Ala His Ala Phe Ala Thr Ser His Leu Glu Ser Ile Ala
180 185 190

Thr His Gln Ile Ser Ser Pro Leu Ala Glu Gln Val Lys His Ala Leu
195 200 205

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

Met Pro Phe Tyr Gln Glu Glu Ala Ser His Asn Glu Ala Leu Leu Thr

225 230 235 240

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

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

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

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

Met Lys Gln Tyr Gly Ala Thr Glu Glu Glu Thr Cys Asn Glu Leu Arg
485 490 495

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

Ser Ile

<210> 28
<211> 553
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 28
Glu Ser Gln Thr Thr Phe Lys Tyr Glu Ser Leu Ala Phe Thr Lys Leu
1 5 10 15
Ser His Cys Gln Trp Thr Asp Tyr Phe Leu Ser Val Pro Ile Asp Glu
20 25 30
Ser Glu Leu Asp Val Ile Thr Arg Glu Ile Asp Ile Leu Lys Pro Glu
35 40 45

Val Met Glu Leu Leu Ser Ser Gln Gly Asp Asp Glu Thr Ser Lys Arg
50 55 60
Lys Val Leu Leu Ile Gln Leu Leu Leu Ser Leu Gly Leu Ala Phe His
65 70 75 80
Phe Glu Asn Glu Ile Lys Asn Ile Leu Glu His Ala Phe Arg Lys Ile
85 90 95
Asp Asp Ile Thr Gly Asp Glu Lys Asp Leu Ser Thr Ile Ser Ile Met

100 105 110

Phe Arg Val Phe Arg Thr Tyr Gly His Asn Leu Pro Ala Glu Val Phe
115 120 125
Glu Arg Phe Lys Asp Gln His Gly Asn Phe Lys Ala Ser Leu Ser Ser
130 135 140
Asp Val Glu Gly Met Leu Ser Leu Tyr Glu Ala Ser Phe Leu Asp Tyr
145 150 155 160
Glu Gly Glu Asp Ile Leu Asp Glu Ala Lys Ala Phe Thr Ser Phe His
165 170 175

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

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

Asp Asp Ala Cys Asp His Tyr Phe Ser Ile His Glu Leu Thr Arg Leu
305 310 315 320
Val Ala Cys Val Glu Arg Trp Ser Pro Asp Gly Ile Asp Thr Leu Glu
325 330 335
Asp Ile Ser Arg Ser Val Phe Lys Leu Met Leu Asp Val Phe Asp Asp
340 345 350

Ile Gly Lys Gly Val Arg Ser Glu Gly Ser Ser Tyr His Leu Lys Glu
355 360 365

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

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

Asn Glu Glu Leu Leu Lys Thr Thr Ser Val Pro Gly Arg Val Leu Lys
500 505 510
Gln Ala Leu Asn Phe Gly Arg Leu Leu Glu Leu Leu Tyr Thr Lys Ser
515 520 525
Asp Asp Ile Tyr Asn Cys Ser Glu Gly Lys Leu Lys Glu Tyr Ile Val
530 535 540
Thr Leu Leu Ile Asp Pro Ile Arg Leu
545 550

<210> 29
<211> 552
<212> PRT

<213> Artificial Sequence
<220><223> Synthetic polypeptide

<400> 29

Ser Ile Gln Val Pro Gln Ile Ser Ser Gln Asn Ala Lys Ser Gln Val
1 5 10 15

Met Arg Arg Thr Ala Asn Phe His Pro Ser Val Trp Gly Asp Arg Phe
20 25 30

Ala Asn Tyr Thr Ala Glu Asp Lys Met Asn His Ala Arg Asp Leu Lys
35 40 45

Glu Leu Lys Ala Leu Lys Glu Glu Val Gly Arg Lys Leu Leu Ala Thr
50 55 60

Ala Gly Pro Ile Val Lys Leu Glu Leu Val Asp Asp Val Lys Arg Leu
65 70 75 80

Gly Ile Gly Tyr Arg Phe Glu Lys Glu Ile Val Glu Ala Leu His Arg
85 90 95

Cys Phe Ile Ser Ser Glu Arg Phe Thr His Arg Asn Leu His Gln Thr
100 105 110

Ala Leu Ser Phe Arg Leu Leu Arg Glu Cys Gly Tyr Asp Val Thr Cys
115 120 125

Asp Lys Phe Asn Lys Phe Thr Asn Lys Glu Gly Lys Phe Asn Ser Lys
130 135 140

Leu Gly Glu Asn Ile Lys Gly Met Ile Asp Leu Tyr Glu Ala Ser Gln
145 150 155 160

Leu Gly Ile Ala Gly Glu Tyr Ile Leu Ala Glu Ala Gly Glu Phe Ser
165 170 175

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

Lys Ala Gln Val Arg His Ala Leu Arg Gln Pro Leu His Arg Gly Leu
195 200 205

Pro Arg Leu Glu His Arg Arg Tyr Ile Ser Ile Tyr Gln Asp Asp Ala
210 215 220

Ser His Tyr Lys Ala Leu Leu Thr Leu Ala Lys Leu Asp Phe Asn Leu
225 230 235 240

Val Gln Ser Leu His Lys Lys Glu Leu Cys Glu Ile Ser Arg Trp Trp

245 250 255

Lys Asp Leu Asp Phe Ala Arg Lys Leu Pro Phe Ala Arg Asp Arg Met

260 265 270

Val Glu Cys Tyr Phe Trp Ile Leu Gly Val Tyr Phe Glu Pro Gln Tyr

275 280 285

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

290 295 300

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

305 310 315 320

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

325 330 335

Pro Glu Tyr Met Gln Thr Phe Phe Gly Ala Leu Leu Asp Leu Tyr Asn

340 345 350

Glu Ile Glu Lys Glu Ile Ala Asn Glu Gly Trp Ser Tyr Arg Val Gln

355 360 365

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

370 375 380

Ser Arg Trp Leu Lys Cys Asn His Ala Pro Thr Met Glu Glu Tyr Met

385 390 395 400

Lys Val Arg Gly Val Ser Ser Gly Tyr Pro Leu Leu Ile Thr Ile Ser

405 410 415

Phe Ile Gly Met Glu Asp Thr Thr Glu Glu Ile Leu Thr Trp Ala Thr

420 425 430

Ser Glu Pro Met Ile Ile Arg Ala Ser Val Ile Val Cys Arg Leu Met

435 440 445

Asp Asp Ile Lys Ser His Lys Phe Glu Gln Glu Arg Gly His Ala Ala

450 455 460

Ser Ala Val Glu Cys Tyr Met Lys Gln His Gly Leu Ser Glu Gln Glu

465 470 475 480

Val Cys Glu Glu Leu Tyr Arg Gln Val Ser Asn Ala Trp Lys Asp Ile

485 490 495

Asn Glu Glu Cys Leu Asn Pro Thr Ala Val Pro Met Pro Leu Leu Met

500 505 510

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

515 520 525

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

530 535 540

Leu Leu Ile Asp Gln Val Pro Ile

545 550

<210> 30

<211> 561

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 30

Ala Leu Gln Asp Ser Glu Val Pro Ser Ser Ile Leu Asn Ala Thr Ala

1 5 10 15

Gly Asn Arg Pro Thr Ala Ser Tyr His Pro Thr Leu Trp Gly Glu Lys

20 25 30

Phe Leu Val Val Ser Thr Gln Ser Thr Ser Gly Ser Met Lys Asn Glu

35 40 45

Pro Thr Thr Gln Gly Glu Tyr Asp Glu Leu Lys Gln Gln Val Thr Lys

50 55 60

Met Leu Thr Asp Ala Thr Thr Asn Asp Pro Ser Lys Lys Leu His Leu

65 70 75 80

Ile Asp Met Val Gln Arg Leu Gly Ile Ala Tyr His Phe Glu Ile Glu

85 90 95

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

100 105 110

Glu Tyr Asp Leu Tyr Thr Ile Ala Leu Gly Phe Arg Leu Leu Arg Gln

115 120 125

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

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

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

Tyr Gly Thr Asn Lys Glu Leu Glu Leu Leu Thr Lys Cys Ile Glu Arg
325 330 335
Trp Asp Ile Asp Val Ile Asp Gln Leu Pro Glu Tyr Met Lys Leu Val
340 345 350
Tyr Gln Ala Leu Leu Asn Val Tyr Ser Glu Met Glu Ala Lys Val Ala
355 360 365
Lys Glu Gly Arg Ser Tyr Ala Ile Asp Tyr Ala Lys Glu Ser Met Lys

370 375 380

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

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

Pro Ala Ile Phe Pro Met Pro Ile Leu Thr Val Val Leu Asn Phe Ala
515 520 525
Arg Val Met Asp Phe Leu Tyr Lys Asp Gly Asp Asn Tyr Thr Asn Ser
530 535 540
His Met Leu Lys Asp Tyr Ile Thr Ser Leu Leu Val Asn Pro Leu Leu
545 550 555 560
Ile

<210> 31
<211> 561
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide

<400> 31

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

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

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

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

245 250 255

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

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

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

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

Glu Asp Val Ala Asn Ala Trp Lys Asp Ile Asn Glu Gly Phe Met Lys
500 505 510

Pro Ala Ile Phe Pro Met Pro Ile Leu Thr Val Val Leu Asn Phe Ala
515 520 525

Arg Val Met Asp Phe Leu Tyr Lys Asp Gly Asp Asn Tyr Thr Asn Ser
530 535 540

His Met Leu Lys Asp Tyr Ile Thr Ser Leu Leu Val Asn Pro Leu Leu
545 550 555 560

Ile

<210> 32

<211> 561

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 32

Ala Leu Gln Asp Ser Glu Val Pro Ser Ser Ile Leu Asn Ala Thr Ala
1 5 10 15

Gly Asn Arg Pro Thr Ala Ser Tyr His Pro Thr Leu Trp Gly Glu Lys
20 25 30

Phe Leu Val Val Ser Thr Gln Ser Thr Ser Gly Ser Met Lys Asn Glu
35 40 45

Pro Thr Thr Gln Gly Glu Tyr Asp Glu Leu Lys Gln Gln Val Thr Lys
50 55 60

Met Leu Thr Asp Ala Thr Thr Asn Asp Pro Ser Lys Lys Leu His Leu
65 70 75 80

Ile Asp Met Val Gln Arg Leu Gly Ile Ala Tyr His Phe Glu Ile Glu
85 90 95

Ile Glu Asn Ala Leu Glu Lys Ile Asn Leu Gly Asp Ala Asn Tyr Phe
100 105 110

Glu Tyr Asp Leu Tyr Thr Ile Ala Leu Gly Phe Arg Leu Leu Arg Gln

115 120 125

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

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

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

Tyr Gly Thr Asn Lys Glu Leu Glu Leu Leu Thr Lys Cys Ile Glu Arg
325 330 335
Trp Asp Ile Asp Val Ile Asp Gln Leu Pro Glu Tyr Met Lys Leu Val
340 345 350
Tyr Gln Ala Leu Leu Asn Val Tyr Ser Glu Met Glu Ala Lys Val Ala
355 360 365

Lys Glu Gly Arg Ser Tyr Ala Ile Asp Tyr Ala Lys Glu Ser Met Lys
370 375 380

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

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

Pro Ala Ile Phe Pro Met Pro Ile Leu Thr Val Val Leu Asn Phe Ala
515 520 525
Arg Val Met Asp Phe Leu Tyr Lys Asp Gly Asp Asn Tyr Thr Asn Ser
530 535 540
His Met Leu Lys Asp Tyr Ile Thr Ser Leu Leu Val Asn Pro Leu Leu
545 550 555 560
Ile

<210> 33
<211> 561
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide

<400> 33

Ala Leu Gln Asp Ser Glu Val Pro Ser Ser Ile Leu Asn Ala Thr Ala
1 5 10 15

Gly Asn Arg Pro Thr Ala Ser Tyr His Pro Thr Leu Trp Gly Glu Lys
20 25 30

Phe Leu Val Val Ser Thr Gln Ser Thr Ser Gly Ser Met Lys Asn Glu
35 40 45

Pro Thr Thr Gln Gly Glu Tyr Asp Glu Leu Lys Gln Gln Val Thr Lys
50 55 60

Met Leu Thr Asp Ala Thr Thr Asn Asp Pro Ser Lys Lys Leu His Leu
65 70 75 80

Ile Asp Met Val Gln Arg Leu Gly Ile Ala Tyr His Phe Glu Ile Glu
85 90 95

Ile Glu Asn Ala Leu Glu Lys Ile Asn Leu Gly Asp Ala Asn Tyr Phe
100 105 110

Glu Tyr Asp Leu Tyr Thr Ile Ala Leu Gly Phe Arg Leu Leu Arg Gln
115 120 125

Gln Gly Ile Lys Val Ser Ser Glu Ile Phe Lys Lys Phe Met Asp Glu
130 135 140

Lys Gly Lys Phe Lys Glu Asp Val Val Asn Asp Val Leu Gly Met Leu
145 150 155 160

Asn Leu Tyr Glu Ala Ala His Leu Arg Leu Arg Gly Glu Asp Ile Leu
165 170 175

Asp Glu Ala Leu Ala Phe Thr Thr Ser His Leu Glu Ser Met Ala Thr
180 185 190

Lys Val Ser Pro Leu Leu Ala Glu Gln Ile Ala His Ala Leu Asn Cys
195 200 205

Pro Ile Gln Lys Gly Leu Pro Arg Ile Glu Ala Arg His Tyr Ile Ser
210 215 220

Leu Tyr Ser Arg Glu Thr His Phe Ala Ser Ser Asn Ala Ala Leu Leu
225 230 235 240

Arg Phe Ala Lys Ile Asp Phe Asn Met Val Gln Ala Leu His Gln Lys

245 250 255

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

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

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

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

Glu Asp Val Ala Asn Ala Trp Lys Asp Ile Asn Glu Gly Phe Met Lys
500 505 510

Pro Ala Ile Phe Pro Met Pro Ile Leu Thr Val Val Leu Asn Phe Ala
515 520 525
Arg Val Met Asp Phe Leu Tyr Lys Asp Gly Asp Asn Tyr Thr Asn Ser
530 535 540
His Met Leu Lys Asp Tyr Ile Thr Ser Leu Leu Val Asn Pro Leu Leu
545 550 555 560
Ile

<210> 34
<211> 561
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide

<400> 34
Ala Leu Gln Asp Ser Glu Val Pro Ser Ser Ile Leu Asn Ala Thr Ala
1 5 10 15
Gly Asn Arg Pro Thr Ala Ser Tyr His Pro Thr Leu Trp Gly Glu Lys
20 25 30
Phe Leu Val Val Ser Thr Gln Ser Thr Ser Gly Ser Met Lys Asn Glu
35 40 45
Pro Thr Thr Gln Gly Glu Tyr Asp Glu Leu Lys Gln Gln Val Thr Lys
50 55 60

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

115 120 125

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

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

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

Tyr Gly Thr Asn Lys Glu Leu Glu Leu Leu Thr Lys Cys Ile Glu Arg
325 330 335
Trp Asp Ile Asp Val Ile Asp Gln Leu Pro Glu Tyr Met Lys Leu Val
340 345 350
Tyr Gln Ala Leu Leu Asn Val Tyr Ser Glu Met Glu Ala Lys Val Ala
355 360 365

Lys Glu Gly Arg Ser Tyr Ala Ile Asp Tyr Ala Lys Glu Ser Met Lys
370 375 380

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

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

Pro Ala Ile Phe Pro Met Pro Ile Leu Thr Val Val Leu Asn Phe Ala
515 520 525
Arg Val Met Asp Phe Leu Tyr Lys Asp Gly Asp Asn Tyr Thr Asn Ser
530 535 540
His Met Leu Lys Asp Tyr Ile Thr Ser Leu Leu Val Asn Pro Leu Leu
545 550 555 560
Ile

<210> 35
<211> 561
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide

<400> 35

Ala Leu Gln Asp Ser Glu Val Pro Ser Ser Ile Leu Asn Ala Thr Ala
1 5 10 15

Gly Asn Arg Pro Thr Ala Ser Tyr His Pro Thr Leu Trp Gly Glu Lys
20 25 30

Phe Leu Val Val Ser Thr Gln Ser Thr Ser Gly Ser Met Lys Asn Glu
35 40 45

Pro Thr Thr Gln Gly Glu Tyr Asp Glu Leu Lys Gln Gln Val Thr Lys
50 55 60

Met Leu Thr Asp Ala Thr Thr Asn Asp Pro Ser Lys Lys Leu His Leu
65 70 75 80

Ile Asp Met Val Gln Arg Leu Gly Ile Ala Tyr His Phe Glu Ile Glu
85 90 95

Ile Glu Asn Ala Leu Glu Lys Ile Asn Leu Gly Asp Ala Asn Tyr Phe
100 105 110

Glu Tyr Asp Leu Tyr Thr Ile Ala Leu Gly Phe Arg Leu Leu Arg Gln
115 120 125

Gln Gly Ile Lys Val Ser Ser Glu Ile Phe Lys Lys Phe Met Asp Glu
130 135 140

Lys Gly Lys Phe Lys Glu Asp Val Val Asn Asp Val Leu Gly Met Leu
145 150 155 160

Asn Leu Tyr Glu Ala Ala His Leu Arg Leu Arg Gly Glu Asp Ile Leu
165 170 175

Asp Glu Ala Leu Ala Phe Thr Thr Ser His Leu Glu Ser Met Ala Thr
180 185 190

Lys Val Ser Pro Leu Leu Ala Glu Gln Ile Ala His Ala Leu Asn Cys
195 200 205

Pro Ile Gln Lys Gly Leu Pro Arg Ile Glu Ala Arg His Tyr Ile Ser
210 215 220

Leu Tyr Ser Arg Glu Thr His Phe Ala Ser Ser Asn Ala Ala Leu Leu
225 230 235 240

Arg Phe Ala Lys Ile Asp Phe Asn Met Val Gln Ala Leu His Gln Lys

245 250 255

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

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

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

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

Glu Asp Val Ala Asn Ala Trp Lys Asp Ile Asn Glu Gly Phe Met Lys
500 505 510

Pro Ala Ile Phe Pro Met Pro Ile Leu Thr Val Val Leu Asn Phe Ala
515 520 525
Arg Val Met Asp Phe Leu Tyr Lys Asp Gly Asp Asn Tyr Thr Asn Ser
530 535 540
His Met Leu Lys Asp Tyr Ile Thr Ser Leu Leu Val Asn Pro Leu Leu
545 550 555 560
Ile

<210> 36
<211> 552
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide

<400> 36
Ala Ser Ala Gln Ala Ser Leu Pro Ser Asn Asn Arg Gln Glu Thr Val
1 5 10 15
Arg Pro Leu Ala Asp Phe Pro Glu Asn Ile Trp Ala Asp Arg Ile Ala
20 25 30
Pro Phe Thr Leu Asp Lys Gln Glu Tyr Glu Met Cys Gln Arg Glu Ile
35 40 45
Glu Met Leu Lys Ala Glu Val Ala Ser Met Leu Leu Ala Thr Gly Lys
50 55 60

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

115 120 125

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

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

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

Ile Leu Thr Asp Ser Ala Glu Arg Trp Asp Gly Ser Gly Val Asp Gln
325 330 335
Leu Ser Asp Tyr Ile Arg Ala Ser Tyr Asn Thr Leu Leu Lys Phe Asn
340 345 350
Lys Glu Val Gly Glu Asp Leu Ala Lys Lys Gln Arg Thr Tyr Ala Phe
355 360 365

Asp Lys Tyr Ile Glu Asp Trp Lys Gln Tyr Met Arg Thr Asn Phe Ser
370 375 380

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

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

Met Leu Leu Asn Ile Ala Arg Val Gly Glu Thr Val Tyr Lys His Arg
515 520 525
Ile Asp Gly Phe Thr Gln Pro His Ala Ile Glu Glu His Ile Arg Ala
530 535 540
Met Leu Val Asp Phe Met Ser Ile
545 550

<210> 37
<211> 552
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 37
Ala Ser Ala Gln Ala Ser Leu Pro Ser Asn Asn Arg Gln Glu Thr Val

1 5 10 15

Arg Pro Leu Ala Asp Phe Pro Glu Asn Ile Trp Ala Asp Arg Ile Ala

20 25 30

Pro Phe Thr Leu Asp Lys Gln Glu Tyr Glu Met Cys Gln Arg Glu Ile

35 40 45

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

50 55 60

Thr Met Met Gln Arg Phe Asp Phe Ile Asp Lys Ile Glu Arg Leu Gly

65 70 75 80

Val Ser His His Phe Asp Ile Glu Ile Glu Asn Gln Leu Gln Glu Phe

85 90 95

Phe Asn Val Tyr Thr Asn Leu Gly Glu Tyr Ser Ala Tyr Asp Leu Ser

100 105 110

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

115 120 125

Ser Cys Gly Ile Phe Asp Gln Phe Ile Asp Ala Lys Gly Lys Phe Lys

130 135 140

Glu Ser Leu Cys Asn Asp Ile Arg Gly Leu Leu Ser Leu Tyr Glu Ala

145 150 155 160

Ala His Val Arg Thr His Gly Asp Lys Ile Leu Glu Glu Ala Leu Ala

165 170 175

Phe Thr Thr Thr His Met Thr Ser Gly Gly Pro His Leu Asp Ser Ser

180 185 190

Leu Ala Lys Gln Val Lys Tyr Ala Leu Glu Gln Pro Leu His Lys Gly

195 200 205

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

210 215 220

Glu Ser Asn Asn Lys Leu Leu Leu Arg Leu Ala Lys Leu Asp Tyr His

225 230 235 240

Leu Leu Gln Met Ser Tyr Lys Gln Glu Leu Cys Glu Ile Thr Arg Trp

245 250 255

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

260 265 270

Phe Val Glu Cys Tyr Phe Trp Ala Val Gly Thr Leu Tyr Glu Pro Gln

275 280 285

Tyr Ser Leu Ala Arg Met Thr Phe Ala Lys Val Ala Ala Leu Ile Thr

290 295 300

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

305 310 315 320

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

325 330 335

Leu Ser Asp Tyr Ile Arg Ala Ser Tyr Asn Thr Leu Leu Lys Phe Asn

340 345 350

Lys Glu Val Gly Glu Asp Leu Ala Lys Lys Gln Arg Thr Tyr Ala Phe

355 360 365

Asp Lys Tyr Ile Glu Asp Trp Lys Gln Tyr Met Arg Thr Asn Phe Ser

370 375 380

Gln Ser Arg Trp Phe Phe Thr Lys Glu Leu Pro Ser Phe Ala Asp Tyr

385 390 395 400

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

405 410 415

Ala Phe Leu Tyr Met Asp Ser Ala Lys Glu Asp Val Ile Asn Trp Met

420 425 430

Ser Thr Asn Pro Lys Leu Val Val Ala Tyr Ser Thr His Ser Arg Leu

435 440 445

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

450 455 460

Thr Ala Ile Glu Cys Tyr Met Lys Asp His Asn Ile Ser Glu Glu Glu

465 470 475 480

Ala Ala Lys Lys Phe Arg Glu Met Ile Glu Asn Thr Trp Lys Val Met

485 490 495

Asn Glu Glu Cys Leu Arg Pro Ile Pro Ile Pro Arg Asp Thr Leu Lys

500 505 510

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

515 520 525

Ile Asp Gly Phe Thr Gln Pro His Ala Ile Glu Glu His Ile Arg Ala

530 535 540

Met Leu Val Asp Phe Met Ser Ile

545 550

<210> 38

<211> 559

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 38

Ser Leu Leu Glu Gly Asn Val Asn His Glu Asn Gly Ile Phe Arg Pro

1 5 10 15

Glu Ala Asn Phe Ser Pro Ser Met Trp Gly Asn Ile Phe Arg Asp Ser

20 25 30

Ser Lys Asp Asn Gln Ile Ser Glu Glu Val Val Glu Glu Ile Glu Ala

35 40 45

Leu Lys Glu Val Val Lys His Met Ile Ile Ser Thr Thr Ser Asn Ala

50 55 60

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

65 70 75 80

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

85 90 95

Asn Ala Asn His Glu Asp Glu Gly Asn His Lys Arg Asn Lys Glu Asp

100 105 110

Leu Tyr Ala Ala Ala Leu Glu Phe Arg Ile Phe Arg Gln His Gly Phe

115 120 125

Asn Val Ser Ser Asp Cys Phe Asn Gln Phe Lys Asp Thr Lys Gly Lys

130 135 140

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

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

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

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

385 390 395 400

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

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

Val Val Tyr Lys Asn Asn Gln Asp Gly Tyr Ser Asn Pro Lys Asn Asn
530 535 540
Val Lys Ser Val Ile Glu Ala Leu Leu Val Asn Pro Ile Asn Met
545 550 555

<210> 39
<211> 542
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 39

Glu Ser Arg Arg Ser Ala Asn Tyr Gln Ala Ser Ile Trp Asp Asp Asn
1 5 10 15
Phe Ile Gln Ser Leu Ala Ser Pro Tyr Ala Gly Glu Lys Tyr Val Ser
20 25 30

Gln Ala Asn Glu Leu Lys Glu Gln Val Lys Met Met Leu Asp Glu Glu

35 40 45

Asp Met Lys Leu Leu Asp Cys Leu Glu Leu Val Asp Asn Leu Glu Arg

50 55 60

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

65 70 75 80

Ser Ala Tyr Asn Ala Asn His Glu Asp Glu Gly Asn His Lys Arg Asn

85 90 95

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

100 105 110

His Gly Phe Asn Val Pro Gln Asp Val Phe Ser Ser Phe Met Asn Lys

115 120 125

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

130 135 140

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

145 150 155 160

Asp Met Ala Lys Asp Phe Ser Ser His His Leu His Lys Met Val Glu

165 170 175

Asp Ala Thr Asp Lys Arg Val Ala Asn Gln Ile Ile His Ser Leu Glu

180 185 190

Met Pro Leu His Arg Arg Val Gln Lys Leu Glu Ala Ile Trp Phe Ile

195 200 205

Gln Phe Tyr Glu Cys Gly Ser Asp Ala Asn Pro Thr Leu Val Glu Leu

210 215 220

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

225 230 235 240

Lys Arg Leu Ser Arg Trp Tyr Glu Glu Thr Gly Leu Gln Glu Lys Leu

245 250 255

Ser Phe Ala Arg His Arg Leu Ala Glu Ala Phe Leu Trp Ser Met Gly

260 265 270

Ile Ile Pro Glu Gly His Phe Gly Tyr Gly Arg Met His Leu Met Lys

275 280 285

Ile Gly Ala Tyr Ile Thr Leu Leu Asp Asp Ile Tyr Asp Val Tyr Gly

290 295 300

Thr Leu Glu Glu Leu Gln Val Leu Thr Glu Ile Ile Glu Arg Trp Asp

305 310 315 320

Ile Asn Leu Leu Asp Gln Leu Pro Glu Tyr Met Gln Ile Phe Phe Leu

325 330 335

Tyr Met Phe Asn Ser Thr Asn Glu Leu Ala Tyr Glu Ile Leu Arg Asp

340 345 350

Gln Gly Ile Asn Val Ile Ser Asn Leu Lys Gly Leu Trp Val Glu Leu

355 360 365

Ser Gln Cys Tyr Phe Lys Glu Ala Thr Trp Phe His Asn Gly Tyr Thr

370 375 380

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

385 390 395 400

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

405 410 415

Lys His Glu Leu Gln Ser Leu Glu Arg His Ala His Ser Leu Ser Met

420 425 430

Ile Leu Arg Leu Ala Asp Asp Leu Gly Thr Ser Ser Asp Glu Met Lys

435 440 445

Arg Gly Asp Val Pro Lys Ala Ile Gln Cys Phe Met Asn Asp Thr Gly

450 455 460

Cys Cys Glu Glu Glu Ala Arg Gln His Val Lys Arg Leu Ile Asp Ala

465 470 475 480

Glu Trp Lys Lys Met Asn Lys Asp Ile Leu Met Glu Lys Pro Phe Lys

485 490 495

Asn Phe Cys Pro Thr Ala Met Asn Leu Gly Arg Ile Ser Met Ser Phe

500 505 510

Tyr Glu His Gly Asp Gly Tyr Gly Gly Pro His Ser Asp Thr Lys Lys

515 520 525

Lys Met Val Ser Leu Phe Val Gln Pro Met Asn Ile Thr Ile

530 535 540

<210> 40

<211> 551

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 40

Ala Ser Thr Glu Ile Ala Val Pro Leu Asn Asn Gln His Glu Ser Val
1 5 10 15

Arg Gln Leu Ala Asp Phe Pro Glu Asn Ile Trp Ala Asp Arg Val Ala
20 25 30

Ser Phe Thr Leu Asp Lys Gln Gly His Asp Met Cys Ala Lys Glu Ile
35 40 45

Glu Met Leu Lys Glu Glu Val Met Ser Met Leu Leu Glu Glu Lys Pro
50 55 60

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

Ser Tyr His Phe Gly Asp Lys Ile Glu Asp Gln Leu Gln Glu Tyr Tyr
85 90 95

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

Ala Ala Leu Gln Phe Arg Leu Phe Arg Gln His Gly Phe Asn Ile Ser
115 120 125

Cys Gly Ile Phe Asp Gly Phe Leu Asp Ala Asn Gly Lys Phe Lys Glu
130 135 140

Ser Leu Cys Asn Asp Ile Lys Gly Leu Leu Ser Leu Tyr Glu Ala Ala
145 150 155 160

His Val Arg Thr His Gly Asp Lys Ile Leu Glu Glu Ala Leu Phe Phe
165 170 175

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

180 185 190

Ala Lys Gln Val Lys Tyr Ala Leu Glu Gln Pro Leu His Lys Gly Ile

195 200 205

Pro Arg Tyr Glu Ala Trp Arg Tyr Ile Ser Ile Tyr Glu Glu Asp Glu

210 215 220

Ser Ser Asn Lys Leu Leu Leu Arg Leu Ala Lys Leu Asp Tyr His Leu

225 230 235 240

Ser Gln Met Leu Asn Lys Gln Asp Leu Cys Glu Ile Ile Arg Trp Gly

245 250 255

Lys Glu Leu Asp Ile Ile Ser Lys Val Pro Tyr Ala Arg Asp Arg Ile

260 265 270

Val Glu Cys Tyr Phe Trp Ala Val Ala Thr Tyr Tyr Glu Pro Gln Tyr

275 280 285

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

290 295 300

Ile Asp Asp Thr Tyr Asp Ala Tyr Gly Thr Leu Asp Glu Leu Lys Ile

305 310 315 320

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

325 330 335

Ser Asp Tyr Met Lys Ala Ala Tyr Thr Leu Val Leu Asn Phe Asn Lys

340 345 350

Glu Val Gly Glu Asp Leu Ala Lys Lys Gln Arg Thr Tyr Ala Phe Asp

355 360 365

Lys Tyr Ile Glu Glu Trp Lys Gln Tyr Ala Arg Thr Ser Phe Thr Gln

370 375 380

Ser Lys Trp Phe Leu Thr Asn Glu Leu Pro Ser Phe Ser Asp Tyr Leu

385 390 395 400

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

405 410 415

Phe Leu Asp Met Asp Ser Ala Ser Glu Asp Val Ile Asn Trp Met Ser

420 425 430

Thr Asn Pro Lys Leu Phe Val Ala Leu Thr Thr His Ala Arg Leu Ala
435 440 445

Asn Asp Val Gly Ser His Lys Phe Glu Lys Glu Arg Gly Ser Gly Thr
450 455 460

Ala Ile Glu Cys Tyr Met Lys Asp Tyr His Val Ser Glu Glu Glu Ala
465 470 475 480

Met Lys Lys Phe Glu Glu Met Cys Asp Asp Ala Trp Lys Val Met Asn
485 490 495

Glu Glu Cys Leu Arg Ser Thr Thr Ile Pro Arg Glu Ile Leu Lys Val
500 505 510

Ile Leu Asn Leu Ala Arg Thr Cys Glu Val Val Tyr Lys His Arg Gly
515 520 525

Asp Gly Phe Thr Asp Gln Arg Arg Ile Glu Ala His Ile Asn Ala Met
530 535 540

Leu Met Asp Ser Val Ser Ile
545 550

<210> 41

<211> 551

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 41

Ala Ser Thr Glu Ile Ala Val Pro Leu Asn Asn Gln His Glu Ser Val
1 5 10 15

Arg Gln Leu Ala Asp Phe Pro Glu Asn Ile Trp Ala Asp Arg Val Ala
20 25 30

Ser Phe Thr Leu Asp Lys Gln Gly His Asp Met Cys Ala Lys Glu Ile
35 40 45

Glu Met Leu Lys Glu Glu Val Met Ser Met Leu Leu Glu Glu Lys Pro
50 55 60

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

Ser Tyr His Phe Gly Asp Lys Ile Glu Asp Gln Leu Gln Glu Tyr Tyr
85 90 95
Asp Ala Cys Thr Asn Phe Glu Lys His Ala Glu Cys Asp Leu Ser Ile
100 105 110
Ala Ala Leu Gln Phe Arg Leu Phe Arg Gln His Gly Phe Asn Ile Ser

115 120 125
Cys Gly Ile Phe Asp Gly Phe Leu Asp Ala Asn Gly Lys Phe Lys Glu
130 135 140
Ser Leu Cys Asn Asp Ile Lys Gly Leu Leu Ser Leu Tyr Glu Ala Ala
145 150 155 160
His Val Arg Thr His Gly Asp Lys Ile Leu Glu Glu Ala Leu Phe Phe
165 170 175
Thr Thr Thr His Leu Thr Arg Glu Ile Pro Asn Val Gly Ser Thr Leu

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

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

305 310 315 320
Phe Thr Glu Ala Val Glu Arg Trp Asp Ser Ser Gly Ile Asp Gln Leu

325 330 335

Ser Asp Tyr Met Lys Ala Ala Tyr Thr Leu Val Leu Asn Phe Asn Lys

340 345 350

Glu Val Gly Glu Asp Leu Ala Lys Lys Gln Arg Thr Tyr Ala Phe Asp

355 360 365

Lys Tyr Ile Glu Glu Trp Lys Gln Tyr Ala Arg Thr Ser Phe Thr Gln

370 375 380

Ser Lys Trp Phe Leu Thr Asn Glu Leu Pro Ser Phe Ser Asp Tyr Leu

385 390 395 400

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

405 410 415

Phe Leu Gly Met Asp Gly Ala Ser Glu Asp Val Ile Asn Trp Met Ser

420 425 430

Thr Asn Pro Lys Leu Phe Val Ala Leu Thr Thr His Ala Arg Leu Ala

435 440 445

Asn Asp Val Gly Ser His Lys Phe Glu Lys Glu Arg Gly Ser Gly Thr

450 455 460

Ala Ile Glu Cys Tyr Met Lys Asp Tyr His Val Ser Glu Glu Glu Ala

465 470 475 480

Met Lys Lys Phe Glu Glu Met Cys Asp Asp Ala Trp Lys Val Met Asn

485 490 495

Glu Glu Cys Leu Arg Ser Thr Thr Ile Pro Arg Glu Ile Leu Lys Val

500 505 510

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

515 520 525

Asp Gly Phe Thr Asp Gln Arg Arg Ile Glu Ala His Ile Asn Ala Met

530 535 540

Leu Met Asp Ser Val Ser Ile

545 550

<210> 42

<211> 551

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 42

Ala Ser Thr Glu Ile Ala Val Pro Leu Asn Asn Gln His Glu Ser Val

1 5 10 15

Arg Gln Leu Ala Asp Phe Pro Glu Asn Ile Trp Ala Asp Arg Val Ala

20 25 30

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

35 40 45

Glu Met Leu Lys Glu Glu Val Met Ser Met Leu Leu Glu Glu Lys Pro

50 55 60

Met Met Glu Lys Phe Asn Leu Ile Asp Asn Ile Glu Arg Leu Gly Ile

65 70 75 80

Ser Tyr His Phe Gly Asp Lys Ile Glu Asp Gln Leu Gln Glu Tyr Tyr

85 90 95

Asp Ala Cys Thr Asn Phe Glu Lys His Ala Glu Cys Asp Leu Ser Ile

100 105 110

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

115 120 125

Cys Gly Ile Phe Asp Gly Phe Leu Asp Ala Asn Gly Lys Phe Lys Glu

130 135 140

Ser Leu Cys Asn Asp Ile Lys Gly Leu Leu Ser Leu Tyr Glu Ala Ala

145 150 155 160

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

165 170 175

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

180 185 190

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

195 200 205

Pro Arg Tyr Glu Ala Tyr Cys Phe Ile Ser Met Tyr Glu Glu Asp Glu

210 215 220

Ser Ser Asn Lys Leu Leu Leu Arg Leu Ala Lys Leu Asp Tyr His Leu
225 230 235 240
Ser Gln Met Leu Asn Lys Gln Asp Leu Cys Glu Ile Ile Arg Trp Gly
245 250 255
Lys Glu Leu Asp Ile Ile Ser Lys Val Pro Tyr Ala Arg Asp Arg Ile

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

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

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

450 455 460
Ala Ile Glu Cys Tyr Met Lys Asp Tyr His Val Ser Glu Glu Glu Ala

465 470 475 480

Met Lys Lys Phe Glu Glu Met Cys Asp Asp Ala Trp Lys Val Met Asn

485 490 495

Glu Glu Cys Leu Arg Ser Thr Thr Ile Pro Arg Glu Ile Leu Lys Val

500 505 510

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

515 520 525

Asp Gly Phe Thr Asp Gln Arg Arg Ile Glu Ala His Ile Asn Ala Met

530 535 540

Leu Met Asp Ser Val Ser Ile

545 550

<210> 43

<211> 552

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 43

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

1 5 10 15

Arg Pro Leu Ala Asp Phe Pro Glu Asn Ile Trp Ala Asp Arg Ile Ala

20 25 30

Pro Phe Thr Leu Asp Lys Gln Glu Tyr Glu Met Cys Gln Arg Glu Ile

35 40 45

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

50 55 60

Thr Met Met Gln Arg Phe Asp Phe Ile Asp Lys Ile Glu Arg Leu Gly

65 70 75 80

Val Ser His His Phe Asp Ile Glu Ile Glu Asn Gln Leu Gln Glu Phe

85 90 95

Phe Asn Val Tyr Thr Asn Leu Gly Glu Tyr Ser Ala Tyr Asp Leu Ser

100 105 110

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

115 120 125

Ser Cys Gly Ile Phe Asp Gln Phe Ile Asp Ala Lys Gly Lys Phe Lys

130 135 140

Glu Ser Leu Cys Asn Asp Ile Arg Gly Leu Leu Ser Leu Tyr Glu Ala

145 150 155 160

Ala His Val Arg Thr His Gly Asp Lys Ile Leu Glu Glu Ala Leu Ala

165 170 175

Phe Thr Thr Thr His Met Thr Ser Gly Gly Pro His Leu Asp Ser Ser

180 185 190

Leu Ala Lys Gln Val Lys Tyr Ala Leu Glu Gln Pro Leu His Lys Gly

195 200 205

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

210 215 220

Glu Ser Asn Asn Lys Leu Leu Leu Arg Leu Ala Lys Leu Asp Tyr His

225 230 235 240

Leu Leu Gln Met Ser Tyr Lys Gln Glu Leu Cys Glu Ile Thr Arg Trp

245 250 255

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

260 265 270

Phe Val Glu Cys Tyr Phe Trp Ala Val Gly Thr Leu Tyr Glu Pro Gln

275 280 285

Tyr Ser Leu Ala Arg Met Thr Phe Ala Lys Val Ala Ala Leu Ile Thr

290 295 300

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

305 310 315 320

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

325 330 335

Leu Ser Asp Tyr Ile Arg Ala Ser Tyr Asn Thr Leu Leu Lys Phe Asn

340 345 350

Lys Glu Val Gly Glu Asp Leu Ala Lys Lys Gln Arg Thr Tyr Ala Phe

355 360 365

Asp Lys Tyr Ile Glu Asp Trp Lys Gln Tyr Met Arg Thr Ser Phe Thr

370 375 380

Gln Ser Lys Trp Phe Leu Thr Asn Glu Leu Pro Ser Phe Ala Asp Tyr

385 390 395 400

Ile Ser Asn Gly Ala Ile Thr Ile Gly Ala Tyr Leu Ile Ala Ser Ala

405 410 415

Gly Phe Leu Asp Met Asp Ser Ala Leu Glu Asp Val Ile Asn Trp Met

420 425 430

Ser Thr Asn Pro Lys Leu Met Val Ala Tyr Ser Thr His Ser Arg Leu

435 440 445

Ile Asn Asp Tyr Gly Gly His Lys Phe Asp Lys Glu Arg Gly Ser Val

450 455 460

Thr Ala Leu Asp Cys Tyr Met Lys Asp Tyr Ser Val Ser Glu Glu Glu

465 470 475 480

Ala Ala Lys Lys Phe Arg Glu Met Cys Glu Asp Asn Trp Lys Val Met

485 490 495

Asn Glu Glu Cys Leu Arg Pro Thr Thr Ile Pro Arg Asp Gly Leu Lys

500 505 510

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

515 520 525

Ile Asp Gly Phe Thr Gln Pro His Ala Ile Glu Glu His Ile Arg Ala

530 535 540

Met Leu Val Asp Phe Met Ser Ile

545 550

<210> 44

<211> 551

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 44

Ala Ser Thr Glu Ile Ala Val Pro Leu Asn Asn Gln His Glu Ser Val

1 5 10 15

Arg Gln Leu Ala Asp Phe Pro Glu Asn Ile Trp Ala Asp Arg Val Ala
20 25 30

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

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

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

Ser Asn Asn Lys Leu Leu Leu Arg Leu Ala Lys Leu Asp Tyr His Leu
225 230 235 240
Leu Gln Met Ser Tyr Lys Arg Glu Leu Ser Glu Ile Ile Arg Trp Gly
245 250 255
Lys Glu Leu Asp Ile Ile Ser Lys Val Pro Tyr Ala Arg Asp Arg Ile

260 265 270

Val Glu Cys Tyr Phe Trp Ala Val Ala Thr Tyr Tyr Glu Pro Gln Tyr

275 280 285

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

290 295 300

Ile Asp Asp Thr Tyr Asp Ala Tyr Gly Thr Leu Asp Glu Leu Lys Ile

305 310 315 320

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

325 330 335

Ser Asp Tyr Met Lys Ala Ala Tyr Thr Leu Val Leu Asn Phe Asn Lys

340 345 350

Glu Val Gly Glu Asp Leu Ala Lys Lys Gln Arg Thr Tyr Ala Phe Asp

355 360 365

Lys Tyr Ile Glu Glu Trp Lys Gln Tyr Ala Arg Thr Ser Phe Thr Gln

370 375 380

Ser Lys Trp Phe Leu Thr Asn Glu Leu Pro Ser Phe Ser Asp Tyr Leu

385 390 395 400

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

405 410 415

Phe Leu Gly Met Asp Gly Ala Ser Glu Asp Val Ile Asn Trp Met Ser

420 425 430

Thr Asn Pro Lys Leu Phe Val Ala Leu Thr Thr His Ala Arg Leu Ala

435 440 445

Asn Asp Val Gly Ser His Lys Phe Glu Lys Glu Arg Gly Ser Ser Thr

450 455 460

Ala Ile Glu Cys Tyr Met Lys Asp Tyr His Val Ser Glu Glu Glu Ala

465 470 475 480

Met Glu Lys Phe Glu Glu Met Cys Asp Asp Ala Trp Lys Val Met Asn

485 490 495

Glu Glu Cys Leu Arg Ser Thr Thr Ile Pro Arg Glu Ile Leu Lys Val

500 505 510

Ile Leu Asn Leu Ala Arg Thr Cys Glu Val Val Tyr Lys His Arg Gly
515 520 525

Asp Gly Phe Thr Asp Gln Arg Arg Ile Glu Ala His Ile Asn Ala Met
530 535 540

Leu Met Asp Ser Val Ser Ile
545 550

<210> 45

<211> 551

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 45

Ala Ser Thr Glu Ile Ala Val Pro Leu Asn Asn Gln His Glu Ser Val
1 5 10 15

Arg Gln Leu Ala Asp Phe Pro Glu Asn Ile Trp Ala Asp Arg Val Ala
20 25 30

Ser Phe Thr Leu Asp Lys Gln Gly His Asp Met Cys Ala Lys Glu Ile
35 40 45

Glu Met Leu Lys Glu Glu Val Met Ser Met Leu Leu Glu Glu Lys Pro
50 55 60

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

Ser Tyr His Phe Gly Asp Lys Ile Glu Asp Gln Leu Gln Glu Tyr Tyr
85 90 95

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

Ala Ala Leu Gln Phe Arg Leu Phe Arg Gln His Gly Phe Asn Ile Ser
115 120 125

Cys Gly Ile Phe Asp Gly Phe Leu Asp Ala Asn Gly Lys Phe Lys Glu
130 135 140

Ser Leu Cys Asn Asp Ile Lys Gly Leu Leu Ser Leu Tyr Glu Ala Ala
145 150 155 160

His Val Arg Thr His Gly Asp Lys Ile Leu Glu Glu Ala Leu Phe Phe
165 170 175

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

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

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

Lys Tyr Ile Glu Glu Trp Lys Gln Tyr Ala Arg Thr Ser Phe Thr Gln
370 375 380
Ser Lys Trp Phe Leu Thr Asn Glu Leu Pro Ser Phe Ala Asp Tyr Leu
385 390 395 400
Ser Asn Gly Met Val Thr Ser Thr Tyr Tyr Leu Leu Ser Ala Ala Ala

405 410 415

Leu Leu Asp Met Asp Ser Ala Leu Glu Asp Val Ile Asn Trp Met Ser
420 425 430

Thr Asn Pro Lys Phe Phe Val Ala Leu Thr Thr His Ala Arg Leu Thr
435 440 445

Asn Asp Val Gly Ser His Lys Phe Glu Lys Glu Arg Gly Ser Gly Thr
450 455 460

Ala Ile Glu Cys Tyr Met Lys Asp Tyr His Val Ser Glu Glu Glu Ala
465 470 475 480

Met Lys Lys Phe Glu Glu Met Cys Asp Asp Ala Trp Lys Val Met Asn
485 490 495

Glu Glu Cys Leu Arg Ser Thr Thr Ile Pro Arg Glu Ile Leu Lys Val
500 505 510

Ile Leu Asn Leu Ala Arg Thr Cys Glu Val Val Tyr Lys His Arg Gly
515 520 525

Asp Gly Phe Thr Asp Gln Arg Arg Ile Glu Ala His Ile Asn Ala Met
530 535 540

Leu Met Asp Ser Val Ser Ile
545 550

<210> 46

<211> 552

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 46

Ala Ser Ala Gln Ala Ser Leu Pro Ser Asn Asn Arg Gln Glu Thr Val
1 5 10 15

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

Pro Phe Thr Leu Asp Lys Gln Glu Tyr Glu Met Cys Gln Arg Glu Ile
35 40 45

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

50 55 60

Thr Met Met Gln Arg Phe Asp Phe Ile Asp Lys Ile Glu Arg Leu Gly

65 70 75 80

Val Ser His His Phe Asp Ile Glu Ile Glu Asn Gln Leu Gln Glu Phe

85 90 95

Phe Asn Val Tyr Thr Asn Leu Gly Glu Tyr Ser Ala Tyr Asp Leu Ser

100 105 110

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

115 120 125

Ser Cys Gly Ile Phe Asp Gln Phe Ile Asp Ala Lys Gly Lys Phe Lys

130 135 140

Glu Ser Leu Cys Asn Asp Ile Arg Gly Leu Leu Ser Leu Tyr Glu Ala

145 150 155 160

Ala His Val Arg Thr His Gly Asp Lys Ile Leu Glu Glu Ala Leu Ala

165 170 175

Phe Thr Thr Thr His Met Thr Ser Gly Gly Pro His Leu Asp Ser Ser

180 185 190

Leu Ala Lys Gln Val Lys Tyr Ala Leu Glu Gln Pro Leu His Lys Gly

195 200 205

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

210 215 220

Glu Ser Asn Asn Lys Leu Leu Leu Arg Leu Ala Lys Leu Asp Tyr His

225 230 235 240

Leu Leu Gln Met Ser Tyr Lys Gln Glu Leu Cys Glu Ile Thr Arg Trp

245 250 255

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

260 265 270

Phe Val Glu Cys Tyr Phe Trp Ala Val Gly Thr Leu Tyr Glu Pro Gln

275 280 285

Tyr Ser Leu Ala Arg Met Thr Phe Ala Lys Val Ala Ala Leu Ile Thr

290 295 300

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

305 310 315 320

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

325 330 335

Leu Ser Asp Tyr Ile Arg Ala Ser Tyr Asn Thr Leu Leu Lys Phe Asn

340 345 350

Lys Glu Val Gly Glu Asp Leu Ala Lys Lys Gln Arg Thr Tyr Ala Phe

355 360 365

Asp Lys Tyr Ile Glu Asp Trp Lys Gln Tyr Met Arg Thr Ser Phe Thr

370 375 380

Gln Ser Lys Trp Phe Leu Thr Asn Glu Leu Pro Ser Phe Ala Asp Tyr

385 390 395 400

Ile Ser Asn Gly Ala Ile Thr Ile Gly Ala Tyr Leu Ile Ala Ser Ala

405 410 415

Gly Phe Leu Asp Met Asp Ser Ala Leu Glu Asp Val Ile Asn Trp Met

420 425 430

Ser Thr Asn Pro Lys Leu Met Val Ala Tyr Ser Thr His Ser Arg Leu

435 440 445

Ile Asn Asp Tyr Gly Gly His Lys Phe Asp Lys Glu Arg Gly Thr Gly

450 455 460

Thr Ala Ile Glu Cys Tyr Met Lys Asp His Asn Ile Ser Glu Glu Glu

465 470 475 480

Ala Ala Lys Lys Phe Arg Glu Met Ile Glu Asn Thr Trp Lys Val Met

485 490 495

Asn Glu Glu Cys Leu Arg Pro Ile Pro Ile Pro Arg Asp Thr Leu Lys

500 505 510

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

515 520 525

Ile Asp Gly Phe Thr Gln Pro His Ala Ile Glu Glu His Ile Arg Ala

530 535 540

Met Leu Val Asp Phe Met Ser Ile
545 550

<210> 47

<211> 551

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 47

Ala Ser Thr Glu Ile Ala Val Pro Leu Asn Asn Gln His Glu Ser Val
1 5 10 15

Arg Gln Leu Ala Asp Phe Pro Glu Asn Ile Trp Ala Asp Arg Val Ala
20 25 30

Ser Phe Thr Leu Asp Lys Gln Gly His Asp Met Cys Ala Lys Glu Ile
35 40 45

Glu Met Leu Lys Glu Glu Val Met Ser Met Leu Leu Glu Glu Lys Pro
50 55 60

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

Ser Tyr His Phe Gly Asp Lys Ile Glu Asp Gln Leu Gln Glu Tyr Tyr
85 90 95

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

Ala Ala Leu Gln Phe Arg Leu Phe Arg Gln His Gly Phe Asn Ile Ser
115 120 125

Cys Gly Ile Phe Asp Gly Phe Leu Asp Ala Asn Gly Lys Phe Lys Glu
130 135 140

Ser Leu Cys Asn Asp Ile Lys Gly Leu Leu Ser Leu Tyr Glu Ala Ala
145 150 155 160

His Val Arg Thr His Gly Asp Lys Ile Leu Glu Glu Ala Leu Phe Phe
165 170 175

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

180 185 190

Ala Lys Gln Val Lys His Ala Leu Glu Gln Pro Leu His Arg Gly Ile
195 200 205

Pro Arg Tyr Glu Ala Tyr Cys Phe Ile Ser Ile Tyr Glu Glu Asp Glu
210 215 220

Ser Asn Asn Lys Leu Leu Leu Arg Leu Ala Lys Leu Asp Tyr His Leu
225 230 235 240

Leu Gln Met Ser Tyr Lys Arg Glu Leu Ser Glu Ile Ile Arg Trp Gly
245 250 255

Lys Glu Leu Asp Ile Ile Ser Lys Val Pro Tyr Ala Arg Asp Arg Ile
260 265 270

Val Glu Cys Tyr Phe Trp Ala Val Ala Thr Tyr Tyr Glu Pro Gln Tyr
275 280 285

Ser Leu Ala Arg Met Thr Leu Thr Lys Ala Thr Val Phe Ala Gly Met
290 295 300

Ile Asp Asp Thr Tyr Asp Ala Tyr Gly Thr Leu Asp Glu Leu Lys Ile
305 310 315 320

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

Ser Asp Tyr Met Lys Ala Ala Tyr Thr Leu Val Leu Asn Phe Asn Lys
340 345 350

Glu Val Gly Glu Asp Leu Ala Lys Lys Gln Arg Thr Tyr Ala Phe Asp
355 360 365

Lys Tyr Ile Glu Glu Trp Lys Gln Tyr Ala Arg Thr Ser Phe Thr Gln
370 375 380

Ser Lys Trp Phe Leu Thr Asn Glu Leu Pro Ser Phe Ser Asp Tyr Leu
385 390 395 400

Ser Asn Gly Met Val Thr Ser Thr Tyr Tyr Leu Leu Ser Ala Ala Ala
405 410 415

Phe Leu Asp Met Asp Ser Ala Ser Glu Asp Val Ile Asn Trp Met Ser
420 425 430

Thr Asn Pro Lys Leu Phe Val Ala Leu Thr Thr His Ala Arg Leu Ala
435 440 445

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

Ile Leu Asn Leu Ala Arg Thr Cys Glu Val Val Tyr Lys His Arg Gly
515 520 525
Asp Gly Phe Thr Asp Gln Arg Arg Ile Glu Ala His Ile Asn Ala Met
530 535 540
Leu Met Asp Ser Val Ser Ile
545 550

<210> 48
<211> 553
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 48
Ala Ser Ala Gln Ala Ser Leu Pro Ser Asn Asn Arg Gln Glu Thr Val
1 5 10 15

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

65 70 75 80

Val Ser His His Phe Asp Ile Glu Ile Glu Asn Gln Leu Gln Glu Phe
85 90 95
Phe Asn Val Tyr Thr Asn Leu Gly Glu Tyr Ser Ala Tyr Asp Leu Ser
100 105 110
Ser Ala Ala Leu Gln Phe Arg Leu Phe Arg Gln His Gly Phe Asn Ile
115 120 125
Ser Cys Gly Ile Phe Asp Gln Phe Ile Asp Ala Lys Gly Lys Phe Lys
130 135 140

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

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

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

Ile Leu Thr Asp Ser Ala Glu Arg Trp Asp Gly Ser Gly Val Asp Gln
325 330 335

Leu Ser Asp Tyr Ile Arg Ala Ser Tyr Asn Thr Leu Leu Lys Phe Asn
340 345 350

Lys Glu Val Gly Glu Asp Leu Ala Lys Lys Gln Arg Thr Tyr Ala Phe
355 360 365

Asp Lys Tyr Ile Glu Asp Trp Lys Gln Tyr Met Arg Thr Asn Phe Ser
370 375 380

Gln Ser Arg Trp Phe Phe Thr Lys Glu Leu Pro Ser Phe Ala Asp Tyr
385 390 395 400

Ile Asn Asn Gly Ala Ile Thr Ile Gly Ala Tyr Leu Val Ala Ser Ala
405 410 415

Ala Phe Leu Tyr Met Asp Ser Ala Lys Glu Asp Val Ile Asn Trp Met
420 425 430

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

Ile Asn Asp Phe Gly Gly His Lys Phe Asp Lys Glu Arg Gly Ser Gly
450 455 460

Thr Ala Leu Glu Cys Tyr Met Lys Asp Tyr Asn Val Ser Glu Glu Glu
465 470 475 480

Ala Ala Asn Lys Phe Arg Glu Met Met Glu Asp Ala Trp Lys Val Met
485 490 495

Asn Glu Asp Cys Leu Arg Pro Thr Ser Ile Pro Arg Asp Val Ser Lys
500 505 510

Val Leu Leu Asn Val Ala Arg Ala Gly Glu Ile Val Tyr Lys His Arg
515 520 525

Ile Asp Gly Phe Thr Glu Pro His Ile Ile Lys Asp His Ile Arg Ala
530 535 540

Thr Leu Val Asp Phe Met Ala Ile Asn
545 550

<210> 49

<211> 553

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 49

Ala Ser Ala Gln Ala Ser Leu Pro Ser Asn Asn Arg Gln Glu Thr Val
1 5 10 15

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

Pro Phe Thr Leu Asp Lys Gln Glu Tyr Glu Met Cys Gln Arg Glu Ile
35 40 45

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

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

Val Ser His His Phe Asp Ile Glu Ile Glu Asn Gln Leu Gln Glu Phe
85 90 95

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

Ser Ala Ala Leu Gln Phe Arg Leu Phe Arg Gln His Gly Phe Asn Ile
115 120 125

Ser Cys Gly Ile Phe Asp Gln Phe Ile Asp Ala Lys Gly Lys Phe Lys
130 135 140

Glu Ser Leu Cys Asn Asp Ile Arg Gly Leu Leu Ser Leu Tyr Glu Ala
145 150 155 160

Ala His Val Arg Thr His Gly Asp Lys Ile Leu Glu Glu Ala Leu Ala
165 170 175

Phe Thr Thr Thr His Met Thr Ser Gly Gly Pro His Leu Asp Ser Ser
180 185 190

Leu Ala Lys Gln Val Lys Tyr Ala Leu Glu Gln Pro Leu His Lys Gly
195 200 205

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

210 215 220

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

275 280 285

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

340 345 350

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

405 410 415

Gly Phe Leu Asp Met Asp Ser Ala Leu Glu Asp Val Ile Asn Trp Met
420 425 430
Ser Thr Asn Pro Lys Leu Met Val Ala Tyr Ser Thr His Ser Arg Leu
435 440 445
Ile Asn Asp Tyr Gly Gly His Lys Phe Asp Lys Glu Arg Gly Ser Val

450 455 460

Thr Ala Leu Asp Cys Tyr Met Lys Asp Tyr Ser Val Ser Glu Glu Glu

465 470 475 480

Ala Ala Lys Lys Phe Arg Glu Met Ile Glu Asn Thr Trp Lys Val Met

485 490 495

Asn Glu Glu Cys Leu Arg Pro Ile Pro Ile Pro Arg Asp Thr Leu Lys

500 505 510

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

515 520 525

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

530 535 540

Met Leu Val Asp Phe Met Ala Ile Asn

545 550

<210> 50

<211> 552

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 50

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

1 5 10 15

Arg Pro Leu Ala Asp Phe Pro Glu Asn Ile Trp Ala Asp Arg Ile Ala

20 25 30

Pro Phe Thr Leu Asp Lys Gln Glu Tyr Glu Met Cys Gln Arg Glu Ile

35 40 45

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

50 55 60

Thr Met Met Gln Arg Phe Asp Phe Ile Asp Lys Ile Glu Arg Leu Gly

65 70 75 80

Val Ser His His Phe Asp Ile Glu Ile Glu Asn Gln Leu Gln Glu Phe

85 90 95

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

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

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

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

340 345 350

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

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

Ala Ala Lys Lys Phe Arg Glu Met Cys Glu Asp Asn Trp Lys Val Met
485 490 495
Asn Glu Glu Cys Leu Arg Pro Thr Thr Ile Pro Arg Asp Gly Leu Lys
500 505 510
Met Leu Leu Asn Ile Ala Arg Val Gly Glu Thr Val Tyr Lys His Arg
515 520 525
Ile Asp Gly Phe Thr Gln Pro His Ala Ile Glu Glu His Ile Arg Ala
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Met Leu Val Asp Phe Met Ser Ile
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<220><223> Synthetic polypeptide

<400> 51

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35 40 45

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

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

Val Ser His His Phe Asp Ile Glu Ile Glu Asn Gln Leu Gln Glu Phe
85 90 95

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

Ser Ala Ala Leu Gln Phe Arg Leu Phe Arg Gln His Gly Phe Asn Ile
115 120 125

Ser Cys Gly Ile Phe Asp Gln Phe Ile Asp Ala Lys Gly Lys Phe Lys
130 135 140

Glu Ser Leu Cys Asn Asp Ile Arg Gly Leu Leu Ser Leu Tyr Glu Ala
145 150 155 160

Ala His Val Arg Thr His Gly Asp Lys Ile Leu Glu Glu Ala Leu Ala
165 170 175

Phe Thr Thr Thr His Met Thr Ser Gly Gly Pro His Leu Asp Ser Ser
180 185 190

Leu Ala Lys Gln Val Lys Tyr Ala Leu Glu Gln Pro Leu His Lys Gly
195 200 205

Ile Leu Arg Tyr Glu Ala Trp Arg Tyr Ile Ser Ile Tyr Glu Glu Asp
210 215 220

Glu Ser Asn Asn Lys Leu Leu Leu Arg Leu Ala Lys Leu Asp Tyr His

225 230 235 240

Leu Leu Gln Met Ser Tyr Lys Gln Glu Leu Cys Glu Ile Thr Arg Trp

245 250 255

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

260 265 270

Phe Val Glu Cys Tyr Phe Trp Ala Val Gly Thr Leu Tyr Glu Pro Gln

275 280 285

Tyr Ser Leu Ala Arg Met Thr Phe Ala Lys Val Ala Ala Leu Ile Thr

290 295 300

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

305 310 315 320

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

325 330 335

Leu Ser Asp Tyr Ile Arg Ala Ser Tyr Asn Thr Leu Leu Lys Phe Asn

340 345 350

Lys Glu Val Gly Glu Asp Leu Ala Lys Lys Gln Arg Thr Tyr Ala Phe

355 360 365

Asp Lys Tyr Ile Glu Asp Trp Lys Gln Tyr Met Arg Thr Asn Phe Ser

370 375 380

Gln Ser Arg Trp Phe Phe Thr Lys Glu Leu Pro Ser Phe Ala Asp Tyr

385 390 395 400

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

405 410 415

Ala Phe Leu Tyr Met Asp Ser Ala Lys Glu Asp Val Ile Asn Trp Met

420 425 430

Ser Thr Asn Pro Lys Leu Val Val Ala Tyr Ser Thr His Ser Arg Leu

435 440 445

Ile Asn Asp Phe Gly Gly His Lys Phe Asp Lys Glu Arg Gly Ser Val

450 455 460

Thr Ala Leu Asp Cys Tyr Met Lys Asp Tyr Ser Val Ser Glu Glu Glu

465 470 475 480

Ala Ala Lys Lys Phe Arg Glu Met Ile Glu Asn Thr Trp Lys Val Met

485 490 495

Asn Glu Glu Cys Leu Arg Pro Ile Pro Ile Pro Arg Asp Thr Leu Lys

500 505 510

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

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530 535 540

Met Leu Val Asp Phe Met Ala Ile Asn

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<211> 355

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 52

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35 40 45

Gln Leu Gln Glu Phe Phe Asn Val Tyr Thr Asn Phe Gly Glu Tyr Ser

50 55 60

Ala Tyr Asp Leu Ser Ser Ala Ala Leu Gln Phe Lys Gln Trp Cys Asp

65 70 75 80

His Asn Arg Ser Leu Ser Cys Ser Ile Thr Arg Gly Leu Leu Ser Leu

85 90 95

Tyr Glu Ala Ala His Val Arg Thr His Gly Asp Lys Ile Leu Glu Glu

100 105 110

Ala Leu His Leu Thr Ser Gly Glu Ser His Leu Asp Ser Thr Leu Ala

115 120 125

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

130 135 140

Arg Tyr Glu Ala Trp Arg Tyr Ile Ser Ile Tyr Glu Glu Asp Glu Ser

145 150 155 160

His Asn Lys Leu Leu Leu Arg Leu Ala Lys Leu Asp Tyr His Phe Leu

165 170 175

Gln Ile Ser Tyr Arg Gln Asp Leu Cys Glu Ile Ile Arg Trp Asp Ser

180 185 190

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

195 200 205

Leu Ala Lys Lys Gln Arg Thr Tyr Ala Phe Gly Thr Phe Leu Gly Met

210 215 220

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

225 230 235 240

Leu Met Phe Ala Cys Ser Thr His Ala Arg Leu Ile Asn Asp Phe Gly

245 250 255

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

260 265 270

Tyr Met Lys Asp Tyr Asn Val Ser Glu Glu Glu Ala Ala Asn Lys Phe

275 280 285

Arg Glu Met Met Glu Asp Ala Trp Lys Val Met Asn Glu Glu Cys Leu

290 295 300

Arg Pro Thr Thr Ile Pro Arg Glu Ile Leu Lys Met Leu Leu Asn Ile

305 310 315 320

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

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Met Ser Val

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<211> 5718

<212> DNA

<213> Artificial Sequence

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gttattaggt gtgaaaccac gaaaagttca ccataacttc gaataaagtc gcggaaaaaa 300

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<212> DNA

<213> Artificial Sequence

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<211> 9

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<223> Xaa may be Asp or Glu

<400> 55

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<211> 450

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

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ctcgtcttca ccggtcgcgt tcctgaaacg cagatgtgcc tcgcgccgca ctgctccgaa 120

caataaagat tctacaatac tagcttttat ggttatgaag aggaaaaatt ggcagtaacc 180

tggccccaca aaccttcaaa tgaacgaatc aaattaacaa ccataggatg ataatgcgat 240

tagtttttta gccttatttc tggggtaatt aatcagcgaa gcgatgattt ttgatctatt 300

aacagatata taaatgcaaa aactgcataa ccactttaac taatactttc aacattttcg 360

gtttgtatta cttcttattc aaatgtaata aaagtatcaa caaaaaattg ttaatatacc 420

tctatacttt aacgtcaagg agaaaaaact 450

<210> 58

<211> 1584

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 58

atggctgcag accaattggt gaagactgaa gtcaccaaga agtcttttac tgctcctgta 60

caaaaggctt ctacaccagt tttaaccaat aaaacagtca tttctggatc gaaagtcaaa 120

agtttatcat ctgcgcaatc gagctcatca ggaccttcat catctagtga ggaagatgat 180

tcccgcgata ttgaaagctt ggataagaaa atacgtcctt tagaagaatt agaagcatta 240

ttaagtagtg gaaatacaaa acaattgaag aacaaagagg tcgctgcctt ggttattcac 300

ggtaagttac ctttgtacgc tttggagaaa aaattaggtg atactacgag agcggttgcg 360

gtacgtagga aggctctttc aattttggca gaagctcctg tattagcatc tgatcgttta 420

ccatataaaa attatgacta cgaccgcgta tttggcgctt gttgtgaaaa tgttataggt 480

tacatgcctt tgcccgttgg tgttataggc cccttggtta tcgatggtac atcttatcat 540

ataccaatgg caactacaga gggttgtttg gtagcttctg ccatgcgtgg ctgtaaggca 600

atcaatgctg gcggtggtgc aacaactgtt ttaactaagg atggtatgac aagaggccca 660

gtagtccgtt tcccaacttt gaaaagatct ggtgcctgta agatatggtt agactcagaa 720

gagggacaaa acgcaattaa aaaagctttt aactctacat caagatttgc acgtctgcaa 780

catattcaaa cttgtctagc aggagattta ctcttcatga gatttagaac aactactggt 840

gacgcaatgg gtatgaatat gatttctaag ggtgtcgaat actcattaaa gcaaatggta 900

gaagagtatg gctgggaaga tatggaggtt gtctccgttt ctggtaacta ctgtaccgac 960

aaaaaaccag ctgccatcaa ctggatcgaa ggtcgtggta agagtgtcgt cgcagaagct 1020

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gcacatgcag ctaatttagt gacagctgtt ttcttggcat taggacaaga tcctgcacaa 1200

aatgtcgaaa gttccaactg tataacattg atgaaagaag tggacggtga tttgagaatt 1260

tccgtatcca tgccatccat cgaagtaggt accatcggtg gtggtactgt tctagaacca 1320

caaggtgcca tgttggactt attaggtgta agaggcccac atgctaccgc tcctggtacc 1380

aacgcacgtc aattagcaag aatagttgcc tgtgccgtct tggcaggtga attatcctta 1440

tgtgctgccc tagcagccgg ccatttggtt caaagttata tgacccacaa caggaaacct 1500

gctgaaccaa caaaacctaa caatttggac gccactgata taaatcgttt gaaagatggg 1560

tccgtcacct gcattaaatc ctaa 1584

<210> 59

<211> 200

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 59

agatccgctc taaccgaaaa ggaaggagtt agacaacctg aagtctaggt ccctatttat 60

ttttttatag ttatgttagt attaagaacg ttatttatat ttcaaatttt tctttttttt 120

ctgtacagac gcgtgtacgc atgtaacatt atactgaaaa ccttgcttga gaaggttttg 180

ggacgctcga agatccagct 200

<210> 60

<211> 200

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 60

agctggatct tcgagcgtcc caaaaccttc tcaagcaagg ttttcagtat aatgttacat 60

gcgtacacgc gtctgtacag aaaaaaaaga aaaatttgaa atataaataa cgttcttaat 120

actaacataa ctataaaaaa ataaataggg acctagactt caggttgtct aactccttcc 180

ttttcggtta gagcggatct 200

<210> 61

<211> 1584

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 61

ttaggattta atgcaggtga cggacccatc tttcaaacga tttatatcag tggcgtccaa 60

attgttaggt tttgttggtt cagcaggttt cctgttgtgg gtcatataac tttgaaccaa 120

atggccggct gctagggcag cacataagga taattcacct gccaagacgg cacaggcaac 180

tattcttgct aattgacgtg cgttggtacc aggagcggta gcatgtgggc ctcttacacc 240

taataagtcc aacatggcac cttgtggttc tagaacagta ccaccaccga tggtacctac 300

ttcgatggat ggcatggata cggaaattct caaatcaccg tccacttctt tcatcaatgt 360

tatacagttg gaactttcga cattttgtgc aggatcttgt cctaatgcca agaaaacagc 420

tgtcactaaa ttagctgcat gtgcgttaaa tccaccaaca gacccagcca ttgcagatcc 480

aaccaaattc ttagcaatgt tcaactcaac caatgcggaa acatcacttt ttaacacttt 540

tctgacaaca tcaccaggaa tagtagcttc tgcgacgaca ctcttaccac gaccttcgat 600

ccagttgatg gcagctggtt ttttgtcggt acagtagtta ccagaaacgg agacaacctc 660

catatcttcc cagccatact cttctaccat ttgctttaat gagtattcga cacccttaga 720

aatcatattc atacccattg cgtcaccagt agttgttcta aatctcatga agagtaaatc 780

tcctgctaga caagtttgaa tatgttgcag acgtgcaaat cttgatgtag agttaaaagc 840

ttttttaatt gcgttttgtc cctcttctga gtctaaccat atcttacagg caccagatct 900

tttcaaagtt gggaaacgga ctactgggcc tcttgtcata ccatccttag ttaaaacagt 960

tgttgcacca ccgccagcat tgattgcctt acagccacgc atggcagaag ctaccaaaca 1020

accctctgta gttgccattg gtatatgata agatgtacca tcgataacca aggggcctat 1080

aacaccaacg ggcaaaggca tgtaacctat aacattttca caacaagcgc caaatacgcg 1140

gtcgtagtca taatttttat atggtaaacg atcagatgct aatacaggag cttctgccaa 1200

aattgaaaga gccttcctac gtaccgcaac cgctctcgta gtatcaccta atttttttctc 1260

caaagcgtac aaaggtaact taccgtgaat aaccaaggca gcgacctctt tgttcttcaa 1320

ttgttttgta tttccactac ttaataatgc ttctaattct tctaaaggac gtattttctt 1380

atccaagctt tcaatatcgc gggaatcatc ttcctcacta gatgatgaag gtcctgatga 1440

gctcgattgc gcagatgata aacttttgac tttcgatcca gaaatgactg ttttattggt 1500

taaaactggt gtagaagcct tttgtacagg agcagtaaaa gacttcttgg tgacttcagt 1560

cttcaccaat tggtctgcag ccat 1584

<210> 62

<211> 451

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 62

agtttttttct ccttgacgtt aaagtataga ggtatattaa caatttttttg ttgatacttt 60

tattacattt gaataagaag taatacaaac cgaaaatgtt gaaagtatta gttaaagtgg 120

ttatgcagtt tttgcattta tatatctgtt aatagatcaa aaatcatcgc ttcgctgatt 180

aattacccca gaaataaggc taaaaaacta atcgcattat catcctatgg ttgttaattt 240

gattcgttca tttgaaggtt tgtggggcca ggttactgcc aatttttcct cttcataacc 300

ataaaagcta gtattgtaga atctttattg ttcggagcag tgcggcgcga ggcacatctg 360

cgtttcagga acgcgaccgg tgaagacgag gacgcacgga ggagagtctt ccttcggagg 420

gctgtcaccc gctcggcggc ttctaatccg t 451

<210> 63

<211> 462

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 63

aatgtgtata ttagtttaaa aagttgtatg taataaaagt aaaatttaat attttggatg 60

aaaaaaacca tttttagact ttttcttaac tagaatgctg gagtagaaat acgccatctc 120

aagatacaaa aagcgttacc ggcactgatt tgtttcaacc agtatataga ttattattgg 180

gtcttgatca actttcctca gacatatcag taacagttat caagctaaat atttacgcga 240

aagaaaaaca aatattttaa ttgtgatact tgtgaatttt attttattaa ggatacaaag 300

ttaagagaaa acaaaattta tatacaatat aagtaatatt catatatatg tgatgaatgc 360

agtcttaacg agaagacatg gccttggtga caactctctt caaaccaact tcagcctttc 420

tcaattcatc agcagatggg tcttcgattt gcaaagcagc ca 462

<210> 64

<211> 573

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 64

atgtccggta aatggagact agtgctgact gggataggca atccagagcc tcagtacgct 60

ggcacccgtc acaatgtagg gctatatatg ctggagctgc tacgaaagcg gcttggtctg 120

caggggagaa cctattcccc tgtgcctaat acgggcggca aagtgcatta tatagaagac 180

gaacattgta cgatactaag atcggatggc cagtacatga atctaagtgg agaacaggtg 240

tgcaaggtct gggcccggta cgccaagtac caagcccgac acgttgttat tcatgacgag 300

ttaagtgtgg cgtgtggaaa agtgcagctc agagccccca gcaccagtat tagaggtcat 360

aatgggctgc gaagtctact gaaatgctcc ggaggccgtg tacccttgc caaattggct 420

attggaatcg gcagagaacc tgggtcccgc tctagagacc ctgcgagcgt ctcccgctgg 480

gttctgggag ctctaactcc gcaggaacta caaaccttgc ttacacagag tgaacctgct 540

gcctggcgtg ctctgactca gtacatttca tag 573

<210> 65

<211> 511

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 65

gatcttgaaa ctgagtaaga tgctcagaat acccgtcaag ataagagtat aatgtagagt 60

aatataccaa gtattcagca tattctcctc ttcttttgta taaatcacgg aagggatgat 120

ttataagaaa aatgaatact attacacttc atttaccacc ctctgatcta gattttccaa 180

cgatatgtac gtagtggtat aaggtgaggg ggtccacaga tataacatcg tttaatttag 240

tactaacaga gacttttgtc acaactacat ataagtgtac aaatatagta cagatatgac 300

acacttgtag cgccaacgcg catcctacgg attgctgaca gaaaaaaagg tcacgtgacc 360

agaaaagtca cgtgtaattt tgtaactcac cgcattctag cggtccctgt cgtgcacact 420

gcactcaaca ccataaacct tagcaacctc caaaggaaat caccgtataa caaagccaca 480

gttttacaac ttagtctctt atgaagtgtc t 511

<210> 66

<211> 1335

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 66

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aagttttgca gaacaccgct attctccatc tatgatcagt ccacgtctcc atatctcttg 120

cactgtttcg aactgttgaa cttgacctcc agatcgtttg ctgctgtgat cagagagctg 180

catccagaat tgagaaactg tgttactctc ttttatttga ttttaagggc tttggatacc 240

atcgaagacg atatgtccat cgaacacgat ttgaaaattg acttgttgcg tcacttccac 300

gagaaattgt tgttaactaa atggagtttc gacggaaatg cccccgatgt gaaggacaga 360

gccgttttga cagatttcga atcgattctt attgaattcc acaaattgaa accagaatat 420

caagaagtca tcaaggagat caccgagaaa atgggtaatg gtatggccga ctacatctta 480

gatgaaaatt acaacttgaa tgggttgcaa accgtccacg actacgacgt gtactgtcac 540

tacgtagctg gtttggtcgg tgatggtttg acccgtttga ttgtcattgc caagtttgcc 600

aacgaatctt tgtattctaa tgagcaattg tatgaaagca tgggtctttt cctacaaaaa 660

accaacatca tcagagatta caatgaagat ttggtcgatg gtagatcctt ctggcccaag 720

gaaatctggt cacaatacgc tcctcagttg aaggacttca tgaaacctga aaacgaacaa 780

ctggggttgg actgtataaa ccacctcgtc ttaaacgcat tgagtcatgt tatcgatgtg 840

ttgacttatt tggccggtat ccacgagcaa tccactttcc aattttgtgc cattccccaa 900

gttatggcca ttgcaacctt ggctttggta ttcaacaacc gtgaagtgct acatggcaat 960

gtaaagattc gtaagggtac tacctgctat ttaattttga aatcaaggac tttgcgtggc 1020

tgtgtcgaga tttttgacta ttacttacgt gatatcaaat ctaaattggc tgtgcaagat 1080

ccaaatttct taaaattgaa cattcaaatc tccaagatcg aacagtttat ggaagaaatg 1140

taccaggata aattacctcc taacgtgaag ccaaatgaaa ctccaatttt cttgaaagtt 1200

aaagaaagat ccagatacga tgatgaattg gttccaaccc aacaagaaga agagtacaag 1260

ttcaatatgg ttttatctat catcttgtcc gttcttcttg ggttttatta tatatacact 1320

ttacacagag cgtga 1335

<210> 67

<211> 1668

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 67

atggccagtc aggcttcaca agttttagca tctccccacc cagctatatc ctctgaaaac 60

cggccaaagg ctgatttcca tcctggtatc tggggcgaca tgtttattat ctgtccagat 120

acggacattg atgccgctac agagctgcaa tatgaagaat tgaaagcgca agtccgcaag 180

atgatcatgg aaccagtaga cgattctaat caaaagctac cattcattga cgctgttcaa 240

aggctcggag tgagctacca ctttgaaaaa gaaattgaag acgaacttga aaacatctac 300

cgtgatacca ataacaacga cgcagacact gatctataca ctaccgcctt gagattcaga 360

ttattgagag agcatggttt tgatatttcc tgcgatgctt tcaacaagtt gaaagacgaa 420

gaaggtaatt tcaaggcttc gttgacttct gacgttcctg gtttgttaga actctatgag 480

gcttcctact tgagagtcca cggtgaagat atcctagatg aagccatatc tttcgctact 540

gctcagttaa ccttggcttt gccaactttg catcacccgc tttcagagca agttggtcac 600

gcattgaagc aaagtatcag aagaggcctg ccaagagttg aagccagaaa ctttatctct 660

atttaccaag atttagaatc ccacaataag gctttgttgc aattcgccaa aattgacttt 720

aacatgttac aattgctaca taggaaggag ctcagcgaaa tttgtagatg gtggaaagat 780

cttgatttta ccagaaagtt acctttcgct cgtgaccgtg tcgtcgaagg ttatttctgg 840

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gcagataaag gtcgacagta cagagtggaa tacgctaaga aagctatgat tcggttggtg 1140

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cacagaaggg aggatgactg ttccgctatt gaatgttaca tggagcaata caaagtcaca 1440

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gaagagttct tgaaaccaac tgaaatgcct actccggtac tgtgtagaag tttgaaccta 1560

gccagagtca tggatgtttt gtacagagaa ggtgacggtt atactcatgt tggaaaagcc 1620

gctaagggtg gtataacatc acttcttatc gatcccattc aaatctaa 1668

<210> 68

<211> 1668

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 68

atggccagtc aggcttcaca agttttagca tctccccacc cagctatatc ctctgaaaac 60

cggccaaagg ctgatttcca tcctggtatc tggggcgaca tgtttattat ctgtccagat 120

acggacattg atgccgctac agagctgcaa tatgaagaat tgaaagcgca agtccgcaag 180

atgatcatgg aaccagtaga cgattctaat caaaagctac cattcattga cgctgttcaa 240

aggctcggag tgagctacca ctttgaaaaa gaaattgaag acgaacttga aaacatctac 300

cgtgatacca ataacaacga cgcagacact gatctataca ctaccgcctt gagattcaga 360

ttattgagag agcatggttt tgatatttcc tgcgaagctt tcaacaagtt gaaagacgaa 420

gagggtaatt tcaaggcttc gttgacttct gatgttagag gtttgttaga actctatcag 480

gcttcctaca tgagaatcca cggtgaagat attcttgatg aagccatatc tttcaccact 540

gctcaattaa ccttggcttt gcctactttg gatcccccat tgtcagagca agtcggtcat 600

gccctaaagc agagtataag aagaggccta ccaagagttg aagccagaaa ctttatctct 660

atttaccaag acttggaatc ccacaataag gctttattgc aattcgctaa aattgacttt 720

aacatgttac aattgctaca taggaaggag ctcagcgaaa tctgtcgttg gtggaaagat 780

cttgatttta ctagaaagtt gcctttcgca cgggaccgtg tcgttgaagg ttatttctgg 840

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gctagagtca tggatgtttt gtacagagaa ggtgacggtt atactcatgt cgggaaagcc 1620

gctaagggtg gtataacctc attgctaatt gatcccattc aaatctaa 1668

<210> 69

<211> 1668

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 69

atggccagtc aggcttcaca agttttagca tctccccacc cagctatatc ctctgaaaac 60

cggccaaagg ctgatttcca tcctggtatc tggggcgaca tgtttattat ctgtccagat 120

acggacattg atgccgctac agagctgcaa tatgaagaat tgaaagcgca agtccgcaag 180

atgatcatgg aaccagtaga cgattctaat caaaagctac cattcattga cgctgttcaa 240

aggctcggag tgagctacca ctttgaaaaa gaaattgaag acgaacttga aaacatctac 300

cgtgatacca ataacaacga cgcagacact gatctataca ctaccgcctt gagattcaga 360

ttattgagag agcatggttt tgatatttcc tgcgatgctt tcaacaagtt gaaagacgaa 420

gaaggtaatt tcaaggcttc gttgacttct gacgttcctg gtttgttaga actctatgag 480

gcttcctact tgagagtcca cggtgaagat atcctagatg aagccatatc tttcgctact 540

gctcagttaa ccttggcttt gccaactttg catcacccgc tttcagagca agttggtcac 600

gcattgaagc aaagtatcag aagaggcctg ccaagagttg aagccagaaa ctttatctct 660

atttaccaag atttagaatc ccacaataag gctttgttgc aattcgccaa aattgacttt 720

aacatgttac aattgctaca taggaaggag ctcagcgaaa tttgtagatg gtggaaagat 780

cttgatttta ccagaaagtt acctttcgct cgtgaccgtg tcgtcgaagg ttatttctgg 840

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tttagagaca atgctttgcc gacatctggg tatgccatgc tagctataac cgcgttcgtt 1260

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cacagaaggg aggatgactg ttccgctatt gaatgttaca tgaagcaata cggtgcaaca 1440

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gaagagttct tgaaaccaac tgaaatgcct actccggtac tgtgtagaag tttgaaccta 1560

gccagagtca tggatgtttt gtacagagaa ggtgacggtt atactcatgt tgggaaagcc 1620

gctaagggtg gtataacatc acttcttatc gatcccattc aaatctaa 1668

<210> 70

<211> 1668

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 70

atggcctcac aggcttccca agttttagca tctcctcacc cagctatatc ttccgaaaac 60

cgtccaaagg ctgatttcca tccaggtatc tggggcgaca tgtttattat ctgtccagat 120

acagacattg atgccgctac cgagttgcaa tatgaagaat tgaaagccca agtcagaaag 180

atgatcatgg aaccagttga cgattctaat caaaagttgc ctttcattga cgctgtccaa 240

agattgggtg tttcatacca ctttgaaaaa gaaattgaag acgaattaga aaacatctac 300

agagatacta ataacaacga cgcagacact gatttgtaca ccactgcctt gagattcaga 360

ttattgcgtg agcatggttt tgatatttct tgcgaagctt tcaacaagtt gaaagacgaa 420

gagggtaatt tcaaggcttc cttaacctct gatgtcagag gtttgttgga attgtatcag 480

gcttcctaca tgagaatcca cggtgaagat attttggatg aagctatatc tttcacaact 540

gctcaattaa ctttagcttt accaactttg gatcctccat tgtctgagca agttggtcat 600

gccttgaagc agtcaatacg tagaggtttg ccaagagttg aagccagaaa ctttatctct 660

atttaccaag acttggaatc ccacaataag tctttattag aatttgctaa aattgatttc 720

aacttattgc aattgttaca cagaaaggag ttgtccgaaa tctgtagatg gtggaaagac 780

ttggatttta ccagaaagtt acctttcgct agagatcgtg tcgttgaagg ttatttctgg 840

atcatgggtg tctacttcga accacaatac tccttgggta gaaagatgtt gaccaaagtt 900

attgctatgg cctctattgt tgacgatact tatgactcat ttgcaaccta cgacgaattg 960

ataccatata cagacgctat tgaaagatgg gatatcaagt gtatgaacca attgccaaat 1020

tatatgcaaa tatcttacaa ggctttgtta gacgtttacg aggaaatgga acaattgttg 1080

gctgataagg gtagacaata tagagtcgag tacgcaaaaa aagccatgat cagattggtt 1140

caggcctact tattagaggc taagtggacc catttgaact acaagcctac ttttgaagag 1200

ttcagagaca atgctttacc aacctccggt tatgccatgt tggctatcac tgcattcgtt 1260

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attaaggctt ctactatcat ctgccgtttc atggatgata ttgctgaaca caaattcaac 1380

cacagaagag aggacgattg ttccgctatt gaatgttaca tggaacaata caaggttaca 1440

gcccaagaag catacgacga atttaacaag catatcgaat catcttggaa ggacgttaat 1500

gaagaatttt taaagcctac cgaaatgcca acaccagtct tgtgtagatc tttgaacttg 1560

gccagagtta tggatgtctt gtaccgtgaa ggtgatggtt atactcatgt cggtaaggct 1620

gctaaaggtg gtatcacctc cttgttgatc gaccctattc aaatttaa 1668

<210> 71

<211> 1668

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 71

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cgtccaaagg ctgatttcca tccaggtatc tggggcgaca tgtttattat ctgtccagat 120

acagacattg atgccgctac cgagttgcaa tatgaagaat tgaaagccca agtcagaaag 180

atgatcatgg aaccagttga cgattctaat caaaagttgc ctttcattga cgctgtccaa 240

agattgggtg tttcatacca ctttgaaaaa gaaattgaag acgaattaga aaacatctac 300

agagatacta ataacaacga cgcagacact gatttgtaca ccactgcctt gagattcaga 360

ttattgcgtg agcatggttt tgatatttct tgcgatgctt tcaacaagtt gaaagacgaa 420

gaaggtaatt tcaaggcttc cttaacctct gacgtcccag gtttgttgga attgtatgag 480

gcttcctact taagagttca cggtgaagat atcttggatg aagctatatc tttcgccact 540

gctcagttaa ccttggcttt accaactttg catcacccat tgtctgagca agttggtcac 600

gcattgaagc aatcaatcag aagaggtttg ccaagagttg aagctagaaa ctttatctct 660

atttaccaag atttagaatc ccacaataag tctttattag aatttgccaa aattgatttc 720

aacttgttgc aattgttaca ccgtaaggag ttgtccgaaa tatgtagatg gtggaaagac 780

ttagatttta caagaaagtt acctttcgct agagatagag tcgttgaagg ttatttctgg 840

attatgggtg tctacttcga accacaatac tccttgggta gaaagatgtt gaccaaagtt 900

attgctatgg cttctatcgt tgacgatact tatgactcat ttgccactta cgacgaattg 960

atcccttata cagacgctat tgaacgttgg gatatcaagt gtatgaacca gttgccaaat 1020

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ttcagagaca atgctttacc aacttccggt tatgccatgt tggctataac cgcattcgtt 1260

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atcaaggctt ctactatcat ctgccgtttc atggatgata ttgccgaaca taaattcaac 1380

cacagaagag aggacgattg ttccgctatt gaatgttaca tggaacaata caaggttaca 1440

gcccaagaag cttacgacga atttaacaag cacatcgaat catcttggaa ggacgtcaat 1500

gaagaatttt tgaagcctac cgaaatgcca actccagtct tgtgtagatc tttgaacttg 1560

gcaagagtta tggatgtctt gtacagagaa ggtgatggtt atactcatgt cggtaaggct 1620

gctaaaggtg gtatcacctc cttgttgatc gaccctattc aaatttaa 1668

<210> 72

<211> 1668

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 72

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cgtccaaagg ctgatttcca tccaggtatc tggggcgaca tgtttattat ctgtccagat 120

acagacattg atgccgctac cgagttgcaa tatgaagaat tgaaagccca agtcagaaag 180

atgatcatgg aaccagttga cgattctaat caaaagttgc ctttcattga cgctgtccaa 240

agattgggtg tttcatacca ctttgaaaaa gaaattgaag acgaattaga aaacatctac 300

agagatacta ataacaacga cgcagacact gatttgtaca ccactgcctt gagattcaga 360

ttattgcgtg agcatggttt tgatatttct tgcgaagctt tcaacaagtt gaaagacgaa 420

gagggtaatt tcaaggcttc cttaacctct gatgtcagag gtttgttgga attgtatcag 480

gcttcctaca tgagaatcca cggtgaagat attttggatg aagctatatc tttcacaact 540

gctcaattaa ctttagcttt accaactttg gatcctccat tgtctgagca agttggtcat 600

gccttgaagc agtcaatacg tagaggtttg ccaagagttg aagccagaaa ctttatctct 660

atttaccaag acttggaatc ccacaataag tctttattag aatttgctaa aattgatttc 720

aacttattgc aattgttaca cagaaaggag ttgtccgaaa tctgtagatg gtggaaagac 780

ttggatttta ccagaaagtt acctttcgct agagatcgtg tcgttgaagg ttatttctgg 840

atcatgggtg tctacttcga accacaatac tccttgggta gaaagatgtt gaccaaagtt 900

attgctatgg cctctattgt tgacgatact tatgactcat ttgcaaccta cgacgaattg 960

ataccatata cagacgctat tgaaagatgg gatatcaagt gtatgaacca attgccaaat 1020

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gctgataagg gtagacaata tagagtcgag tacgcaaaaa aagccatgat cagattggtt 1140

caggcctact tattagaggc taagtggacc catttgaact acaagcctac ttttgaagag 1200

ttcagagaca atgctttacc aacctccggt tatgccatgt tggctatcac tgcattcgtt 1260

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attaaggctt ctactatcat ctgccgtttc atggatgata ttgctgaaca caaattcaac 1380

cacagaagag aggacgattg ttccgctatt gaatgttaca tgaaacaata cggtgctaca 1440

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gaagaatttt taaagcctac cgaaatgcca acaccagtct tgtgtagatc tttgaacttg 1560

gcaagagtta tggatgtctt gtaccgtgaa ggtgatggtt atactcatgt cggtaaggct 1620

gctaaaggtg gcatcacctc cttgttgatc gaccctattc aaatttaa 1668

<210> 73

<211> 1668

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 73

atggcctcac aggcttccca agttttagca tctcctcacc cagctatatc ttccgaaaac 60

cgtccaaagg ctgatttcca tccaggtatc tggggcgaca tgtttattat ctgtccagat 120

acagacattg atgccgctac cgagttgcaa tatgaagaat tgaaagccca agtcagaaag 180

atgatcatgg aaccagttga cgattctaat caaaagttgc ctttcattga cgctgtccaa 240

agattgggtg tttcatacca ctttgaaaaa gaaattgaag acgaattaga aaacatctac 300

agagatacta ataacaacga cgcagacact gatttgtaca ccactgcctt gagattcaga 360

ttattgcgtg agcatggttt tgatatttct tgcgatgctt tcaacaagtt gaaagacgaa 420

gaaggtaatt tcaaggcttc cttaacctct gacgtcccag gtttgttgga attgtatgag 480

gcttcctact taagagttca cggtgaagat atcttggatg aagctatatc tttcgccact 540

gctcagttaa ccttggcttt accaactttg catcacccat tgtctgagca agttggtcac 600

gcattgaagc aatcaatcag aagaggtttg ccaagagttg aagctagaaa ctttatctct 660

atttaccaag atttagaatc ccacaataag tctttattag aatttgccaa aattgatttc 720

aacttgttgc aattgttaca ccgtaaggag ttgtccgaaa tatgtagatg gtggaaagac 780

ttagatttta caagaaagtt acctttcgct agagatagag tcgttgaagg ttatttctgg 840

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attgctatgg cttctatcgt tgacgatact tatgactcat ttgccactta cgacgaattg 960

atcccttata cagacgctat tgaacgttgg gatatcaagt gtatgaacca gttgccaaat 1020

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cacagaagag aggacgattg ttccgctatt gaatgttaca tgaaacaata cggtgctaca 1440

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gaagaatttt tgaagcctac cgaaatgcca actccagtct tgtgtagatc tttgaacttg 1560

gccagagtta tggatgtctt gtacagagaa ggtgatggtt atactcatgt cggtaaggct 1620

gctaaaggtg gcatcacctc cttgttgatc gaccctattc aaatttaa 1668

<210> 74

<211> 1674

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 74

atgtccatac aggttcccca aatttcttcg caaaatgcaa agtcacaagt aatgcgtaga 60

accgccaact ttcatccatc tgtgtgggga gacagattcg ctaactacac ggctgaggat 120

aaaatgaacc acgctcgcga cttgaaggaa cttaaagcgt taaaggaaga agttggtaga 180

aagctgttgg ccacagctgg cccaattcaa ctcaatctaa tcgatgctat ccaaagattg 240

ggtgtcggtt atcacttcga acgagaattg gaacaagctt tgcaacattt atacaacgag 300

aagtatagcg atgacgacac tgaagatgat ttgtacagga tttctctgag atttagattg 360

ttaagacagc acggttacaa tgtctcctgc gacaaattca acatgtttaa ggatgacaaa 420

ggtaacttca aggaaagttt ggcttctgat gccttgggta tgctctcctt atacgaagcg 480

gctcatttgg gcgttcacgg tgaagatatc ttagacgaag ctattgcatt taccactact 540

catctaaagt ccgtcgctac tcacttatct aatcctctaa aggcccaagt tcgtcatgcc 600

ttgagacaac cgcttcacag aggtttgcca agattggaac acagaaggta tatcagcatt 660

taccaggatg acgcttctca ttacaaagct ttgttgaccc ttgcgaagtt ggatttcaat 720

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gacttcgctc gtaagttgcc ttttgctaga gatagaatgg tcgaatgtta tttctggatc 840

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gctatgactt ctattattga tgacatctat gacgtttacg ggacaccaga agaattgaag 960

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aacgaaggtt ggtcttacag agtccaatat gcaaaagaag ctatgaagat tttagttgag 1140

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gaaagaggtc actgtgcgtc cgctgtcgaa tgttatatga gggaacatgg cgtgtctgaa 1440

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aacttgacga gagttattga tgtcgtctac aaggaaggtg atggttatac tcatgtgggt 1620

aatgaaatga aacaaaacgt tgctgctctt ttgatcgacc aagtcccaat ttaa 1674

<210> 75

<211> 1668

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 75

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tcaaagtacc atcctagtat ttggggtgac tatttcatcc aaaattccag cttaacccac 120

gccaaagaat ctactcaaag gatgatcaag agagttgaag aactaaaggt acaagtcaaa 180

tctatgttca aggacacttc tgatttgttg caactgatga acttaattaa ctctattcaa 240

atgctaggac ttgactacca ctttgaaaat gaaatcgatg aggctctccg cttgatctat 300

gaagttgacg ataagtcata cggtctgtac gaaacgagct tgagattcca gttgttgaga 360

caacatggtt accacgtgga tggtgaagaa gctttcaaca tgcttaaaga cgaagagggt 420

aactttaagg cgtccttgac ctctgatgtt ccaggtttat tggaattata tcaagctagc 480

tacatgagaa tacatggtga agatattttg gatgaagcca ttagtttcac taccgctcaa 540

ttgactttag ctcttcccac cttagacccg ccattgtcgg cacaagtctc tttgttcttg 600

gagctaccat tatgcagaag aaacaagatt ttgcttgcca gaaaatacat cttgatatat 660

caagaagatg ctatgcgtaa taatgttatt ctcgagttgg ctaagcttaa ctttaactta 720

ttgcaatcct tgtaccaaga agaactgaag aaaatctcta tctggtggaa tgacttagct 780

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ctaaacccta ctaaggttcc aagattgatg atagaaagaa tagtaaactt gtcaaagtcc 1560

aacgaagaaa tttacaaata caacgacacc tacactaatt ctgatactac aatgaaggac 1620

aatattagtc tagtattggt tgagtcctgt gattatttca acaaataa 1668

<210> 76

<211> 1674

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 76

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atgagaccaa aggctgactt tcaaccctcg atatggggcg atttgttcct gaattgccca 120

gacaagaaca ttgatgctga aaccgaaaag cgtcatcaac aattgaaaga agaagtcaga 180

aagatgatcg tggcaccaat ggctaattct acacaaaagt tggctttcat tgactctgtt 240

cagaggcttg gagtatccta ccactttact aaagaaattg aggatgaatt agaaaacatc 300

tatcacaaca ataacgacgc agaaaacgat ttgtacacga cttccctaag attcagatta 360

ttgagagaac atggtttcaa tgtctcttgt gacgttttta acaagtttaa ggatgagcaa 420

ggtaatttca agtcaagtgt tacctctgac gtccgcggtc tcttggaatt ataccaagcg 480

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<210> 77

<211> 1668

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 77

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atgagaccaa aggctgactt tcaaccctcg atatggggcg atttgttcct gaattgccca 120

gacaagaaca ttgatgctga aaccgaaaag cgtcatcaac aattgaaaga agaagtcaga 180

aagatgatcg tggcaccaat ggctaattct acacaaaagt tggctttcat tgactctgtt 240

cagaggcttg gagtatccta ccactttact aaagaaattg aggatgaatt agaaaacatc 300

tatcacaaca ataacgacgc agaaaacgat ttgtacacga cttccataag attcagatta 360

ttgagagaac atggttacca cgtcgatggt gaggaagcct tcaacatgct caaggacgaa 420

gaaggtaatt ttaaggcttc tttgacctca gacgttcctg gtttgttaga actatatcaa 480

gcctcataca tgcgaatcca tggtgaagat attttggacg aagcgatctc ttttactact 540

gctcaattaa ccttggcttt gccaaccctg gatccaccgc tctctgaaga ggtcagtcac 600

gcgctaaagc aaagtattag aagaggttta ccacgtgtag aagctagaca ttatctgtcc 660

gtttaccaag acatcgaatc tcacaataaa gctctattgg aatttgccaa gattgatttc 720

aacatgttgc agttcctcca cagaaaggaa ctttcagaaa tatgtcgttg gtggaaagat 780

ttggacttcc aacgcaagtt accatatgct agagatcgcg ttgtcgaggg ttacttctgg 840

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caagaatttc tcaagccaac tgaaatgcca acagaggtgt tgaacagatc acttaacctc 1560

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<210> 78

<211> 1677

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 78

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acggacattg atgccgctac agagctgcaa tatgaagaat tgaaagcgca agtccgcaag 180

atgatcatgg aaccagtaga cgattctaat caaaagctac cattcattga cgctgttcaa 240

aggctcggag tgagctacca ctttgaaaaa gaaattgaag acgaacttga aaacatctac 300

cgtgatacca ataacaacga cgcagacact gatctataca ctaccgcctt gagattcaga 360

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gctggtaatt tcaaggcttc gttgacttct gacgttcaag gtttgttgga attgtatgag 480

gcctcctaca tgagagtcca cggtgaagat atcctagatg aagctatatc ttttaccact 540

gctcagttaa ccttggcttt acctactttg catcacccgt tgtcagagca agttggtcac 600

gcactcaagc agagtatcag aagaggcctg ccaagagttg aagccagaaa ctttatctct 660

atttaccaag atttggaatc ccacaataag tccttgttac aattcgctaa aattgacttt 720

aacctttttac aattgctcca taggaaggaa ctcagcgaaa tttgtagatg gtggaaagat 780

cttgatttca ctagaaagtt gccttttgca cgtgaccgtg tcgtcgaagg ttatttctgg 840

attatgggag tttacttcga accacaatat agcttgggta gaaagatgtt gaccaaggtt 900

attgctatgg cttctatcgt cgatgataca tacgattctt acgctacata tgacgaattg 960

ataccatata ctaacgccat cgaaagatgg gacatcaagt gtatgaatca actgccaaac 1020

tacatgaaga ttagttacaa agcattattg aatgtatatg aggagatgga acaattgctt 1080

gcgaatcaag gtcgacagta cagagtggaa tacgctaaga aagctatgat tcggttggtg 1140

caagcctact tattagaagc gaagtggact catcaaaact acaagccaac cttcgaagaa 1200

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caagaaaggg ggcactgtgc ttccgctgtc gaatgttaca tgagagaaca cggtgtctca 1440

gaagaagagg cctgttctga attgaaaaag caggtcgaca acgcctggaa ggatattaac 1500

catgagatga ttttttagtga aacatccaaa gctgtcccaa tgagtgttct aaccagagtt 1560

ttgaacctta ctagagttat ggacgtattg tacagagaag gtgatggtta tacgcatgtc 1620

ggtaaggctg caaagggtgg tatcacctct ttgttgattg accccattca aatctaa 1677

<210> 79

<211> 1650

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 79

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gaatacaagg aaacaattcg taagatgttg gttgaagccc ctgaagggtc cgagcaaaaa 180

ttggtcttaa tcgacgctat gcaaagattg ggtgttgcat atcactttca taacgaaatt 240

gaaacctcta ttcaaaatat cttcgatgct ccaaagcaaa acaacgacga taacttgcac 300

attgtctctt taagattcag attggtccgt caacagggtc attacatgtc ctctgacgtt 360

tttaagcaat tcactaacca agatggtaaa ttcaaggaaa ccttgactaa tgatgtccaa 420

ggtttgttgt cattatatga agcttctcac ttgagagtta gaaatgaaga aatattagag 480

gaagctttga cttttaccac aactcatttg gaatccatcg tttctaactt atcaaacaaa 540

aataactctt taaaggttga agtttctgaa gctttgtccc aaccaatcag aatgactttg 600

ccaagaattg gtgccagaaa gtacatttcc atatacgaaa acaatgacgc ccacaaccat 660

ttgttgttaa agttcgctaa gttggatttt aatatgttac aaaagttcca ccaaagagaa 720

ttgtccgact tgaccagatg gtggaaagac ttggactttg ctaacaagat cccatatgct 780

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tttgatgctt acgccaattt cgacgaattg gttccattca atgacgccat ccaaagatgg 960

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gatatatatg gtgaaatgga ccaagtttta tccaaagagg gtaagttgga tagagtctac 1080

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gcaatggatg atatcgtcgg tcacgaggtt gaacaagaac gtggtcattg tgcttcagca 1380

gtcgaatgtt acatgagaga gcatggtgtt tctgaagaag aagcttgctc cgaattaaag 1440

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aaagctgtcc caatgtctgt cttaaccaga gttttaaact tgacaagagt tattgatact 1560

ttgtaccagg aagaagatga atacaccaac gctaagggta aattaaaaaa tatgatccac 1620

tccatcttga ttgagtcagt caagatctaa 1650

<210> 80

<211> 1677

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 80

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tccaagtacc atccttctat ttggggcgac tatttcatcc aaaattcctc tttaacccac 120

gccaaagaat ctactcaaag aatgatcaag agagttgaag aattgaaggt ccaagttaaa 180

tcaatgttca aggacacttc cgatttattg caattgatga acttaattaa ctctattcaa 240

atgttgggtt tggactacca ctttgaaaat gaaatcgatg aggctttgag attgatctat 300

gaagtcgacg ataagtccta cggtttgtac gaaacatcat taagattcca gttgttaaga 360

caacatggtt accacgttga tggtgaagaa gctttcaaca tgttgaagga tgaggaaggt 420

aactttaaag cttctttaac ctccgacgtt ccaggtttgt tagagttgta tcaagcctct 480

tacatgcgta ttcatggtga agatatattg gatgaagcta tttcattcac taccgctcaa 540

ttaactttgg ctttgccaac tttagaccca ccattgtccg cacaagtctc tttgttcttg 600

gagttgccat tatgcagaag aaacaagatt ttgttggcca gaaaatacat cttgatatat 660

caagaagatg ctatgcgtaa taatgttatt ttggagttag ccaagttgaa ctttaactta 720

ttgcaatctt tataccaaga agaattgaag aaaatctcta tctggtggaa tgacttagct 780

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atattctctg aaacatctaa ggccgttcct atgtcagtct tgaccagagt tttgaacttg 1560

acccgtggta atgaagaaat ctacaagtac aacgatactt atactaattc agacaccacc 1620

atgaaagaca acatctcctt ggtcttggtt gaatcttgtg actatttcaa caagtaa 1677

<210> 81

<211> 1665

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 81

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accgccaact ttcatccatc tgtgtgggga gacagattcg ctaactacac ggctgaggat 120

aaaatgaacc acgctcgcga cttgaaggaa cttaaagcgt taaaggaaga agttggtaga 180

aagctgttgg ccacagctgg cccaattcaa ctcaatctaa tcgatgctat ccaaagattg 240

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aagtatagcg atgacgacac tgaagatgat ttgtacagga tttctctgag atttagattg 360

ttaagacagc acggttacaa tgtctcctgc gacgccttca acagatttaa agataccaag 420

ggtagtttca aggaagactt gatcaaagat gttaactcta tgctctgttt atacgaagca 480

actcatttgc gggttcacgg tgaagatatt ttggacgaag ctttgggatt tacaacttcc 540

caactaaagt ccatcttacc taagttaaaa ccattgctgg cttctcaagt catgcatgcc 600

ttgaagcaac cgctacaccg tggtttgcca agactcgaac acagaaggta tattagcatt 660

taccaggatg acgcttctca ttacaaagcc ttgttgactc ttgcgaagtt ggatttcaat 720

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cgagccagtg aaattattgg tagattcatg gacgatatca aatctcataa gtttgaacaa 1380

gagagaggtc acgctgcaag cgctgtcgaa tgttatatga agcaacacgg tctctcagaa 1440

caagaagtct gtgaagaact ttacagacaa gtctccaacg cttggaagga catcaatgag 1500

gaatgcttga atccaaccgc tgttccaatg ccattgttga tgagagcact aaacttggca 1560

cgcgtaatcg acgtagttta taaagaaggt gacggttaca ctcacgttgg taacgaaatg 1620

aagcaaaacg tggctgctct acttattgat caagtaccaa tctaa 1665

<210> 82

<211> 1680

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 82

atgtccgcag cgcaagtcag tcctgctcca gttccagccc acaatgctgc tgcttctaag 60

gaagaggtgc gtagatcggc cggatatcat ccatcattct ggggtgaatt tttccttact 120

cacacaagcg aatacgctaa aaaggacgat aagattcaga aacaacatga agaattgaag 180

caagaggtta agggcatgct agtagatgct acgaccgaac ccactaaaaa gttagaattg 240

atagacgcca tcctgagatt gggtgtcggt taccactttg aagatgagat tcaagctgaa 300

ttggaaagga tccacagact cggtgactta gattgcgact tgtataacac ctgtatttgg 360

ttcagagttc ttagaggtca aggttttact gtctctgctg aagaatttaa caagttcaaa 420

aattccgacg gaaacttcaa ggaagatttg atcaatgacg tttctggtat gttgtgttta 480

tacgaagcca cccatttgcg ggttcacggt gaggatattt tggatgaagc gctcgaattt 540

actaccacac gtttaaagtc tatcttacca gacttggaac cgccattggc tactcaagta 600

atgcacgcac tagaactacc ttaccataag ggtatgcaga gattggaagc ccgacaatac 660
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gccttgaact tcactagaat gatggaggtc ctttaccaaa atattgatgg ttatacaaat 1620
tccggtggta gaaccaagga cagaatcacc tctttgttgg ttcacccaat tactatttaa 1680

<210> 83
<211> 1653
<212> DNA
<213> Artificial Sequence
<220><223> Synthetic polynucleotide
<400> 83

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catccaaccg tttggggaga tttcttttta acacactcct ctaacttctt ggagaacaat 120

gactcaatat tggaaaagca cgaagaattg aagcaagagg ttagaaactt attggtcgtt 180
gaaacttctg acttgccttc caagattcag ttgactgatg aaattatcag attaggtgtc 240
ggttatcatt ttgagaccga aatcaaagcc caattagaaa agttgcacga tcatcaattg 300
cacttgaact tcgacttgtt gaccacatct gtttggttca gattattgag aggtcacggt 360

ttttccattt cttccgacat cttcaataag ttcaaaaatt cagatggtaa ctttaaggaa 420

gatttaatca acgacgtttc tggtatgttg tgcttgtacg aagctactca tttgcgtgtc 480

cacggtgaag atattttaga cgaagccttg gaatttacta ctaccagatt gaagtctatt 540

ttgccagatt tagaaccacc attaaatgaa tgtgtcagag acgctttgca tattccttat 600

cacagaaacg ttcaacgttt ggctgcaaga caatacatac cacagtacga tgccgaacca 660

acaaaaatcg agtctttgtc attattcgct aagattgatt tcaacatgtt gcaagctttg 720

catcaaagag aattgagaga ggcttccaga tggtggaaag aatttgactt cccttctaag 780

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gaaccaaagt tctcattgtc tcgtaagttc ttaaacagaa tcattggtat cacttcttta 900

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gctgacgaaa tttcttcatc tgtcgttatt ccatcattga acttcaccag agttttggag 1560

gtcatgtacg ataagggtga tggttactct gattcccaag gtgttactaa agaccgtatc 1620

gccgctttat tgagacacgc catcgaaatc taa 1653

<210> 84

<211> 1665

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 84

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atgagaccaa aggctgactt tcaaccctcg atatggggcg atttgttcct gaattgccca 120

gacaagaaca ttgatgctga aaccgaaaag cgtcatcaac aattgaaaga agaagtcaga 180

aagatgatcg tggcaccaat ggctaattct acacaaaagt tggctttcat tgactctgtt 240

cagaggcttg gagtatccta ccactttact aaagaaattg aggatgaatt agaaaacatc 300

tatcacaaca ataacgacgc agaaaacgat ttgtacacga cttccctaag attcagatta 360

ttgagagaac atggtttcaa tgtctcttgt gacgccttta acagatttaa ggataccaaa 420

ggttcattca aggaagactt gatcaaggat gttaattcca tgttgtgttt atacgaagcg 480

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gaatttttga agcccaccga gatgcctacg gaagtgctga acagatcttt gaacctcgca 1560

agagttatgg atgtcttgta cagagaaggt gatggttata cttatgtggg taaggctgct 1620

aaaggtggga ttacctccct attgatcgaa ccagtcgctt tataa 1665

<210> 85

<211> 1665

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 85

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atgagaccaa aggctgactt tcaaccctcg atatggggcg atttgttcct gaattgccca 120

gacaagaaca ttgatgctga aaccgaaaag cgtcatcaac aattgaaaga agaagtcaga 180

aagatgatcg tggcaccaat ggctaattct acacaaaagt tggctttcat tgactctgtt 240

cagaggcttg gagtatccta ccactttact aaagaaattg aggatgaatt agaaaacatc 300

tatcacaaca ataacgacgc agaaaacgat ttgtacacga cttccataag attcagatta 360

ttgagagaac atggttacaa tgtctcttgt gacatcttta acaagttcaa gaatagcgat 420

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cgcctaaaat ctattttgcc tgacttagaa ccacccctgg ccacccaagt catgcacgct 600

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gaatttctaa aacccactga gatgccaaca gaagttctca acagaagttt gaacttggct 1560

agagtaatgg acgttttgta tagagagggt gatggttata cttatgttgg taaagccgct 1620

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<210> 86

<211> 1629

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 86

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tctccacttt tatctaagtt gcaaaatgaa ctgtcggtcg cccatctcga agaattgaaa 120

ctagaggtga agcaattaat ctggagcacg aaggatccct tattcctttt gaaattcatt 180

gactccattc aaagattggg cgttgcttac cactttgaag aagaaatcaa ggaatctttg 240

cacctggtct acctggaaga gcgaaacggt gatcatcaac actataagga aaaaggattg 300

catttcaccg ctttgagatt cagaatattg agacaggacg gttaccacgt accacaagat 360

gtttttttct cattcatgaa taaggctggt gactttgaag aaagtttatc caaagacact 420

aagggtttgg tctctttgta cgaagcctcc tacctctcta tggaaggtga aaccattttg 480

gatatggcca aggatttctc ctctcaccat ttacacaaga tggttgaaga tgctactgac 540

aaaagagttg ctaaccaaat cattcatagc ttggagatgc ctttgcatag aagagttcaa 600

aagctagagg ctatctggtt catccaattt tatgaatgcg gttccgacgc caacccgacc 660

ttggtcgaat tggcgaaatt agattttaat atggtgcaag ctacttacca agaagaatta 720

aagcgtctat ctaggtggta cgaggaaacc ggtctccaag aaaagttgtc tttcgctcgt 780

cacagattgg ctgaagcttt cttgtggtct atgggcatta ttcctgaagg tcatttcgga 840

tatggcagaa tgcaccttat gaagatcggt gcatacatta ccttattgga tgatatttat 900

gacgtttatg gtactttgga agaattgcaa gtattgacag aaatcatcga aagatgggat 960

attaaccttt tggaccagtt gccagaatac atgcaaatat tcttcctcta catgtttaac 1020

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cttaaaggtc tttgggtcga actgtcacaa tgttatttca aagaagccac gtggttccac 1140

aacggttata ccccaaccac tgaggaatac ctaaacgttg cttgtatttc agcgtccggt 1200

ccagttatct tgttttcggg atactttact actacaaatc caatcaacaa gcatgaattg 1260

caatctttag aaagacacgc tcactcctta agtatgatct taagactagc ggatgaccta 1320

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actgcaatga atttaggccg tatcagtatg tctttctacg agcacggtga cggttacggc 1560

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accatttaa 1629

<210> 87

<211> 1665

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 87

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caatggactg attacttctt gtctgttcca atagacgaat ccgaattgga cgtcatcacc 120

agagaaattg atattttaaa gcctgaggtt atggaattgt tatcttcaca aggtgatgac 180

gaaacatcta agcgtaaagt cttgttgatc caattgttgt tatctttggg attagccttt 240

cacttcgaaa acgagattaa gaatatcttg gaacacgctt tcagaaagat tgatgacatc 300

actggtgacg aaaaggattt gtccaccatt tccataatgt ttagagtttt cagaacttac 360

ggtcataact tgccatcctc tatctttaat aaattcaaaa actcagatgg taatttcaag 420

gaagacttga taaacgatgt ttctggtatg ttgtgtttat acgaagctac tcacttgaga 480

gtccatggtg aagacatttt agatgaagct ttagagttta ccactacccg tttgaagtct 540

atcttgccag gtggtacttg tagacctcac attttaagat tgattagaaa cactttatat 600

ttgccacaaa gatggaacat ggaagccgtc atcgctcgtg aatacatatc cttttacgaa 660

caagaggaag accacgataa gatgttattg agattggcta agttgaattt caaattgtta 720

cagttgcatt atattaagga attgaagtca ttcatcaaat ggtggatgga attgggttta 780

acatctaaat ggccatctca atttagagag cgtatcgttg aagcctggtt agctggtttg 840

atgatgtact ttgaaccaca attctccggt ggtagagtta ttgcagctaa gttcaactat 900

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gaaggttctt cctatcactt gaaagaaatg ttggaagaat taaatacttt agttagagca 1140

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aacggtttcg ctgctaacgc aattaactat tacatgaagc aattcgtcgt taccaaggaa 1440

gaagccatct tagaatgcca gagaatgatc gtcgacatca acaagaccat taatgaagag 1500

ttgttaaaaa ctacatctgt tcctggtaga gtcttgaagc aagctttgaa cttcggtaga 1560

ttattggaat tgttgtacac taaatctgac gacatctata attgttccga aggtaagtta 1620

aaggaataca ttgttacttt gttgatcgat ccaataagat tgtaa 1665

<210> 88

<211> 1644

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 88

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catccaaccg tttggggaga tttcttttta acacactcct ctaacttctt ggagaacaat 120

gactcaatat tggaaaagca cgaaggtttg gaacaaaaga ttagaactat gttaatctct 180

cctaccgata ctatctccaa gaaattatct ttgattgacg ccgttcagag attgggtgtc 240

gcttatcatt ttgagaagga aattgaagat gaaatcgaaa agttatcatg taaagagtac 300

aacgacggta atgacttgca aaccgtcgcc ttgagattca gattattgag acaacaaggt 360

tatttcgttt cctgcgatgt ttttaagcgt ttcaagaaca ctaagggtga atttgagact 420

gaagatgcta gaacattgtg gtgtttatac gaagctactc acttgagagt tgacggtgaa 480

gatattttgg aagaagctat ccaattctct cgtaagaaat tagaagcatt gttgccagaa 540

ttatcctttc cattgaatga atgtgttaga gatgccttgc atatcccata ccacagaaac 600

gtccagagat tggctgcacg tcaatatata ccacaatacg acgctgagcc taccaagatt 660

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gcccgtgata gaatcgctga aggttactac tggatgatgg gtgctcattt cgaaccaaaa 840

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tgggatattg aggctgtcaa agacatccca aagtacatgc aagttatata cacaggtatg 1020

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atcgattacg ctatcgaagt tttcaaggag attgtcagat cttaccaaag agaagcagaa 1140

tactttcaca ctggttacgt tccatcttat gacgaataca tggaaaactc aattatctca 1200

ggtggttaca aaatgtttat aatcttgatg ttaatcggta gaggtgagtt cgaattgaaa 1260

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atttcttctt ccgttgttat tccatctttg aactttacta gagtcttgga agtcatgtat 1560

gacaagggag acggttattc tgattcccaa ggtgttacca aggatcgtat tgctgctttg 1620

ttaagacacg ccattgagat ataa 1644

<210> 89

<211> 1704

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 89

atgcgtgact tgaaatccgt cttatcttca aaggaatcta caaaggcaga tgttaataga 60

agatcctcta actatcaccc ttccatctgg ggtgatcatt tcattaacgt ttcttcaaat 120

gagaagtaca ctaacactga agtcgaaaaa agatttgaaa ccttgaaggc cgaaatagaa 180

aagttgttag tttctaacaa caccgcttgg aagaccttgg aggaaattgt cgctatcgtt 240

aatcagttgc aaagattagg gttggcttac cacttcgaaa accaaatcaa agaagccttg 300

caatccattt atgactctca tgtcaacggt aattgcgacg ttaattacga tcacaacaac 360

gatttgtaca tagtcgcttt aagatttcgt ttgttgagac aacacggtta taaagtctct 420

gctgacattt tcaagaagtt tagagatgaa aagggtgaat ttaaggctat gttaacaaat 480

gacgccaaag gtttgttgtg tttatacgaa gcatcctatt tgagagttca aggtgaaaat 540

atcttagaag aggcttgtga attttctcgt aagcatttga agtcattatt gtctcacttg 600

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gaattgatat tagagttggc aaagttggac ttcaacttgt tgcaggcctt acacagaaga 780

gaattgggtg aaatttctcg ttggtggaaa gatattgatt tcgctactaa attgccattc 840

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aagggtatgg ttgaaattga atggatgaat ataaacgagg aaatccagga tccaaaccac 1560

ccacctttac aatggttgtt gccatctttg aacttagctc gtatgatggt cgttttgtac 1620

caaaatggtg acaactatac aaactcctcc ggtaaaacca aggatagaat tgcttccttg 1680

ttggtcgacc ctttgccaat gtaa 1704

<210> 90

<211> 1704

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 90

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agatcctcta actatcaccc ttccatctgg ggtgatcatt tcattaacgt ttcttcaaat 120

gagaagtaca ctaacactga agtcgaaaaa agatttgaaa ccttgaaggc cgaaatagaa 180

aagttgttag tttctaacaa caccgcttgg aagaccttgg aggaaattgt cgctatcgtt 240

aatcagttgc aaagattagg gttggcttac cacttcgaaa accaaatcaa agaagccttg 300

caatccattt atgactctca tgtcaacggt aattgcgacg ttaattacga tcacaacaac 360

gatttgtaca tagtcgcttt aagatttcgt ttgttgagac aacacggtta taaagtctct 420

gctgacattt tcaagaagtt taaagatgaa aagggtgaat ttaaggatat gatcagaaat 480

gacgccagag gtttattgtg tttatacgaa gcatcccatt tgagagttaa gggtgaagat 540

attttagaag aggctactga attttctcgt aagcacttga agtcattgtt accacaattg 600

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ccaagattgg aagctagaca ttacatttct atttatgagg aaaacaactc ctctcgtaat 720

gaattgttgt tagagttggc aaagttggac ttcaacttgt tgcaggcttt acacagaaga 780

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ccacctttac aatggttgtt gccatctttg aacttagctc gtatgatggt tgttttgtac 1620

caaaatggtg acaactacac aaactcctcc ggtaaaacca aggatagaat tgcttccttg 1680

ttggtcgacc ctttgccaat gtaa 1704

<210> 91

<211> 1704

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 91

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gagaagtaca ctaacactga agtcgaaaaa agatttgaaa ccttgaaggc cgaaatagaa 180

aagttgttag tttctaacaa caccgcttgg aagaccttgg aggaaattgt cgctatcgtt 240

aatcagttgc aaagattagg gttggcttac cacttcgaaa accaaatcaa agaagccttg 300

caatccattt atgactctca tgtcaacggt aattgcgacg ttaattacga tcacaacaac 360

gatttgtaca tagtcgcttt aagatttcgt ttgttgagac aacacggtta taaagtctct 420

gctgacattt tcaagaagtt taaagatgaa aagggtgaat ttaaggatat gatcagaaat 480

gacgccagag gtttattgtg tttatacgaa gcatcccatt tgagagttaa gggtgaagat 540

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caaaatggtg acaactacac caactcctcc ggtaaaacca aggatagaat tgcctctttg 1680

ttggtcgacc ctttgcctat gtaa 1704

<210> 92

<211> 1704

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 92

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agatcctcta actatcaccc ttccatctgg ggtgatcatt tcattaacgt ttcttcaaat 120

gagaagtaca ctaacactga agtcgaaaaa agatttgaaa ccttgaaggc cgaaatagaa 180

aagttgttag tttctaacaa caccgcttgg aagaccttgg aggaaattgt cgctatcgtt 240

aatcagttgc aaagattagg gttggcttac cacttcgaaa accaaatcaa agaagccttg 300

caatccattt atgactctca tgtcaacggt aattgcgacg ttaattacga tcacaacaac 360

gatttgtaca tagtcgcttt aagatttcgt ttgttgagac aacacggtta taaagtctct 420

gctgacattt tcaagaagtt taaagatgaa aagggtgaat ttaaggatat gatcagaaat 480

gacgccagag gtttattgtg tttatacgaa gcatcccatt tgagagttaa gggtgaagat 540

attttagaag aggctactga attttctcgt aagcacttga agtcattgtt accacaattg 600
tccacatcat tggctgagca agttaagcac tctttggaaa tcccattaca tagaggtatg 660
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ttggtcgacc ctttgccaat gtaa 1704

<210> 93
<211> 1692
<212> DNA
<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 93

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tgcgactcac aagaaccaga tgatgacggg tctgttaagc atcaacaatt aaaggaagaa 180
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atccaaagat tgggtgtcgc ttatcacttc gaatctgaaa tcgatgagat tttaggtaga 300

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aacaaattca gagatatcga tggtaatttt aagccatcct tggctagaaa cgttagaggt 480

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gtttccatct aa 1692

<210> 94

<211> 1665

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 94

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caatggactg attacttctt gtctgttcca atagacgaat ccgaattgga cgtcatcacc 120

agagaaattg atattttaaa gcctgaggtt atggaattgt tatcttcaca aggtgatgac 180

gaaacatcta agcgtaaagt cttgttgatc caattgttgt tatctttggg attagccttt 240

cacttcgaaa acgagattaa gaatatcttg gaacacgctt tcagaaagat tgatgacatc 300

actggtgacg aaaaggattt gtccaccatt tccataatgt ttagagtttt cagaacttac 360

ggtcataact tgccagctga agtctttgaa agattcaaag accaacacgg taatttcaaa 420

gcttctttgt catccgatgt tgaaggtatg ttgtctttat acgaagcctc tttcttggac 480

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gctttggctg gtggtacctg tagacctcac atcttaagat tgatcagaaa cactttatac 600

ttgccacaaa gatggaacat ggaggccgtc atagctcgtg aatatatctc cttttacgaa 660

caagaggaag accacgataa gatgttattg agattagcta agttgaattt caagttgtta 720

cagttgcatt acattaagga attgaaatca ttcatcaagt ggtggatgga attgggttta 780

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ttgttaaaaa ctacctctgt tccaggtaga gtcttgaaac aagctttgaa cttcggtaga 1560

ttattggaat tgttgtatac taagtccgac gacatttaca actgttctga aggtaaatta 1620

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<211> 1662

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 95

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aaaatgaacc acgctcgcga cttgaaggaa cttaaagcgt taaaggaaga agttggtaga 180

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agttccgaaa gattcactca taggaatttg caccaaaccg ccttgagctt cagattgtta 360

cgggaatgtg gttacgacgt cacttgtgat aagtttaata agttcactaa caaagagggt 420

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caacttggta ttgctggtga atacatcttg gctgaagcag gtgaattttc gggcttagtt 540

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gtcattgacg tagtttataa agaaggtgac ggctacaccc acgttggtaa tgaaatgaag 1620

caaaacgtag ctgctctcct aatcgatcaa gtaccaatct aa 1662

<210> 96

<211> 1689

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 96

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tctacctctg gttccatgaa gaacgaacca actacacaag gtgaatatga cgaattgaag 180

caacaagtca ccaagatgtt gactgatgct accactaacg acccatccaa aaagttgcac 240

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ggtattacaa agtggtggaa aaatttggat ttctcaacta agttgccata cgctagagac 840

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<210> 97

<211> 1689

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 97

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tctacctcag gttctatgaa aaacgaacca accactcaag gtgaatacga cgaattaaag 180

caacaagtca caaagatgtt gactgatgcc actactaatg acccatccaa aaagttgcat 240

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gctttggaaa aaataaactt aggtgacgct aattatttcg aatacgattt gtacaccatt 360

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aactatacta actctcatat gttaaaagac tacattacct cattattggt taatccatta 1680

ttgatttaa 1689

<210> 98

<211> 1689

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 98

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tccacctctg ggtccatgaa gaacgaacca actacccaag gtgaatacga tgaattaaag 180

caacaagtca caaagatgtt gactgatgct accactaatg acccatctaa aaagttgcac 240

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<210> 99

<211> 1689

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 99

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gctttagaaa aaattaactt gggtgacgct aactacttcg aatatgattt gtacactatc 360

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<210> 100

<211> 1689

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 100

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<210> 101

<211> 1689

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 101

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<210> 102

<211> 1662

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 102

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gaatacgaaa tgtgtcaaag agaaatagag atgttaaaag ctgaagttgc ttctatgttg 180
ttggcaactg gtaagactat gatgcaaaga ttcgacttca ttgataagat cgaaagattg 240
ggggtctccc accattttga cattgaaatc gaaaatcaat tgcaagagtt tttcaacgtt 300
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actcacatga cctccggtgg tccacattta gattcttcat tggccaagca agttaaatac 600
gcattggaac agccattgca taagggtata ttgagatatg aagcttggag atacatatct 660
atctacgaag aggacgaatc caacaataag ttattattgc gtttggctaa gttggactat 720
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gtcggtgaaa ctgtttacaa gcatagaatc gatggtttta cccaaccaca tgctattgaa 1620
gaacacataa gagccatgtt ggtcgatttc atgtctattt aa 1662

<210> 103
<211> 1662
<212> DNA
<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 103

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gaatacgaaa tgtgtcaaag agaaatagag atgttaaaag ctgaagttgc ttctatgttg 180

ttggcaactg gtaagactat gatgcaaaga ttcgacttca ttgataagat cgaaagattg 240

ggggtctccc accattttga cattgaaatc gaaaatcaat tgcaagagtt tttcaacgtt 300

tataccaact taggtgaata ctctgcctat gatttgtcat ctgctgcctt gcagttccgt 360

ttatttagac aacacggttt caatatttcc tgcggtattt tcgaccaatt tatcgacgct 420

aaaggtaagt tcaaggaatc tttatgtaac gatatcagag gtttgttgtc tttgtacgaa 480

gctgctcatg ttagaactca cggtgataaa attttggaag aagctttagc tttcaccact 540

actcacatga cctccggtgg tccacattta gattcttcat tggccaagca agttaaatac 600

gcattggaac agccattgca taagggtata ttgagatatg aagcttggag atacatatct 660

atctacgaag aggacgaatc caacaataag ttattattgc gtttggctaa gttggactat 720

cacttgttac aaatgtcata caagcaagag ttgtgtgaaa ttacaagatg gggtaaaggt 780

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caaatattaa ctgactctgc cgaaagatgg gatggttccg gtgtcgatca gttgtctgac 1020

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tatatggact ccgcaaaaga agatgttatc aactggatgt ccacaaaccc taagttggtc 1320

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gagagaggta ccggtactgc tattgaatgc tacatgaagg accataatat atccgaagaa 1440

gaagccgcaa agaagtttag agaaatgatc gagaacacct ggaaggtcat gaatgaagaa 1500

tgtttaagac caattccaat ccctagagac acattgaaga tgttgttaaa catcgccaga 1560

gttggtgaaa ctgtctacaa gcatagaatc gatggtttta ctcaaccaca tgctattgaa 1620

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<210> 104

<211> 1683

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 104

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gaagaagtcg ttgaagaaat cgaggcattg aaggaagtcg ttaagcatat gattatttct 180

acaacctcca acgccatcga acagaaatta gagttggtcg ataatttgga aagattgggt 240

ttggcttacc acttcgaagg tcaaatcaac agattattat catctgccta taatgctaac 300

catgaagacg aaggtaacca caagagaaat aaggaggact tgtacgcagc tgctttggaa 360

tttagaattt tcagacaaca tggttttaac gtttcctctg attgctttaa tcaattcaaa 420

gatactaagg gtaagttcaa aaagactttg ttgattgatg tcaagggtat gttgtccttg 480

tatgaagctg cccacgttcg tgaacatggt gacgacatct tagaagaagc tttgatcttt 540

gctaccttcc acttagaaag aattactcca aattctttgg attccacatt ggaaaaacaa 600

gttggtcacg cattgatgca atcattacac agaggtattc caagagccga agctcatttt 660

aacatatcta tttacgaaga gtgtggttct tctaatgaaa agttgttaag attggctaag 720

ttggactaca acttagtcca agtcttgcac aaggaggaat tatcagaatt gaccaaatgg 780

tggaaagatt tagacttcgc ttctaagttg tcctacgttc gtgatagaat ggttgaatgt 840

tttttctgga ctgtcggtgt ttatttcgaa ccacagtact ccagagccag agttatgtta 900

gctaagtgta ttgctatgat ctctgttatc gacgatactt acgattccta tggtaccttg 960

gacgagttaa ttatattcac tgaagtcgtt gatagatggg atatatccga ggtcgaccgt 1020

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agagaaatta acgaacaaga ccgtttcaat ggtgttaact acgttaagga agctatgaag 1140

gaaatcgtca gatcttatta catcgaggcc gaatggttca tagaaggtaa aatcccatct 1200

ttcgaagagt acttgaacaa tgcattggtt acaggtacct attacttatt ggccccagca 1260

tctttgttgg gtatggaatc cacctcaaag agaacttttg attggatgat gaagaagcca 1320

aaaattttgg tcgcttctgc tatcattggt agagttattg atgatattgc tacttacaag 1380

atagaaaagg aaaagggaca gttagtcact ggtattgaat gctacatgca agagaacaac 1440

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ttgaataaag aatgtatcaa aactaccacc tccaacattc ctaacgaaat attgatgaga 1560

gttgtcaact tgacaagatt aattgacgtt gtctacaaga ataatcaaga tggttattct 1620

aaccctaaga acaatgttaa gtcagtcatc gaagctttgt tggttaatcc aatcaatatg 1680

taa 1683

<210> 105

<211> 1632

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 105

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caagtgaaga tgatgttaga cgaagaggat atgaaactgt tagattgctt ggaattggtt 180

gacaacttgg aaagactagg cttggcttat cacttcgagg gtcaaatcaa tagactcttg 240

agcagtgcct acaacgctaa ccatgaagat gaaggtaatc acaagagaaa taaggaagac 300

ttatacgcgg cggctttgga gttcagaatt tttagacaac atggtttcaa cgttccacag 360

gacgtcttct cttcctttat gaataaggcc ggtgattttg aagaatccct ttctaaggat 420

acaaaaggtt tggtttcatt gtatgaagct tcttacctat caatggaagg tgaaaccatc 480

ttagacatgg ctaaggattt ctcctctcac catttacaca aaatggtcga agatgctact 540

gataagcgag ttgctaacca aatcattcac agccttgaaa tgccattgca cagaagggta 600

caaaaactcg aagcaatatg gttcattcaa ttctacgaat gtggttctga cgccaacccc 660

actttggtag aattggctaa gttagacttc aacatggttc aagctacgta tcaagaagaa 720

ctaaagagat tgtcgagatg gtacgaagag accggactgc aagaaaagtt atcttttgca 780

cgtcatcgtt tggccgaagc ttttttgtgg tctatgggta tcattccaga aggccatttc 840

ggttacggta gaatgcactt gatgaagatc ggtgcctata ttactttatt ggatgatatt 900

tatgatgtct acggtacctt ggaagagttg caagttctaa ctgaaatcat cgaacgttgg 960

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cataacggtt acactccaac tacagaggaa tacttgaacg ttgcttgtat tagtgcatct 1200

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atgaatgaca ctggttgttg tgaagaagag gcaagacaac acgtcaaaag actcatagac 1440

gctgaatgga agaagatgaa caaggacatc ttgatggaaa aacccttaa gaacttctgt 1500

ccaactgcta tgaatttagg taggataagc atgtcctttt acgagcacgg tgatggttac 1560

ggtggtccac actctgatac caaaaaaaag atggttagct tgttcgttca acctatgaac 1620

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<210> 106

<211> 1659

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 106

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ggtcatgaca tgtgtgctaa agaaatagaa atgttaaagg aagaagtcat gtctatgttg 180

ttggaggaaa agccaatgat ggaaaaattc aacttgatcg ataatattga aagattaggc 240

atctcctacc acttcggtga caagattgaa gatcaattac aagaatatta cgacgcctgc 300

actaactttg agaagcatgc tgaatgtgat ttgtcaatag ctgccttgca attcagattg 360

tttagacaac acggtttcaa tatttcttgt ggtatctttg acggtttctt ggatgcaaac 420

ggtaaattca aggaatcttt atgtaatgac attaagggtt tgttgtcctt atacgaagcc 480

gctcatgtta gaactcacgg tgataaaatt ttggaggaag ctttgttttt taccactact 540

catttgaccc gtgaaatccc aaacgttggt tctactttgg ctaagcaggt caaatatgct 600

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gctatgaaga aattcgagga aatgtgtgac gatgcttgga aggtcatgaa cgaagaatgc 1500

ttgcgttcca ctacaatccc aagagagatt ttgaaggtta ttttgaactt ggcaagaact 1560

tgtgaagtcg tttacaagca tcgtggtgat ggcttcaccg atcaaagaag aattgaagct 1620

cacatcaacg ccatgttaat ggactccgtt tccatctaa 1659

<210> 107

<211> 1659

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 107

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ggtcatgaca tgtgtgctaa agaaatagaa atgttaaagg aagaagtcat gtctatgttg 180

ttggaggaaa agccaatgat ggaaaaattc aacttgatcg ataatattga aagattaggc 240

atctcctacc acttcggtga caagattgaa gatcaattac aagaatatta cgacgcctgc 300

actaactttg agaagcatgc tgaatgtgat ttgtcaatag ctgccttgca attcagattg 360

tttagacaac acggtttcaa tatttcttgt ggtatctttg acggtttctt ggatgcaaac 420

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aagaaacaaa gaacttacgc cttcgacaag tacatcgaag aatggaagca atatgctaga 1140

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ttgcgttcta ctaccatccc aagagagatt ttgaaggtta ttttgaactt ggccagaacc 1560

tgtgaagtcg tttacaagca tcgtggtgat ggtttcactg atcagagaag aattgaagct 1620

cacatcaacg ctatgttaat ggactccgtt tccatctaa 1659

<210> 108

<211> 1659

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 108

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ggtcatgaca tgtgtgctaa agaaatagaa atgttaaagg aagaagtcat gtctatgttg 180

ttggaggaaa agccaatgat ggaaaaattc aacttgatcg ataatattga aagattaggc 240

atctcctacc acttcggtga caagattgaa gatcaattac aagaatatta cgacgcctgc 300

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tttagacaac acggtttcaa tatttcttgt ggtatctttg acggtttctt ggatgcaaac 420

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ttgcgttcta ctaccatccc aagagagatt ttgaaggtta ttttgaactt ggccagaacc 1560

tgtgaagtcg tttacaagca tcgtggtgat ggtttcactg accaaagaag aatcgaagct 1620

cacattaacg ctatgttaat ggactccgtt tccatctaa 1659

<210> 109

<211> 1662

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 109

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gaatacgaaa tgtgtcaaag agaaatagag atgttaaaag ctgaagttgc ttctatgttg 180

ttggcaactg gtaagactat gatgcaaaga ttcgacttca ttgataagat cgaaagattg 240

ggggtctccc accattttga cattgaaatc gaaaatcaat tgcaagagtt tttcaacgtt 300

tataccaact taggtgaata ctctgcctat gatttgtcat ctgctgcctt gcagttccgt 360

ttatttagac aacacggttt caatatttcc tgcggtattt tcgaccaatt tatcgacgct 420

aaaggtaagt tcaaggaatc tttatgtaac gatatcagag gtttgttgtc tttgtacgaa 480

gctgctcatg ttagaactca cggtgataaa attttggaag aagctttagc tttcaccact 540

actcacatga cctccggtgg tccacattta gattcttcat tggccaagca agttaaatac 600

gcattggaac agccattgca taagggtata ttgagatatg aagcttggag atacatatct 660

atctacgaag aggacgaatc caacaataag ttattattgc gtttggctaa gttggactat 720

cacttgttac aaatgtcata caagcaagag ttgtgtgaaa ttacaagatg gggtaaaggt 780

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gaaagagggt cagttactgc tttggattgc tacatgaagg attactccgt ctctgaggaa 1440

gaagctgcaa agaagttcag agaaatgtgt gaagacaact ggaaggttat gaatgaagaa 1500

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<210> 110

<211> 1659

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 110

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ggtcatgaca tgtgtgctaa agaaatagaa atgttaaagg aagaagtcat gtctatgttg 180

ttggaggaaa agccaatgat ggaaaaattc aacttgatcg ataatattga aagattaggc 240

atctcctacc acttcggtga caagattgaa gatcaattac aagaatatta cgacgcctgc 300

actaactttg agaagcatgc tgaatgtgat ttgtcaatag ctgccttgca attcagattg 360

tttagacaac acggtttcaa tatttcttgt ggtatctttg acggtttctt ggatgcaaac 420

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ttgttgcaaa tgtcctacaa aagagaattg tccgagatca ttagatgggg taaggaatta 780

gacattattt ctaaggttcc ttatgctaga gatagaatcg tcgaatgtta tttctgggct 840

gttgccacat actacgagcc acaatactcc ttggctagaa tgacattgac caaagctact 900

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atgaaagcag cttacacctt agtcttaaat tttaacaagg aagttggtga ggatttagcc 1080

aagaaacaaa gaacttacgc cttcgacaag tacatcgaag aatggaagca atatgctaga 1140

acctctttca cccaatctaa gtggttcttg accaatgaat tgccatcctt ttctgattat 1200

ttgtctaacg gtatggttac ttcaacatac tacttattgt ctgccgctac attcttgggt 1260

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ttgcgttcca ctaccatccc aagagagatt ttgaaggtta ttttgaactt ggccagaacc 1560

tgtgaagtcg tttacaagca tcgtggtgat ggtttcactg atcagagaag aattgaagct 1620

cacatcaacg ctatgttaat ggactcagtt tccatctaa 1659

<210> 111

<211> 1659

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 111

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ggtcatgaca tgtgtgctaa agaaatagaa atgttaaagg aagaagtcat gtctatgttg 180

ttggaggaaa agccaatgat ggaaaaattc aacttgatcg ataatattga aagattaggc 240

atctcctacc acttcggtga caagattgaa gatcaattac aagaatatta cgacgcctgc 300

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gttgccacat actacgagcc acaatactcc ttggctagaa tgacattgac caaagctact 900

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ttgcgttcta ctacaatccc aagagagatt ttgaaggtta ttttgaactt ggccagaacc 1560

tgtgaagtcg tttacaagca tcgtggtgat ggcttcactg accagagaag aattgaagct 1620

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<210> 112

<211> 1662

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 112

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gaatacgaaa tgtgtcaaag agaaatagag atgttgaaag ctgaagtggc ctctatgttg 180

cttgccactg gaaagactat gatgcaacga ttcgacttca ttgataagat cgaaagattg 240

ggcgtatcgc accattttga cattgaaatc gaaaatcaac tccaagagtt tttcaacgtt 300

tataccaact tgggtgaata cagcgcgtat gatctgtcat ctgctgcatt gcagttcaga 360

ttatttagac aacacggttt caatatttcc tgcggtattt tcgaccaatt tatcgacgct 420

aaaggtaagt tcaaggaatc tttatgtaac gatatccggg gtttgttgtc tctctacgaa 480

gctgctcatg ttagaacgca cggtgataaa attttggaag aagcattggc ttttactact 540

acccatatga cttccggtgg tccacaccta gactctagct tggctaagca agtcaagtac 600

gcgcttgagc aaccattaca caaggggatt ttgagatacg aagcttggcg ttatatatcc 660

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gctgccttga ttactatgat tgacgatatc tacgatgcct atggtacctt ggacgagtta 960

caaatattga ccgattctgc tgaaagatgg gatggttcgg gagtcgacca attgtctgac 1020

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gccaaaaagc aaagaacgta cgcatttgac aaatacatcg aagattggaa gcaatacatg 1140

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<210> 113

<211> 1659

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 113

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ggtcatgaca tgtgtgctaa agaaatagaa atgttaaagg aagaagtcat gtctatgttg 180

ttggaggaaa agccaatgat ggaaaaattc aacttgatcg ataatattga aagattaggc 240

atctcctacc acttcggtga caagattgaa gatcaattac aagaatatta cgacgcctgc 300

actaactttg agaagcatgc tgaatgtgat ttgtcaatag ctgccttgca attcagattg 360

tttagacaac acggtttcaa tatttcttgt ggtatctttg acggtttctt ggatgcaaac 420

ggtaaattca aggaatcttt atgtaatgac attaagggtt tgttgtcctt atacgaagcc 480

gctcatgtta gaactcacgg tgataaaatt ttggaggaag ctttgttttt taccactact 540

catttgaccc gtgaaatccc aaacgttggt tctactttgg ctaagcaggt caaacacgct 600

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ttgttgcaaa tgtcctacaa aagagaattg tccgagatca ttagatgggg taaggaatta 780

gacattattt ctaaggttcc ttatgctaga gatagaatcg tcgaatgtta cttttgggct 840

gttgccacat attacgagcc acaatactcc ttggctagaa tgacattgac caaagctact 900

gttttcgctg gtatgatcga tgatacctat gacgcttacg gtactttaga cgaattgaag 960

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ttgcgttcca ctacaatccc aagagagatt ttgaaggtta ttttgaactt ggccagaacc 1560

tgtgaagtcg tttacaagca tcgtggtgac ggcttcactg atcagagaag aattgaagct 1620

cacatcaatg ctatgttaat ggactccgtt tccatctaa 1659

<210> 114

<211> 1665

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 114

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gaatacgaaa tgtgtcaaag agaaatagag atgttaaaag ctgaagttgc ttctatgttg 180

ttggcaactg gtaagactat gatgcaaaga ttcgacttca ttgataagat cgaaagattg 240

ggggtctccc accattttga cattgaaatc gaaaatcaat tgcaagagtt tttcaacgtt 300

tataccaact taggtgaata ctctgcctat gatttgtcat ctgctgcctt gcagttccgt 360

ttatttagac aacacggttt caatatttcc tgcggtattt tcgaccaatt tatcgacgct 420

aaaggtaagt tcaaggaatc tttatgtaac gatatcagag gtttgttgtc tttgtacgaa 480

gctgctcatg ttagaactca cggtgataaa attttggaag aagctttagc tttcaccact 540

actcacatga cctccggtgg tccacattta gattcttcat tggccaagca agttaaatac 600

gcattggaac agccattgca taagggtata ttgagatatg aagcttggag atacatatct 660

atctacgaag aggacgaatc caacaataag ttattattgc gtttggctaa gttggactat 720

cacttgttac aaatgtcata caagcaagag ttgtgtgaaa ttacaagatg gggtaaaggt 780

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gaagccgcaa acaagtttag agaaatgatg gaggacgctt ggaaggttat gaatgaagac 1500

tgtttaagac caacttccat ccctagagat gtctccaagg ttttgttaaa cgtcgccaga 1560

gctggtgaaa ttgtttacaa gcatagaatc gatggtttta ccgaaccaca tatcattaaa 1620

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<210> 115

<211> 1665

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 115

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gaatacgaaa tgtgtcaaag agaaatagag atgttgaaag ctgaagtggc ctctatgttg 180

cttgccactg gaaagactat gatgcaacga ttcgacttca ttgataagat cgaaagattg 240

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tataccaact tgggtgaata cagcgcgtat gatctgtcat ctgctgcatt gcagttcaga 360

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aaaggtaagt tcaaggaatc tttatgtaac gatatccggg gtttgttgtc tctctacgaa 480

gctgctcatg ttagaacgca cggtgataaa attttggaag aagcattggc ttttactact 540

acccatatga cttccggtgg tccacaccta gactctagct tggctaagca agtcaagtac 600

gcgcttgagc aaccattaca caaggggatt ttgagatacg aagcttggcg ttatatatcc 660

atctacgaag aagacgaatc taataacaaa cttctgttaa gattggctaa actcgattat 720

catttgcttc aaatgtccta caagcaggaa ttatgtgaaa tcacgagatg gggcaagggt 780

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gccaaaaagc aaagaacgta cgcatttgac aaatacatcg aagattggaa gcaatacatg 1140

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<210> 116

<211> 1662

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 116

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gaatacgaaa tgtgtcaaag agaaatagag atgttaaaag ctgaagttgc ttctatgttg 180

ttggcaactg gtaagactat gatgcaaaga ttcgacttca ttgataagat cgaaagattg 240

ggggtctccc accattttga cattgaaatc gaaaatcaat tgcaagagtt tttcaacgtt 300

tataccaact taggtgaata ctctgcctat gatttgtcat ctgctgcctt gcagttccgt 360

ttatttagac aacacggttt caatatttcc tgcggtattt tcgaccaatt tatcgacgct 420

aaaggtaagt tcaaggaatc tttatgtaac gatatcagag gtttgttgtc tttgtacgaa 480

gctgctcatg ttagaactca cggtgataaa attttggaag aagctttagc tttcaccact 540

actcacatga cctccggtgg tccacattta gattcttcat tggccaagca agttaaatac 600

gcattggaac agccattgca taagggtata ttgagatatg aagcttggag atacatatct 660

atctacgaag aggacgaatc caacaataag ttattattgc gtttggctaa gttggactat 720

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gagagaggtt ccgttactgc tttggactgc tacatgaagg actactctgt ctccgaagaa 1440

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<210> 117

<211> 1665

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 117

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gaatacgaaa tgtgtcaaag agaaatagag atgttaaaag ctgaagttgc ttctatgttg 180

ttggcaactg gtaagactat gatgcaaaga ttcgacttca ttgataagat cgaaagattg 240

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tataccaact taggtgaata ctctgcctat gatttgtcat ctgctgcctt gcagttccgt 360

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gctgctcatg ttagaactca cggtgataaa attttggaag aagctttagc tttcaccact 540

actcacatga cctccggtgg tccacattta gattcttcat tggccaagca agttaaatac 600

gcattggaac agccattgca taagggtata ttgagatatg aagcttggag atacatatct 660

atctacgaag aggacgaatc caacaataag ttattattgc gtttggctaa gttggactat 720

cacttgttac aaatgtcata caagcaagag ttgtgtgaaa ttacaagatg gggtaaaggt 780

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<210> 118

<211> 1071

<212> DNA

<213> Artificial Sequence

<220><223> Synthetic polynucleotide

<400> 118

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caccatttcg atattgaaat cgagaaccaa ttacaagaat ttttcaatgt ttacactaac 180

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gaccacaata gatcattatc ttgctctatt actagaggtt tgttatcctt gtatgaggct 300

gctcatgtca gaacccacgg tgataagatc ttggaagaag ctttacactt gacttctggt 360

gaatcccatt tggactccac cttggctaaa caagttaaat gtgcattaga acaaccattg 420

cacaagggta tacctcgtta cgaagcctgg agatatattt ctatctacga agaggatgaa 480

tcacataaca agttgttgtt gagattagct aaattggatt atcacttctt acagatttct 540

tacagacaag atttgtgtga aatcattcgt tgggactcat ctggtgtcga ccaattatct 600

gattacatca gagcagttgg tgaggaattg gctaagaagc aaagaacata cgctttcggt 660

actttttag gtatggatgg tgcctctgaa gatgttatta actggatgtc cactatccca 720

aagttgatgt tcgcttgctc tacacatgcc agattgatta atgactttgg tggtcataaa 780

ttcgataagg aaagaggtac tggtaccgct ttagagtgtt atatgaaaga ctataacgtc 840

tccgaagaag aagccgccaa caagtttaga gaaatgatgg aggacgcttg gaaagttatg 900

aatgaagaat gtttgcgtcc aaccactatt ccaagagaaa tattaaagat gttgttgaac 960

atcgtccgtg ttggtgaaac tactaataag cacagaatcg atggtttcac acagcctcac 1020

gctattgagg aacacattag agctatgttg gttgacttta tgtccgtcta a 1071

<210> 119

<211> 43

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 119

Leu Lys Asp Glu Glu Gly Asn Phe Lys Ala Ser Leu Thr Ser Asp Val
1 5 10 15

Pro Gly Leu Leu Glu Leu Tyr Glu Ala Ser Tyr Leu Arg Val His Gly
20 25 30

Glu Asp Ile Leu Asp Glu Ala Ile Ser Phe Ala
35 40

<210> 120

<211> 40

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 120

Asn Lys Ala Leu Leu Gln Phe Ala Lys Ile Asp Phe Asn Met Leu Gln
1 5 10 15

Leu Leu His Arg Lys Glu Leu Ser Glu Ile Cys Arg Trp Trp Lys Asp
20 25 30

Leu Asp Phe Thr Arg Lys Leu Pro
35 40

<210> 121

<211> 58

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 121

Asp Arg Val Val Glu Gly Tyr Phe Trp Ile Met Gly Val Tyr Phe Glu

1 5 10 15

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

20 25 30

Ala Ser Ile Val Asp Asp Thr Tyr Asp Ser Phe Ala Thr Tyr Asp Glu

35 40 45

Leu Ile Pro Tyr Thr Asp Ala Ile Glu Arg

50 55

<210> 122

<211> 31

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 122

Tyr Met Gln Ile Ser Tyr Lys Ala Leu Leu Asp Val Tyr Glu Glu Met

1 5 10 15

Glu Gln Leu Leu Ala Asp Lys Gly Arg Gln Tyr Arg Val Glu Tyr

20 25 30

<210> 123

<211> 29

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 123

Trp Thr His Leu Asn Tyr Lys Pro Thr Phe Glu Glu Phe Arg Asp Asn

1 5 10 15

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

20 25

<210> 124

<211> 27

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 124

Thr Phe Glu Trp Ala Ala Ser Asp Pro Lys Ile Ile Lys Ala Ser Thr
1 5 10 15

Ile Ile Cys Arg Phe Met Asp Asp Ile Ala Glu
20 25

<210> 125

<211> 42

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 125

Glu Asp Asp Cys Ser Ala Ile Glu Cys Tyr Met Glu Gln Tyr Lys Val
1 5 10 15

Thr Ala Gln Glu Ala Tyr Asp Glu Phe Asn Lys His Ile Glu Ser Ser
20 25 30

Trp Lys Asp Val Asn Glu Glu Phe Leu Lys
35 40

<210> 126

<211> 62

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 126

Glu Ala Phe Asn Lys Leu Lys Asp Glu Glu Gly Asn Phe Lys Ala Ser
1 5 10 15

Leu Thr Ser Asp Val Arg Gly Leu Leu Glu Leu Tyr Gln Ala Ser Tyr
20 25 30

Met Arg Ile His Gly Glu Asp Ile Leu Asp Glu Ala Ile Ser Phe Thr
35 40 45

Thr Ala Gln Leu Thr Leu Ala Leu Pro Thr Leu Asp Pro Pro
50 55 60

<210> 127

<211> 40

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 127

Asn Lys Ala Leu Leu Gln Phe Ala Lys Ile Asp Phe Asn Met Leu Gln
1 5 10 15

Leu Leu His Arg Lys Glu Leu Ser Glu Ile Cys Arg Trp Trp Lys Asp
20 25 30

Leu Asp Phe Thr Arg Lys Leu Pro
35 40

<210> 128

<211> 58

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 128

Asp Arg Val Val Glu Gly Tyr Phe Trp Ile Met Gly Val Tyr Phe Glu
1 5 10 15

Pro Gln Tyr Ser Leu Gly Arg Lys Met Leu Thr Lys Val Ile Ala Met
20 25 30

Ala Ser Ile Val Asp Asp Thr Tyr Asp Ser Phe Ala Thr Tyr Asp Glu
35 40 45

Leu Ile Pro Tyr Thr Asp Ala Ile Glu Arg
50 55

<210> 129

<211> 31

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 129

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

Glu Gln Leu Leu Ala Asp Lys Gly Arg Gln Tyr Arg Val Glu Tyr

20 25 30

<210> 130

<211> 29

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 130

Trp Thr His Leu Asn Tyr Lys Pro Thr Phe Glu Glu Phe Arg Asp Asn

1 5 10 15

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

20 25

<210> 131

<211> 27

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 131

Thr Phe Glu Trp Ala Ala Ser Asp Pro Lys Ile Ile Lys Ala Ser Thr

1 5 10 15

Ile Ile Cys Arg Phe Met Asp Asp Ile Ala Glu

20 25

<210> 132

<211> 30

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 132

Ser Ala Ile Glu Cys Tyr Met Lys Gln Tyr Gly Ala Thr Ala Gln Glu

1 5 10 15

Ala Tyr Asp Glu Phe Asn Lys His Ile Glu Ser Ser Trp Lys

20 25 30

<210> 133

<211> 43

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 133

Leu Lys Asp Glu Glu Gly Asn Phe Lys Ala Ser Leu Thr Ser Asp Val

1 5 10 15

Pro Gly Leu Leu Glu Leu Tyr Glu Ala Ser Tyr Leu Arg Val His Gly

20 25 30

Glu Asp Ile Leu Asp Glu Ala Ile Ser Phe Ala

35 40

<210> 134

<211> 40

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 134

Asn Lys Ala Leu Leu Gln Phe Ala Lys Ile Asp Phe Asn Met Leu Gln

1 5 10 15

Leu Leu His Arg Lys Glu Leu Ser Glu Ile Cys Arg Trp Trp Lys Asp

20 25 30

Leu Asp Phe Thr Arg Lys Leu Pro

35 40

<210> 135

<211> 58

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 135

Asp Arg Val Val Glu Gly Tyr Phe Trp Ile Met Gly Val Tyr Phe Glu

1 5 10 15

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

20 25 30

Ala Ser Ile Val Asp Asp Thr Tyr Asp Ser Phe Ala Thr Tyr Asp Glu

35 40 45

Leu Ile Pro Tyr Thr Asp Ala Ile Glu Arg

50 55

<210> 136

<211> 31

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 136

Tyr Met Gln Ile Ser Tyr Lys Ala Leu Leu Asp Val Tyr Glu Glu Met

1 5 10 15

Glu Gln Leu Leu Ala Asp Lys Gly Arg Gln Tyr Arg Val Glu Tyr

20 25 30

<210> 137

<211> 29

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 137

Trp Thr His Leu Asn Tyr Lys Pro Thr Phe Glu Glu Phe Arg Asp Asn

1 5 10 15

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

20 25

<210> 138

<211> 27

<212>

PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 138

Thr Phe Glu Trp Ala Ala Ser Asp Pro Lys Ile Ile Lys Ala Ser Thr

1 5 10 15

Ile Ile Cys Arg Phe Met Asp Asp Ile Ala Glu

20 25

<210> 139

<211> 30

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 139

Ser Ala Ile Glu Cys Tyr Met Lys Gln Tyr Gly Ala Thr Ala Gln Glu

1 5 10 15

Ala Tyr Asp Glu Phe Asn Lys His Ile Glu Ser Ser Trp Lys

20 25 30

<210> 140

<211> 62

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 140

Glu Ala Phe Asn Lys Leu Lys Asp Glu Glu Gly Asn Phe Lys Ala Ser

1 5 10 15

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

20 25 30

Met Arg Ile His Gly Glu Asp Ile Leu Asp Glu Ala Ile Ser Phe Thr

35 40 45

Thr Ala Gln Leu Thr Leu Ala Leu Pro Thr Leu Asp Pro Pro

50 55 60

<210> 141

<211> 29

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 141

Leu Leu Glu Phe Ala Lys Ile Asp Phe Asn Leu Leu Gln Leu Leu His

1 5 10 15

Arg Lys Glu Leu Ser Glu Ile Cys Arg Trp Trp Lys Asp

20 25

<210> 142

<211> 58

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 142

Asp Arg Val Val Glu Gly Tyr Phe Trp Ile Met Gly Val Tyr Phe Glu

1 5 10 15

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

20 25 30

Ala Ser Ile Val Asp Asp Thr Tyr Asp Ser Phe Ala Thr Tyr Asp Glu

35 40 45

Leu Ile Pro Tyr Thr Asp Ala Ile Glu Arg

50 55

<210> 143

<211> 31

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 143

Tyr Met Gln Ile Ser Tyr Lys Ala Leu Leu Asp Val Tyr Glu Glu Met

1 5 10 15

Glu Gln Leu Leu Ala Asp Lys Gly Arg Gln Tyr Arg Val Glu Tyr

20 25 30

<210> 144

<211> 29

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 144

Trp Thr His Leu Asn Tyr Lys Pro Thr Phe Glu Glu Phe Arg Asp Asn
1 5 10 15

Ala Leu Pro Thr Ser Gly Tyr Ala Met Leu Ala Ile Thr
20 25

<210> 145

<211> 27

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 145

Thr Phe Glu Trp Ala Ala Ser Asp Pro Lys Ile Ile Lys Ala Ser Thr
1 5 10 15

Ile Ile Cys Arg Phe Met Asp Asp Ile Ala Glu
20 25

<210> 146

<211> 42

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 146

Glu Asp Asp Cys Ser Ala Ile Glu Cys Tyr Met Glu Gln Tyr Lys Val
1 5 10 15

Thr Ala Gln Glu Ala Tyr Asp Glu Phe Asn Lys His Ile Glu Ser Ser
20 25 30

Trp Lys Asp Val Asn Glu Glu Phe Leu Lys
35 40

<210> 147

<211> 43

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 147

Leu Lys Asp Glu Glu Gly Asn Phe Lys Ala Ser Leu Thr Ser Asp Val

1 5 10 15

Pro Gly Leu Leu Glu Leu Tyr Glu Ala Ser Tyr Leu Arg Val His Gly

20 25 30

Glu Asp Ile Leu Asp Glu Ala Ile Ser Phe Ala

35 40

<210> 148

<211> 29

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 148

Leu Leu Glu Phe Ala Lys Ile Asp Phe Asn Leu Leu Gln Leu Leu His

1 5 10 15

Arg Lys Glu Leu Ser Glu Ile Cys Arg Trp Trp Lys Asp

20 25

<210> 149

<211> 58

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 149

Asp Arg Val Val Glu Gly Tyr Phe Trp Ile Met Gly Val Tyr Phe Glu

1 5 10 15

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

20 25 30

Ala Ser Ile Val Asp Asp Thr Tyr Asp Ser Phe Ala Thr Tyr Asp Glu

35 40 45

Leu Ile Pro Tyr Thr Asp Ala Ile Glu Arg

50 55

<210> 150

<211> 31

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 150

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

Glu Gln Leu Leu Ala Asp Lys Gly Arg Gln Tyr Arg Val Glu Tyr
20 25 30

<210> 151

<211> 29

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 151

Trp Thr His Leu Asn Tyr Lys Pro Thr Phe Glu Glu Phe Arg Asp Asn
1 5 10 15

Ala Leu Pro Thr Ser Gly Tyr Ala Met Leu Ala Ile Thr
20 25

<210> 152

<211> 27

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 152

Thr Phe Glu Trp Ala Ala Ser Asp Pro Lys Ile Ile Lys Ala Ser Thr
1 5 10 15

Ile Ile Cys Arg Phe Met Asp Asp Ile Ala Glu
20 25

<210> 153

<211> 42

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 153

Glu Asp Asp Cys Ser Ala Ile Glu Cys Tyr Met Glu Gln Tyr Lys Val
1 5 10 15

Thr Ala Gln Glu Ala Tyr Asp Glu Phe Asn Lys His Ile Glu Ser Ser
20 25 30

Trp Lys Asp Val Asn Glu Glu Phe Leu Lys
35 40

<210> 154

<211> 62

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 154

Glu Ala Phe Asn Lys Leu Lys Asp Glu Glu Gly Asn Phe Lys Ala Ser
1 5 10 15

Leu Thr Ser Asp Val Arg Gly Leu Leu Glu Leu Tyr Gln Ala Ser Tyr
20 25 30

Met Arg Ile His Gly Glu Asp Ile Leu Asp Glu Ala Ile Ser Phe Thr
35 40 45

Thr Ala Gln Leu Thr Leu Ala Leu Pro Thr Leu Asp Pro Pro
50 55 60

<210> 155

<211> 29

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 155

Leu Leu Glu Phe Ala Lys Ile Asp Phe Asn Leu Leu Gln Leu Leu His
1 5 10 15

Arg Lys Glu Leu Ser Glu Ile Cys Arg Trp Trp Lys Asp
20 25

<210> 156

<211> 58

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 156

Asp Arg Val Val Glu Gly Tyr Phe Trp Ile Met Gly Val Tyr Phe Glu

1 5 10 15

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

20 25 30

Ala Ser Ile Val Asp Asp Thr Tyr Asp Ser Phe Ala Thr Tyr Asp Glu

35 40 45

Leu Ile Pro Tyr Thr Asp Ala Ile Glu Arg

50 55

<210> 157

<211> 31

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 157

Tyr Met Gln Ile Ser Tyr Lys Ala Leu Leu Asp Val Tyr Glu Glu Met

1 5 10 15

Glu Gln Leu Leu Ala Asp Lys Gly Arg Gln Tyr Arg Val Glu Tyr

20 25 30

<210> 158

<211> 29

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 158

Trp Thr His Leu Asn Tyr Lys Pro Thr Phe Glu Glu Phe Arg Asp Asn

1 5 10 15

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

20 25

<210> 159

<211> 27

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 159

Thr Phe Glu Trp Ala Ala Ser Asp Pro Lys Ile Ile Lys Ala Ser Thr
1 5 10 15

Ile Ile Cys Arg Phe Met Asp Asp Ile Ala Glu
20 25

<210> 160

<211> 30

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 160

Ser Ala Ile Glu Cys Tyr Met Lys Gln Tyr Gly Ala Thr Ala Gln Glu
1 5 10 15

Ala Tyr Asp Glu Phe Asn Lys His Ile Glu Ser Ser Trp Lys
20 25 30

<210> 161

<211> 43

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 161

Leu Lys Asp Glu Glu Gly Asn Phe Lys Ala Ser Leu Thr Ser Asp Val
1 5 10 15

Pro Gly Leu Leu Glu Leu Tyr Glu Ala Ser Tyr Leu Arg Val His Gly
20 25 30

Glu Asp Ile Leu Asp Glu Ala Ile Ser Phe Ala
35 40

<210> 162

<211> 29

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 162

Leu Leu Glu Phe Ala Lys Ile Asp Phe Asn Leu Leu Gln Leu Leu His
1 5 10 15

Arg Lys Glu Leu Ser Glu Ile Cys Arg Trp Trp Lys Asp
20 25

<210> 163

<211> 58

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 163

Asp Arg Val Val Glu Gly Tyr Phe Trp Ile Met Gly Val Tyr Phe Glu
1 5 10 15

Pro Gln Tyr Ser Leu Gly Arg Lys Met Leu Thr Lys Val Ile Ala Met
20 25 30

Ala Ser Ile Val Asp Asp Thr Tyr Asp Ser Phe Ala Thr Tyr Asp Glu
35 40 45

Leu Ile Pro Tyr Thr Asp Ala Ile Glu Arg
50 55

<210> 164

<211> 31

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 164

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

Glu Gln Leu Leu Ala Asp Lys Gly Arg Gln Tyr Arg Val Glu Tyr
20 25 30

<210> 165

<211> 29

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 165

Trp Thr His Leu Asn Tyr Lys Pro Thr Phe Glu Glu Phe Arg Asp Asn
1 5 10 15

Ala Leu Pro Thr Ser Gly Tyr Ala Met Leu Ala Ile Thr
20 25

<210> 166

<211> 27

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 166

Thr Phe Glu Trp Ala Ala Ser Asp Pro Lys Ile Ile Lys Ala Ser Thr
1 5 10 15

Ile Ile Cys Arg Phe Met Asp Asp Ile Ala Glu
20 25

<210> 167

<211> 30

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 167

Ser Ala Ile Glu Cys Tyr Met Lys Gln Tyr Gly Ala Thr Ala Gln Glu
1 5 10 15

Ala Tyr Asp Glu Phe Asn Lys His Ile Glu Ser Ser Trp Lys
20 25 30

<210> 168

<211> 67

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 168

Phe Glu Gln Glu Arg Gly His Cys Ala Ser Ala Val Glu Cys Tyr Met
1 5 10 15

Arg Glu His Gly Val Ser Glu Glu Glu Ala Cys Ser Glu Leu Lys Lys
20 25 30

Gln Val Asp Asn Ala Trp Lys Asp Ile Asn His Glu Met Ile Phe Ser
35 40 45

Glu Thr Ser Lys Ala Val Pro Met Ser Val Leu Thr Arg Val Leu Asn
50 55 60

Leu Thr Arg
65

<210> 169

<211> 71

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 169

Gly Tyr His Val Asp Gly Glu Glu Ala Phe Asn Met Leu Lys Asp Glu
1 5 10 15

Glu Gly Asn Phe Lys Ala Ser Leu Thr Ser Asp Val Pro Gly Leu Leu
20 25 30

Glu Leu Tyr Gln Ala Ser Tyr Met Arg Ile His Gly Glu Asp Ile Leu
35 40 45

Asp Glu Ala Ile Ser Phe Thr Thr Ala Gln Leu Thr Leu Ala Leu Pro
50 55 60

Thr Leu Asp Pro Pro Leu Ser
65 70

<210> 170

<211> 67

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 170

Phe Glu Gln Glu Arg Gly His Cys Ala Ser Ala Val Glu Cys Tyr Met
1 5 10 15
Arg Glu His Gly Val Ser Glu Glu Glu Ala Cys Ser Glu Leu Lys Lys

20 25 30
Gln Val Asp Asn Ala Trp Lys Asp Ile Asn His Glu Met Ile Phe Ser
35 40 45
Glu Thr Ser Lys Ala Val Pro Met Ser Val Leu Thr Arg Val Leu Asn
50 55 60
Leu Thr Arg
65

<210> 171

<211> 72

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 171

Gly Tyr His Val Asp Gly Glu Glu Ala Phe Asn Met Leu Lys Asp Glu

1 5 10 15
Glu Gly Asn Phe Lys Ala Ser Leu Thr Ser Asp Val Pro Gly Leu Leu
20 25 30
Glu Leu Tyr Gln Ala Ser Tyr Met Arg Ile His Gly Glu Asp Ile Leu
35 40 45
Asp Glu Ala Ile Ser Phe Thr Thr Ala Gln Leu Thr Leu Ala Leu Pro
50 55 60
Thr Leu Asp Pro Pro Leu Ser Glu
65 70

<210> 172

<211> 67

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 172

Phe Glu Gln Glu Arg Gly His Cys Ala Ser Ala Val Glu Cys Tyr Met
1 5 10 15

Arg Glu His Gly Val Ser Glu Glu Glu Ala Cys Ser Glu Leu Lys Lys
20 25 30

Gln Val Asp Asn Ala Trp Lys Asp Ile Asn His Glu Met Ile Phe Ser
35 40 45

Glu Thr Ser Lys Ala Val Pro Met Ser Val Leu Thr Arg Val Leu Asn
50 55 60

Leu Thr Arg
65

<210> 173

<211> 66

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 173

Glu Gln Glu Arg Gly His Cys Ala Ser Ala Val Glu Cys Tyr Met Arg
1 5 10 15

Glu His Gly Val Ser Glu Glu Glu Ala Cys Ser Glu Leu Lys Lys Gln
20 25 30

Val Asp Asn Ala Trp Lys Asp Ile Asn His Glu Met Ile Phe Ser Glu
35 40 45

Thr Ser Lys Ala Val Pro Met Ser Val Leu Thr Arg Val Leu Asn Leu
50 55 60

Thr Arg
65

<210> 174

<211> 71

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 174

Gly Tyr His Val Asp Gly Glu Glu Ala Phe Asn Met Leu Lys Asp Glu
1 5 10 15

Glu Gly Asn Phe Lys Ala Ser Leu Thr Ser Asp Val Pro Gly Leu Leu
20 25 30

Glu Leu Tyr Gln Ala Ser Tyr Met Arg Ile His Gly Glu Asp Ile Leu
35 40 45

Asp Glu Ala Ile Ser Phe Thr Thr Ala Gln Leu Thr Leu Ala Leu Pro
50 55 60

Thr Leu Asp Pro Pro Leu Ser
65 70

<210> 175

<211> 68

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 175

Phe Glu Gln Glu Arg Gly His Cys Ala Ser Ala Val Glu Cys Tyr Met
1 5 10 15

Arg Glu His Gly Val Ser Glu Glu Glu Ala Cys Ser Glu Leu Lys Lys
20 25 30

Gln Val Asp Asn Ala Trp Lys Asp Ile Asn His Glu Met Ile Phe Ser
35 40 45

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

50 55 60

Leu Thr Arg Gly
65

<210> 176

<211> 75

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 176

Asp Ala Phe Asn Arg Phe Lys Asp Thr Lys Gly Ser Phe Lys Glu Asp
1 5 10 15

Leu Ile Lys Asp Val Asn Ser Met Leu Cys Leu Tyr Glu Ala Thr His
20 25 30

Leu Arg Val His Gly Glu Asp Ile Leu Asp Glu Ala Leu Gly Phe Thr
35 40 45

Thr Ser Gln Leu Lys Ser Ile Leu Pro Lys Leu Lys Pro Leu Leu Ala
50 55 60

Ser Gln Val Met His Ala Leu Lys Gln Pro Leu
65 70 75

<210> 177

<211> 68

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 177

Phe Asn Lys Phe Lys Asn Ser Asp Gly Asn Phe Lys Glu Asp Leu Ile
1 5 10 15

Asn Asp Val Ser Gly Met Leu Cys Leu Tyr Glu Ala Thr His Leu Arg
20 25 30

Val His Gly Glu Asp Ile Leu Asp Glu Ala Leu Glu Phe Thr Thr Thr
35 40 45

Arg Leu Lys Ser Ile Leu Pro Asp Leu Glu Pro Pro Leu Ala Thr Gln
50 55 60

Val Met His Ala
65

<210> 178

<211> 62

<212> PRT

<213> Artificial Sequence

<220><223>

Synthetic polypeptide

<400> 178

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

<210> 179

<211> 75

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 179

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

Thr Ser Gln Leu Lys Ser Ile Leu Pro Lys Leu Lys Pro Leu Leu Ala
50 55 60
Ser Gln Val Met His Ala Leu Lys Gln Pro Leu
65 70 75

<210> 180

<211> 69

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 180

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

1 5 10 15

Ile Asn Asp Val Ser Gly Met Leu Cys Leu Tyr Glu Ala Thr His Leu

20 25 30

Arg Val His Gly Glu Asp Ile Leu Asp Glu Ala Leu Glu Phe Thr Thr

35 40 45

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

50 55 60

Gln Val Met His Ala

65

<210> 181

<211> 72

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 181

Glu Thr Asn Phe Thr Asn Ser Pro Leu Leu Ser Lys Leu Gln Asn Glu

1 5 10 15

Leu Ser Val Ala His Leu Glu Glu Leu Lys Leu Glu Val Lys Gln Leu

20 25 30

Ile Trp Ser Thr Lys Asp Pro Leu Phe Leu Leu Lys Phe Ile Asp Ser

35 40 45

Ile Gln Arg Leu Gly Val Ala Tyr His Phe Glu Glu Glu Ile Lys Glu

50 55 60

Ser Leu His Leu Val Tyr Leu Glu

65 70

<210> 182

<211> 56

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 182

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

1 5 10 15

Ile Asn Asp Val Ser Gly Met Leu Cys Leu Tyr Glu Ala Thr His Leu

20 25 30

Arg Val His Gly Glu Asp Ile Leu Asp Glu Ala Leu Glu Phe Thr Thr

35 40 45

Thr Arg Leu Lys Ser Ile Leu Pro

50 55

<210> 183

<211> 78

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 183

Glu Gly Leu Glu Gln Lys Ile Arg Thr Met Leu Ile Ser Pro Thr Asp

1 5 10 15

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

20 25 30

Val Ala Tyr His Phe Glu Lys Glu Ile Glu Asp Glu Ile Glu Lys Leu

35 40 45

Ser Cys Lys Glu Tyr Asn Asp Gly Asn Asp Leu Gln Thr Val Ala Leu

50 55 60

Arg Phe Arg Leu Leu Arg Gln Gln Gly Tyr Phe Val Ser Cys

65 70 75

<210> 184

<211> 21

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 184

Leu Gln Arg Leu Gly Leu Ala Tyr His Phe Glu Asn Gln Ile Lys Glu

1 5 10 15

Ala Leu Gln Ser Ile

20

<210> 185

<211> 42

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 185

Leu Ser His Leu Ser Thr Ser Leu Ala Glu Gln Val Lys His Ser Leu
1 5 10 15

Glu Ile Pro Leu His Arg Gly Met Pro Arg Leu Glu Ala Arg His Tyr
20 25 30

Ile Ser Ile Tyr Glu Glu Asp Asn Ser Ser
35 40

<

210> 186

<211> 223

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 186

Glu Leu Ala Lys Leu Asp Phe Asn Leu Leu Gln Ala Leu His Arg Arg
1 5 10 15

Glu Leu Gly Glu Ile Ser Arg Trp Trp Lys Asp Ile Asp Phe Ala Thr
20 25 30

Lys Leu Pro Phe Ala Arg Asp Arg Leu Val Glu Cys Tyr Phe Trp Ile
35 40 45

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

Thr Lys Val Ile Ala Ile Ala Ser Val Ile Asp Asp Ile Tyr Asp Val
65 70 75 80

Tyr Gly Thr Leu Glu Glu Leu Lys Leu Phe Thr His Ala Ile Glu Arg
85 90 95

Trp Glu Thr Val Ala Ala Asn Glu Leu Pro Lys Tyr Met Gln Val Cys

100 105 110

Tyr Phe Ala Leu Leu Asp Val Phe Lys Glu Met Glu Asp Lys Leu Val
115 120 125
Asn Lys Gly Leu Leu Tyr Ser Met Pro Cys Ala Lys Glu Ala Val Lys
130 135 140
Gly Leu Val Arg Ala Tyr Phe Val Glu Ala Glu Trp Phe Asn Ala Asn
145 150 155 160
Tyr Met Pro Thr Phe Glu Glu Tyr Met Glu Asn Ser Thr Met Ser Ser
165 170 175

Gly Tyr Pro Met Leu Ala Val Glu Ala Leu Ile Gly Ile Glu Asp Ala
180 185 190
Thr Ile Ser Lys Glu Ala Phe Asp Trp Ala Ile Ser Val Pro Lys Ile
195 200 205
Ile Arg Ser Cys Ala Leu Ile Ala Arg Leu Val Asp Asp Ile His
210 215 220

<210> 187
<211> 32
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 187
Asp Ala Pro Ser Ser Val Glu Cys Tyr Met Gln Gln Tyr Asp Val Ser

1 5 10 15
Glu Glu Glu Ala Cys Asn Arg Ile Lys Gly Met Val Glu Ile Glu Trp
20 25 30

<210> 188
<211> 32
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 188
Asn Leu Ala Arg Met Met Val Val Leu Tyr Gln Asn Gly Asp Asn Tyr

1 5 10 15

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

20 25 30

<210> 189

<211> 21

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 189

Leu Gln Arg Leu Gly Leu Ala Tyr His Phe Glu Asn Gln Ile Lys Glu

1 5 10 15

Ala Leu Gln Ser Ile

20

<210> 190

<211> 322

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 190

Lys Phe Lys Asp Glu Lys Gly Glu Phe Lys Asp Met Ile Arg Asn Asp

1 5 10 15

Ala Arg Gly Leu Leu Cys Leu Tyr Glu Ala Ser His Leu Arg Val Lys

20 25 30

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

35 40 45

Lys Ser Leu Leu Pro Gln Leu Ser Thr Ser Leu Ala Glu Gln Val Lys

50 55 60

His Ser Leu Glu Ile Pro Leu His Arg Gly Met Pro Arg Leu Glu Ala

65 70 75 80

Arg His Tyr Ile Ser Ile Tyr Glu Glu Asn Asn Ser Ser Arg Asn Glu

85 90 95

Leu Leu Leu Glu Leu Ala Lys Leu Asp Phe Asn Leu Leu Gln Ala Leu

100 105 110

His Arg Arg Glu Leu Gly Asp Ile Ser Arg Trp Trp Lys Asp Ile Asp

115 120 125

Phe Ala Thr Lys Leu Pro Phe Ala Arg Asp Arg Leu Val Glu Cys Tyr

130 135 140

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

145 150 155 160

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

165 170 175

Tyr Asp Val Tyr Gly Thr Leu Glu Glu Leu Lys Leu Phe Thr His Ala

180 185 190

Ile Glu Arg Trp Glu Thr Val Ala Ala Asn Glu Leu Pro Lys Tyr Met

195 200 205

Gln Val Cys Tyr Phe Ala Leu Leu Asp Val Phe Lys Glu Met Glu Asp

210 215 220

Lys Leu Val Asn Lys Gly Leu Leu Tyr Ser Met Pro Cys Ala Lys Glu

225 230 235 240

Ala Val Lys Gly Leu Val Arg Ala Tyr Phe Val Glu Ala Glu Trp Phe

245 250 255

Asn Ala Asn Tyr Met Pro Thr Phe Glu Glu Tyr Met Glu Asn Ser Thr

260 265 270

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

275 280 285

Glu Asp Ala Thr Ile Ser Lys Glu Ala Phe Asp Trp Ala Ile Ser Val

290 295 300

Pro Lys Ile Ile Arg Ser Cys Ala Leu Ile Ala Arg Leu Val Asp Asp

305 310 315 320

Ile His

<210> 191

<211> 19

<212

> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 191

Lys Val Glu Gln Glu Arg Gly Asp Ala Pro Ser Ser Val Gln Cys Tyr

1 5 10 15

Val Gln Gln

<210> 192

<211> 32

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 192

Asn Leu Ala Arg Met Met Val Val Leu Tyr Gln Asn Gly Asp Asn Tyr

1 5 10 15

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

20 25 30

<210> 193

<211> 21

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 193

Leu Gln Arg Leu Gly Leu Ala Tyr His Phe Glu Asn Gln Ile Lys Glu

1 5 10 15

Ala Leu Gln Ser Ile

20

<210> 194

<211> 242

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 194

Lys Phe Lys Asp Glu Lys Gly Glu Phe Lys Asp Met Ile Arg Asn Asp

1 5 10 15

Ala Arg Gly Leu Leu Cys Leu Tyr Glu Ala Ser His Leu Arg Val Lys

20 25 30

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

35 40 45

Lys Ser Leu Leu Pro Gln Leu Ser Thr Ser Leu Ala Glu Gln Val Lys

50 55 60

His Ser Leu Glu Ile Pro Leu His Arg Gly Met Pro Arg Leu Glu Ala

65 70 75 80

Arg His Tyr Ile Ser Ile Tyr Glu Glu Asn Asn Ser Ser Arg Asn Glu

85 90 95

Leu Leu Leu Glu Leu Ala Lys Leu Asp Phe Asn Leu Leu Gln Ala Leu

100 105 110

His Arg Arg Glu Leu Gly Asp Ile Ser Arg Trp Trp Lys Asp Ile Asp

115 120 125

Phe Ala Thr Lys Leu Pro Phe Ala Arg Asp Arg Leu Val Glu Cys Tyr

130 135 140

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

145 150 155 160

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

165 170 175

Tyr Asp Val Tyr Gly Thr Leu Glu Glu Leu Lys Leu Phe Thr His Ala

180 185 190

Ile Glu Arg Trp Glu Thr Val Ala Ala Asn Glu Leu Pro Lys Tyr Met

195 200 205

Gln Val Cys Tyr Phe Ala Leu Leu Asp Val Phe Lys Glu Met Glu Asp

210 215 220

Lys Leu Val Asn Lys Gly Leu Leu Tyr Ser Met Pro Cys Ala Lys Glu

225 230 235 240

Ala Val

<210> 195

<211> 27

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 195

Tyr Val Pro Thr Phe Glu Glu Tyr Met Glu Asn Ser Thr Met Ser Ser

1 5 10 15

Gly Tyr Pro Met Leu Ala Val Glu Ala Leu Val

20 25

<210> 196

<211> 17

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 196

Asp Trp Ala Ile Ser Val Pro Lys Ile Ile Arg Ser Cys Ala Leu Ile

1 5 10 15

Ala

<210> 197

<211> 52

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 197

Lys Val Glu Gln Glu Arg Gly Asp Ala Pro Ser Ser Val Gln Cys Tyr

1 5 10 15

Met Gln Gln Tyr Asp Val Ser Glu Glu Glu Ala Cys Asn Arg Ile Lys

20 25 30

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

35 40 45

Thr Asn His Leu

50

<210> 198

<211> 32

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 198

Asn Leu Ala Arg Met Met Val Val Leu Tyr Gln Asn Gly Asp Asn Tyr

1 5 10 15

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

20 25 30

<210> 199

<211> 21

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 199

Leu Gln Arg Leu Gly Leu Ala Tyr His Phe Glu Asn Gln Ile Lys Glu

1 5 10 15

Ala Leu Gln Ser Ile

20

<210> 200

<211> 242

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 200

Lys Phe Lys Asp Glu Lys Gly Glu Phe Lys Asp Met Ile Arg Asn Asp

1 5 10 15

Ala Arg Gly Leu Leu Cys Leu Tyr Glu Ala Ser His Leu Arg Val Lys

20 25 30

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

35 40 45

Lys Ser Leu Leu Pro Gln Leu Ser Thr Ser Leu Ala Glu Gln Val Lys
50 55 60
His Ser Leu Glu Ile Pro Leu His Arg Gly Met Pro Arg Leu Glu Ala
65 70 75 80
Arg His Tyr Ile Ser Ile Tyr Glu Glu Asn Asn Ser Ser Arg Asn Glu
85 90 95
Leu Leu Leu Glu Leu Ala Lys Leu Asp Phe Asn Leu Leu Gln Ala Leu
100 105 110

His Arg Arg Glu Leu Gly Asp Ile Ser Arg Trp Trp Lys Asp Ile Asp
115 120 125
Phe Ala Thr Lys Leu Pro Phe Ala Arg Asp Arg Leu Val Glu Cys Tyr
130 135 140
Phe Trp Ile Leu Gly Val Tyr Phe Glu Pro Lys Tyr Ser Ile Thr Arg
145 150 155 160
Lys Phe Met Thr Lys Val Ile Ala Ile Ala Ser Val Ile Asp Asp Ile
165 170 175

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

Ala Val

<210> 201
<211> 27
<212> PRT
<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 201

Tyr Val Pro Thr Phe Glu Glu Tyr Met Glu Asn Ser Thr Met Ser Ser
1 5 10 15

Gly Tyr Pro Met Leu Ala Val Glu Ala Leu Val
20 25

<210> 202

<211> 17

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 202

Asp Trp Ala Ile Ser Val Pro Lys Ile Ile Arg Ser Cys Ala Leu Ile

1 5 10 15

Ala

<210> 203

<211> 32

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 203

Asp Ala Pro Ser Ser Val Glu Cys Tyr Met Gln Gln Tyr Asp Val Ser
1 5 10 15

Glu Glu Glu Ala Cys Asn Arg Ile Lys Gly Met Val Glu Ile Glu Trp
20 25 30

<210> 204

<211> 32

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 204

Asn Leu Ala Arg Met Met Val Val Leu Tyr Gln Asn Gly Asp Asn Tyr

1 5 10 15

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

20 25 30

<210> 205

<211> 25

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 205

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

1 5 10 15

Phe His Pro Ser Ile Trp Gly Asp His

20 25

<210> 206

<211> 51

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 206

Asp Asp Gly Ser Val Lys His Gln Gln Leu Lys Glu Glu Ile Arg Lys

1 5 10 15

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

20 25 30

Ala Ile Gln Arg Leu Gly Val Ala Tyr His Phe Glu Ser Glu Ile Asp

35 40 45

Glu Ile Leu

50

<210> 207

<211> 29

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 207

Ser Leu Ala Arg Asn Val Arg Gly Met Leu Ser Leu Tyr Glu Ala Thr
1 5 10 15
His Leu Arg Val His Gly Glu Asn Ile Leu Asp Glu Ala
20 25

<210> 208
<211> 44
<212> PRT
<213> Artificial Sequence

<220><223> Synthetic polypeptide
<400> 208
Leu Glu Ala Arg Asn Tyr Met Pro Phe Tyr Gln Glu Glu Ala Ser His
1 5 10 15
Asn Glu Ala Leu Leu Thr Phe Ala Lys Leu Asp Phe Asn Lys Leu Gln
20 25 30
Lys Leu His Gln Lys Glu Leu Ser Glu Ile Thr Arg
35 40

<210> 209
<211> 63
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide

<400> 209
Phe Glu Gln Ser Arg Glu His Val Ala Ser Ser Ile Glu Cys Tyr Met
1 5 10 15
Lys Gln Tyr Gly Ala Thr Glu Glu Glu Thr Cys Asn Glu Leu Arg Lys
20 25 30
Gln Val Ser Asn Ala Trp Lys Asp Ile Asn Glu Glu Cys Leu Cys Pro
35 40 45
Thr Ala Val Pro Met Pro Leu Ile Val Arg Ile Leu Asn Leu Thr
50 55 60

<210> 210
<211> 57

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 210

Ala Glu Val Phe Glu Arg Phe Lys Asp Gln His Gly Asn Phe Lys Ala
1 5 10 15

Ser Leu Ser Ser Asp Val Glu Gly Met Leu Ser Leu Tyr Glu Ala Ser
20 25 30

Phe Leu Asp Tyr Glu Gly Glu Asp Ile Leu Asp Glu Ala Lys Ala Phe
35 40 45

Thr Ser Phe His Leu Arg Gly Ala Leu
50 55

<210> 211

<211> 59

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 211

Val Lys Leu Glu Leu Val Asp Asp Val Lys Arg Leu Gly Ile Gly Tyr
1 5 10 15

Arg Phe Glu Lys Glu Ile Val Glu Ala Leu His Arg Cys Phe Ile Ser
20 25 30

Ser Glu Arg Phe Thr His Arg Asn Leu His Gln Thr Ala Leu Ser Phe
35 40 45

Arg Leu Leu Arg Glu Cys Gly Tyr Asp Val Thr
50 55

<210> 212

<211> 59

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 212

Phe Asn Lys Phe Thr Asn Lys Glu Gly Lys Phe Asn Ser Lys Leu Gly

1 5 10 15

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

20 25 30

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

35 40 45

Val Leu Lys Glu Lys Val Ala Cys Ile Asn Asn

50 55

<210> 213

<211> 51

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 213

Val Tyr Phe Glu Pro Gln Tyr Ser Val Pro Arg Arg Thr Thr Thr Lys

1 5 10 15

Val Ile Gly Leu Cys Ser Val Ile Asp Asp Met Tyr Asp Ala Tyr Gly

20 25 30

Thr Ile Asp Glu Leu Glu Leu Phe Thr Asn Ala Ile Glu Arg Leu Asp

35 40 45

Thr Ser Thr

50

<210> 214

<211> 66

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 214

Arg Trp Leu Lys Cys Asn His Ala Pro Thr Met Glu Glu Tyr Met Lys

1 5 10 15

Val Arg Gly Val Ser Ser Gly Tyr Pro Leu Leu Ile Thr Ile Ser Phe

20 25 30

Ile Gly Met Glu Asp Thr Thr Glu Glu Ile Leu Thr Trp Ala Thr Ser

35 40 45

Glu Pro Met Ile Ile Arg Ala Ser Val Ile Val Cys Arg Leu Met Asp

50 55 60

Asp Ile

65

<210> 215

<211> 48

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 215

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

1 5 10 15

Leu Gly Met Leu Asn Leu Tyr Glu Ala Ala His Leu Arg Leu Arg Gly

20 25 30

Glu Asp Ile Leu Asp Glu Ala Leu Ala Phe Thr Thr Ser His Leu Glu

35 40 45

<210> 216

<211> 31

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 216

Trp Trp Lys Asn Leu Asp Phe Ser Thr Lys Leu Pro Tyr Ala Arg Asp

1 5 10 15

Arg Ile Val Glu Cys Tyr Phe Trp Ile Met Gly Ala Tyr Phe Glu

20 25 30

<210> 217

<211> 25

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 217

Ser Leu Ala Arg Thr Phe Leu Thr Lys Val Ile Ala Met Thr Ser Ile
1 5 10 15
Leu Asp Asp Thr Tyr Asp Asn Tyr Gly
20 25

<210> 218
<211> 61
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 218
Asp Tyr Val Pro Pro Ile Glu Glu Tyr Met Gln Val Ala Arg Ile Ser
1 5 10 15
Ser Ala Tyr Pro Met Leu Ile Thr Asn Ser Phe Val Gly Met Gly Glu
20 25 30
Val Ala Thr Lys Glu Ala Phe Asp Trp Ile Ser Asn Asp Pro Lys Ile
35 40 45

Leu Lys Ala Ser Thr Thr Ile Cys Arg Leu Met Asp Asp
50 55 60
<210> 219
<211> 29
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 219
Glu Phe Glu Gln Thr Arg Asp His Val Ala Ser Gly Val Glu Cys Tyr
1 5 10 15
Met Lys Gln Tyr Gly Val Ser Arg Glu Glu Thr Val Lys
20 25
<210> 220
<211> 48
<212> PRT
<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 220

Phe Met Asp Glu Lys Gly Lys Phe Lys Glu Asp Val Val Asn Asp Val
1 5 10 15

Leu Gly Met Leu Asn Leu Tyr Glu Ala Ala His Leu Arg Leu Arg Gly
20 25 30

Glu Asp Ile Leu Asp Glu Ala Leu Ala Phe Thr Thr Ser His Leu Glu
35 40 45

<210> 221

<211> 31

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 221

Trp Trp Lys Asn Leu Asp Phe Ser Thr Lys Leu Pro Tyr Ala Arg Asp
1 5 10 15

Arg Ile Val Glu Cys Tyr Phe Trp Ile Met Gly Ala Tyr Phe Glu
20 25 30

<210> 222

<211> 25

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 222

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

Leu Asp Asp Thr Tyr Asp Asn Tyr Gly
20 25

<210> 223

<211> 47

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 223

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

Asn Ser Phe Val Gly Met Gly Glu Val Ala Thr Lys Glu Ala Phe Asp
20 25 30

Trp Ile Ser Asn Asn Pro Lys Met Leu Lys Ala Ser Thr Ile Ile
35 40 45

<210> 224

<211> 29

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 224

Glu Phe Glu Gln Thr Arg Asp His Val Ala Ser Gly Val Glu Cys Tyr
1 5 10 15

Met Lys Gln Tyr Gly Val Ser Arg Glu Glu Thr Val Lys
20 25

<210> 225

<211> 48

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 225

Phe Met Asp Glu Lys Gly Lys Phe Lys Glu Asp Val Val Asn Asp Val
1 5 10 15

Leu Gly Met Leu Asn Leu Tyr Glu Ala Ala His Leu Arg Leu Arg Gly
20 25 30

Glu Asp Ile Leu Asp Glu Ala Leu Ala Phe Thr Thr Ser His Leu Glu
35 40 45

<210> 226

<211> 31

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 226

Trp Trp Lys Asn Leu Asp Phe Ser Thr Lys Leu Pro Tyr Ala Arg Asp
1 5 10 15

Arg Ile Val Glu Cys Tyr Phe Trp Ile Met Gly Ala Tyr Phe Glu
20 25 30

<210> 227

<211> 25

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 227

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

Leu Asp Asp Thr Tyr Asp Asn Tyr Gly
20 25

<210> 228

<211> 16

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 228

Asp Tyr Val Pro Pro Ile Glu Glu Tyr Met Gln Val Ala Arg Ile Ser
1 5 10 15

<210> 229

<211> 36

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 229

Gly Tyr Pro Met Leu Ile Thr Asn Ser Leu Val Gly Met Gly Glu Val
1 5 10 15

Ala Thr Lys Glu Ala Phe Asp Leu Ile Ser Asn Asp Pro Lys Met Leu
20 25 30
Lys Ala Ser Thr
35

<210> 230
<211> 29
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 230
Glu Phe Glu Gln Thr Arg Asp His Val Ala Ser Gly Val Glu Cys Tyr
1 5 10 15
Met Lys Gln Tyr Gly Val Ser Arg Glu Glu Thr Val Lys
20 25

<210> 231
<211> 48
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 231
Phe Met Asp Glu Lys Gly Lys Phe Lys Glu Asp Val Val Asn Asp Val
1 5 10 15
Leu Gly Met Leu Asn Leu Tyr Glu Ala Ala His Leu Arg Leu Arg Gly
20 25 30
Glu Asp Ile Leu Asp Glu Ala Leu Ala Phe Thr Thr Ser His Leu Glu
35 40 45

<210> 232
<211> 31
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 232
Trp Trp Lys Asn Leu Asp Phe Ser Thr Lys Leu Pro Tyr Ala Arg Asp

1 5 10 15

Arg Ile Val Glu Cys Tyr Phe Trp Ile Met Gly Ala Tyr Phe Glu

20 25 30

<210> 233

<211> 25

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 233

Ser Leu Ala Arg Thr Phe Leu Thr Lys Val Ile Ala Met Thr Ser Ile

1 5 10 15

Leu Asp Asp Thr Tyr Asp Asn Tyr Gly

20 25

<210> 234

<211> 59

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 234

Val Pro Pro Met Asp Glu Tyr Met Gln Val Ala Leu Ile Ser Cys Gly

1 5 10 15

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

20 25 30

Thr Lys Glu Ala Phe Asp Trp Ile Ser Asn Asp Pro Lys Ile Leu Lys

35 40 45

Ala Ser Thr Thr Ile Cys Arg Leu Met Asp Asp

50 55

<210> 235

<211> 29

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 235

Glu Phe Glu Gln Thr Arg Asp His Val Ala Ser Gly Val Glu Cys Tyr
1 5 10 15
Met Lys Gln Tyr Gly Val Ser Arg Glu Glu Thr Val Lys

20 25

<210> 236
<211> 48
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 236
Phe Met Asp Glu Lys Gly Lys Phe Lys Glu Asp Val Val Asn Asp Val
1 5 10 15
Leu Gly Met Leu Asn Leu Tyr Glu Ala Ala His Leu Arg Leu Arg Gly
20 25 30
Glu Asp Ile Leu Asp Glu Ala Leu Ala Phe Thr Thr Ser His Leu Glu
35 40 45

<210> 237
<211> 59
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 237
Trp Trp Lys Asn Leu Asp Phe Ala Thr Met Leu Pro Tyr Ala Arg Asp
1 5 10 15
Arg Ile Val Glu Cys Tyr Phe Trp Ile Met Gly Val Tyr Phe Glu Pro
20 25 30
Lys Tyr Ser Leu Ala Arg Thr Phe Leu Thr Lys Val Ile Ala Met Thr
35 40 45

Ser Ile Leu Asp Asp Thr Tyr Asp Asn Tyr Gly
50 55
<210> 238
<211> 47

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 238

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

Asn Ser Phe Val Gly Met Gly Glu Val Ala Thr Lys Glu Ala Phe Asp
20 25 30

Trp Ile Ser Asn Asn Pro Lys Met Leu Lys Ala Ser Thr Ile Ile
35 40 45

<210> 239

<211> 29

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 239

Glu Phe Glu Gln Thr Arg Asp His Val Ala Ser Gly Val Glu Cys Tyr
1 5 10 15

Met Lys Gln Tyr Gly Val Ser Arg Glu Glu Thr Val Lys
20 25

<210> 240

<211> 48

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 240

Phe Met Asp Glu Lys Gly Lys Phe Lys Glu Asp Val Val Asn Asp Val
1 5 10 15

Leu Gly Met Leu Asn Leu Tyr Glu Ala Ala His Leu Arg Leu Arg Gly
20 25 30

Glu Asp Ile Leu Asp Glu Ala Leu Ala Phe Thr Thr Ser His Leu Glu
35 40 45

<210> 241

<211> 59

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 241

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

<210> 242

<211> 16

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 242

Asp Tyr Val Pro Pro Ile Glu Glu Tyr Met Gln Val Ala Arg Ile Ser
1 5 10 15

<210> 243

<211> 36

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 243

Gly Tyr Pro Met Leu Ile Thr Asn Ser Leu Val Gly Met Gly Glu Val
1 5 10 15
Ala Thr Lys Glu Ala Phe Asp Leu Ile Ser Asn Asp Pro Lys Met Leu
20 25 30
Lys Ala Ser Thr

35

<210> 244

<211> 29

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 244

Glu Phe Glu Gln Thr Arg Asp His Val Ala Ser Gly Val Glu Cys Tyr
1 5 10 15

Met Lys Gln Tyr Gly Val Ser Arg Glu Glu Thr Val Lys
20 25

<210> 245

<211> 27

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 245

Ser Asn Asn Arg Gln Glu Thr Val Arg Pro Leu Ala Asp Phe Pro Glu
1 5 10 15

Asn Ile Trp Ala Asp Arg Ile Ala Pro Phe Thr
20 25

<210> 246

<211> 45

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 246

Glu Met Cys Gln Arg Glu Ile Glu Met Leu Lys Ala Glu Val Ala Ser
1 5 10 15

Met Leu Leu Ala Thr Gly Lys Thr Met Met Gln Arg Phe Asp Phe Ile
20 25 30

Asp Lys Ile Glu Arg Leu Gly Val Ser His His Phe Asp
35 40 45

<210> 247

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 247

Ile Phe Asp Gln Phe Ile Asp Ala Lys Gly Lys Phe Lys Glu Ser Leu
1 5 10 15

Cys Asn Asp Ile Arg Gly Leu Leu Ser Leu Tyr Glu Ala Ala His Val
20 25 30

Arg Thr His Gly Asp Lys Ile Leu Glu Glu Ala Leu Ala Phe Thr Thr
35 40 45

Thr His Met Thr Ser Gly Gly Pro His Leu Asp Ser Ser Leu Ala Lys
50 55 60

Gln Val Lys Tyr Ala Leu Glu Gln Pro Leu His Lys Gly Ile Leu Arg
65 70 75 80

Tyr Glu Ala Trp Arg Tyr Ile Ser Ile Tyr Glu Glu Asp Glu Ser Asn
85 90 95

Asn Lys Leu Leu Leu Arg Leu Ala Lys Leu Asp Tyr His Leu Leu Gln
100 105 110

Met Ser Tyr Lys Gln Glu Leu
115

<210> 248

<211> 47

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 248

Arg Trp Gly Lys Gly Leu Glu Ser Val Ser Asn Phe Pro Tyr Ala Arg
1 5 10 15

Asp Arg Phe Val Glu Cys Tyr Phe Trp Ala Val Gly Thr Leu Tyr Glu
20 25 30

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

<210> 249

<211> 179

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 249

Arg Trp Asp Gly Ser Gly Val Asp Gln Leu Ser Asp Tyr Ile Arg Ala
1 5 10 15

Ser Tyr Asn Thr Leu Leu Lys Phe Asn Lys Glu Val Gly Glu Asp Leu
20 25 30

Ala Lys Lys Gln Arg Thr Tyr Ala Phe Asp Lys Tyr Ile Glu Asp Trp
35 40 45

Lys Gln Tyr Met Arg Thr Asn Phe Ser Gln Ser Arg Trp Phe Phe Thr
50 55 60

Lys Glu Leu Pro Ser Phe Ala Asp Tyr Ile Asn Asn Gly Ala Ile Thr
65 70 75 80

Ile Gly Ala Tyr Leu Val Ala Ser Ala Ala Phe Leu Tyr Met Asp Ser
85 90 95

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

Val Ala Tyr Ser Thr His Ser Arg Leu Ile Asn Asp Phe Gly Gly His
115 120 125

Lys Phe Glu Lys Glu Arg Gly Ser Ser Thr Ala Ile Glu Cys Tyr Met
130 135 140

Lys Asp His Asn Val Ser Glu Glu Glu Ala Ala Asn Lys Phe Arg Glu
145 150 155 160

Met Met Glu Asp Ala Trp Lys Val Met Asn Glu Glu Cys Leu Arg Pro
165 170 175

Thr Thr Ile

<210> 250

<211> 31

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 250

Glu Thr Val Tyr Lys His Arg Ile Asp Gly Phe Thr Gln Pro His Ala

1 5 10 15

Ile Glu Glu His Ile Arg Ala Met Leu Val Asp Phe Met Ser Ile

20 25 30

<210> 251

<211> 27

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 251

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

1 5 10 15

Asn Ile Trp Ala Asp Arg Ile Ala Pro Phe Thr

20 25

<210> 252

<211> 45

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 252

Glu Met Cys Gln Arg Glu Ile Glu Met Leu Lys Ala Glu Val Ala Ser

1 5 10 15

Met Leu Leu Ala Thr Gly Lys Thr Met Met Gln Arg Phe Asp Phe Ile

20 25 30

Asp Lys Ile Glu Arg Leu Gly Val Ser His His Phe Asp

35 40 45

<210> 253

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 253

Ile Phe Asp Gln Phe Ile Asp Ala Lys Gly Lys Phe Lys Glu Ser Leu
1 5 10 15

Cys Asn Asp Ile Arg Gly Leu Leu Ser Leu Tyr Glu Ala Ala His Val
20 25 30

Arg Thr His Gly Asp Lys Ile Leu Glu Glu Ala Leu Ala Phe Thr Thr
35 40 45

Thr His Met Thr Ser Gly Gly Pro His Leu Asp Ser Ser Leu Ala Lys
50 55 60

Gln Val Lys Tyr Ala Leu Glu Gln Pro Leu His Lys Gly Ile Leu Arg
65 70 75 80

Tyr Glu Ala Trp Arg Tyr Ile Ser Ile Tyr Glu Glu Asp Glu Ser Asn
85 90 95

Asn Lys Leu Leu Leu Arg Leu Ala Lys Leu Asp Tyr His Leu Leu Gln
100 105 110

Met Ser Tyr Lys Gln Glu Leu
115

<210> 254

<211> 47

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 254

Arg Trp Gly Lys Gly Leu Glu Ser Val Ser Asn Phe Pro Tyr Ala Arg
1 5 10 15

Asp Arg Phe Val Glu Cys Tyr Phe Trp Ala Val Gly Thr Leu Tyr Glu
20 25 30

Pro Gln Tyr Ser Leu Ala Arg Met Thr Phe Ala Lys Val Ala Ala

35 40 45

<210> 255

<211> 129

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 255

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

20 25 30
Ala Lys Lys Gln Arg Thr Tyr Ala Phe Asp Lys Tyr Ile Glu Asp Trp
35 40 45
Lys Gln Tyr Met Arg Thr Asn Phe Ser Gln Ser Arg Trp Phe Phe Thr
50 55 60
Lys Glu Leu Pro Ser Phe Ala Asp Tyr Ile Asn Asn Gly Ala Ile Thr
65 70 75 80
Ile Gly Ala Tyr Leu Val Ala Ser Ala Ala Phe Leu Tyr Met Asp Ser

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

<210> 256

<211> 17

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 256

Lys Glu Arg Gly Thr Gly Thr Ala Ile Glu Cys Tyr Met Lys Asp His

1 5 10 15

Asn

<210> 257

<211> 28

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 257

Glu Met Ile Glu Asn Thr Trp Lys Val Met Asn Glu Glu Cys Leu Arg

1 5 10 15

Pro Ile Pro Ile Pro Arg Asp Thr Leu Lys Met Leu

20 25

<210> 258

<211> 31

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 258

Glu Thr Val Tyr Lys His Arg Ile Asp Gly Phe Thr Gln Pro His Ala

1 5 10 15

Ile Glu Glu His Ile Arg Ala Met Leu Val Asp Phe Met Ser Ile

20 25 30

<210> 259

<211> 62

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 259

Leu Glu Leu Val Asp Asn Leu Glu Arg Leu Gly Leu Ala Tyr His Phe

1 5 10 15

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

20 25 30

Glu Asp Glu Gly Asn His Lys Arg Asn Lys Glu Asp Leu Tyr Ala Ala

35 40 45

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

50 55 60

<210> 260

<211> 90

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 260

Tyr Val Ser Gln Ala Asn Glu Leu Lys Glu Gln Val Lys Met Met Leu

1 5 10 15

Asp Glu Glu Asp Met Lys Leu Leu Asp Cys Leu Glu Leu Val Asp Asn

20 25 30

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

35 40 45

Leu Leu Ser Ser Ala Tyr Asn Ala Asn His Glu Asp Glu Gly Asn His

50 55 60

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

65 70 75 80

Phe Arg Gln His Gly Phe Asn Val Pro Gln

85 90

<210> 261

<211> 22

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 261

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

1 5 10 15

Ile Trp Ala Asp Arg Val

20

<210> 262

<211> 23

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 262

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

1 5 10 15

Val Met Ser Met Leu Leu Glu

20

<210> 263

<211> 34

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 263

Ser Thr Leu Ala Lys Gln Val Lys Tyr Ala Leu Glu Gln Pro Leu His

1 5 10 15

Lys Gly Ile Pro Arg Tyr Glu Ala Trp Arg Tyr Ile Ser Ile Tyr Glu

20 25 30

Glu Asp

<210> 264

<211> 20

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 264

Leu Ala Lys Leu Asp Tyr His Leu Ser Gln Met Leu Asn Lys Gln Asp

1 5 10 15

Leu Cys Glu Ile

20

<210> 265

<211> 26

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 265

Arg Asp Arg Ile Val Glu Cys Tyr Phe Trp Ala Val Ala Thr Tyr Tyr

1 5 10 15

Glu Pro Gln Tyr Ser Leu Ala Arg Met Thr

20 25

<210> 266

<211> 20

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 266

Glu Val Gly Glu Asp Leu Ala Lys Lys Gln Arg Thr Tyr Ala Phe Asp

1 5 10 15

Lys Tyr Ile Glu

20

<210> 267

<211> 24

<212> PRT

<213> Artificial Sequence

<220><223

> Synthetic polypeptide

<400> 267

Tyr Ala Arg Thr Ser Phe Thr Gln Ser Lys Trp Phe Leu Thr Asn Glu

1 5 10 15

Leu Pro Ser Phe Ser Asp Tyr Leu

20

<210> 268

<211> 84

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 268

Ala Ala Phe Leu Asp Met Asp Ser Ala Ser Glu Asp Val Ile Asn Trp
1 5 10 15

Met Ser Thr Asn Pro Lys Leu Phe Val Ala Leu Thr Thr His Ala Arg

20 25 30

Leu Ala Asn Asp Val Gly Ser His Lys Phe Glu Lys Glu Arg Gly Ser
35 40 45

Gly Thr Ala Ile Glu Cys Tyr Met Lys Asp Tyr His Val Ser Glu Glu
50 55 60

Glu Ala Met Lys Lys Phe Glu Glu Met Cys Asp Asp Ala Trp Lys Val
65 70 75 80

Met Asn Glu Glu

<210> 269

<211> 22

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 269

Asn Asn Gln His Glu Ser Val Arg Gln Leu Ala Asp Phe Pro Glu Asn
1 5 10 15

Ile Trp Ala Asp Arg Val

20

<210> 270

<211> 23

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 270

Gln Gly His Asp Met Cys Ala Lys Glu Ile Glu Met Leu Lys Glu Glu
1 5 10 15

Val Met Ser Met Leu Leu Glu

20

<210> 271

<211> 54

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 271

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

1 5 10 15

Tyr Glu Ala Tyr Cys Phe Ile Ser Ile Tyr Glu Glu Asp Glu Ser Asn

20 25 30

Asn Lys Leu Leu Leu Arg Leu Ala Lys Leu Asp Tyr His Leu Leu Gln

35 40 45

Met Ser Tyr Lys Arg Glu

50

<210> 272

<211> 26

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 272

Arg Asp Arg Ile Val Glu Cys Tyr Phe Trp Ala Val Ala Thr Tyr Tyr

1 5 10 15

Glu Pro Gln Tyr Ser Leu Ala Arg Met Thr

20 25

<210> 273

<211> 20

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 273

Glu Val Gly Glu Asp Leu Ala Lys Lys Gln Arg Thr Tyr Ala Phe Asp

1 5 10 15

Lys Tyr Ile Glu

20

<210> 274

<211> 24

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 274

Tyr Ala Arg Thr Ser Phe Thr Gln Ser Lys Trp Phe Leu Thr Asn Glu

1 5 10 15

Leu Pro Ser Phe Ser Asp Tyr Leu

20

<210> 275

<211> 25

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 275

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

1 5 10 15

Ser Thr Asn Pro Lys Leu Phe Val Ala

20 25

<210> 276

<211> 44

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 276

Lys Phe Glu Lys Glu Arg Gly Ser Gly Thr Ala Ile Glu Cys Tyr Met

1 5 10 15

Lys Asp Tyr His Val Ser Glu Glu Glu Ala Met Lys Lys Phe Glu Glu

20 25 30

Met Cys Asp Asp Ala Trp Lys Val Met Asn Glu Glu

35 40

<210> 277

<211> 22

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 277

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

1 5 10 15

Ile Trp Ala Asp Arg Val

20

<210> 278

<211> 23

<212> PRT

<213>

Artificial Sequence

<220><223> Synthetic polypeptide

<400> 278

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

1 5 10 15

Val Met Ser Met Leu Leu Glu

20

<210> 279

<211> 22

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 279

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

1 5 10 15

Tyr Glu Ala Tyr Cys Phe

20

<210> 280

<211> 20

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 280

Leu Ala Lys Leu Asp Tyr His Leu Ser Gln Met Leu Asn Lys Gln Asp

1 5 10 15

Leu Cys Glu Ile

20

<210> 281

<211> 26

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 281

Arg Asp Arg Ile Val Glu Cys Tyr Phe Trp Ala Val Ala Thr Tyr Tyr

1 5 10 15

Glu Pro Gln Tyr Ser Leu Ala Arg Met Thr

20 25

<210> 282

<211> 20

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 282

Glu Val Gly Glu Asp Leu Ala Lys Lys Gln Arg Thr Tyr Ala Phe Asp

1 5 10 15

Lys Tyr Ile Glu

20

<210> 283

<211> 24

<212> PRT

<213> Artificial Sequence

<220><223

> Synthetic polypeptide

<400> 283

Tyr Ala Arg Thr Ser Phe Thr Gln Ser Lys Trp Phe Leu Thr Asn Glu
1 5 10 15

Leu Pro Ser Phe Ser Asp Tyr Leu
20

<210> 284

<211> 25

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 284

Thr Phe Leu Gly Met Asp Gly Ala Ser Glu Asp Val Ile Asn Trp Met
1 5 10 15

Ser Thr Asn Pro Lys Leu Phe Val Ala
20 25

<210> 285

<211> 44

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 285

Lys Phe Glu Lys Glu Arg Gly Ser Gly Thr Ala Ile Glu Cys Tyr Met
1 5 10 15

Lys Asp Tyr His Val Ser Glu Glu Glu Ala Met Lys Lys Phe Glu Glu
20 25 30

Met Cys Asp Asp Ala Trp Lys Val Met Asn Glu Glu
35 40

<210> 286

<211> 27

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 286

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

1 5 10 15

Asn Ile Trp Ala Asp Arg Ile Ala Pro Phe Thr

20 25

<210> 287

<211> 45

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 287

Glu Met Cys Gln Arg Glu Ile Glu Met Leu Lys Ala Glu Val Ala Ser

1 5 10 15

Met Leu Leu Ala Thr Gly Lys Thr Met Met Gln Arg Phe Asp Phe Ile

20 25 30

Asp Lys Ile Glu Arg Leu Gly Val Ser His His Phe Asp

35 40 45

<210> 288

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 288

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

1 5 10 15

Cys Asn Asp Ile Arg Gly Leu Leu Ser Leu Tyr Glu Ala Ala His Val

20 25 30

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

35 40 45

Thr His Met Thr Ser Gly Gly Pro His Leu Asp Ser Ser Leu Ala Lys

50 55 60

Gln Val Lys Tyr Ala Leu Glu Gln Pro Leu His Lys Gly Ile Leu Arg

65 70 75 80

Tyr Glu Ala Trp Arg Tyr Ile Ser Ile Tyr Glu Glu Asp Glu Ser Asn
85 90 95
Asn Lys Leu Leu Leu Arg Leu Ala Lys Leu Asp Tyr His Leu Leu Gln
100 105 110
Met Ser Tyr Lys Gln Glu Leu
115

<210> 289
<211> 47
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 289
Arg Trp Gly Lys Gly Leu Glu Ser Val Ser Asn Phe Pro Tyr Ala Arg
1 5 10 15

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

<210> 290
<211> 73
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 290
Arg Trp Asp Gly Ser Gly Val Asp Gln Leu Ser Asp Tyr Ile Arg Ala
1 5 10 15
Ser Tyr Asn Thr Leu Leu Lys Phe Asn Lys Glu Val Gly Glu Asp Leu

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

65 70

<210> 291

<211> 24

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 291

Leu Asp Met Asp Ser Ala Leu Glu Asp Val Ile Asn Trp Met Ser Thr

1 5 10 15

Asn Pro Lys Leu Met Val Ala Tyr

20

<210> 292

<211> 51

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 292

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

1 5 10 15

Lys Asp Tyr Ser Val Ser Glu Glu Glu Ala Ala Lys Lys Phe Arg Glu

20 25 30

Met Cys Glu Asp Asn Trp Lys Val Met Asn Glu Glu Cys Leu Arg Pro

35 40 45

Thr Thr Ile

50

<210> 293

<211> 31

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 293

Glu Thr Val Tyr Lys His Arg Ile Asp Gly Phe Thr Gln Pro His Ala

1 5 10 15

Ile Glu Glu His Ile Arg Ala Met Leu Val Asp Phe Met Ser Ile

20 25 30

<210> 294

<211> 22

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 294

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

1 5 10 15

Ile Trp Ala Asp Arg Val

20

<210> 295

<211> 23

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 295

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

1 5 10 15

Val Met Ser Met Leu Leu Glu

20

<210> 296

<211> 59

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 296

Ser Thr Leu Ala Lys Gln Val Lys Tyr Ala Leu Glu Gln Pro Leu His

1 5 10 15

Lys Gly Ile Pro Arg Tyr Glu Ala Trp Arg Tyr Ile Ser Ile Tyr Glu

20 25 30

Glu Asp Glu Ser Asn Asn Lys Leu Leu Leu Arg Leu Ala Lys Leu Asp

35 40 45

Tyr His Leu Leu Gln Met Ser Tyr Lys Arg Glu

50 55

<210> 297

<211> 26

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 297

Arg Asp Arg Ile Val Glu Cys Tyr Phe Trp Ala Val Ala Thr Tyr Tyr

1 5 10 15

Glu Pro Gln Tyr Ser Leu Ala Arg Met Thr

20 25

<210> 298

<211> 20

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 298

Glu Val Gly Glu Asp Leu Ala Lys Lys Gln Arg Thr Tyr Ala Phe Asp

1 5 10 15

Lys Tyr Ile Glu

20

<210> 299

<211> 24

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 299

Tyr Ala Arg Thr Ser Phe Thr Gln Ser Lys Trp Phe Leu Thr Asn Glu

1 5 10 15

Leu Pro Ser Phe Ser Asp Tyr Leu

20

<210> 300

<211> 25

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 300

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

1 5 10 15

Ser Thr Asn Pro Lys Leu Phe Val Ala

20 25

<210> 301

<211> 36

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 301

Ser Thr Ala Ile Glu Cys Tyr Met Lys Asp Tyr His Val Ser Glu Glu

1 5 10 15

Glu Ala Met Glu Lys Phe Glu Glu Met Cys Asp Asp Ala Trp Lys Val

20 25 30

Met Asn Glu Glu

35

<210> 302

<211> 22

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 302

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

1 5 10 15

Ile Trp Ala Asp Arg Val

20

<210> 303

<211> 23

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 303

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

1 5 10 15

Val Met Ser Met Leu Leu Glu

20

<210> 304

<211> 59

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 304

Ser Thr Leu Ala Lys Gln Val Lys Tyr Ala Leu Glu Gln Pro Leu His

1 5 10 15

Lys Gly Ile Pro Arg Tyr Glu Ala Trp Arg Tyr Ile Ser Ile Tyr Glu

20 25 30

Glu Asp Glu Ser Asn Asn Lys Leu Leu Leu Arg Leu Ala Lys Leu Asp

35 40 45

Tyr His Leu Leu Gln Met Ser Tyr Lys Arg Glu

50 55

<210> 305

<211> 26

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 305

Arg Asp Arg Ile Val Glu Cys Tyr Phe Trp Ala Val Ala Thr Tyr Tyr

1 5 10 15

Glu Pro Gln Tyr Ser Leu Ala Arg Met Thr

20 25

<210> 306

<211> 20

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 306

Glu Val Gly Glu Asp Leu Ala Lys Lys Gln Arg Thr Tyr Ala Phe Asp

1 5 10 15

Lys Tyr Ile Glu

20

<210> 307

<211> 25

<212> PRT

<213> Artificial Sequence

<220><223

> Synthetic polypeptide

<400> 307

Tyr Ala Arg Thr Ser Phe Thr Gln Ser Lys Trp Phe Leu Thr Asn Glu

1 5 10 15

Leu Pro Ser Phe Ala Asp Tyr Leu Ser

20 25

<210> 308

<211> 84

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 308

Ala Ala Leu Leu Asp Met Asp Ser Ala Leu Glu Asp Val Ile Asn Trp

1 5 10 15

Met Ser Thr Asn Pro Lys Phe Phe Val Ala Leu Thr Thr His Ala Arg

20 25 30

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

<210> 309

<211> 27
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 309
Ser Asn Asn Arg Gln Glu Thr Val Arg Pro Leu Ala Asp Phe Pro Glu
1 5 10 15
Asn Ile Trp Ala Asp Arg Ile Ala Pro Phe Thr
20 25
<210> 310
<211> 45
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 310
Glu Met Cys Gln Arg Glu Ile Glu Met Leu Lys Ala Glu Val Ala Ser
1 5 10 15

Met Leu Leu Ala Thr Gly Lys Thr Met Met Gln Arg Phe Asp Phe Ile
20 25 30
Asp Lys Ile Glu Arg Leu Gly Val Ser His His Phe Asp
35 40 45
<210> 311
<211> 119
<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 311

Ile Phe Asp Gln Phe Ile Asp Ala Lys Gly Lys Phe Lys Glu Ser Leu
1 5 10 15

Cys Asn Asp Ile Arg Gly Leu Leu Ser Leu Tyr Glu Ala Ala His Val
20 25 30

Arg Thr His Gly Asp Lys Ile Leu Glu Glu Ala Leu Ala Phe Thr Thr
35 40 45

Thr His Met Thr Ser Gly Gly Pro His Leu Asp Ser Ser Leu Ala Lys
50 55 60

Gln Val Lys Tyr Ala Leu Glu Gln Pro Leu His Lys Gly Ile Leu Arg
65 70 75 80

Tyr Glu Ala Trp Arg Tyr Ile Ser Ile Tyr Glu Glu Asp Glu Ser Asn
85 90 95

Asn Lys Leu Leu Leu Arg Leu Ala Lys Leu Asp Tyr His Leu Leu Gln
100 105 110

Met Ser Tyr Lys Gln Glu Leu
115

<210> 312

<211> 47

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 312

Arg Trp Gly Lys Gly Leu Glu Ser Val Ser Asn Phe Pro Tyr Ala Arg
1 5 10 15

Asp Arg Phe Val Glu Cys Tyr Phe Trp Ala Val Gly Thr Leu Tyr Glu
20 25 30

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

<210> 313

<211> 73

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 313

Arg Trp Asp Gly Ser Gly Val Asp Gln Leu Ser Asp Tyr Ile Arg Ala

1 5 10 15

Ser Tyr Asn Thr Leu Leu Lys Phe Asn Lys Glu Val Gly Glu Asp Leu

20 25 30

Ala Lys Lys Gln Arg Thr Tyr Ala Phe Asp Lys Tyr Ile Glu Asp Trp

35 40 45

Lys Gln Tyr Met Arg Thr Ser Phe Thr Gln Ser Lys Trp Phe Leu Thr

50 55 60

Asn Glu Leu Pro Ser Phe Ala Asp Tyr

65 70

<210> 314

<211> 24

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 314

Leu Asp Met Asp Ser Ala Leu Glu Asp Val Ile Asn Trp Met Ser Thr

1 5 10 15

Asn Pro Lys Leu Met Val Ala Tyr

20

<210> 315

<211> 17

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 315

Lys Glu Arg Gly Thr Gly Thr Ala Ile Glu Cys Tyr Met Lys Asp His

1 5 10 15

Asn

<210> 316

<211> 28

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 316

Glu Met Ile Glu Asn Thr Trp Lys Val Met Asn Glu Glu Cys Leu Arg
1 5 10 15
Pro Ile Pro Ile Pro Arg Asp Thr Leu Lys Met Leu
20 25

<210> 317

<211> 31

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 317

Glu Thr Val Tyr Lys His Arg Ile Asp Gly Phe Thr Gln Pro His Ala
1 5 10 15
Ile Glu Glu His Ile Arg Ala Met Leu Val Asp Phe Met Ser Ile
20 25 30

<210> 318

<211> 22

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 318

Asn Asn Gln His Glu Ser Val Arg Gln Leu Ala Asp Phe Pro Glu Asn
1 5 10 15
Ile Trp Ala Asp Arg Val
20

<210> 319

<211> 23

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 319

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

1 5 10 15

Val Met Ser Met Leu Leu Glu

20

<210> 320

<211> 54

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 320

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

1 5 10 15

Tyr Glu Ala Tyr Cys Phe Ile Ser Ile Tyr Glu Glu Asp Glu Ser Asn

20 25 30

Asn Lys Leu Leu Leu Arg Leu Ala Lys Leu Asp Tyr His Leu Leu Gln

35 40 45

Met Ser Tyr Lys Arg Glu

50

<210> 321

<211> 26

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 321

Arg Asp Arg Ile Val Glu Cys Tyr Phe Trp Ala Val Ala Thr Tyr Tyr

1 5 10 15

Glu Pro Gln Tyr Ser Leu Ala Arg Met Thr

20 25

<210> 322

<211> 20

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 322

Glu Val Gly Glu Asp Leu Ala Lys Lys Gln Arg Thr Tyr Ala Phe Asp
1 5 10 15

Lys Tyr Ile Glu
20

<210> 323

<211> 24

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 323

Tyr Ala Arg Thr Ser Phe Thr Gln Ser Lys Trp Phe Leu Thr Asn Glu
1 5 10 15

Leu Pro Ser Phe Ser Asp Tyr Leu
20

<210> 324

<211> 41

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 324

Ala Ala Phe Leu Asp Met Asp Ser Ala Ser Glu Asp Val Ile Asn Trp
1 5 10 15

Met Ser Thr Asn Pro Lys Leu Phe Val Ala Leu Thr Thr His Ala Arg
20 25 30

Leu Ala Asn Asp Val Gly Ser His Lys
35 40

<210> 325

<211> 39

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 325

Arg Gly Ser Gly Thr Ala Ile Glu Cys Tyr Met Lys Asp Tyr Asn Val

1 5 10 15

Ser Glu Glu Glu Ala Leu Lys Lys Phe Glu Glu Met Cys Glu Asp Thr

20 25 30

Trp Lys Val Met Asn Glu Glu

35

<210> 326

<211> 27

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 326

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

1 5 10 15

Asn Ile Trp Ala Asp Arg Ile Ala Pro Phe Thr

20 25

<210> 327

<211> 45

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 327

Glu Met Cys Gln Arg Glu Ile Glu Met Leu Lys Ala Glu Val Ala Ser

1 5 10 15

Met Leu Leu Ala Thr Gly Lys Thr Met Met Gln Arg Phe Asp Phe Ile

20 25 30

Asp Lys Ile Glu Arg Leu Gly Val Ser His His Phe Asp

35 40 45

<210> 328

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 328

Ile Phe Asp Gln Phe Ile Asp Ala Lys Gly Lys Phe Lys Glu Ser Leu
1 5 10 15

Cys Asn Asp Ile Arg Gly Leu Leu Ser Leu Tyr Glu Ala Ala His Val
20 25 30

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

35 40 45

Thr His Met Thr Ser Gly Gly Pro His Leu Asp Ser Ser Leu Ala Lys
50 55 60

Gln Val Lys Tyr Ala Leu Glu Gln Pro Leu His Lys Gly Ile Leu Arg
65 70 75 80

Tyr Glu Ala Trp Arg Tyr Ile Ser Ile Tyr Glu Glu Asp Glu Ser Asn
85 90 95

Asn Lys Leu Leu Leu Arg Leu Ala Lys Leu Asp Tyr His Leu Leu Gln

100 105 110

Met Ser Tyr Lys Gln Glu Leu

115

<210> 329

<211> 226

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 329

Arg Trp Asp Gly Ser Gly Val Asp Gln Leu Ser Asp Tyr Ile Arg Ala
1 5 10 15

Ser Tyr Asn Thr Leu Leu Lys Phe Asn Lys Glu Val Gly Glu Asp Leu
20 25 30

Ala Lys Lys Gln Arg Thr Tyr Ala Phe Asp Lys Tyr Ile Glu Asp Trp

35 40 45

Lys Gln Tyr Met Arg Thr Asn Phe Ser Gln Ser Arg Trp Phe Phe Thr

50 55 60

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

65 70 75 80

Ile Gly Ala Tyr Leu Val Ala Ser Ala Ala Phe Leu Tyr Met Asp Ser

85 90 95

Ala Lys Glu Asp Val Ile Asn Trp Met Ser Thr Asn Pro Lys Leu Val

100 105 110

Val Ala Tyr Ser Thr His Ser Arg Leu Ile Asn Asp Phe Gly Gly His

115 120 125

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

130 135 140

Lys Asp Tyr Asn Val Ser Glu Glu Glu Ala Ala Asn Lys Phe Arg Glu

145 150 155 160

Met Met Glu Asp Ala Trp Lys Val Met Asn Glu Asp Cys Leu Arg Pro

165 170 175

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

180 185 190

Ala Gly Glu Ile Val Tyr Lys His Arg Ile Asp Gly Phe Thr Glu Pro

195 200 205

His Ile Ile Lys Asp His Ile Arg Ala Thr Leu Val Asp Phe Met Ala

210 215 220

Ile Asn

225

<210> 330

<211> 47

<

212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 330

Arg Trp Gly Lys Gly Leu Glu Ser Val Ser Asn Phe Pro Tyr Ala Arg
1 5 10 15

Asp Arg Phe Val Glu Cys Tyr Phe Trp Ala Val Gly Thr Leu Tyr Glu
20 25 30

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

<210> 331

<211> 27

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 331

Ser Asn Asn Arg Gln Glu Thr Val Arg Pro Leu Ala Asp Phe Pro Glu
1 5 10 15

Asn Ile Trp Ala Asp Arg Ile Ala Pro Phe Thr
20 25

<210> 332

<211> 45

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 332

Glu Met Cys Gln Arg Glu Ile Glu Met Leu Lys Ala Glu Val Ala Ser
1 5 10 15

Met Leu Leu Ala Thr Gly Lys Thr Met Met Gln Arg Phe Asp Phe Ile
20 25 30

Asp Lys Ile Glu Arg Leu Gly Val Ser His His Phe Asp
35 40 45

<210> 333

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 333

Ile Phe Asp Gln Phe Ile Asp Ala Lys Gly Lys Phe Lys Glu Ser Leu
1 5 10 15

Cys Asn Asp Ile Arg Gly Leu Leu Ser Leu Tyr Glu Ala Ala His Val
20 25 30

Arg Thr His Gly Asp Lys Ile Leu Glu Glu Ala Leu Ala Phe Thr Thr
35 40 45

Thr His Met Thr Ser Gly Gly Pro His Leu Asp Ser Ser Leu Ala Lys
50 55 60

Gln Val Lys Tyr Ala Leu Glu Gln Pro Leu His Lys Gly Ile Leu Arg
65 70 75 80

Tyr Glu Ala Trp Arg Tyr Ile Ser Ile Tyr Glu Glu Asp Glu Ser Asn
85 90 95

Asn Lys Leu Leu Leu Arg Leu Ala Lys Leu Asp Tyr His Leu Leu Gln
100 105 110

Met Ser Tyr Lys Gln Glu Leu
115

<210> 334

<211> 47

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 334

Arg Trp Gly Lys Gly Leu Glu Ser Val Ser Asn Phe Pro Tyr Ala Arg
1 5 10 15

Asp Arg Phe Val Glu Cys Tyr Phe Trp Ala Val Gly Thr Leu Tyr Glu
20 25 30

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

<210> 335

<211> 73

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 335

Arg Trp Asp Gly Ser Gly Val Asp Gln Leu Ser Asp Tyr Ile Arg Ala

1 5 10 15

Ser Tyr Asn Thr Leu Leu Lys Phe Asn Lys Glu Val Gly Glu Asp Leu

20 25 30

Ala Lys Lys Gln Arg Thr Tyr Ala Phe Asp Lys Tyr Ile Glu Asp Trp

35 40 45

Lys Gln Tyr Met Arg Thr Ser Phe Thr Gln Ser Lys Trp Phe Leu Thr

50 55 60

Asn Glu Leu Pro Ser Phe Ala Asp Tyr

65 70

<210> 336

<211> 24

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 336

Leu Asp Met Asp Ser Ala Leu Glu Asp Val Ile Asn Trp Met Ser Thr

1 5 10 15

Asn Pro Lys Leu Met Val Ala Tyr

20

<210> 337

<211> 59

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 337

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

1 5 10 15

Lys Asp Tyr Ser Val Ser Glu Glu Glu Ala Ala Lys Lys Phe Arg Glu

20 25 30

Met Ile Glu Asn Thr Trp Lys Val Met Asn Glu Glu Cys Leu Arg Pro
35 40 45
Ile Pro Ile Pro Arg Asp Thr Leu Lys Met Leu
50 55

<210> 338
<211> 19
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 338
Glu Pro His Ile Ile Lys Asp His Ile Arg Ala Met Leu Val Asp Phe
1 5 10 15
Met Ala Ile

<210> 339

<211> 27
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 339
Ser Asn Asn Arg Gln Glu Thr Val Arg Pro Leu Ala Asp Phe Pro Glu
1 5 10 15
Asn Ile Trp Ala Asp Arg Ile Ala Pro Phe Thr
20 25

<210> 340
<211> 45
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 340
Glu Met Cys Gln Arg Glu Ile Glu Met Leu Lys Ala Glu Val Ala Ser

1 5 10 15

Met Leu Leu Ala Thr Gly Lys Thr Met Met Gln Arg Phe Asp Phe Ile
20 25 30
Asp Lys Ile Glu Arg Leu Gly Val Ser His His Phe Asp
35 40 45

<210> 341
<211> 119
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 341

Ile Phe Asp Gln Phe Ile Asp Ala Lys Gly Lys Phe Lys Glu Ser Leu
1 5 10 15
Cys Asn Asp Ile Arg Gly Leu Leu Ser Leu Tyr Glu Ala Ala His Val
20 25 30
Arg Thr His Gly Asp Lys Ile Leu Glu Glu Ala Leu Ala Phe Thr Thr
35 40 45
Thr His Met Thr Ser Gly Gly Pro His Leu Asp Ser Ser Leu Ala Lys
50 55 60
Gln Val Lys Tyr Ala Leu Glu Gln Pro Leu His Lys Gly Ile Leu Arg
65 70 75 80
Tyr Glu Ala Trp Arg Tyr Ile Ser Ile Tyr Glu Glu Asp Glu Ser Asn
85 90 95
Asn Lys Leu Leu Leu Arg Leu Ala Lys Leu Asp Tyr His Leu Leu Gln
100 105 110
Met Ser Tyr Lys Gln Glu Leu
115

<210> 342
<211> 47
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide

<400> 342

Arg Trp Gly Lys Gly Leu Glu Ser Val Ser Asn Phe Pro Tyr Ala Arg
1 5 10 15
Asp Arg Phe Val Glu Cys Tyr Phe Trp Ala Val Gly Thr Leu Tyr Glu

20 25 30
Pro Gln Tyr Ser Leu Ala Arg Met Thr Phe Ala Lys Val Ala Ala
35 40 45

<210> 343

<211> 179

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 343

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

20 25 30
Ala Lys Lys Gln Arg Thr Tyr Ala Phe Asp Lys Tyr Ile Glu Asp Trp
35 40 45
Lys Gln Tyr Met Arg Thr Asn Phe Ser Gln Ser Arg Trp Phe Phe Thr
50 55 60
Lys Glu Leu Pro Ser Phe Ala Asp Tyr Ile Asn Asn Gly Ala Ile Thr
65 70 75 80
Ile Gly Ala Tyr Leu Val Ala Ser Ala Ala Phe Leu Tyr Met Asp Ser
85 90 95

Ala Lys Glu Asp Val Ile Asn Trp Met Ser Thr Asn Pro Lys Leu Val

100 105 110
Val Ala Tyr Ser Thr His Ser Arg Leu Ile Asn Asp Phe Gly Gly His
115 120 125
Lys Phe Asp Lys Glu Arg Gly Ser Val Thr Ala Leu Asp Cys Tyr Met
130 135 140
Lys Asp Tyr Ser Val Ser Glu Glu Glu Ala Ala Lys Lys Phe Arg Glu

145 150 155 160

Met Cys Glu Asp Asn Trp Lys Val Met Asn Glu Glu Cys Leu Arg Pro
165 170 175
Thr Thr Ile

<210> 344
<211> 31
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 344
Glu Thr Val Tyr Lys His Arg Ile Asp Gly Phe Thr Gln Pro His Ala
1 5 10 15
Ile Glu Glu His Ile Arg Ala Met Leu Val Asp Phe Met Ser Ile
20 25 30

<210> 345
<211> 27
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 345
Ser Asn Asn Arg Gln Glu Thr Val Arg Pro Leu Ala Asp Phe Pro Glu
1 5 10 15
Asn Ile Trp Ala Asp Arg Ile Ala Pro Phe Thr
20 25
<210> 346
<211> 45
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 346
Glu Met Cys Gln Arg Glu Ile Glu Met Leu Lys Ala Glu Val Ala Ser

1 5 10 15

Met Leu Leu Ala Thr Gly Lys Thr Met Met Gln Arg Phe Asp Phe Ile

20 25 30

Asp Lys Ile Glu Arg Leu Gly Val Ser His His Phe Asp

35 40 45

<210> 347

<211> 119

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 347

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

1 5 10 15

Cys Asn Asp Ile Arg Gly Leu Leu Ser Leu Tyr Glu Ala Ala His Val

20 25 30

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

35 40 45

Thr His Met Thr Ser Gly Gly Pro His Leu Asp Ser Ser Leu Ala Lys

50 55 60

Gln Val Lys Tyr Ala Leu Glu Gln Pro Leu His Lys Gly Ile Leu Arg

65 70 75 80

Tyr Glu Ala Trp Arg Tyr Ile Ser Ile Tyr Glu Glu Asp Glu Ser Asn

85 90 95

Asn Lys Leu Leu Leu Arg Leu Ala Lys Leu Asp Tyr His Leu Leu Gln

100 105 110

Met Ser Tyr Lys Gln Glu Leu

115

<210> 348

<211> 47

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 348

Arg Trp Gly Lys Gly Leu Glu Ser Val Ser Asn Phe Pro Tyr Ala Arg
1 5 10 15

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

<210> 349
<211> 187
<212> PRT
<213> Artificial Sequence
<220><223> Synthetic polypeptide
<400> 349
Arg Trp Asp Gly Ser Gly Val Asp Gln Leu Ser Asp Tyr Ile Arg Ala
1 5 10 15
Ser Tyr Asn Thr Leu Leu Lys Phe Asn Lys Glu Val Gly Glu Asp Leu

20 25 30
Ala Lys Lys Gln Arg Thr Tyr Ala Phe Asp Lys Tyr Ile Glu Asp Trp
35 40 45
Lys Gln Tyr Met Arg Thr Asn Phe Ser Gln Ser Arg Trp Phe Phe Thr
50 55 60
Lys Glu Leu Pro Ser Phe Ala Asp Tyr Ile Asn Asn Gly Ala Ile Thr
65 70 75 80
Ile Gly Ala Tyr Leu Val Ala Ser Ala Ala Phe Leu Tyr Met Asp Ser

85 90 95
Ala Lys Glu Asp Val Ile Asn Trp Met Ser Thr Asn Pro Lys Leu Val
100 105 110
Val Ala Tyr Ser Thr His Ser Arg Leu Ile Asn Asp Phe Gly Gly His
115 120 125
Lys Phe Asp Lys Glu Arg Gly Ser Val Thr Ala Leu Asp Cys Tyr Met
130 135 140
Lys Asp Tyr Ser Val Ser Glu Glu Glu Ala Ala Lys Lys Phe Arg Glu

145 150 155 160

Met Ile Glu Asn Thr Trp Lys Val Met Asn Glu Glu Cys Leu Arg Pro

165 170 175

Ile Pro Ile Pro Arg Asp Thr Leu Lys Met Leu

180 185

<210> 350

<211> 19

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 350

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

1 5 10 15

Met Ala Ile

<210> 351

<211> 62

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 351

Glu Ala Phe Asn Lys Leu Lys Asp Glu Glu Gly Asn Phe Lys Ala Ser

1 5 10 15

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

20 25 30

Met Arg Ile His Gly Glu Asp Ile Leu Asp Glu Ala Ile Ser Phe Thr

35 40 45

Thr Ala Gln Leu Thr Leu Ala Leu Pro Thr Leu Asp Pro Pro

50 55 60

<210> 352

<211> 40

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 352

Asn Lys Ala Leu Leu Gln Phe Ala Lys Ile Asp Phe Asn Met Leu Gln
1 5 10 15

Leu Leu His Arg Lys Glu Leu Ser Glu Ile Cys Arg Trp Trp Lys Asp
20 25 30

Leu Asp Phe Thr Arg Lys Leu Pro

35 40

<210> 353

<211> 58

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 353

Asp Arg Val Val Glu Gly Tyr Phe Trp Ile Met Gly Val Tyr Phe Glu
1 5 10 15

Pro Gln Tyr Ser Leu Gly Arg Lys Met Leu Thr Lys Val Ile Ala Met
20 25 30

Ala Ser Ile Val Asp Asp Thr Tyr Asp Ser Phe Ala Thr Tyr Asp Glu
35 40 45

Leu Ile Pro Tyr Thr Asp Ala Ile Glu Arg
50 55

<210> 354

<211> 31

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 354

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

Glu Gln Leu Leu Ala Asp Lys Gly Arg Gln Tyr Arg Val Glu Tyr
20 25 30

<210> 355

<211> 29

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 355

Trp Thr His Leu Asn Tyr Lys Pro Thr Phe Glu Glu Phe Arg Asp Asn
1 5 10 15

Ala Leu Pro Thr Ser Gly Tyr Ala Met Leu Ala Ile Thr
20 25

<210> 356

<211> 27

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 356

Thr Phe Glu Trp Ala Ala Ser Asp Pro Lys Ile Ile Lys Ala Ser Thr
1 5 10 15

Ile Ile Cys Arg Phe Met Asp Asp Ile Ala Glu
20 25

<210> 357

<211> 42

<212> PRT

<213> Artificial Sequence

<220><223> Synthetic polypeptide

<400> 357

Glu Asp Asp Cys Ser Ala Ile Glu Cys Tyr Met Glu Gln Tyr Lys Val
1 5 10 15

Thr Ala Gln Glu Ala Tyr Asp Glu Phe Asn Lys His Ile Glu Ser Ser
20 25 30

Trp Lys Asp Val Asn Glu Glu Phe Leu Lys

35 40