

1793449\_Seq\_list\_17Sep21  
SEQUENCE LISTING

<110> Theraneutrics, LLC  
Theraneutrics LLC

<120> Therapeutic Engineered Microbial Cell Systems and Methods for  
Treating Hyperuricemia and Gout

<130> HL20070

<140> PCT/US 21/070014  
<141> 2021-01-08

<150> 62959991  
<151> 2020-01-12

<150> US 62/959,991  
<151> 2020-01-12

<160> 26

<170> PatentIn version 3.5

<210> 1  
<211> 313  
<212> PRT  
<213> Candida utilis

<400> 1

Met Ser Thr Thr Leu Ser Ser Ser Thr Tyr Gly Lys Asp Asn Val Lys  
1 5 10 15

Phe Leu Lys Val Lys Lys Asp Pro Gln Asn Pro Lys Lys Gln Glu Val  
20 25 30

Met Glu Ala Thr Val Thr Cys Leu Leu Glu Gly Gly Phe Asp Thr Ser  
35 40 45

Tyr Thr Glu Ala Asp Asn Ser Ser Ile Val Pro Thr Asp Thr Val Lys  
50 55 60

Asn Thr Ile Leu Val Leu Ala Lys Thr Thr Glu Ile Trp Pro Ile Glu  
65 70 75 80

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Arg Phe Ala Ala Lys Leu Ala Thr His Phe Val Glu Lys Tyr Ser His  
85 90 95

Val Ser Gly Val Ser Val Lys Ile Val Gln Asp Arg Trp Val Lys Tyr  
100 105 110

Ala Val Asp Gly Lys Pro His Asp His Ser Phe Ile His Glu Gly Gly  
115 120 125

Glu Lys Arg Ile Thr Asp Leu Tyr Tyr Lys Arg Ser Gly Asp Tyr Lys  
130 135 140

Leu Ser Ser Ala Ile Lys Asp Leu Thr Val Leu Lys Ser Thr Gly Ser  
145 150 155 160

Met Phe Tyr Gly Tyr Asn Lys Cys Asp Phe Thr Thr Leu Gln Pro Thr  
165 170 175

Thr Asp Arg Ile Leu Ser Thr Asp Val Asp Ala Thr Trp Val Trp Asp  
180 185 190

Asn Lys Lys Ile Gly Thr Val Tyr Asp Ile Ala Lys Ala Ala Asp Lys  
195 200 205

Gly Ile Phe Asp Asn Val Tyr Asn Gln Ala Arg Glu Ile Thr Leu Thr  
210 215 220

Thr Phe Ala Leu Glu Asn Ser Pro Ser Val Gln Ala Thr Met Phe Asn  
225 230 235 240

Met Ala Thr Gln Ile Leu Glu Lys Ala Cys Ser Val Tyr Ser Val Ser  
245 250 255

Tyr Ala Leu Pro Asn Lys His Tyr Phe Leu Ile Asp Leu Lys Trp Lys  
260 265 270

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His Tyr Phe Leu Ile Asp Leu Lys Trp Lys Gly Leu Glu Asn Asp Asn  
275 280 285

Glu Leu Phe Tyr Pro Ser Pro His Pro Asn Gly Leu Ile Lys Cys Thr  
290 295 300

Val Val Arg Lys Glu Lys Thr Lys Leu  
305 310

<210> 2

<211> 302

<212> PRT

<213> Unknown

<220>

<223> Aspergillus flavus

<400> 2

Met Ser Ala Val Lys Ala Ala Arg Tyr Gly Lys Asp Asn Val Arg Val  
1 5 10 15

Tyr Lys Val His Lys Asp Glu Lys Thr Gly Val Gln Thr Val Tyr Glu  
20 25 30

Met Thr Val Cys Val Leu Leu Glu Gly Glu Ile Glu Thr Ser Tyr Thr  
35 40 45

Lys Ala Asp Asn Ser Val Ile Val Ala Thr Asp Ser Ile Lys Asn Thr  
50 55 60

Ile Tyr Ile Thr Ala Lys Gln Asn Pro Val Thr Pro Pro Glu Leu Phe  
65 70 75 80

Gly Ser Ile Leu Gly Thr His Phe Ile Glu Lys Tyr Asn His Ile His  
85 90 95

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Ala Ala His Val Asn Ile Val Cys His Arg Trp Thr Arg Met Asp Ile  
100 105 110

Asp Gly Lys Pro His Pro His Ser Phe Ile Arg Asp Ser Glu Glu Lys  
115 120 125

Arg Asn Val Gln Val Asp Val Val Glu Gly Lys Gly Ile Asp Ile Lys  
130 135 140

Ser Ser Leu Ser Gly Leu Thr Val Leu Lys Ser Thr Asn Ser Gln Phe  
145 150 155 160

Trp Gly Phe Leu Arg Asp Glu Tyr Thr Thr Leu Lys Glu Thr Trp Asp  
165 170 175

Arg Ile Leu Ser Thr Asp Val Asp Ala Thr Trp Gln Trp Lys Asn Phe  
180 185 190

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

Trp Ala Thr Ala Arg Glu Val Thr Leu Lys Thr Phe Ala Glu Asp Asn  
210 215 220

Ser Ala Ser Val Gln Ala Thr Met Tyr Lys Met Ala Glu Gln Ile Leu  
225 230 235 240

Ala Arg Gln Gln Leu Ile Glu Thr Val Glu Tyr Ser Leu Pro Asn Lys  
245 250 255

His Tyr Phe Glu Ile Asp Leu Ser Trp His Lys Gly Leu Gln Asn Thr  
260 265 270

Gly Lys Asn Ala Glu Val Phe Ala Pro Gln Ser Asp Pro Asn Gly Leu  
275 280 285

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Ile Lys Cys Thr Val Gly Arg Ser Ser Leu Lys Ser Lys Leu  
 290 295 300

<210> 3  
 <211> 302  
 <212> PRT  
 <213> *Arthrobacter globiformis*

<400> 3

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

Gln Asn Gln Tyr Gly Lys Ala Glu Val Arg Leu Val Lys Val Thr Arg  
 20 25 30

Asn Thr Ala Arg His Glu Ile Gln Asp Leu Asn Val Thr Ser Gln Leu  
 35 40 45

Arg Gly Asp Phe Glu Ala Ala His Thr Ala Gly Asp Asn Ala His Val  
 50 55 60

Val Ala Thr Asp Thr Gln Lys Asn Thr Val Tyr Ala Phe Ala Arg Asp  
 65 70 75 80

Gly Phe Ala Thr Thr Glu Glu Phe Leu Leu Arg Leu Gly Lys His Phe  
 85 90 95

Thr Glu Gly Phe Asp Trp Val Thr Gly Gly Arg Trp Ala Ala Gln Gln  
 100 105 110

Phe Phe Trp Asp Arg Ile Asn Asp His Asp His Ala Phe Ser Arg Asn  
 115 120 125

Lys Ser Glu Val Arg Thr Ala Val Leu Glu Ile Ser Gly Ser Glu Gln  
 130 135 140

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

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 145 |     | 150 |     | 155 |     | 160 |     |     |     |     |     |     |     |     |     |
| Ser | Glu | Phe | His | Gly | Phe | Pro | Arg | Asp | Lys | Tyr | Thr | Thr | Leu | Gln | Glu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Thr | Thr | Asp | Arg | Ile | Leu | Ala | Thr | Asp | Val | Ser | Ala | Arg | Trp | Arg | Tyr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asn | Thr | Val | Glu | Val | Asp | Phe | Asp | Ala | Val | Tyr | Ala | Ser | Val | Arg | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Leu | Leu | Lys | Ala | Phe | Ala | Glu | Thr | His | Ser | Leu | Ala | Leu | Gln | Gln |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Thr | Met | Tyr | Glu | Met | Gly | Arg | Ala | Val | Ile | Glu | Thr | His | Pro | Glu | Ile |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Asp | Glu | Ile | Lys | Met | Ser | Leu | Pro | Asn | Lys | His | His | Phe | Leu | Val | Asp |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Leu | Gln | Pro | Phe | Gly | Gln | Asp | Asn | Pro | Asn | Glu | Val | Phe | Tyr | Ala | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asp | Arg | Pro | Tyr | Gly | Leu | Ile | Glu | Ala | Thr | Ile | Gln | Arg | Glu | Gly | Ser |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Arg | Ala | Asp | His | Pro | Ile | Trp | Ser | Asn | Ile | Ala | Gly | Phe | Cys |     |     |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |

<210> 4  
 <211> 304  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic construct / Chimeric porcine / baboon

<400> 4

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | His | Tyr | Arg | Asn | Asp | Tyr | Lys | Lys | Asn | Asp | Glu | Val | Glu | Phe | 1   | 5   | 10  | 15  |
| Val | Arg | Thr | Gly | Tyr | Gly | Lys | Asp | Met | Ile | Lys | Val | Leu | His | Ile | Gln | 20  | 25  | 30  |     |
| Arg | Asp | Gly | Lys | Tyr | His | Ser | Ile | Lys | Glu | Val | Ala | Thr | Ser | Val | Gln | 35  | 40  | 45  |     |
| Leu | Thr | Leu | Ser | Ser | Lys | Lys | Asp | Tyr | Leu | His | Gly | Asp | Asn | Ser | Asp | 50  | 55  | 60  |     |
| Val | Ile | Pro | Thr | Asp | Thr | Ile | Lys | Asn | Thr | Val | Asn | Val | Leu | Ala | Lys | 65  | 70  | 75  | 80  |
| Phe | Lys | Gly | Ile | Lys | Ser | Ile | Glu | Thr | Phe | Ala | Val | Thr | Ile | Cys | Glu | 85  | 90  | 95  |     |
| His | Phe | Leu | Ser | Ser | Phe | Lys | His | Val | Ile | Arg | Ala | Gln | Val | Tyr | Val | 100 | 105 | 110 |     |
| Glu | Glu | Val | Pro | Trp | Lys | Arg | Phe | Glu | Lys | Asn | Gly | Val | Lys | His | Val | 115 | 120 | 125 |     |
| His | Ala | Phe | Ile | Tyr | Thr | Pro | Thr | Gly | Thr | His | Phe | Cys | Glu | Val | Glu | 130 | 135 | 140 |     |
| Gln | Ile | Arg | Asn | Gly | Pro | Pro | Val | Ile | His | Ser | Gly | Ile | Lys | Asp | Leu | 145 | 150 | 155 | 160 |
| Lys | Val | Leu | Lys | Thr | Thr | Gln | Ser | Gly | Phe | Glu | Gly | Phe | Ile | Lys | Asp | 165 | 170 | 175 |     |
| Gln | Phe | Thr | Thr | Leu | Pro | Glu | Val | Lys | Asp | Arg | Cys | Phe | Ala | Thr | Gln | 180 | 185 | 190 |     |

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Val Tyr Cys Lys Trp Arg Tyr His Gln Gly Arg Asp Val Asp Phe Glu  
195 200 205

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

Pro Tyr Asp Lys Gly Glu Tyr Ser Pro Ser Val Gln Lys Thr Leu Tyr  
225 230 235 240

Asp Ile Gln Val Leu Ser Leu Ser Arg Val Pro Glu Ile Glu Asp Met  
245 250 255

Glu Ile Ser Leu Pro Asn Ile His Tyr Phe Asn Ile Asp Met Ser Lys  
260 265 270

Met Gly Leu Ile Asn Lys Glu Glu Val Leu Leu Pro Leu Asp Asn Pro  
275 280 285

Tyr Gly Lys Ile Thr Gly Thr Val Lys Arg Lys Leu Ser Ser Arg Leu  
290 295 300

<210> 5  
<211> 296  
<212> PRT  
<213> Schizosaccharomyces pombe

<400> 5

Met Ser Glu Thr Thr Tyr Val Lys Gln Cys Ala Tyr Gly Lys Thr Leu  
1 5 10 15

Val Arg Phe Met Lys Lys Asp Ile Cys Pro Lys Thr Lys Thr His Thr  
20 25 30

Val Tyr Glu Met Asp Val Gln Ser Leu Leu Thr Gly Glu Leu Glu Glu  
35 40 45

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

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Ile Asn Thr Tyr Pro Ala Ile Asn Glu Val Tyr Tyr Ala Leu Pro Asn  
245 250 255

Lys His Tyr Phe Glu Ile Asn Leu Ala Pro Phe Asn Ile Asp Asn Leu  
260 265 270

Gly Ser Asn Cys Ser Leu Tyr Gln Pro Gln Ala Tyr Pro Ser Gly Tyr  
275 280 285

Ile Thr Cys Thr Val Ala Arg Lys  
290 295

<210> 6

<211> 494

<212> PRT

<213> Bacillus subtilis

<400> 6

Met Phe Thr Met Asp Asp Leu Asn Gln Met Asp Thr Gln Thr Leu Thr  
1 5 10 15

Asp Thr Leu Gly Ser Ile Phe Glu His Ser Ser Trp Ile Ala Glu Arg  
20 25 30

Ser Ala Ala Leu Arg Pro Phe Ser Ser Leu Ser Asp Leu His Arg Lys  
35 40 45

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

Ile Lys Lys His Pro Arg Leu Gly Thr Lys Lys Thr Met Ser Gly Asp  
65 70 75 80

Ser Val Arg Glu Gln Gln Asn Ala Gly Leu Ser Lys Leu Glu Gln Gln  
85 90 95

Glu Tyr Glu Glu Phe Leu Met Leu Asn Glu His Tyr Tyr Asp Arg Phe

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100

105

110

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

His Gln Ala Leu Leu Ala Arg Leu Glu Ser Glu Arg Glu Thr Glu Phe  
130 135 140

Gln Gln Ala Leu Ile Glu Ile Tyr Arg Ile Ala Arg Phe Arg Leu Ala  
145 150 155 160

Asp Ile Ile Thr Glu Lys Gly Glu Thr Gln Met Lys Arg Thr Met Ser  
165 170 175

Tyr Gly Lys Gly Asn Val Phe Ala Tyr Arg Thr Phe Leu Lys Pro Leu  
180 185 190

Thr Gly Val Lys Gln Ile Pro Glu Ser Ser Phe Ala Gly Arg Ser Asn  
195 200 205

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

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

Ser Met Lys Asn Phe Ile Gln Arg His Leu Ala Ser Tyr Glu Gly Thr  
245 250 255

Thr Thr Glu Gly Phe Leu His Tyr Val Ala His Arg Phe Leu Asp Thr  
260 265 270

Tyr Ser His Met Asp Lys Ile Thr Leu Thr Gly Glu Asp Ile Pro Phe  
275 280 285

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

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290

295

300

Val Phe Arg Arg Ser Arg Asn Glu Arg Ser Arg Ser Val Leu Lys Ala  
305 310 315 320

Glu Arg Ser Gly Asn Thr Ile Thr Ile Thr Glu Gln Tyr Ser Glu Ile  
325 330 335

Met Asp Leu Gln Leu Val Lys Val Ser Gly Asn Ser Phe Val Gly Phe  
340 345 350

Ile Arg Asp Glu Tyr Thr Thr Leu Pro Glu Asp Gly Asn Arg Pro Leu  
355 360 365

Phe Val Tyr Leu Asn Ile Ser Trp Gln Tyr Glu Asn Thr Asn Asp Ala  
370 375 380

Tyr Ala Phe Asp Pro Ser Arg Tyr Val Ala Ala Glu Gln Val Arg Asp  
385 390 395 400

Leu Ala Ser Thr Val Phe His Glu Leu Glu Thr Pro Ser Ile Gln Asn  
405 410 415

Leu Ile Tyr His Ile Gly Cys Arg Ile Leu Ala Arg Phe Pro Gln Leu  
420 425 430

Thr Asp Val Ser Phe Gln Ser Gln Asn His Thr Trp Asp Thr Val Val  
435 440 445

Glu Glu Ile Pro Gly Ser Lys Gly Lys Val Tyr Thr Glu Pro Arg Pro  
450 455 460

Pro Tyr Gly Phe Gln His Phe Thr Val Thr Arg Glu Asp Ala Glu Lys  
465 470 475 480

Glu Lys Gln Lys Thr Ala Glu Lys Cys Arg Ser Leu Lys Ala

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485

490

<210> 7  
<211> 305  
<212> PRT  
<213> Unknown

<220>  
<223> Zygosaccharomyces parabailii

<400> 7

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1 5 10 15

Leu Lys Val Lys Lys Asp Pro Ser Asn Pro Lys Leu Gln Gln Val Met  
20 25 30

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

Thr Glu Ala Asp Asn Ser Pro Ile Val Pro Thr Asp Thr Val Lys Asn  
50 55 60

Thr Ile Leu Ile Leu Ala Arg Gln Asn Asp Thr Trp Pro Thr Glu Lys  
65 70 75 80

Phe Ala Ala Lys Leu Ala Leu His Phe Thr Gly Lys Tyr Ser His Val  
85 90 95

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

Val Asp Gly Arg Pro Ser Gln His Ser Phe Val His Gln Gly Pro Glu  
115 120 125

Lys Lys Ile Val Glu Leu Glu Tyr Asp Lys Val Asn Gly Pro Thr His  
130 135 140

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Tyr Lys Leu Ser Thr Ser Ile Lys Asp Leu Thr Val Leu Lys Ser Thr  
145 150 155 160

Asn Ser Met Phe Tyr Asp Tyr Asn Val Cys Glu Tyr Thr Thr Leu Lys  
165 170 175

Pro Thr Thr Asp Arg Val Leu Ser Thr Asp Ile Phe Ala Val Trp Asp  
180 185 190

Trp Ser Ala Ser Lys Leu Gly Pro Leu Thr Ala Ile Ala Ala Gly Ala  
195 200 205

Ser Asp Leu Val Phe Asp Lys Val Phe Asn Asp Ala Arg Asp Ile Thr  
210 215 220

Leu Asp Ile Phe Ala Lys Glu Asn Ser Val Ser Val Gln Ala Thr Met  
225 230 235 240

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

Val Ser Tyr Glu Leu Pro Asn Lys His Tyr Ile Leu Phe Asp Leu Lys  
260 265 270

Trp Phe Gln Gly Leu Ser Asn Asp Asn Glu Leu Phe Tyr Pro Ser Pro  
275 280 285

His Pro Asn Gly Leu Ile Arg Cys Lys Val Gly Arg Lys Thr Ser Lys  
290 295 300

Leu  
305

<210> 8  
<211> 281  
<212> PRT

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<213> Unknown

<220>

<223> Spirosoma sp. KCTC 42546

<400> 8

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

Leu Ser Lys Ile Ile Arg His Pro Asn Tyr His Glu Phe Arg Gln Ile  
20 25 30

Ser Val Asn Val Ser Leu Glu Gly Asp Phe Glu Thr Ala His Thr Leu  
35 40 45

Gly Asp Asn Ser Lys Ile Val Pro Thr Asp Thr Gln Lys Asn Thr Val  
50 55 60

Tyr Ala Leu Ala Lys Glu His Phe Val Asp Ser Ile Glu Asn Phe Gly  
65 70 75 80

Leu Tyr Leu Ala Asn Tyr Phe Ile Thr Asn Asn Pro Gln Val Ser Gln  
85 90 95

Ala Thr Val His Ile Ile Glu His Pro Trp Ala Arg Met Ala Phe Asp  
100 105 110

Gly Glu Pro His His His Ala Tyr Val Gly Gly Gly Ser Glu Lys Arg  
115 120 125

Thr Thr Thr Leu Val Gln Thr Thr Glu Ala Ile Arg Val Thr Ser Gly  
130 135 140

Ile Lys Asp Leu Leu Ile Leu Lys Thr Thr Asp Ser Gly Phe Glu Gly  
145 150 155 160

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

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165

170

175

Phe Ala Thr Gln Cys Glu Ala Asn Trp Val Tyr Thr Ser His Asn Leu  
180 185 190

Asp Phe Thr Ser Leu Phe Gly Lys Ile Arg Glu Thr Leu Leu Lys Thr  
195 200 205

Phe Ala His His Lys Ser Leu Ser Val Gln Gln Thr Leu Leu Ala Met  
210 215 220

Gly Ser Ala Val Leu Glu Glu Asn Gln Glu Val Ser Glu Ile Ser Leu  
225 230 235 240

Ile Met Pro Asn Lys His His Ile Pro Phe Asn Leu Glu Gln Phe Gly  
245 250 255

Met Asp Asn Gln Asn Glu Ile Phe Ile Ala Thr Asp Glu Pro Tyr Gly  
260 265 270

Tyr Ile Thr Gly Thr Val Thr Arg Glu  
275 280

<210> 9

<211> 574

<212> PRT

<213> Unknown

<220>

<223> Aspergillus nidulans

<400> 9

Met Asp Asn Ser Ile His Ser Thr Asp Gly Pro Asp Ser Val Ile Pro  
1 5 10 15

Asn Ser Asn Pro Lys Lys Thr Val Arg Gln Arg Val Arg Leu Leu Ala  
20 25 30

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

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Pro Thr Val Met Leu Ile Gly Ile Ser Leu Ile Gly Thr Gly Phe Lys  
225 230 235 240

Asp Trp Ala Gly Gly Ser Ala Cys Met Asp Asp Gly Met Leu Cys Pro  
245 250 255

Ser Ala Thr Ala Pro Arg Pro Leu Pro Trp Gly Ser Pro Glu Phe Ile  
260 265 270

Gly Leu Gly Phe Leu Val Phe Val Ser Ile Ile Leu Cys Glu Arg Phe  
275 280 285

Gly Ala Pro Ile Met Lys Ser Cys Ser Val Val Ile Gly Leu Leu Val  
290 295 300

Gly Cys Ile Val Ala Ala Ala Cys Gly Tyr Phe Ser His Ala Asp Ile  
305 310 315 320

Asp Ala Ala Pro Ala Ala Ser Phe Ile Trp Val Lys Thr Phe Pro Leu  
325 330 335

Ser Val Tyr Gly Pro Met Val Leu Pro Ile Ile Ala Val Phe Ile Ile  
340 345 350

Cys Ala Cys Glu Cys Ile Gly Asp Val Thr Ala Thr Cys Asp Val Ser  
355 360 365

Arg Leu Glu Val Arg Gly Gly Thr Phe Glu Ser Arg Ile Gln Gly Ala  
370 375 380

Val Leu Ala Asp Gly Ile Asn Ser Val Val Ala Ala Leu Ala Thr Met  
385 390 395 400

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

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Arg Cys Ala Asn Arg Trp Ala Gly Tyr Cys Cys Cys Leu Ile Leu Ile  
420 425 430

Val Ala Gly Ile Phe Ala Lys Phe Ala Ala Ala Ile Val Ala Ile Pro  
435 440 445

Asn Ser Val Met Gly Gly Met Lys Thr Phe Leu Phe Ala Ser Val Val  
450 455 460

Ile Ser Gly Gln Ala Ile Val Ala Lys Ala Pro Phe Thr Arg Arg Asn  
465 470 475 480

Arg Phe Ile Leu Thr Ala Ser Met Ala Leu Gly Tyr Gly Ala Thr Leu  
485 490 495

Val Pro Thr Trp Phe Gly Asn Val Phe Pro Gln Thr Glu Asn Arg Asp  
500 505 510

Leu Glu Gly Phe Glu Asn Ala Ile Glu Leu Val Leu Glu Thr Gly Phe  
515 520 525

Ala Val Thr Ala Phe Val Ala Met Leu Leu Asn Ala Ile Met Pro Ala  
530 535 540

Glu Val Glu Glu Ile Gly Ala Val Thr Pro Met Pro Val Ser Ala His  
545 550 555 560

Asp Asn Arg Asp Gly Glu Ala Glu Tyr Gln Ser Lys Gln Ala  
565 570

<210> 10

<211> 580

<212> PRT

<213> Unknown

<220>

<223> Aspergillus nidulans

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<400> 10

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

Phe Gly Asp Arg Val Arg Arg Ala Ala Arg Ala Phe Thr Thr Arg Asp  
20 25 30

Gly Leu Ile Gly Asp Tyr Asp Tyr Gly Phe Leu Phe Thr Pro Arg Leu  
35 40 45

Pro Phe Val Lys Gln Lys Arg Arg Ala Ala Pro Phe Phe Gly Leu Glu  
50 55 60

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

Leu Ala Met Leu Ala Gly Val Ile Thr Pro Pro Ile Leu Leu Ala Gly  
85 90 95

Ser Ser Gly Ala Asn Phe Gly Ala Asp Glu Ser Gln Tyr Leu Val Ser  
100 105 110

Thr Ser Leu Ile Val Ser Gly Leu Leu Ser Ala Val Gln Met Phe Arg  
115 120 125

Leu His Val Tyr Lys Thr Arg Tyr Tyr Val Gly Thr Gly Leu Val Ser  
130 135 140

Val Val Gly Thr Ser Phe Ala Thr Ile Thr Val Ala Thr Gly Thr Phe  
145 150 155 160

Asn Gln Met Tyr Ser Thr Gly Tyr Cys Pro Val Asp Gly Ser Gly Asn  
165 170 175

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

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180

185

190

Leu Cys Ser Leu Leu Glu Ile Gly Leu Ser Phe Met Ser Ser Arg Leu  
195 200 205

Leu Lys Ala Leu Phe Pro Pro Ile Val Thr Gly Pro Thr Val Phe Leu  
210 215 220

Ile Gly Ala Ser Leu Ile Gly Asn Ala Met Lys Asp Trp Ala Gly Gly  
225 230 235 240

Ser Gly Thr Cys Ser Ser Asn Pro Gly Asn Gly Ala Leu Cys Pro Ser  
245 250 255

Ala Asp Ala Pro His Pro Leu Pro Trp Gly Ser Ala Glu Phe Ile Gly  
260 265 270

Leu Gly Phe Leu Val Phe Ala Thr Ile Ile Leu Cys Glu Arg Phe Gly  
275 280 285

Ser Pro Ile Met Lys Ser Cys Ala Val Ile Val Gly Leu Leu Val Gly  
290 295 300

Cys Ile Val Ala Ala Ala Cys Gly Tyr Phe Asp Arg Ser Gly Ile Asp  
305 310 315 320

Ala Ala Pro Val Ala Ser Phe Ile Trp Val Lys Thr Phe Pro Leu Thr  
325 330 335

Ile Tyr Ala Pro Leu Ile Leu Pro Leu Leu Ala Val Tyr Met Val Ile  
340 345 350

Met Met Glu Ser Ile Gly Asp Ile Thr Ala Thr Cys Asp Val Ser Arg  
355 360 365

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

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370

375

380

Leu Gly Asn Gly Ile Thr Cys Leu Leu Ala Gly Leu Cys Thr Ile Thr  
385 390 395 400

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

Cys Ala Asn Arg Lys Ala Gly Tyr Cys Cys Cys Phe Phe Leu Val Val  
420 425 430

Met Gly Ile Phe Ala Lys Phe Ala Ala Ala Leu Val Ala Ile Pro Ser  
435 440 445

Ser Val Leu Gly Gly Met Thr Thr Phe Leu Phe Ser Ser Val Ala Ile  
450 455 460

Ser Gly Val Arg Ile Met Cys Ser Val Asp Trp Thr Arg Arg Asn Arg  
465 470 475 480

Phe Ile Leu Thr Ala Ser Phe Ala Val Gly Met Ala Ala Thr Leu Val  
485 490 495

Pro Asp Trp Phe Ser Tyr Phe Phe Thr Tyr Ser Gly Asp Asn His Ala  
500 505 510

Leu Glu Gly Leu Leu Gln Ala Val Glu Leu Val Met Ala Asn Gly Phe  
515 520 525

Ala Val Thr Gly Phe Leu Gly Leu Leu Leu Asn Leu Ile Leu Pro Glu  
530 535 540

Asp Met Glu Glu Asp Val Val Glu Ser Glu Glu Asp Tyr Glu Ala Thr  
545 550 555 560

Thr Val Val Gly Met Gln Gly Gly Ser Glu Pro Gly Ser Ser Gly Gln

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565

570

575

Asn Val Lys Ala  
580

<210> 11

<211> 583

<212> PRT

<213> Unknown

<220>

<223> *Aspergillus fumigatus*

<400> 11

Met Asp Gly Pro Asp Arg Ile Gly Pro Asp His Ser Pro Arg Arg Thr  
1 5 10 15

Leu Arg Asp Lys Ala Arg Arg Leu Val Lys Thr Trp Thr Thr Lys Glu  
20 25 30

Gly Leu Val Gly Asp Tyr Asn Tyr Ala Tyr Leu Phe Thr Pro Arg Ile  
35 40 45

Pro Phe Thr Lys Asn Ile Arg Arg Thr Ala Pro Phe Phe Gly Leu His  
50 55 60

Asp Arg Leu Pro Val Leu Leu Ala Phe Ile Leu Gly Leu Gln His Ala  
65 70 75 80

Leu Ala Met Leu Ala Gly Val Ile Ser Pro Pro Ile Ile Leu Gly Gly  
85 90 95

Ser Ser Gly Ala Asn Phe Gly Asp Ala Glu Tyr Gln Tyr Leu Val Ser  
100 105 110

Thr Ser Leu Ile Ala Ser Gly Leu Leu Ser Ala Val Gln Met Ala Arg  
115 120 125

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Leu Arg Ile Trp Lys Thr Arg Tyr Phe Ile Gly Thr Gly Leu Ile Ser  
130 135 140

Val Val Gly Thr Ser Phe Ser Thr Ile Thr Val Ala Ser Gly Thr Phe  
145 150 155 160

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

Arg Leu Pro Cys Pro Arg Gly Tyr Gly Ala Ile Leu Gly Thr Ala Cys  
180 185 190

Leu Cys Ser Leu Leu Thr Ile Gly Leu Ser Phe Met Ser Pro Arg Ile  
195 200 205

Leu Lys Arg Ile Phe Pro Pro Met Val Thr Gly Pro Thr Val Leu Leu  
210 215 220

Ile Gly Ala Ser Leu Ile Glu Ser Gly Met Lys Asp Trp Ala Gly Gly  
225 230 235 240

Ser Gly Cys Gly Ser Asp Pro Ser Ala Arg Ala Leu Cys Pro Ser Ala  
245 250 255

Gly Ala Pro His Ala Leu Pro Trp Gly Ser Ala Glu Phe Ile Gly Leu  
260 265 270

Gly Phe Leu Val Phe Val Thr Ile Ile Leu Cys Glu Arg Phe Gly Ser  
275 280 285

Pro Ile Met Lys Ser Cys Ala Val Val Val Gly Leu Leu Val Gly Cys  
290 295 300

Ile Val Ala Ala Ala Cys Gly Tyr Phe Asp Arg Ser Gly Ile Asp Ser  
305 310 315 320

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Ala Pro Val Val Ser Phe Ile Trp Val Lys Thr Phe Pro Leu Thr Ile  
325 330 335

Tyr Ala Pro Leu Ile Leu Pro Phe Leu Ala Leu Tyr Ile Val Ile Met  
340 345 350

Met Glu Ser Ile Gly Asp Ile Thr Ala Thr Cys Asp Val Ser Gln Leu  
355 360 365

Glu Val Glu Gly Ala Asp Phe Asp Ser Arg Val Gln Gly Gly Val Leu  
370 375 380

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

Met Ser Val Phe Ala Gln Asn Asn Gly Val Ile Ala Leu Thr Lys Cys  
405 410 415

Ala Asn Arg Lys Ala Gly Tyr Cys Cys Cys Phe Phe Leu Val Val Met  
420 425 430

Gly Val Phe Ala Lys Phe Ala Ala Ala Ile Val Ala Ile Pro Lys Pro  
435 440 445

Val Leu Gly Gly Met Thr Thr Phe Leu Phe Ser Ser Val Ala Ile Ser  
450 455 460

Gly Ile Arg Ile Ile Ser Thr Ile Pro Phe Thr Arg Arg Asn Arg Phe  
465 470 475 480

Ile Leu Thr Ala Ser Phe Ala Val Gly Met Ala Ala Thr Leu Val Pro  
485 490 495

Asp Trp Phe Ser Tyr Phe Phe Thr Tyr Ser Gly Asp Asn His Ala Leu  
500 505 510

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Glu Gly Leu Leu Asn Ala Val Glu Leu Val Met Glu Asn Gly Phe Ala  
515 520 525

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

Pro Glu Asp Glu Ala Ala Ile Val Glu Ala Thr Ala Arg Asp Ala Pro  
545 550 555 560

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

Pro Ser Gly Ser Leu Ala Val  
580

<210> 12  
<211> 591  
<212> PRT  
<213> Candida albicans

<400> 12

Met Ser Ala Ile Gln Lys Thr Leu Lys Arg Met Val Arg Lys Trp Thr  
1 5 10 15

Thr Lys Asp Gly Leu Leu Gly Asp Tyr Asp Tyr Lys Tyr Leu Phe Thr  
20 25 30

Pro Asp Ile Pro Phe Ile Thr Lys Glu Leu Lys Thr Gln Pro Phe Phe  
35 40 45

Gly Val Asp Thr Asp Met Pro Ile Leu Leu Gly Ala Ile Leu Gly Phe  
50 55 60

Gln His Ala Leu Ala Met Leu Ala Gly Ile Val Thr Val Pro Ile Met  
65 70 75 80

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

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Ser Cys Ala Val Ile Phe Gly Leu Leu Ile Gly Cys Ile Val Ala Ala  
275 280 285

Ala Ala Gly Tyr Phe Ser Ser Asp Asn Val Asp Ala Ala Pro Ala Ala  
290 295 300

Ser Phe Met Trp Val His Thr Phe Lys Leu Thr Val Tyr Gly Pro Val  
305 310 315 320

Val Leu Pro Phe Leu Ala Val Tyr Ile Val Leu Met Met Glu Cys Ile  
325 330 335

Gly Asp Val Thr Ala Thr Ser Asp Val Ser Arg Leu Pro Val Ser Gly  
340 345 350

Glu Met Tyr Glu Ser Arg Ile Gln Gly Gly Val Leu Gly Asp Gly Ile  
355 360 365

Cys Gly Ile Leu Ser Thr Leu Met Thr Met Thr Pro Met Ser Val Phe  
370 375 380

Ala Gln Asn Asn Gly Val Ile Ser Ile Thr Lys Cys Ala Asn Arg Lys  
385 390 395 400

Val Gly Tyr Trp Cys Ala Phe Phe Leu Ile Val Met Gly Val Phe Ala  
405 410 415

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

Met Thr Ser Phe Leu Phe Cys Ser Val Ala Ile Ser Gly Ile Lys Ile  
435 440 445

Ile Ser Thr Thr Glu Phe Thr Arg Arg Asp Arg Phe Val Leu Thr Ala  
450 455 460

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Ala Val Ser Pro Gly Leu Gly Ala Thr Met Leu Pro Asn Trp Phe Glu  
465 470 475 480

His Val Phe Thr Tyr Gln Gly Gly Asn Lys Ser Leu Lys Gly Phe Phe  
485 490 495

Asn Ala Ile Ile Val Val Val Glu Ser Gly Phe Cys Leu Ser Gly Val  
500 505 510

Ile Ala Val Ile Leu Asn Leu Leu Ile Pro Gln Val Glu Asp Asp Val  
515 520 525

Glu Glu Ile Asn Glu Leu Val Leu Asp Val Val Gly Ser Ala Thr Glu  
530 535 540

Ser Ala Arg Gln Lys Phe Glu Glu Lys Glu Gly Val Lys Leu Glu Ala  
545 550 555 560

Leu Arg Ser Gln Leu Ser Asn Ile Lys Ser Asn Gly Gly Ser Arg Asp  
565 570 575

Ala Ile Thr Val Leu His Arg Asn Asp Gly Phe Pro Asp Leu Lys  
580 585 590

<210> 13  
<211> 601  
<212> PRT  
<213> Schizosaccharomyces pombe

<400> 13

Met Ser Glu Ser Ile Gln Asp Gln Asp His Glu Lys Thr Thr Ile Ile  
1 5 10 15

Glu Lys Thr Arg Arg Phe Val Leu Ser Ile Phe Thr Lys Asp Phe Trp  
20 25 30

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

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35

40

45

Lys Gln Lys Pro Lys Ser Pro Pro Phe Phe Ser Leu Asn Ala Lys Val  
50 55 60

Pro Val Leu Leu Ala Leu Leu Gly Phe Gln His Ala Leu Ala Met  
65 70 75 80

Val Gly Gly Val Thr Ser Pro Pro Arg Ile Ile Ala Ala Ser Ala Asn  
85 90 95

Leu Thr Thr Glu Gln Thr Asn Tyr Leu Val Ser Ala Gly Leu Ile Ser  
100 105 110

Ser Gly Ile Met Thr Leu Ile Gln Ile Ala Arg Val His Ile Pro Lys  
115 120 125

Thr Lys Tyr Tyr Ile Gly Thr Gly Met Leu Ser Val Leu Gly Ile Ser  
130 135 140

Phe Thr Ser Val Ser Val Ala Pro Lys Val Leu Ser Gln Met Tyr Glu  
145 150 155 160

Asn Gly Tyr Cys Pro Lys Asp Glu Asn Gly Thr Lys Leu Pro Cys Pro  
165 170 175

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

Glu Ile Phe Met Ser Phe Ile Pro Pro Arg Ile Leu Lys Arg Leu Phe  
195 200 205

Pro Pro Ile Val Thr Gly Pro Val Val Leu Leu Ile Gly Thr Ser Leu  
210 215 220

Ile Ser Ser Gly Leu Asn Asp Trp Ala Gly Gly Glu Gly Ser Cys Thr

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

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420

425

430

Met Gly Leu Phe Ala Lys Phe Ala Ala Val Phe Val Ala Ile Pro Ser  
435 440 445

Pro Val Leu Gly Gly Met Thr Thr Phe Leu Phe Ser Ser Val Ala Val  
450 455 460

Ser Gly Ile Ala Ile Ile Ser Gln Ile Pro Phe Asn Arg Arg Asn Arg  
465 470 475 480

Phe Ile Leu Thr Ala Ser Met Thr Leu Gly Met Gly Ala Ile Leu Val  
485 490 495

Pro Asp Trp Phe Thr Tyr Phe Phe Glu Tyr Ser Gly Pro Asn Lys Ala  
500 505 510

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

Ala Ile Gly Ala Phe Ile Ser Ile Phe Leu Asn Leu Ile Leu Pro Tyr  
530 535 540

Glu Phe Asp Pro Asp Leu Thr Asn Asp Ser Pro Gly Leu Ser Thr Thr  
545 550 555 560

Asn Gly Val Asn Asn Gly Ile Val Glu Val Arg Gly Ile Asp Pro Asn  
565 570 575

Asp Ser Leu Ser Asn Thr Asp Thr Glu Tyr Ala Asn Glu Asn Lys Lys  
580 585 590

Asp Glu Val Asp Val Asp Lys Val Val  
595 600

<210> 14

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<211> 430

<212> PRT

<213> Bacillus subtilis

<400> 14

Met Lys Glu Gln His Asn Ala Leu Gln Leu Met Met Leu Gly Leu Gln  
1 5 10 15

His Met Leu Ala Met Tyr Ala Gly Ala Ile Leu Val Pro Leu Ile Val  
20 25 30

Gly Ala Ala Ile Gly Leu Asn Ala Gly Gln Leu Thr Tyr Leu Ile Ala  
35 40 45

Ile Asp Leu Phe Met Cys Gly Ala Ala Thr Leu Leu Gln Leu Trp Arg  
50 55 60

Asn Arg Tyr Phe Gly Ile Gly Leu Pro Val Val Leu Gly Cys Thr Phe  
65 70 75 80

Thr Ala Val Gly Pro Met Ile Ser Ile Gly Ser Thr Tyr Gly Val Pro  
85 90 95

Ala Ile Tyr Gly Ala Ile Ile Ala Ala Gly Leu Ile Val Val Leu Ala  
100 105 110

Ala Gly Phe Phe Gly Lys Leu Val Arg Phe Phe Pro Pro Val Val Thr  
115 120 125

Gly Ser Val Val Met Ile Ile Gly Ile Ser Leu Ile Pro Thr Ala Met  
130 135 140

Asn Asn Leu Ala Gly Gly Glu Gly Ser Lys Glu Phe Gly Ser Leu Asp  
145 150 155 160

Asn Val Leu Leu Gly Phe Gly Val Thr Ala Phe Ile Leu Leu Leu Phe  
165 170 175

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Tyr Phe Phe Lys Gly Phe Ile Arg Ser Ile Ala Ile Leu Leu Gly Leu  
180 185 190

Ile Ala Gly Thr Ala Ala Ala Tyr Phe Met Gly Lys Val Asp Phe Ser  
195 200 205

Glu Val Leu Glu Ala Ser Trp Leu His Val Pro Ser Leu Phe Tyr Phe  
210 215 220

Gly Pro Pro Thr Phe Glu Leu Pro Ala Val Val Thr Met Leu Leu Val  
225 230 235 240

Ala Ile Val Ser Leu Val Glu Ser Thr Gly Val Tyr Phe Ala Leu Ala  
245 250 255

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

Arg Ala Glu Gly Leu Ala Ile Leu Leu Gly Gly Leu Phe Asn Ala Phe  
275 280 285

Pro Tyr Thr Ala Phe Ser Gln Asn Val Gly Ile Val Gln Leu Ser Lys  
290 295 300

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

Ile Gly Leu Val Pro Lys Ala Ala Ala Leu Thr Thr Val Ile Pro Thr  
325 330 335

Pro Val Leu Gly Gly Ala Met Ile Val Met Phe Gly Met Val Ile Ser  
340 345 350

Tyr Gly Ile Lys Met Leu Ser Ser Val Asp Leu Asp Ser Gln Gly Asn  
355 360 365

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Leu Leu Ile Ile Ala Ser Ser Val Ser Leu Gly Leu Gly Ala Thr Thr  
370 375 380

Val Pro Ala Leu Phe Ser Ser Leu Ser Gly Ala Ala Ser Val Leu Ala  
385 390 395 400

Gly Ser Gly Ile Val Ile Gly Ser Leu Thr Ala Ile Ala Leu His Ala  
405 410 415

Phe Phe Gln Thr Lys Gln Pro Asn Ser Ala Asp Ile Lys Thr  
420 425 430

<210> 15  
<211> 450  
<212> PRT  
<213> Bacillus subtilis

<400> 15

Met Val Lys Lys Arg Ser Phe Lys Val Phe Thr Leu Gly Leu Gln His  
1 5 10 15

Val Leu Ala Met Tyr Ala Gly Ala Ile Leu Val Pro Leu Leu Val Gly  
20 25 30

Arg Ala Leu Asn Val Thr Thr Glu Gln Leu Ser Tyr Leu Leu Ala Ile  
35 40 45

Asp Leu Leu Thr Cys Gly Val Ala Thr Leu Leu Gln Thr Leu Arg Gly  
50 55 60

Ala Tyr Ile Gly Ile Gly Leu Pro Val Met Leu Gly Ser Ser Phe Val  
65 70 75 80

Ala Val Thr Pro Met Ile Ala Ile Gly Ser Asn Tyr Gly Ile His Ala  
85 90 95

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Ile Tyr Gly Ser Ile Ile Ala Ala Gly Val Phe Ile Phe Leu Phe Ala  
100 105 110

Arg Phe Phe Gly Lys Leu Thr Val Leu Phe Pro Pro Val Val Thr Gly  
115 120 125

Thr Val Val Thr Leu Ile Gly Leu Ser Leu Val Pro Thr Gly Val Lys  
130 135 140

Asn Met Ala Gly Gly Glu Lys Ile Asn Gly Ser Ala Asn Pro Glu Tyr  
145 150 155 160

Gly Ser Leu Glu Asn Leu Leu Leu Ser Val Gly Val Leu Val Leu Ile  
165 170 175

Leu Val Leu Asn Arg Phe Leu Lys Gly Phe Ala Arg Thr Leu Ser Val  
180 185 190

Leu Ile Gly Ile Ala Ala Gly Thr Ala Ala Ala Ala Ile Met Gly Lys  
195 200 205

Val Ser Phe Ser Ser Val Thr Glu Ala Pro Phe Phe Gln Ile Pro Lys  
210 215 220

Pro Phe Tyr Phe Gly Ala Pro Thr Phe Glu Ile Gly Pro Ile Leu Thr  
225 230 235 240

Met Leu Ile Val Gly Ile Val Ile Ile Val Glu Ser Thr Gly Val Phe  
245 250 255

Tyr Ala Ile Gly Lys Ile Cys Gly Arg Pro Leu Thr Glu Lys Asp Leu  
260 265 270

Val Lys Gly Tyr Arg Ala Glu Gly Ile Ala Ile Leu Ile Gly Gly Leu  
275 280 285

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Phe Asn Ala Phe Pro Tyr Asn Thr Phe Ala Gln Asn Ala Gly Leu Leu  
290 295 300

Gln Leu Thr Lys Val Lys Thr Arg Asn Ile Val Val Thr Ala Gly Cys  
305 310 315 320

Ile Leu Val Cys Leu Gly Leu Ile Pro Lys Ile Ala Ala Leu Ala Ser  
325 330 335

Ala Val Pro Ala Ala Val Leu Gly Gly Ala Thr Val Val Met Phe Gly  
340 345 350

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

Asn Gln Tyr His Leu Leu Thr Ile Ala Cys Ser Ile Ala Leu Gly Ile  
370 375 380

Gly Ala Ser Thr Ala Pro Gly Ile Phe Ala Glu Phe Pro Ala Pro Ile  
385 390 395 400

Arg Ile Leu Val Ser Asp Gly Thr Ile Thr Gly Ser Leu Thr Ala Ile  
405 410 415

Phe Leu Asn Leu Phe Phe Ser Leu Arg Asp Lys Lys Glu Leu Thr Ala  
420 425 430

Gln Gln Thr Glu Leu Pro Val Leu Glu His Thr Leu Ala Leu Glu Lys  
435 440 445

Glu Val  
450

<210> 16  
<211> 525  
<212> PRT

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<213> Escherichia coli

<400> 16

Met Pro Pro Gln Phe Leu Ser Leu Thr Pro Leu Pro Arg Lys Asn Trp  
1 5 10 15

His Ser Thr Ser Met Cys Leu Asp Ser Phe Met Asn Ile Asn Gly Cys  
20 25 30

Phe Leu Leu Trp Arg Ala Lys Gly Glu Thr Leu Met Asn Ala Ile Asp  
35 40 45

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

Asp Arg Ile Leu Ser Pro Gly Lys Leu Ile Ile Leu Gly Leu Gln His  
65 70 75 80

Val Leu Val Met Tyr Ala Gly Ala Val Ala Val Pro Leu Met Ile Gly  
85 90 95

Asp Arg Leu Gly Leu Ser Lys Glu Ala Ile Ala Met Leu Ile Ser Ser  
100 105 110

Asp Leu Phe Cys Cys Gly Ile Val Thr Leu Leu Gln Cys Ile Gly Ile  
115 120 125

Gly Arg Phe Met Gly Ile Arg Leu Pro Val Ile Met Ser Val Thr Phe  
130 135 140

Ala Ala Val Thr Pro Met Ile Ala Ile Gly Met Asn Pro Asp Ile Gly  
145 150 155 160

Leu Leu Gly Ile Phe Gly Ala Thr Ile Ala Ala Gly Phe Ile Thr Thr  
165 170 175

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Leu Leu Ala Pro Leu Ile Gly Arg Leu Met Pro Leu Phe Pro Pro Leu  
180 185 190

Val Thr Gly Val Val Ile Thr Ser Ile Gly Leu Ser Ile Ile Gln Val  
195 200 205

Gly Ile Asp Trp Ala Ala Gly Gly Lys Gly Asn Pro Gln Tyr Gly Asn  
210 215 220

Pro Val Tyr Leu Gly Ile Ser Phe Ala Val Leu Ile Phe Ile Leu Leu  
225 230 235 240

Ile Thr Arg Tyr Ala Lys Gly Phe Met Ser Asn Val Ala Val Leu Leu  
245 250 255

Gly Ile Val Phe Gly Phe Leu Leu Ser Trp Met Met Asn Glu Val Asn  
260 265 270

Leu Ser Gly Leu His Asp Ala Ser Trp Phe Ala Ile Val Thr Pro Met  
275 280 285

Ser Phe Gly Met Pro Ile Phe Asp Pro Val Ser Ile Leu Thr Met Thr  
290 295 300

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Ser Phe Pro His Thr Ser Phe Ser Gln Asn Val Gly Leu Val Ser Val  
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Arg Tyr Asn Leu Tyr Ile Val Ala Ile Ser Leu Gly Val Gly Met Thr  
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Leu Asn Val Phe Phe Asn Gly Tyr Gln His His Ala Asp Leu Val Lys  
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Val Cys Gly Leu Thr Ala Ile Ile Leu Asn Leu Leu Ile Pro Gln Glu  
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Cys Leu Gly Leu Phe Pro Pro Val Gly Arg Trp Ile Thr Val Met Pro  
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Ser Cys Val Leu Gly Ala Leu Ala Ile Met Leu Phe Gly Leu Val Ala  
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Val Ser Gly Leu Arg Leu Met Val Ser Gly Gly Leu Ser Gln Arg Asp  
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Ala Leu Ile Ala Ala Ile Ser Leu Gly Val Gly Ile Gly Val Pro Ser  
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Gln Glu Glu Trp Leu Lys Thr Leu Pro Thr Val Val Gln Thr Phe Leu  
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| ataggtccat tctcttagcg caactacaca gaacaggggc acaaacaggc aaaaaacggg  | 360  |
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| ggaaaaagct gaaaaaaaaag gttgaaacca gttccctgaa attattcccc tatttgacta | 540  |
| ataagtatat aaagacggta ggtattgatt gtaattctgt aaatctattt cttaaacttc  | 600  |
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| ccttgcaacc aaccactgac agaatcttgt ccaccgacgt cgatgccacc tgggtttggg  | 1260 |
| ataacaagaa gattggcact gtctacgaca tcgccaaggc tgcagacaag gggatctttg  | 1320 |
| acaacgttta caaccaggct agagagatca ccttgaccac cttcgccctg gagaactctc  | 1380 |
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| atatcctact acaaaaaatc ataaatgaca ctgaattgga cacatgctag cgtcaaatac   | 7620 |
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| atactccgcc tcgccatccc gattatcatg agcagagacc ggcatagggg tgacggcacc   | 7740 |
| gatctcttcg acttcagcag gcatgattgc gttcaagagc atagcaacaa atgccgtgac   | 7800 |
| cgcaaacccc gtctcaagca cgagctcgat cgcattttca aaccctcca ggtctctatt    | 7860 |
| ctcggtctga gggaatacat tcccaaacca agtgggcacc agcgctcgccc cgtatcccag  | 7920 |
| ggccattgac gcggtgagga taaaccgatt tcgccttgtg aacggcgcct tggccacgat   | 7980 |
| cgctgttccg ctaataacga ccgaagcgaa gagaaacgtc ttcatcccgc ccatgacact   | 8040 |
| gttgggtatg gcaacaatgg ctgcagcgaa tttagcaaag ataccggcta ctatcaatat   | 8100 |
| cagacagcag cagtatccgg cccagcggtt tgcgcagcga gtgagggcaa tcacgccgtt   | 8160 |
| gttctgcgca aaggtcgtca tgggggtcat tgtcgcaagg gcagcgacta ccgagttgat   | 8220 |
| cccgtctgct aggacggcgc cctggatgcg cgactcgaat gtgccgccgc ggacttcgag   | 8280 |
| acgcgagacg tcgcaggtgg cggttacatc accgatgcac tcgcaggcgc agatgatgaa   | 8340 |
| aaccgcgatg atcgggagaa ccatcggacc atagacagag agagggaag tcttgacca     | 8400 |
| gatgaatgag gcggcagggg cagcgtcaat atcggcgtgg ctgaagtagc cgcaggctgc   | 8460 |
| agcgactata caaccgacga gcagcccgat gacaacagaa caggacttca taatcggggc   | 8520 |
| tccaaatcgt tcgcagagga tgatcgatac aaagactaga aaaccaggc cgatgaactc    | 8580 |
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|--------------------------------------------------------------------|------|
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| cacgaaagcg aggaggatct ccaccaaagc acagcaggcc gaggtgccaa tcaaggcgcc  | 8820 |
| gtacgcttcg gggcaaggga gtctgtttcc agcctcgtcg agttgacaga acccgttcga  | 8880 |
| gtacatctgg ttgaaggcgc cgctggcgac ggagatgatg gagaacgaga cccccataac  | 8940 |
| tgagaggacg ccactgccga tatagtacgg tgtctttag atagaaatc gcgttatctg    | 9000 |
| gaccatcgac agcagcccgc agacgataag cgaggtcgaa acgagatact gctggagatc  | 9060 |
| ggacggcagg ctcagcgagc ttgatatgat cagaggagga gtgaccacac ccgccaacat  | 9120 |
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| gcggactctc tgtcggacgg tcttcttggg gttggagttg gggatgacgg agtcggggcc  | 9360 |
| gtcggttgaa tggatggagt tgtccattgt tttatatattg ttgtaaaaag tagataatta | 9420 |
| cttccttgat gatctgtaaa aaagagaaaa agaaagcatc taagaacttg aaaaactaag  | 9480 |
| aattagaaaa gaccaaatat gtatttcttg cattgaccaa tttatgcaag tttatatata  | 9540 |
| tgtaaagtga agtttcacga ggttctacta aactaaacca ccccttggt tagaagaaaa   | 9600 |
| gagtgtgtga gaacaggctg ttgttgtcac acgattcgga caattctgtt tgaaagagag  | 9660 |
| agagtaacag tacgatcgaa cgaactttgc tctggagatc acagtgggca tcatagcatg  | 9720 |
| tggtactaaa ccctttcccg ccattccaga accttcgatt gcttgttaca aaacctgtga  | 9780 |
| gccgtcgcta ggaccttggt gtgtgacgaa attggaagct gcaatcaata ggaagacagg  | 9840 |
| aagtcgagcg tgtctgggtt ttttcagttt tgttcttttt gcaaacaaat cacgagcgac  | 9900 |
| ggtaatttct ttctcgataa gaggcggtac                                   | 9930 |

<210> 20

<211> 1272

1793449\_Seq\_list\_17Sep21

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct / Exemplary E. coli malE/K expression cassette

<400> 20

|                                                                   |      |
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| aaaagcaatt tttccggctg tctgtataca aaaacgccgc aaagtttgag cgaagtcaat | 180  |
| aaactctcta ccattcagg gcaatatctc tcttgatcc aaagtgaact ctagaaataa   | 240  |
| ttttgtttta ctttaagaag gagatataca tatgactgcc accgcagaaa cctcaaccgg | 300  |
| caccaaggtc gtgctcggac agaaccagta cggcaaggcc gaagtccgcc tcgtcaaggt | 360  |
| cacgcgcaat accgcccggc acgagatcca ggacctgaat gtcacctcgc agctgcgcgg | 420  |
| cgacttcgag gccgcacaca ccgccggcga caacgcgcac gtggtcgcca ccgacacgca | 480  |
| gaagaacacc gtctacgcct tcgcccgcga cggcttcgcc accaccgagg agttcctgct | 540  |
| ccggctgggc aaacacttca ccgagggcct cgactgggta accggcgggc gctgggcggc | 600  |
| gcagcagttc ttctgggacc gcatcaacga ccacgaccac gccttctccc ggaacaagag | 660  |
| cgaggtccgc accgccgtgc tcgagatctc gggcagcgag caggccatcg tcgccgggat | 720  |
| cgagggcctg acggtcctga agtccaccgg ttcggaattc cacggcttcc cgcgggacaa | 780  |
| gtacaccacc ctgcaggaaa ccaccgaccg tctcctcgcc acggatgtca gcgcccgctg | 840  |
| gcgctacaac accgtcgagg ttgacttcga cgccgtctac gcgagcgtcc gcgggctgct | 900  |
| gctcaaggcc ttcgccgaga cccactcgct ggccctgcag cagaccatgt atgagatggg | 960  |
| ccgggccgct atcgagacgc acccggaat cgacgaaatc aagatgtccc tgccgaacaa  | 1020 |
| gcaccatttc ctggtggacc tgcagccctt cggacaggac aaccggaatg aggtgttcta | 1080 |
| cgccgccgac cgtccctacg gactgatcga agccaccatc cagcgcgagg gctcgcgcgc | 1140 |
| cgaccacccg atctggtcga acatcgccgg attctgctag cgcaaaaaac cccgcttcgg | 1200 |

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<210> 21  
<211> 1960  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthetic construct / Exemplary E. coli LacZ expression cassette

<400> 21  
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cgccatagat tcccaacttc cctcatcttc tgggcaagac cgccaactg atgaggttga 480  
ccgcatatta tcaccaggaa agctgatcat actcggctctg caacacgtcc ttgtcatgta 540  
cgcaggtgca gtcgctgttc ctcttatgat tggtagccga ctgggcctct caaaagatgc 600  
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cattcaggtg ggtattgact gggccgctgg aggtaaaggg aatccgcaat atggtaatcc 960  
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|                                                                    |      |
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| gtggatgatg aatgaagtca atttatccgg gctacatgat gcctcgtggg ttgcgattgt  | 1140 |
| caccccgatg tcgttttgta tgccgatttt cgatcccgtt tccattctga ccatgactgc  | 1200 |
| cgtgttaatc atcgtgttta tcgagtcgat ggggatgttc ctggcactgg gtgaaatagt  | 1260 |
| cggtcgtaaa ctctcttcac acgatattat ttgcgggctg cgtgtcgatg gcgtagggac  | 1320 |
| aatgataggc ggcacgttta acagcttccc ccacacgtca ttttctcaaa acgttggcct  | 1380 |
| ggtttagcgtg atgcgcgttc atagccgctg ggtgtgtatt tcttcgggaa ttatattaat | 1440 |
| cctgtttggc atggtgccaa aaatggcggt gctggtagcc tccattccgc aatttgtgct  | 1500 |
| gggcggcgct ggtctagtga tgttcggcat ggtactggcg acagggattc gaattctgtc  | 1560 |
| gcgctgtaac tacaccacca accgttacia cctctatatt gtggcgatca gtctcggcgt  | 1620 |
| tggcatgact ccgacgtctc ctcacgattt cttttctaag ttaccggccg tactgcaacc  | 1680 |
| gctgctacat agcggcatta tgctcgcaac ccttagcgcc gttgtgctga acgtcttctt  | 1740 |
| taatggctat cagcatcatg ctgacctggt gaaggaatcc gtctctgata aagatttaga  | 1800 |
| agtcaggaca gtacgtatgt ggcttctgat gcgcaagctg aagaaaaatg agcatggaga  | 1860 |
| ataaaaaaaaa aaaccccgcc cctgacaggg cgggggtttt tttttgccgt tttcatcata | 1920 |
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<210> 22

<211> 11378

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct / Exemplary Bacteroides transformation vector

<400> 22

|                                                                   |     |
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| attctaccta ttctgatccg gaggaagtga agagaatgaa cgagccgttg cagggaact  | 120 |
| tcgaaggatc cgggtatacag tttaatatgg cggaggacac ttgctggtg atacagcctg | 180 |

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|                                                                    |      |
|--------------------------------------------------------------------|------|
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| aagatacgct gatagccggg gtaaagatga gtaccgagga tattatgcgt cgcctccgtg  | 300  |
| gtcctaaaga ttcaaaagtg aatctgaaaa tacttcgccg aggggtgaag gaactgctcc  | 360  |
| cctttacggg gaaaagggat aaaaccgttt tgccgccact acccatgagg agttcaagaa  | 420  |
| agcgctgacc gggttgcaga agaaaggaat gaaagacttg attcttgatt tgcagggcaa  | 480  |
| tggcgggggg tatttgaatg ctgctatcga tattgccaat gaatTTTTTg gtaaaaagga  | 540  |
| actgattgtc tatacggagg gccgtcgtaa tcctcgtagc gagTTTTTTg ccaaaggtag  | 600  |
| gggcgagttt cagaacggtc gtctgatggg attggttgat gaatTTTcgg cttctgccag  | 660  |
| tgagattgtg accggagctg ttcaggattg ggacagaggc gttgtggtag gccgtcgcag  | 720  |
| TTTTggtaaa ggcttggtgc agcgtcccat tgatttgccg gacggttcga tgatccgtct  | 780  |
| gacggtggcc cgctattata cgcctgccgg acgttgtatc cagaaacctt acgagagcat  | 840  |
| tgaaaagtat aatgaagacc tgatagaccg ttataataaa ggagaaatga tgagtgaaga  | 900  |
| cagcatccac tttccggatt cactgaagtt caagactcat aggttggccc gtacggtata  | 960  |
| tggtggcgga gggatcatgc ccgattatTT tgtgccgatt gatacgactc tctatactaa  | 1020 |
| ataccatcgt cagttgcgtg ataaaggagc attgatgaaa gctcatttcc atTTTattga  | 1080 |
| tgcccatcgt aaagaatggc tgggcaaata caagactttc aatgagttct acaaacgttt  | 1140 |
| tgaagtgact ccggatatgt tgacacaact gggttctacc ggcaaggaga tgggagtgga  | 1200 |
| atataatgaa gaagagtatc aaaaggccct gcctctgctg aggttgcaga tgaaagcatt  | 1260 |
| gatagcccgt gatttatggg atatgaatga atattatcac gtcattaatg acgcgaatga  | 1320 |
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| aaagcgatag tcaagacttt atattaactg caggggcgca tagttgcact cctgcagttg  | 1440 |
| tctgaaaaac ttgtaggata aaacgaaagg ctgagtcgaa agactgggcc tttcgTTTTa  | 1500 |
| caattgggct acctTTTTTT tgTTTTgttt gcaatgggtta atctattgtt aaaatttaaa | 1560 |
| gtttcacttg aactttcaaa taatgttctt atatttgcag tgtcgaaaga aacaaagtag  | 1620 |

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|-------------------------------------------------------------------|------|
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| cattcggcac cctaactacc atgaattcag acagatctcc gtcaacgtat cgctggaagg | 1800 |
| agactttgaa acggcccaca cgctcggcga caattcaaaa atagtaccta ccgatacgca | 1860 |
| gaaaaacacg gtgtatgcgc tggccaaaga gcattttgtg gattctatcg aaaatttcgg | 1920 |
| cctctattta gccaatatt ttatcaccaa taatccgcag gtatcgagg ccaccgtcca   | 1980 |
| tattatcgag catccctggg ctgcgatggc cttcgatgga gagccgcac atcatgccta  | 2040 |
| tgtgggtggc ggttctgaaa aacggacaac aaccttagta cagactaccg aagcaattcg | 2100 |
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| ctacgtcaaa gaccaatata caaccctgaa agaaacggcc gaccgcattt tcgcgacca  | 2220 |
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| aatccgcgaa acgctactaa aaaccttcgc gcatcacaag agtctgtcgg tgcagcaaac | 2340 |
| gttgctggct atgggatcgg ccgtcttgga agagaatcag gaagtaagcg aaataagcct | 2400 |
| gatcatgccc aacaaacatc acatcccgtt taacctggaa cagttcggca tggacaacca | 2460 |
| aaacgagatt ttcatagcca ccgacgagcc gtacgggtac attacgggaa cggtagcgag | 2520 |
| ggagtaaaaa ttataaataa attataaac ttttattaaa aaaaaattac aaaatgagcg  | 2580 |
| aaccggttaa cgcgcaatct acccgctcgc tttacggctt ggaagacaag gttcctttgg | 2640 |
| ttccggcgct tttagttagt ttacaacagg ttggggctat ggtggtcggc accatcacac | 2700 |
| cagcgctgat attgtcgggt atccttcact ttgaccaca ggataccgct tatttagtaa  | 2760 |
| gcatggcggt ggtagcgtcg gcactgggta cgtttttgca aacgatgcgg ctcggtttca | 2820 |
| ttggctctgg cttactgagc atcacgggta ccagcttcgc ttttttgga ccgcttattc  | 2880 |
| aggcgggtgt aacgggcggc ttgccgtta tggctgggtat gtcgctggca ggaacgccgg | 2940 |
| tacagctggc attagcccct tttctgcca aactaaaacg agtcttcaca cccttagttt  | 3000 |
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| tcgttggcgt ggttacgggt tatacgattt gtggactcat gggttggctt caatctcctg   | 3240 |
| ctccgagcaa tggttcctgg ctcacccttc cgcagctgtt tccatatggc ttggccttta   | 3300 |
| aatgggaatt actgtttcca ttcgcgttta tatacctcgt ttgcgtgctg gaagcgatgg   | 3360 |
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| tataagaaaa ataatccttt ggcgtttcat ttagtttggc atttgttcag tgcaaagata   | 4860 |
| ggaaaataat gtaattcgca tttacccttc cccgaattaa agaataatct ccataattcc   | 4920 |
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| attcttggga gctaactggt acgcgttggg tgcaactgcc gggctggctg ctctgtttgt   | 5220 |
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| acgttatgca gtgaacgtta aacctaaaac tgtggaatgg gcatctcaga acatgcttgt   | 5340 |
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| cgccggcggg agccggccag cctcgcagag caggattccc gttgagcacc gccaggtgcg   | 5820 |
| aataagggac agtgaagaag gaacacccgc tcgcgggtgg gcctacttca cctatcctgc   | 5880 |
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|---------------------------------------------------------------------|------|
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| gaacaataaa attaatataa atcagcaact taaatagcct ctaaggtttt  | aagttttata | 11220 |
| agaaaaaaaa gaatatataa ggctttttaa gcttttaagg tttaacggtt  | gtggacaaca | 11280 |
| agccagggat gtaacgcact gagaagccct tagagcctct caaagcaatt  | ttgagtgaca | 11340 |
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| ccgctttcag aagactctcc attcgtggca ctgcagtccg tcacttcaga aaatcttgcg  | 180  |
| tttatcgtcg taagtccgtt tatctttttt aagaattatg aatttgatct tgatgaatca  | 240  |
| actgctgaac ttttg gatat cgataatatt caagacgtag aagtcatgac aatattgact | 300  |
| atggcagagc catttgaaaa gtctactgcg aattttattgg ctcccattat tgtgaatcgc | 360  |
| aagaacatga tggctaagca agtcgtttta cacgactcct catatacgac aaagcatccg  | 420  |
| attggaggag aatcatgcta gttttatcgc ggaaaataaa cgaagcgatt caaatagggtg | 480  |
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| accgtgcagc agcgttatcc agcgatgtga tctccgcatt atcctcacia aaaaagtgag  | 660  |
| gattttttta tttttgtatt aacaaaatca gagacaatcc gatattaatg atgtagccgg  | 720  |
| gaggaggcgc aaaagactca gccagttaca aaataagggc acaagaacgt gccttaacaa  | 780  |
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| ttcccgtcat gcttggcagt tcatttgtgg ccgtcacccc aatgattgca atcggcagca  | 1020 |
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| aaataaacgg cagcgccaac cccgaatacg gttcgctcga aaaccttctt ctctctgtcg  | 1260 |
| gtgtccttgt tctgatctta gtcctcaacc gctttctcaa aggatttgcc cgaacactgt  | 1320 |
| ccgttctgat cggcatcgcc gccggaacag cggcagcagc gatcatgggc aaagtcagct  | 1380 |
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| atctcgtcaa aggctatcga gcggaaggaa tcgccattct catcggcggg ctgttcaatg   | 1620 |
| cctttcctta taataccttt gcgcaaaacg ccggcttatt gcagctgacc aaagtgaaaa   | 1680 |
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| accacctctt gaccatcgca tgctcaatcg cactcggcat cggcgccagc acggcccccg   | 1920 |
| ggatTTTTgc tgaattcccc gctccgatcc ggattctggg cagtgcggc accatcacg     | 1980 |
| gaagcctaac cgccatcttt ttgaatctat ttttcagctt gcgcgacaaa aaagaattaa   | 2040 |
| cagcacagca aacagaactt ccggtattag aacatacact cgcattagaa aaagaggtgt   | 2100 |
| aaaaaagatg aaggaacagc acaatgcctt acagctaata atgctggggc ttcagcacat   | 2160 |
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| aagtcaccac cataagcata agctttatgc aacttaccat ctgcagtact aacatcttcg  | 600 |
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| accacttta gtggctgccc gccctcctg cgcttccctt gcgcttccct tgggaccaca    | 1200 |
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| tctggcatag tctgggtgtct ggtgtctggt gtcttttggg aactgaacag tggaaagtgg | 1440 |
| aagtgtaaaa ttgtataaat ataggtgtcc cattcgtggt ttggtggatg tgtccttgac  | 1500 |
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| catgtgtcca                                                          | 2410 |