

33847-BUT-P-WO-2009001860
SEQUENCE LISTING

<110> BUTALCO GmbH

<120> Fermentative Produktion von Isobutanol mit Hefe

<130> 33847-BUT-P-WO

<150> 10 2008 010 121.4

<151> 20.02.2008

<160> 50

<210> 1

<211> 2064

<212> DNA

<213> *Saccharomyces cerevisiae*

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<213> Saccharomyces cerevisiae

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35 40 45

Leu Pro Ala Ser Lys Arg Pro Glu Pro Ala Pro Ser Phe Asn Val Asp
50 55 60

Pro Leu Glu Gln Pro Ala Glu Pro Ser Lys Leu Ala Lys Lys Leu Arg
65 70 75 80

Ala Glu Pro Asp Met Asp Thr Ser Phe Val Gly Leu Thr Gly Gly Gln
85 90 95

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

Tyr Pro Gly Gly Ala Ile Leu Pro Val Tyr Asp Ala Ile His Asn Ser
115 120 125

Asp Lys Phe Asn Phe Val Leu Pro Lys His Glu Gln Gly Ala Gly His
130 135 140

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Met Ala Glu Gly Tyr Ala Arg Ala Ser Gly Lys Pro Gly Val Val Leu
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Val Thr Ser Gly Pro Gly Ala Thr Asn Val Val Thr Pro Met Ala Asp
165 170 175

Ala Phe Ala Asp Gly Ile Pro Met Val Val Phe Thr Gly Gln Val Pro
180 185 190

Thr Ser Ala Ile Gly Thr Asp Ala Phe Gln Glu Ala Asp Val Val Gly
195 200 205

Ile Ser Arg Ser Cys Thr Lys Trp Asn Val Met Val Lys Ser Val Glu
210 215 220

Glu Leu Pro Leu Arg Ile Asn Glu Ala Phe Glu Ile Ala Thr Ser Gly
225 230 235 240

Arg Pro Gly Pro Val Leu Val Asp Leu Pro Lys Asp Val Thr Ala Ala
245 250 255

Ile Leu Arg Asn Pro Ile Pro Thr Lys Thr Thr Leu Pro Ser Asn Ala
260 265 270

Leu Asn Gln Leu Thr Ser Arg Ala Gln Asp Glu Phe Val Met Gln Ser
275 280 285

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290 295 300

Tyr Val Gly Ala Gly Ile Leu Asn His Ala Asp Gly Pro Arg Leu Leu
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325 330 335

Gly Leu Gly Ser Phe Asp Gln Glu Asp Pro Lys Ser Leu Asp Met Leu
340 345 350

Gly Met His Gly Cys Ala Thr Ala Asn Leu Ala Val Gln Asn Ala Asp
355 360 365

Leu Ile Ile Ala Val Gly Ala Arg Phe Asp Asp Arg Val Thr Gly Asn
370 375 380

Ile Ser Lys Phe Ala Pro Glu Ala Arg Arg Ala Ala Ala Glu Gly Arg
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405 410 415

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Val Gln Thr Gln Ile Ala Val Glu Gly Asp Ala Thr Thr Asn Leu Gly
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Lys Met Met Ser Lys Ile Phe Pro Val Lys Glu Arg Ser Glu Trp Phe
435 440 445

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

Val Gly Gln His Gln Met Trp Ala Ala Gln His Trp Thr Trp Arg Asn
500 505 510

Pro His Thr Phe Ile Thr Ser Gly Gly Leu Gly Thr Met Gly Tyr Gly
515 520 525

Leu Pro Ala Ala Ile Gly Ala Gln Val Ala Lys Pro Glu Ser Leu Val
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Ile Asp Ile Asp Gly Asp Ala Ser Phe Asn Met Thr Leu Thr Glu Leu
545 550 555 560

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

Asn Glu Glu Gln Gly Met Val Thr Gln Trp Gln Ser Leu Phe Tyr Glu
580 585 590

His Arg Tyr Ser His Thr His Gln Leu Asn Pro Asp Phe Ile Lys Leu
595 600 605

Ala Glu Ala Met Gly Leu Lys Gly Leu Arg Val Lys Lys Gln Glu Glu
610 615 620

Leu Asp Ala Lys Leu Lys Glu Phe Val Ser Thr Lys Gly Pro Val Leu
625 630 635 640

Leu Glu Val Glu Val Asp Lys Lys Val Pro Val Leu Pro Met Val Ala
645 650 655

Gly Gly Ser Gly Leu Asp Glu Phe Ile Asn Phe Asp Pro Glu Val Glu
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 <213> *Saccharomyces cerevisiae*

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 <213> *Saccharomyces cerevisiae*

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

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

Thr Glu Val Lys Asp Leu Ser Arg Met Thr Ile Val Leu Gln Gly Gln
 115 120 125

Asp Gly Val Val Glu Gln Ala Arg Arg Gln Ile Glu Asp Leu Val Pro
 130 135 140

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

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

Leu Leu Leu His His His Thr Ser Thr Asn Ala Gly Ala Ala Asp Ser
 180 185 190

Gln Glu Leu Val Ala Glu Ile Arg Glu Lys Gln Phe His Pro Ala Asn
 195 200 205

Leu Pro Ala Ser Glu Val Leu Arg Leu Lys His Glu His Leu Asn Asp
 210 215 220

Ile Thr Asn Leu Thr Asn Asn Phe Gly Gly Arg Val Val Asp Ile Ser
 225 230 235 240

Glu Thr Ser Cys Ile Val Glu Leu Ser Ala Lys Pro Thr Arg Ile Ser
 245 250 255

Ala Phe Leu Lys Leu Val Glu Pro Phe Gly Val Leu Glu Cys Ala Arg
 260 265 270

Ser Gly Met Met Ala Leu Pro Arg Thr Pro Leu Lys Thr Ser Thr Glu
 275 280 285

Glu Ala Ala Asp Glu Asp Glu Lys Ile Ser Glu Ile Val Asp Ile Ser
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Gln Leu Pro Pro Gly
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 <213> *Saccharomyces cerevisiae*

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 <213> *Saccharomyces cerevisiae*

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35 40 45

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

Ala Leu Ile Gly Tyr Gly Ser Gln Gly Tyr Gly Gln Gly Leu Asn Leu
85 90 95

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Arg Asp Asn Gly Leu Asn Val Ile Ile Gly Val Arg Lys Asp Gly Ala
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Ser Trp Lys Ala Ala Ile Glu Asp Gly Trp Val Pro Gly Lys Asn Leu
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Phe Thr Val Glu Asp Ala Ile Lys Arg Gly Ser Tyr Val Met Asn Leu
130 135 140

Leu Ser Asp Ala Ala Gln Ser Glu Thr Trp Pro Ala Ile Lys Pro Leu
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Leu Thr Lys Gly Lys Thr Leu Tyr Phe Ser His Gly Phe Ser Pro Val
165 170 175

Phe Lys Asp Leu Thr His Val Glu Pro Pro Lys Asp Leu Asp Val Ile
180 185 190

Leu Val Ala Pro Lys Gly Ser Gly Arg Thr Val Arg Ser Leu Phe Lys
195 200 205

Glu Gly Arg Gly Ile Asn Ser Ser Tyr Ala Val Trp Asn Asp Val Thr
210 215 220

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

Gly Tyr Val Tyr Gln Thr Thr Phe Glu Arg Glu Val Asn Ser Asp Leu
245 250 255

Tyr Gly Glu Arg Gly Cys Leu Met Gly Gly Ile His Gly Met Phe Leu
260 265 270

Ala Gln Tyr Asp Val Leu Arg Glu Asn Gly His Ser Pro Ser Glu Ala
275 280 285

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

Gly Lys Tyr Gly Met Asp Tyr Met Tyr Asp Ala Cys Ser Thr Thr Ala
305 310 315 320

Arg Arg Gly Ala Leu Asp Trp Tyr Pro Ile Phe Lys Asn Ala Leu Lys
325 330 335

Pro Val Phe Gln Asp Leu Tyr Glu Ser Thr Lys Asn Gly Thr Glu Thr
340 345 350

Lys Arg Ser Leu Glu Phe Asn Ser Gln Pro Asp Tyr Arg Glu Lys Leu
355 360 365

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<213> *Saccharomyces cerevisiae*

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<211> 585
<212> PRT
<213> *Saccharomyces cerevisiae*

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35 40 45

Lys Lys Glu Asp Phe Lys Lys Pro Gln Val Gly Val Gly Ser Cys Trp
50 55 60

Trp Ser Gly Asn Pro Cys Asn Met His Leu Leu Asp Leu Asn Asn Arg
65 70 75 80

Cys Ser Gln Ser Ile Glu Lys Ala Gly Leu Lys Ala Met Gln Phe Asn
85 90 95

Thr Ile Gly Val Ser Asp Gly Ile Ser Met Gly Thr Lys Gly Met Arg
100 105 110

Tyr Ser Leu Gln Ser Arg Glu Ile Ile Ala Asp Ser Phe Glu Thr Ile
115 120 125

Met Met Ala Gln His Tyr Asp Ala Asn Ile Ala Ile Pro Ser Cys Asp
130 135 140

Lys Asn Met Pro Gly Val Met Met Ala Met Gly Arg His Asn Arg Pro
145 150 155 160

Ser Ile Met Val Tyr Gly Gly Thr Ile Leu Pro Gly His Pro Thr Cys
165 170 175

Gly Ser Ser Lys Ile Ser Lys Asn Ile Asp Ile Val Ser Ala Phe Gln
180 185 190

Ser Tyr Gly Glu Tyr Ile Ser Lys Gln Phe Thr Glu Glu Glu Arg Glu
195 200 205

Asp Val Val Glu His Ala Cys Pro Gly Pro Gly Ser Cys Gly Gly Met

210

215

220

Tyr Thr Ala Asn Thr Met Ala Ser Ala Ala Glu Val Leu Gly Leu Thr
 225 230 235 240

Ile Pro Asn Ser Ser Ser Phe Pro Ala Val Ser Lys Glu Lys Leu Ala
 245 250 255

Glu Cys Asp Asn Ile Gly Glu Tyr Ile Lys Lys Thr Met Glu Leu Gly
 260 265 270

Ile Leu Pro Arg Asp Ile Leu Thr Lys Glu Ala Phe Glu Asn Ala Ile
 275 280 285

Thr Tyr Val Val Ala Thr Gly Gly Ser Thr Asn Ala Val Leu His Leu
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Val Ala Val Ala His Ser Ala Gly Val Lys Leu Ser Pro Asp Asp Phe
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Gln Arg Ile Ser Asp Thr Thr Pro Leu Ile Gly Asp Phe Lys Pro Ser
 325 330 335

Gly Lys Tyr Val Met Ala Asp Leu Ile Asn Val Gly Gly Thr Gln Ser
 340 345 350

Val Ile Lys Tyr Leu Tyr Glu Asn Asn Met Leu His Gly Asn Thr Met
 355 360 365

Thr Val Thr Gly Asp Thr Leu Ala Glu Arg Ala Lys Lys Ala Pro Ser
 370 375 380

Leu Pro Glu Gly Gln Glu Ile Ile Lys Pro Leu Ser His Pro Ile Lys
 385 390 395 400

Ala Asn Gly His Leu Gln Ile Leu Tyr Gly Ser Leu Ala Pro Gly Gly
 405 410 415

Ala Val Gly Lys Ile Thr Gly Lys Glu Gly Thr Tyr Phe Lys Gly Arg
 420 425 430

Ala Arg Val Phe Glu Glu Glu Gly Ala Phe Ile Glu Ala Leu Glu Arg
 435 440 445

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

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

Ala Leu Met Gly Tyr Gly Leu Gly Lys Asp Val Ala Leu Leu Thr Asp
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Pro Glu Ala Ala Glu Gly Gly Pro Ile Gly Leu Val Arg Asp Gly Asp
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Asp Lys Glu Met Ala Gln Arg Lys Gln Ser Trp Val Ala Pro Pro Pro
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Ala Ser Asn Gly Cys Val Leu Asp Ala
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<211> 1182
<212> DNA
<213> *Saccharomyces cerevisiae*

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 <213> *Saccharomyces cerevisiae*

<400> 10

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

Leu Ala Thr Gly Ala Pro Leu Asp Ala Ser Lys Leu Lys Ile Thr Arg
20 25 30

Asn Pro Asn Pro Ser Lys Pro Arg Pro Asn Glu Glu Leu Val Phe Gly
35 40 45

Gln Thr Phe Thr Asp His Met Leu Thr Ile Pro Trp Ser Ala Lys Glu
50 55 60

Gly Trp Gly Thr Pro His Ile Lys Pro Tyr Gly Asn Leu Ser Leu Asp
65 70 75 80

Pro Ser Ala Cys Val Phe His Tyr Ala Phe Glu Leu Phe Glu Gly Leu
85 90 95

Lys Ala Tyr Arg Thr Pro Gln Asn Thr Ile Thr Met Phe Arg Pro Asp
100 105 110

Lys Asn Met Ala Arg Met Asn Lys Ser Ala Ala Arg Ile Cys Leu Pro
115 120 125

Thr Phe Glu Ser Glu Glu Leu Ile Lys Leu Thr Gly Lys Leu Ile Glu
130 135 140

Gln Asp Lys His Leu Val Pro Gln Gly Asn Gly Tyr Ser Leu Tyr Ile
145 150 155 160

Arg Pro Thr Met Ile Gly Thr Ser Lys Gly Leu Gly Val Gly Thr Pro
165 170 175

Ser Glu Ala Leu Leu Tyr Val Ile Thr Ser Pro Val Gly Pro Tyr Tyr
180 185 190

Lys Thr Gly Phe Lys Ala Val Arg Leu Glu Ala Thr Asp Tyr Ala Thr
195 200 205

Arg Ala Trp Pro Gly Gly Val Gly Asp Lys Lys Leu Gly Ala Asn Tyr
210 215 220

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Ala Pro Cys Ile Leu Pro Gln Leu Gln Ala Ala Lys Arg Gly Tyr Gln
225 230 235 240

Gln Asn Leu Trp Leu Phe Gly Pro Glu Lys Asn Ile Thr Glu Val Gly
245 250 255

Thr Met Asn Val Phe Phe Val Phe Leu Asn Lys Val Thr Gly Lys Lys
260 265 270

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

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

Trp Asp Ile Asn Glu Arg Tyr Tyr Thr Ile Thr Glu Val Ala Thr Arg
305 310 315 320

Ala Lys Gln Gly Glu Leu Leu Glu Ala Phe Gly Ser Gly Thr Ala Ala
325 330 335

Val Val Ser Pro Ile Lys Glu Ile Gly Trp Asn Asn Glu Asp Ile His
340 345 350

Val Pro Leu Leu Pro Gly Glu Gln Cys Gly Ala Leu Thr Lys Gln Val
355 360 365

Ala Gln Trp Ile Ala Asp Ile Gln Tyr Gly Arg Val Asn Tyr Gly Asn
370 375 380

Trp Ser Lys Thr Val Ala Asp Leu Asn
385 390

<210> 11
<211> 1131
<212> DNA
<213> Saccharomyces cerevisiae

<400> 11
atgaccttgg caccctaga cgcctccaaa gttaagataa ctaccacaca acatgcatct 60
aagccaaaac cgaacagtga gttagtgttt ggcaagagct tcacggacca catgttaact 120
gcggaatgga cagctgaaaa aggggtgggg accccagaga ttaaacctta tcaaactctg 180
tcttttagacc cttccgcggt ggttttccat tatgcttttg agctattcga agggatgaag 240
gcttacagaa cgggtggacaa caaaattaca atgtttcgtc cagatatgaa tatgaagcgc 300
atgaataagt ctgctcagag aatctgtttg ccaacgttcg acccagaaga gttgattacc 360
ctaattggga aactgatcca gcaagataag tgcttagttc ctgaaggaaa aggttactct 420
ttatatatca ggcctacatt aatcggcact acggccggtt taggggtttc cacgcctgat 480
agagccttgc tatatgtcat ttgctgccct gtgggtcctt attacaaaac tggatttaag 540

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gcggtcagac tggaagccac tgattatgcc acaagagctt ggccaggagg ctgtggtgac 600
aagaaactag gtgcaaaacta cgccccctgc gtcctgccac aattgcaagc tgcttcaagg 660
ggttaccaac aaaatttatg gctatttggg ccaaataaca acattactga agtcggcacc 720
atgaatgctt ttttcgtggt taaagatagt aaaacgggca agaaggaact agttactgct 780
ccactagacg gtaccattttt ggaaggtggt actagggatt ccattttaaa tcttgctaaa 840
gaaagactcg aaccaagtga atggaccatt agtgaacgct acttcactat aggcgaagtt 900
actgagagat ccaagaacgg tgaactactt gaagcctttg gttctggtac tgctgcgatt 960
gtttctccca ttaaggaaaat cggctggaaa ggcgaacaaa ttaatatcc gttgttgccc 1020
ggcgaacaaa ccggtccatt ggccaaagaa gttgcacaat ggattaatgg aatccaatat 1080
ggcgagactg agcatggcaa ttggtcaagg gttgttactg atttgaactg a 1131

<210> 12
<211> 376
<212> PRT
<213> Saccharomyces cerevisiae

<400> 12

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

Gln His Ala Ser Lys Pro Lys Pro Asn Ser Glu Leu Val Phe Gly Lys
20 25 30

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

Trp Gly Thr Pro Glu Ile Lys Pro Tyr Gln Asn Leu Ser Leu Asp Pro
50 55 60

Ser Ala Val Val Phe His Tyr Ala Phe Glu Leu Phe Glu Gly Met Lys
65 70 75 80

Ala Tyr Arg Thr Val Asp Asn Lys Ile Thr Met Phe Arg Pro Asp Met
85 90 95

Asn Met Lys Arg Met Asn Lys Ser Ala Gln Arg Ile Cys Leu Pro Thr
100 105 110

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

Asp Lys Cys Leu Val Pro Glu Gly Lys Gly Tyr Ser Leu Tyr Ile Arg
130 135 140

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

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Arg Ala Leu Leu Tyr Val Ile Cys Cys Pro Val Gly Pro Tyr Tyr Lys
165 170 175

Thr Gly Phe Lys Ala Val Arg Leu Glu Ala Thr Asp Tyr Ala Thr Arg
180 185 190

Ala Trp Pro Gly Gly Cys Gly Asp Lys Lys Leu Gly Ala Asn Tyr Ala
195 200 205

Pro Cys Val Leu Pro Gln Leu Gln Ala Ala Ser Arg Gly Tyr Gln Gln
210 215 220

Asn Leu Trp Leu Phe Gly Pro Asn Asn Asn Ile Thr Glu Val Gly Thr
225 230 235 240

Met Asn Ala Phe Phe Val Phe Lys Asp Ser Lys Thr Gly Lys Lys Glu
245 250 255

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

Asp Ser Ile Leu Asn Leu Ala Lys Glu Arg Leu Glu Pro Ser Glu Trp
275 280 285

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

Lys Asn Gly Glu Leu Leu Glu Ala Phe Gly Ser Gly Thr Ala Ala Ile
305 310 315 320

Val Ser Pro Ile Lys Glu Ile Gly Trp Lys Gly Glu Gln Ile Asn Ile
325 330 335

Pro Leu Leu Pro Gly Glu Gln Thr Gly Pro Leu Ala Lys Glu Val Ala
340 345 350

Gln Trp Ile Asn Gly Ile Gln Tyr Gly Glu Thr Glu His Gly Asn Trp
355 360 365

Ser Arg Val Val Thr Asp Leu Asn
370 375

<210> 13

<211> 1692

<212> DNA

<213> Saccharomyces cerevisiae

<400> 13

atgtctgaaa ttactttggg taaatatttg ttcgaaagat taaagcaagt caacgttaac 60

accgttttcg gtttgccagg tgacttcaac ttgtccttgt tggacaagat ctacgaagtt 120

gaaggatga gatgggctgg taacgccaac gaattgaacg ctgcttacgc cgctgatggt 180

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tacgctcgta tcaaggggtat gtcttgatc atcaccacct tcggtgtcgg tgaattgtct	240
gctttgaacg gtattgccgg ttcttacgct gaacacgtcg gtgttttgca cgttgttggt	300
gtcccatcca tctctgctca agctaagcaa ttgttggtgc accacacctt gggtaacggt	360
gacttcactg ttttccacag aatgtctgcc aacatttctg aaaccactgc tatgatcact	420
gacattgcta ccgccccagc tgaaattgac agatgtatca gaaccactta cgtcacccaa	480
agaccagtct acttaggttt gccagctaac ttggtcgact tgaacgtccc agctaagttg	540
ttgcaaaactc caattgacat gtctttgaag ccaaacgatg ctgaatccga aaaggaagtc	600
attgacacca tcttggtctt ggtcaaggat gctaagaacc cagttatctt ggctgatgct	660
tggtgttcca gacacgacgt caaggctgaa actaagaagt tgattgactt gactcaattc	720
ccagctttcg tcacccaat gggtaagggt tccattgacg aacaacaccc aagatacggg	780
gggtgtttacg tcggtacctt gtccaagcca gaagttaagg aagccgttga atctgctgac	840
ttgattttgt ctgtcggtgc tttgttgctt gatttcaaca ccggttcttt ctcttactct	900
tacaagacca agaacattgt cgaattccac tccgaccaca tgaagatcag aaacgccact	960
ttcccagggtg tccaaatgaa attcgttttg caaaagttgt tgaccactat tgctgacgcc	1020
gctaagggtt acaagccagt tgctgtccca gctagaactc cagctaacgc tgctgtccca	1080
gcttctaccc cattgaagca agaatggatg tggaaccaat tgggtaactt cttgcaagaa	1140
gggtgatgttgc tcatgtgctga aaccgggtacc tccgctttcg gtatcaacca aaccactttc	1200
ccaaacaaca cctacgggtat ctctcaagtc ttatgggggt ccattgggtt caccactggt	1260
gctaccttgg gtgctgcttt cgctgctgaa gaaattgatc caaagaagag agttatctta	1320
ttcattgggtg acggttcttt gcaattgact gttcaagaaa tctccaccat gatcagatgg	1380
ggcttgaagc catacttggt cgtcttgaac aacgatgggt acaccattga aaagttgatt	1440
cacgggtccaa aggctcaata caacgaaatt caagggtggg accacctatc cttgttgcca	1500
actttcgggtg ctaaggacta tgaaaccac agagtcgcta ccaccgggtga atgggacaag	1560
ttgaccaag acaagtcttt caacgacaac tctaagatca gaatgattga aatcatgttg	1620
ccagtccttcg atgctccaca aaacttggtt gaacaagcta agttgactgc tgctaccaac	1680
gctaagcaat aa	1692

<210> 14

<211> 563

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 14

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

Val	Asn	Val	Asn	Thr	Val	Phe	Gly	Leu	Pro	Gly	Asp	Phe	Asn	Leu	Ser
			20					25					30		

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Leu Leu Asp Lys Ile Tyr Glu Val Glu Gly Met Arg Trp Ala Gly Asn
 35 40 45
 Ala Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Ile
 50 55 60
 Lys Gly Met Ser Cys Ile Ile Thr Thr Phe Gly Val Gly Glu Leu Ser
 65 70 75 80
 Ala Leu Asn Gly Ile Ala Gly Ser Tyr Ala Glu His Val Gly Val Leu
 85 90 95
 His Val Val Gly Val Pro Ser Ile Ser Ala Gln Ala Lys Gln Leu Leu
 100 105 110
 Leu His His Thr Leu Gly Asn Gly Asp Phe Thr Val Phe His Arg Met
 115 120 125
 Ser Ala Asn Ile Ser Glu Thr Thr Ala Met Ile Thr Asp Ile Ala Thr
 130 135 140
 Ala Pro Ala Glu Ile Asp Arg Cys Ile Arg Thr Thr Tyr Val Thr Gln
 145 150 155 160
 Arg Pro Val Tyr Leu Gly Leu Pro Ala Asn Leu Val Asp Leu Asn Val
 165 170 175
 Pro Ala Lys Leu Leu Gln Thr Pro Ile Asp Met Ser Leu Lys Pro Asn
 180 185 190
 Asp Ala Glu Ser Glu Lys Glu Val Ile Asp Thr Ile Leu Ala Leu Val
 195 200 205
 Lys Asp Ala Lys Asn Pro Val Ile Leu Ala Asp Ala Cys Cys Ser Arg
 210 215 220
 His Asp Val Lys Ala Glu Thr Lys Lys Leu Ile Asp Leu Thr Gln Phe
 225 230 235 240
 Pro Ala Phe Val Thr Pro Met Gly Lys Gly Ser Ile Asp Glu Gln His
 245 250 255
 Pro Arg Tyr Gly Gly Val Tyr Val Gly Thr Leu Ser Lys Pro Glu Val
 260 265 270
 Lys Glu Ala Val Glu Ser Ala Asp Leu Ile Leu Ser Val Gly Ala Leu
 275 280 285
 Leu Ser Asp Phe Asn Thr Gly Ser Phe Ser Tyr Ser Tyr Lys Thr Lys
 290 295 300

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Asn Ile Val Glu Phe His Ser Asp His Met Lys Ile Arg Asn Ala Thr
 305 310 315 320
 Phe Pro Gly Val Gln Met Lys Phe Val Leu Gln Lys Leu Leu Thr Thr
 325 330 335
 Ile Ala Asp Ala Ala Lys Gly Tyr Lys Pro Val Ala Val Pro Ala Arg
 340 345 350
 Thr Pro Ala Asn Ala Ala Val Pro Ala Ser Thr Pro Leu Lys Gln Glu
 355 360 365
 Trp Met Trp Asn Gln Leu Gly Asn Phe Leu Gln Glu Gly Asp Val Val
 370 375 380
 Ile Ala Glu Thr Gly Thr Ser Ala Phe Gly Ile Asn Gln Thr Thr Phe
 385 390 395 400
 Pro Asn Asn Thr Tyr Gly Ile Ser Gln Val Leu Trp Gly Ser Ile Gly
 405 410 415
 Phe Thr Thr Gly Ala Thr Leu Gly Ala Ala Phe Ala Ala Glu Glu Ile
 420 425 430
 Asp Pro Lys Lys Arg Val Ile Leu Phe Ile Gly Asp Gly Ser Leu Gln
 435 440 445
 Leu Thr Val Gln Glu Ile Ser Thr Met Ile Arg Trp Gly Leu Lys Pro
 450 455 460
 Tyr Leu Phe Val Leu Asn Asn Asp Gly Tyr Thr Ile Glu Lys Leu Ile
 465 470 475 480
 His Gly Pro Lys Ala Gln Tyr Asn Glu Ile Gln Gly Trp Asp His Leu
 485 490 495
 Ser Leu Leu Pro Thr Phe Gly Ala Lys Asp Tyr Glu Thr His Arg Val
 500 505 510
 Ala Thr Thr Gly Glu Trp Asp Lys Leu Thr Gln Asp Lys Ser Phe Asn
 515 520 525
 Asp Asn Ser Lys Ile Arg Met Ile Glu Ile Met Leu Pro Val Phe Asp
 530 535 540
 Ala Pro Gln Asn Leu Val Glu Gln Ala Lys Leu Thr Ala Ala Thr Asn
 545 550 555 560
 Ala Lys Gln

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<210> 15
 <211> 1692
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 15
 atgtctgaaa taaccttagg taaatattta tttgaaagat tgagccaagt caactgtaac 60
 accgtcttcg gtttgccagg tgactttaac ttgtctcttt tggataagct ttatgaagtc 120
 aaaggatga gatgggctgg taacgctaac gaattgaacg ctgcctatgc tgctgatggt 180
 tacgctcgta tcaagggtat gtcctgtatt attaccacct tcggtgttgg tgaattgtct 240
 gctttgaatg gtattgccgg ttcttacgct gaacatgtcg gtgttttgca cggtgttgg 300
 gttccatcca tctcttctca agctaagcaa ttgtgttgc atcatacctt gggtaacgg 360
 gacttcactg ttttccacag aatgtctgcc aacatttctg aaaccactgc catgatcact 420
 gatattgcta acgctccagc tgaaattgac agatgtatca gaaccaccta cactacccaa 480
 agaccagtct acttgggttt gccagctaac ttggttgact tgaacgtccc agccaagtta 540
 ttggaaactc caattgactt gtctttgaag ccaaacgacg ctgaagctga agctgaagtt 600
 gttagaactg ttgttgaatt gatcaaggat gctaagaacc cagttatctt ggctgatgct 660
 tgtgtctcta gacatgatgt caaggctgaa actaagaagt tgatggactt gactcaattc 720
 ccagtttacg tcacccaat gggtaagggt gctattgacg aacaacaccc aagatacgg 780
 ggtgtttacg ttggtacctt gtctagacca gaagttaaga aggctgtaga atctgctgat 840
 ttgatattgt ctatcggtgc tttgttgtct gatttcaata ccggttcttt ctcttactcc 900
 tacaagacca aaaatatcgt tgaattccac tctgaccaca tcaagatcag aaacgccacc 960
 ttcccagggtg ttcaaataaa atttgccttg caaaaattgt tggatgctat tccagaagtc 1020
 gtcaaggact acaaacctgt tgctgtccca gctagagttc caattaccaa gtctactcca 1080
 gctaacactc caatgaagca agaattgatg tgggaaccatt tgggtaactt cttgagagaa 1140
 ggtgatattg ttattgctga aaccgggtact tccgccttcg gtattaacca aactactttc 1200
 ccaacagatg tatacgctat cgtccaagtc ttgtgggggt ccattgggtt cacagtcggc 1260
 gctctattgg gtgctactat ggccgctgaa gaacttgatc caaagaagag agttatttta 1320
 ttcatgggtg acggttctct acaattgact gttcaagaaa tctctaccat gattagatgg 1380
 gggttgaagc catacatttt tgtcttgaat aacaacgggt acaccattga aaaattgatt 1440
 cacggtcctc atgccgaata taatgaaatt caagggtggg accacttggc cttattgcc 1500
 acttttggtg ctagaaacta cgaaaccac agagttgcta cactgggtga atgggaaaag 1560
 ttgactcaag acaaggactt ccaagacaac tctaagatta gaatgattga agttatgttg 1620
 ccagtccttg atgtccaca aaacttgggt aaacaagctc aattgactgc cgctactaac 1680
 gctaaacaat aa 1692

<210> 16
 <211> 563

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<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 16

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

Val Asn Cys Asn Thr Val Phe Gly Leu Pro Gly Asp Phe Asn Leu Ser
20 25 30

Leu Leu Asp Lys Leu Tyr Glu Val Lys Gly Met Arg Trp Ala Gly Asn
35 40 45

Ala Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Ile
50 55 60

Lys Gly Met Ser Cys Ile Ile Thr Thr Phe Gly Val Gly Glu Leu Ser
65 70 75 80

Ala Leu Asn Gly Ile Ala Gly Ser Tyr Ala Glu His Val Gly Val Leu
85 90 95

His Val Val Gly Val Pro Ser Ile Ser Ser Gln Ala Lys Gln Leu Leu
100 105 110

Leu His His Thr Leu Gly Asn Gly Asp Phe Thr Val Phe His Arg Met
115 120 125

Ser Ala Asn Ile Ser Glu Thr Thr Ala Met Ile Thr Asp Ile Ala Asn
130 135 140

Ala Pro Ala Glu Ile Asp Arg Cys Ile Arg Thr Thr Tyr Thr Thr Gln
145 150 155 160

Arg Pro Val Tyr Leu Gly Leu Pro Ala Asn Leu Val Asp Leu Asn Val
165 170 175

Pro Ala Lys Leu Leu Glu Thr Pro Ile Asp Leu Ser Leu Lys Pro Asn
180 185 190

Asp Ala Glu Ala Glu Ala Glu Val Val Arg Thr Val Val Glu Leu Ile
195 200 205

Lys Asp Ala Lys Asn Pro Val Ile Leu Ala Asp Ala Cys Ala Ser Arg
210 215 220

His Asp Val Lys Ala Glu Thr Lys Lys Leu Met Asp Leu Thr Gln Phe
225 230 235 240

Pro Val Tyr Val Thr Pro Met Gly Lys Gly Ala Ile Asp Glu Gln His
245 250 255

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Pro Arg Tyr Gly Gly Val Tyr Val Gly Thr Leu Ser Arg Pro Glu Val
260 265 270

Lys Lys Ala Val Glu Ser Ala Asp Leu Ile Leu Ser Ile Gly Ala Leu
275 280 285

Leu Ser Asp Phe Asn Thr Gly Ser Phe Ser Tyr Ser Tyr Lys Thr Lys
290 295 300

Asn Ile Val Glu Phe His Ser Asp His Ile Lys Ile Arg Asn Ala Thr
305 310 315 320

Phe Pro Gly Val Gln Met Lys Phe Ala Leu Gln Lys Leu Leu Asp Ala
325 330 335

Ile Pro Glu Val Val Lys Asp Tyr Lys Pro Val Ala Val Pro Ala Arg
340 345 350

Val Pro Ile Thr Lys Ser Thr Pro Ala Asn Thr Pro Met Lys Gln Glu
355 360 365

Trp Met Trp Asn His Leu Gly Asn Phe Leu Arg Glu Gly Asp Ile Val
370 375 380

Ile Ala Glu Thr Gly Thr Ser Ala Phe Gly Ile Asn Gln Thr Thr Phe
385 390 395 400

Pro Thr Asp Val Tyr Ala Ile Val Gln Val Leu Trp Gly Ser Ile Gly
405 410 415

Phe Thr Val Gly Ala Leu Leu Gly Ala Thr Met Ala Ala Glu Glu Leu
420 425 430

Asp Pro Lys Lys Arg Val Ile Leu Phe Ile Gly Asp Gly Ser Leu Gln
435 440 445

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

Tyr Ile Phe Val Leu Asn Asn Asn Gly Tyr Thr Ile Glu Lys Leu Ile
465 470 475 480

His Gly Pro His Ala Glu Tyr Asn Glu Ile Gln Gly Trp Asp His Leu
485 490 495

Ala Leu Leu Pro Thr Phe Gly Ala Arg Asn Tyr Glu Thr His Arg Val
500 505 510

Ala Thr Thr Gly Glu Trp Glu Lys Leu Thr Gln Asp Lys Asp Phe Gln
515 520 525

Asp Asn Ser Lys Ile Arg Met Ile Glu Val Met Leu Pro Val Phe Asp
 530 535 540

Ala Pro Gln Asn Leu Val Lys Gln Ala Gln Leu Thr Ala Ala Thr Asn
 545 550 555 560

Ala Lys Gln

<210> 17
 <211> 1692
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 17
 atgtctgaaa ttactcttgg aaaatactta tttgaaagat tgaagcaagt taatgttaac 60
 accatttttg ggctaccagg cgacttcaac ttgtccctat tggacaagat ttacgaggta 120
 gatggattga gatgggctgg taatgcaaata gagctgaacg ccgcctatgc cgccgatggg 180
 tacgcacgca tcaagggttt atctgtgctg gtaactactt ttggcgtagg tgaattatcc 240
 gccttgaatg gtattgcagg atcgtatgca gaacacgtcg gtgtactgca tgttgttggg 300
 gtccccctcta tctccgctca ggctaagcaa ttgttgttgc atcatacctt gggtaacggg 360
 gattttaccg tttttcacag aatgtccgcc aatatctcag aaactacatc aatgattaca 420
 gacattgcta cagccccctc agaaatcgat aggttgatca ggacaacatt tataacacaa 480
 aggcctagct acttgggggt gccagcgaat ttggtagatc taaagggtcc tggttctctt 540
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 attgataccg tactagaatt gatccagaat tcgaaaaacc ctgttatact atcggatgcc 660
 tgtgtcttcta ggcacaacgt taaaaaagaa acccagaagt taattgattt gacgcaattc 720
 ccagcttttg tgacacctct aggtaaaggg tcaatagatg aacagcatcc cagatatggc 780
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 tacaagacta aaaatgtagt ggagtttcat tccgattacg taaagggtgaa gaacgctacg 960
 ttcctcgggtg taaaaatgaa atttgcaact caaaacttac tgaagggttat tcccgatggt 1020
 gtttaagggt acaagagcgt tcccgtacca accaaaactc ccgcaaacaa aggtgtacct 1080
 gctagcacgc ccttgaaaca agagtgggtg tggaacgaat tgtccaaatt cttgcaagaa 1140
 ggtgatgtta tcatttccga gaccggcacg tctgccttcg gtatcaatca aactatcttt 1200
 cctaaggacg cctacggtat ctgcaggtg ttgtgggggt ccatcggttt tacaacagga 1260
 gcaactttag gtgctgcctt tgccgctgag gagattgacc ccaacaagag agtcatctta 1320
 ttcataagggt acgggtcttt gcagttaacc gtccaagaaa tctccaccat gatcagatgg 1380
 gggttaaagc cgtatctttt tgtccttaac aacgacggct acactatcga aaagctgatt 1440
 catgggcctc acgcagagta caacgaaatc cagacctggg atcacctcgc cctgttgccc 1500

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gcatttggtg cgaaaaagta cgaaaatcac aagatcgcca ctacgggtga gtgggatgcc 1560
 ttaaccactg attcagagtt ccagaaaaac tcggtgatca gactaattga actgaaactg 1620
 cccgtctttg atgctccgga aagtttgatc aaacaagcgc aattgactgc cgctacaaat 1680
 gccaaacaat aa 1692

<210> 18
 <211> 563
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 18

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

Val Asn Val Asn Thr Ile Phe Gly Leu Pro Gly Asp Phe Asn Leu Ser
 20 25 30

Leu Leu Asp Lys Ile Tyr Glu Val Asp Gly Leu Arg Trp Ala Gly Asn
 35 40 45

Ala Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Ile
 50 55 60

Lys Gly Leu Ser Val Leu Val Thr Thr Phe Gly Val Gly Glu Leu Ser
 65 70 75 80

Ala Leu Asn Gly Ile Ala Gly Ser Tyr Ala Glu His Val Gly Val Leu
 85 90 95

His Val Val Gly Val Pro Ser Ile Ser Ala Gln Ala Lys Gln Leu Leu
 100 105 110

Leu His His Thr Leu Gly Asn Gly Asp Phe Thr Val Phe His Arg Met
 115 120 125

Ser Ala Asn Ile Ser Glu Thr Thr Ser Met Ile Thr Asp Ile Ala Thr
 130 135 140

Ala Pro Ser Glu Ile Asp Arg Leu Ile Arg Thr Thr Phe Ile Thr Gln
 145 150 155 160

Arg Pro Ser Tyr Leu Gly Leu Pro Ala Asn Leu Val Asp Leu Lys Val
 165 170 175

Pro Gly Ser Leu Leu Glu Lys Pro Ile Asp Leu Ser Leu Lys Pro Asn
 180 185 190

Asp Pro Glu Ala Glu Lys Glu Val Ile Asp Thr Val Leu Glu Leu Ile
 195 200 205

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Gln Asn Ser Lys Asn Pro Val Ile Leu Ser Asp Ala Cys Ala Ser Arg
210 215 220

His Asn Val Lys Lys Glu Thr Gln Lys Leu Ile Asp Leu Thr Gln Phe
225 230 235 240

Pro Ala Phe Val Thr Pro Leu Gly Lys Gly Ser Ile Asp Glu Gln His
245 250 255

Pro Arg Tyr Gly Gly Val Tyr Val Gly Thr Leu Ser Lys Gln Asp Val
260 265 270

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

Leu Ser Asp Phe Asn Thr Gly Ser Phe Ser Tyr Ser Tyr Lys Thr Lys
290 295 300

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

Phe Leu Gly Val Gln Met Lys Phe Ala Leu Gln Asn Leu Leu Lys Val
325 330 335

Ile Pro Asp Val Val Lys Gly Tyr Lys Ser Val Pro Val Pro Thr Lys
340 345 350

Thr Pro Ala Asn Lys Gly Val Pro Ala Ser Thr Pro Leu Lys Gln Glu
355 360 365

Trp Leu Trp Asn Glu Leu Ser Lys Phe Leu Gln Glu Gly Asp Val Ile
370 375 380

Ile Ser Glu Thr Gly Thr Ser Ala Phe Gly Ile Asn Gln Thr Ile Phe
385 390 395 400

Pro Lys Asp Ala Tyr Gly Ile Ser Gln Val Leu Trp Gly Ser Ile Gly
405 410 415

Phe Thr Thr Gly Ala Thr Leu Gly Ala Ala Phe Ala Ala Glu Glu Ile
420 425 430

Asp Pro Asn Lys Arg Val Ile Leu Phe Ile Gly Asp Gly Ser Leu Gln
435 440 445

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

Tyr Leu Phe Val Leu Asn Asn Asp Gly Tyr Thr Ile Glu Lys Leu Ile
465 470 475 480

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His Gly Pro His Ala Glu Tyr Asn Glu Ile Gln Thr Trp Asp His Leu
485 490 495

Ala Leu Leu Pro Ala Phe Gly Ala Lys Lys Tyr Glu Asn His Lys Ile
500 505 510

Ala Thr Thr Gly Glu Trp Asp Ala Leu Thr Thr Asp Ser Glu Phe Gln
515 520 525

Lys Asn Ser Val Ile Arg Leu Ile Glu Leu Lys Leu Pro Val Phe Asp
530 535 540

Ala Pro Glu Ser Leu Ile Lys Gln Ala Gln Leu Thr Ala Ala Thr Asn
545 550 555 560

Ala Lys Gln

<210> 19
<211> 1908
<212> DNA
<213> Saccharomyces cerevisiae

<400> 19
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aaatcagttt tcggtgttcc tgggtgacttc aacttatctc tattagaata tctctattca 180
cctagtgttg aatcagctgg cctaagatgg gtcggcacgt gtaatgaact gaacgccgct 240
tatgcggccg acggatattc ccgttactct aataagattg gctgtttaat aaccacgtat 300
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gttttgcaca ttgttggtgt ggccaagtcc atagattcgc gttcaagtaa ctttagtgat 420
cggaacctac atcatttggt cccacagcta catgattcaa attttaaagg gccaaatcat 480
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cctggttata tttttgttcc tgcagatttt gcggatatgt ctgttacatg tgataatttg 660
gttaatgttc cacgtatatc tcaacaagat tgtatagtat acccttctga aaaccaattg 720
tctgacataa tcaacaagat tactagttagg atatattcca gtaaaacacc tgcgatcctt 780
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ctgtgcgact tgggtcttgca ttttgagtc gacatcaatg aaattaataa tgggcattat 1020
acttttactt ataaacaaaa tgctaaaatc attcaatttc atccgaatta tattcgctt 1080
gtggacacta ggcagggcaa tgagcaaatg ttcaaaggaa tcaattttgc ccctatttta 1140

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aaagaactat acaagcgc	at tgacgtttct aaactttctt	tgcaatatga ttcaa	atgta	1200
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gactataagc caagattaat	tttgtttgaa ggtgacggtg	cagcacagat gacaatccaa		1560
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ggctacacta ttgaaagagc	catcatgggc cctaccaggt	cgtataacga cgttatgtct		1680
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aaaagaagcg ggatagaact	tttagaagtc aaattaggcg	aattggattt ccccgaacag		1860
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<210> 20
 <211> 635
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 20

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Leu Val Ser Asn Arg Ser Ala Thr Ile Pro Phe Gly Glu Tyr Ile Phe
 20 25 30

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

Asp Phe Asn Leu Ser Leu Leu Glu Tyr Leu Tyr Ser Pro Ser Val Glu
 50 55 60

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

Tyr Ala Ala Asp Gly Tyr Ser Arg Tyr Ser Asn Lys Ile Gly Cys Leu
 85 90 95

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

Gly Ser Phe Ala Glu Asn Val Lys Val Leu His Ile Val Gly Val Ala
 115 120 125

Lys Ser Ile Asp Ser Arg Ser Ser Asn Phe Ser Asp Arg Asn Leu His
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130

135

140

His Leu Val Pro Gln Leu His Asp Ser Asn Phe Lys Gly Pro Asn His
 145 150 155 160
 Lys Val Tyr His Asp Met Val Lys Asp Arg Val Ala Cys Ser Val Ala
 165 170 175
 Tyr Leu Glu Asp Ile Glu Thr Ala Cys Asp Gln Val Asp Asn Val Ile
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 Arg Asp Ile Tyr Lys Tyr Ser Lys Pro Gly Tyr Ile Phe Val Pro Ala
 195 200 205
 Asp Phe Ala Asp Met Ser Val Thr Cys Asp Asn Leu Val Asn Val Pro
 210 215 220
 Arg Ile Ser Gln Gln Asp Cys Ile Val Tyr Pro Ser Glu Asn Gln Leu
 225 230 235 240
 Ser Asp Ile Ile Asn Lys Ile Thr Ser Trp Ile Tyr Ser Ser Lys Thr
 245 250 255
 Pro Ala Ile Leu Gly Asp Val Leu Thr Asp Arg Tyr Gly Val Ser Asn
 260 265 270
 Phe Leu Asn Lys Leu Ile Cys Lys Thr Gly Ile Trp Asn Phe Ser Thr
 275 280 285
 Val Met Gly Lys Ser Val Ile Asp Glu Ser Asn Pro Thr Tyr Met Gly
 290 295 300
 Gln Tyr Asn Gly Lys Glu Gly Leu Lys Gln Val Tyr Glu His Phe Glu
 305 310 315 320
 Leu Cys Asp Leu Val Leu His Phe Gly Val Asp Ile Asn Glu Ile Asn
 325 330 335
 Asn Gly His Tyr Thr Phe Thr Tyr Lys Pro Asn Ala Lys Ile Ile Gln
 340 345 350
 Phe His Pro Asn Tyr Ile Arg Leu Val Asp Thr Arg Gln Gly Asn Glu
 355 360 365
 Gln Met Phe Lys Gly Ile Asn Phe Ala Pro Ile Leu Lys Glu Leu Tyr
 370 375 380
 Lys Arg Ile Asp Val Ser Lys Leu Ser Leu Gln Tyr Asp Ser Asn Val
 385 390 395 400
 Thr Gln Tyr Thr Asn Glu Thr Met Arg Leu Glu Asp Pro Thr Asn Gly

405

410

415

Gln Ser Ser Ile Ile Thr Gln Val His Leu Gln Lys Thr Met Pro Lys
 420 425 430

Phe Leu Asn Pro Gly Asp Val Val Val Cys Glu Thr Gly Ser Phe Gln
 435 440 445

Phe Ser Val Arg Asp Phe Ala Phe Pro Ser Gln Leu Lys Tyr Ile Ser
 450 455 460

Gln Gly Phe Phe Leu Ser Ile Gly Met Ala Leu Pro Ala Ala Leu Gly
 465 470 475 480

Val Gly Ile Ala Met Gln Asp His Ser Asn Ala His Ile Asn Gly Gly
 485 490 495

Asn Val Lys Glu Asp Tyr Lys Pro Arg Leu Ile Leu Phe Glu Gly Asp
 500 505 510

Gly Ala Ala Gln Met Thr Ile Gln Glu Leu Ser Thr Ile Leu Lys Cys
 515 520 525

Asn Ile Pro Leu Glu Val Ile Ile Trp Asn Asn Asn Gly Tyr Thr Ile
 530 535 540

Glu Arg Ala Ile Met Gly Pro Thr Arg Ser Tyr Asn Asp Val Met Ser
 545 550 555 560

Trp Lys Trp Thr Lys Leu Phe Glu Ala Phe Gly Asp Phe Asp Gly Lys
 565 570 575

Tyr Thr Asn Ser Thr Leu Ile Gln Cys Pro Ser Lys Leu Ala Leu Lys
 580 585 590

Leu Glu Glu Leu Lys Asn Ser Asn Lys Arg Ser Gly Ile Glu Leu Leu
 595 600 605

Glu Val Lys Leu Gly Glu Leu Asp Phe Pro Glu Gln Leu Lys Cys Met
 610 615 620

Val Glu Ala Ala Ala Leu Lys Arg Asn Lys Lys
 625 630 635

<210> 21

<211> 1830

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 21

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120

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ctcataacaa cctttggtgt aggcgaatta tcggcaatca atggcgtggc cggatcttac	300
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caactactac tgcatacat tctgggcaat ggtgatttca cggtatttca tagaatagcc	420
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gataagtgc tcaaaaaggc ttggatagaa cagaggccag tatacatggg catgcctgtc	540
aaccaggtaa atctcccgat tgaatcagca aggcttaata cacctctgga tttacaattg	600
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aaaagccaga atccggcaat catcgtagat gcatgtacta gtcgacagaa tttaatcgag	720
gagactaaag agctttgtaa taggcctaaa tttccagttt ttgttacacc tatgggtaag	780
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ctacagaaaa tattagcaaa tcttgatgaa tctaaactgt cttaccaacc aagcgaacaa	1080
cccagtatga tggttccaag accttaccga gcaggaaatg tcctcttgag acaagaatgg	1140
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agggatgttc cacaggctct gcttgacagg tgggtggtag aaaaagaaca gagcaaacaa	1740
gtgcaagagg agaacgaaaa ttctagcgca gtaaatacgc caactccaga attccaacca	1800
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<210> 22

<211> 609

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 22

Met Asn Ser Ser Tyr Thr Gln Arg Tyr Ala Leu Pro Lys Cys Ile Ala

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 Ile Ser Asp Tyr₂₀ Leu Phe His Arg Leu₂₅ Asn Gln Leu Asn Ile₃₀ His Thr
 Ile Phe Gly₃₅ Leu Ser Gly Glu Phe₄₀ Ser Met Pro Leu₄₅ Asp Lys Leu
 Tyr Asn Ile₅₀ Pro Asn Leu Arg₅₅ Trp Ala Gly Asn Ser₆₀ Asn Glu Leu Asn
 Ala Ala Tyr Ala Ala Asp₇₀ Gly Tyr Ser Arg Leu₇₅ Lys Gly Leu Gly Cys₈₀
 Leu Ile Thr Thr₈₅ Phe Gly Val Gly Glu Leu₉₀ Ser Ala Ile Asn Gly₉₅ Val
 Ala Gly Ser Tyr₁₀₀ Ala Glu His Val Gly₁₀₅ Ile Leu His Ile Val₁₁₀ Gly Met
 Pro Pro Thr₁₁₅ Ser Ala Gln Thr Lys₁₂₀ Gln Leu Leu Leu His₁₂₅ His Thr Leu
 Gly Asn Gly Asp Phe Thr Val₁₃₅ Phe His Arg Ile Ala₁₄₀ Ser Asp Val Ala
 Cys Tyr Thr Thr Leu₁₄₅ Ile₁₅₀ Ile Asp Ser Glu Leu₁₅₅ Cys Ala Asp Glu Val₁₆₀
 Asp Lys Cys Ile Lys₁₆₅ Lys Ala Trp Ile Glu₁₇₀ Gln Arg Pro Val Tyr₁₇₅ Met
 Gly Met Pro Val₁₈₀ Asn Gln Val Asn Leu₁₈₅ Pro Ile Glu Ser Ala₁₉₀ Arg Leu
 Asn Thr Pro₁₉₅ Leu Asp Leu Gln Leu₂₀₀ His Lys Asn Asp Pro₂₀₅ Asp Val Glu
 Lys Glu Val Ile Ser Arg Ile₂₁₅ Leu Ser Phe Ile Tyr₂₂₀ Lys Ser Gln Asn
 Pro Ala Ile Ile Val Asp₂₃₀ Ala Cys Thr Ser Arg₂₃₅ Gln Asn Leu Ile Glu₂₄₀
 Glu Thr Lys Glu Leu₂₄₅ Cys Asn Arg Leu Lys₂₅₀ Phe Pro Val Phe Val₂₅₅ Thr
 Pro Met Gly Lys₂₆₀ Gly Thr Val Asn Glu₂₆₅ Thr Asp Pro Gln Phe₂₇₀ Gly Gly
 Val Phe Thr Gly Ser Ile Ser Ala Pro Glu Val Arg Glu Val Val Asp

275

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280

285

Phe Ala Asp Phe Ile Ile Val Ile Gly Cys Met Leu Ser Glu Phe Ser
290 295 300

Thr Ser Thr Phe His Phe Gln Tyr Lys Thr Lys Asn Cys Ala Leu Leu
305 310 315 320

Tyr Ser Thr Ser Val Lys Leu Lys Asn Ala Thr Tyr Pro Asp Leu Ser
325 330 335

Ile Lys Leu Leu Leu Gln Lys Ile Leu Ala Asn Leu Asp Glu Ser Lys
340 345 350

Leu Ser Tyr Gln Pro Ser Glu Gln Pro Ser Met Met Val Pro Arg Pro
355 360 365

Tyr Pro Ala Gly Asn Val Leu Leu Arg Gln Glu Trp Val Trp Asn Glu
370 375 380

Ile Ser His Trp Phe Gln Pro Gly Asp Ile Ile Ile Thr Glu Thr Gly
385 390 395 400

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

Gly Ile Ser Gln Ala Leu Trp Gly Ser Val Gly Tyr Thr Met Gly Ala
420 425 430

Cys Leu Gly Ala Glu Phe Ala Val Gln Glu Ile Asn Lys Asp Lys Phe
435 440 445

Pro Ala Thr Lys His Arg Val Ile Leu Phe Met Gly Asp Gly Ala Phe
450 455 460

Gln Leu Thr Val Gln Glu Leu Ser Thr Ile Val Lys Trp Gly Leu Thr
465 470 475 480

Pro Tyr Ile Phe Val Met Asn Asn Gln Gly Tyr Ser Val Asp Arg Phe
485 490 495

Leu His His Arg Ser Asp Ala Ser Tyr Tyr Asp Ile Gln Pro Trp Asn
500 505 510

Tyr Leu Gly Leu Leu Arg Val Phe Gly Cys Thr Asn Tyr Glu Thr Lys
515 520 525

Lys Ile Ile Thr Val Gly Glu Phe Arg Ser Met Ile Ser Asp Pro Asn
530 535 540

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

Gly Lys Leu Glu Tyr Lys Asp Ile Pro Val Pro Lys Pro Lys Ala Asn
20 25 30

Glu Leu Leu Ile Asn Val Lys Tyr Ser Gly Val Cys His Thr Asp Leu
35 40 45

His Ala Trp His Gly Asp Trp Pro Leu Pro Val Lys Leu Pro Leu Val
50 55 60

Gly Gly His Glu Gly Ala Gly Val Val Val Gly Met Gly Glu Asn Val
65 70 75 80

Lys Gly Trp Lys Ile Gly Asp Tyr Ala Gly Ile Lys Trp Leu Asn Gly
85 90 95

Ser Cys Met Ala Cys Glu Tyr Cys Glu Leu Gly Asn Glu Ser Asn Cys
100 105 110

Pro His Ala Asp Leu Ser Gly Tyr Thr His Asp Gly Ser Phe Gln Gln
115 120 125

Tyr Ala Thr Ala Asp Ala Val Gln Ala Ala His Ile Pro Gln Gly Thr
130 135 140

Asp Leu Ala Gln Val Ala Pro Ile Leu Cys Ala Gly Ile Thr Val Tyr
145 150 155 160

Lys Ala Leu Lys Ser Ala Asn Leu Met Ala Gly His Trp Val Ala Ile
165 170 175

Ser Gly Ala Ala Gly Gly Leu Gly Ser Leu Ala Val Gln Tyr Ala Lys
180 185 190

Ala Met Gly Tyr Arg Val Leu Gly Ile Asp Gly Gly Glu Gly Lys Glu
195 200 205

Glu Leu Phe Arg Ser Ile Gly Gly Glu Val Phe Ile Asp Phe Thr Lys
210 215 220

Glu Lys Asp Ile Val Gly Ala Val Leu Lys Ala Thr Asp Gly Gly Ala
225 230 235 240

His Gly Val Ile Asn Val Ser Val Ser Glu Ala Ala Ile Glu Ala Ser
245 250 255

Thr Arg Tyr Val Arg Ala Asn Gly Thr Thr Val Leu Val Gly Met Pro
260 265 270

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Ala Gly Ala Lys Cys Cys Ser Asp Val Phe Asn Gln Val Val Lys Ser
275 280 285

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

Ala Leu Asp Phe Phe Ala Arg Gly Leu Val Lys Ser Pro Ile Lys Val
305 310 315 320

Val Gly Leu Ser Thr Leu Pro Glu Ile Tyr Glu Lys Met Glu Lys Gly
325 330 335

Gln Ile Val Gly Arg Tyr Val Val Asp Thr Ser Lys
340 345

<210> 25
<211> 1047
<212> DNA
<213> Saccharomyces cerevisiae

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tctggtgtct gccacaccga ttgacacgct tggcatggtg actggccatt gccaaactaag 180
ttaccattag ttggtggtca cgaaggtgcc ggtgtcgttg tcggcatggg tgaaaacgtt 240
aagggctgga agatcgggtga ctacgccggt atcaaatggt tgaacggttc ttgtatggcc 300
tgtgaatact gtgaattggg taacgaatcc aactgtcctc acgctgactt gtctggttac 360
accacgacg gttctttcca agaatacgtc accgctgacg ctgttcaagc cgctcacatt 420
cctcaaggta ctgacttggc tgaagtcgcg ccaatcttgt gtgctggtat caccgtatac 480
aaggctttga agtctgccaa cttgagagca ggccactggg cggccatttc tgggtgctgct 540
gggtggtctag gttctttggc tggtcaatat gctaaggcga tgggttacag agtcttaggt 600
attgatggtg gtccaggaaa ggaagaattg ttacctcgc tcggtggtga agtattcatc 660
gacttcacca aagagaagga cattgttagc gcagtcgtta aggctaccaa cggcgggtgcc 720
cacggtatca tcaatgtttc cgtttccgaa gccgctatcg aagcttctac cagatactgt 780
agggcgaacg gtactgttgt cttggttggt ttgccagccg gtgcaaagtg ctcctctgat 840
gtcttcaacc acgttgtcaa gtctatctcc attgtcggct cttacgtggg gaacagagct 900
gataccagag aagccttaga tttctttgcc agaggtctag tcaagtctcc aataaaggta 960
gttggttat ccagtttacc agaaatttac gaaaagatgg agaagggcca aattgctggt 1020
agatacgttg ttgacacttc taaataa 1047

<210> 26
<211> 348
<212> PRT
<213> Saccharomyces cerevisiae

<400> 26

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Gly Lys Leu Glu His Lys Asp Ile Pro Val Pro Lys Pro Lys Pro Asn
 20 25 30

Glu Leu Leu Ile Asn Val Lys Tyr Ser Gly Val Cys His Thr Asp Leu
 35 40 45

His Ala Trp His Gly Asp Trp Pro Leu Pro Thr Lys Leu Pro Leu Val
 50 55 60

Gly Gly His Glu Gly Ala Gly Val Val Val Gly Met Gly Glu Asn Val
 65 70 75 80

Lys Gly Trp Lys Ile Gly Asp Tyr Ala Gly Ile Lys Trp Leu Asn Gly
 85 90 95

Ser Cys Met Ala Cys Glu Tyr Cys Glu Leu Gly Asn Glu Ser Asn Cys
 100 105 110

Pro His Ala Asp Leu Ser Gly Tyr Thr His Asp Gly Ser Phe Gln Glu
 115 120 125

Tyr Ala Thr Ala Asp Ala Val Gln Ala Ala His Ile Pro Gln Gly Thr
 130 135 140

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

Lys Ala Leu Lys Ser Ala Asn Leu Arg Ala Gly His Trp Ala Ala Ile
 165 170 175

Ser Gly Ala Ala Gly Gly Leu Gly Ser Leu Ala Val Gln Tyr Ala Lys
 180 185 190

Ala Met Gly Tyr Arg Val Leu Gly Ile Asp Gly Gly Pro Gly Lys Glu
 195 200 205

Glu Leu Phe Thr Ser Leu Gly Gly Glu Val Phe Ile Asp Phe Thr Lys
 210 215 220

Glu Lys Asp Ile Val Ser Ala Val Val Lys Ala Thr Asn Gly Gly Ala
 225 230 235 240

His Gly Ile Ile Asn Val Ser Val Ser Glu Ala Ala Ile Glu Ala Ser
 245 250 255

Thr Arg Tyr Cys Arg Ala Asn Gly Thr Val Val Leu Val Gly Leu Pro
 Seite 36

260

265

270

Ala Gly Ala Lys Cys Ser Ser Asp Val Phe Asn His Val Val Lys Ser
 275 280 285

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

Ala Leu Asp Phe Phe Ala Arg Gly Leu Val Lys Ser Pro Ile Lys Val
 305 310 315 320

Val Gly Leu Ser Ser Leu Pro Glu Ile Tyr Glu Lys Met Glu Lys Gly
 325 330 335

Gln Ile Ala Gly Arg Tyr Val Val Asp Thr Ser Lys
 340 345

<210> 27
 <211> 1128
 <212> DNA
 <213> *Saccharomyces cerevisiae*

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 gagaataagg ggaagctgca ttacaaagat atccctgtcc ccgagcctaa gccaaatgaa 180
 attttaatca acgttaaata ttctgggtgta tgtcacaccg atttacatgc ttggcacggc 240
 gattggccat tacctgttaa actaccatta gtaggtggtc atgaagggtgc tgggtgtagtt 300
 gtcaaactag gttccaatgt caagggctgg aaagtcggtg atttagcagg tatcaaattg 360
 ctgaacggtt cttgtatgac atgcgaattc tgtgaatcag gtcattgaatc aaattgtcca 420
 gatgctgatt tatctgggta cactcatgat gggtctttcc aacaatttgc gaccgctgat 480
 gctattcaag ccgccaaaat tcaacagggg accgacttgg ccgaagtagc cccaatatta 540
 tgtgctgggtg ttactgtata taaagcacta aaagaggcag acttgaaagc tgggtgactgg 600
 gttgccatct ctgggtgctgc aggtggcttg gggttccttg ccgttcaata tgcaactgcg 660
 atgggttaca gagttctagg tattgatgca ggtgaggaaa aggaaaaact tttcaagaaa 720
 ttgggggggtg aagtattcat cgactttact aaaacaaaga atatgggtttc tgacattcaa 780
 gaagctacca aaggtggccc tcatgggtgtc attaacgttt ccgtttctga agccgctatt 840
 tctctatcta cggaatatgt tagaccatgt ggtaccgtcg ttttggttg tttgcccgt 900
 aacgcctacg ttaaatacaga ggtattctct catgtggtga agtccatcaa tatcaagggt 960
 tcttatgttg gtaacagagc tgatacgaga gaagccttag acttcttttag cagagggttg 1020
 atcaaatac caataaaaat tggttgatta tctgaattac caaagggtta tgacttgatg 1080
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<210> 28
<211> 375
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 28

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1 5 10 15

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

Thr Gln Lys Gly Val Ile Phe Tyr Glu Asn Lys Gly Lys Leu His Tyr
35 40 45

Lys Asp Ile Pro Val Pro Glu Pro Lys Pro Asn Glu Ile Leu Ile Asn
50 55 60

Val Lys Tyr Ser Gly Val Cys His Thr Asp Leu His Ala Trp His Gly
65 70 75 80

Asp Trp Pro Leu Pro Val Lys Leu Pro Leu Val Gly Gly His Glu Gly
85 90 95

Ala Gly Val Val Val Lys Leu Gly Ser Asn Val Lys Gly Trp Lys Val
100 105 110

Gly Asp Leu Ala Gly Ile Lys Trp Leu Asn Gly Ser Cys Met Thr Cys
115 120 125

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

Ser Gly Tyr Thr His Asp Gly Ser Phe Gln Gln Phe Ala Thr Ala Asp
145 150 155 160

Ala Ile Gln Ala Ala Lys Ile Gln Gln Gly Thr Asp Leu Ala Glu Val
165 170 175

Ala Pro Ile Leu Cys Ala Gly Val Thr Val Tyr Lys Ala Leu Lys Glu
180 185 190

Ala Asp Leu Lys Ala Gly Asp Trp Val Ala Ile Ser Gly Ala Ala Gly
195 200 205

Gly Leu Gly Ser Leu Ala Val Gln Tyr Ala Thr Ala Met Gly Tyr Arg
210 215 220

Val Leu Gly Ile Asp Ala Gly Glu Glu Lys Glu Lys Leu Phe Lys Lys
225 230 235 240

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

245

250

255

Ser Asp Ile Gln Glu Ala Thr Lys Gly Gly Pro His Gly Val Ile Asn
 260 265 270

Val Ser Val Ser Glu Ala Ala Ile Ser Leu Ser Thr Glu Tyr Val Arg
 275 280 285

Pro Cys Gly Thr Val Val Leu Val Gly Leu Pro Ala Asn Ala Tyr Val
 290 295 300

Lys Ser Glu Val Phe Ser His Val Val Lys Ser Ile Asn Ile Lys Gly
 305 310 315 320

Ser Tyr Val Gly Asn Arg Ala Asp Thr Arg Glu Ala Leu Asp Phe Phe
 325 330 335

Ser Arg Gly Leu Ile Lys Ser Pro Ile Lys Ile Val Gly Leu Ser Glu
 340 345 350

Leu Pro Lys Val Tyr Asp Leu Met Glu Lys Gly Lys Ile Leu Gly Arg
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Tyr Val Val Asp Thr Ser Lys
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<210> 29

<211> 1149

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 29

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ttaaacgttg ctatctatga caaaactcaa ccaaacccaa atattgccaa tgtcacagct      240
ggtttgaagg ttttgaagga acaaaactct gaaattgttg tttccattgg tgggtggttct      300
gctcacgaca atgctaaggc cattgcttta ttggctacta acggtgggga aatcggagac      360
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<210> 30
<211> 382
<212> PRT
<213> *Saccharomyces cerevisiae*
<400> 30

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20 25 30

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

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

Ile Tyr Asp Lys Thr Gln Pro Asn Pro Asn Ile Ala Asn Val Thr Ala
65 70 75 80

Gly Leu Lys Val Leu Lys Glu Gln Asn Ser Glu Ile Val Val Ser Ile
85 90 95

Gly Gly Gly Ser Ala His Asp Asn Ala Lys Ala Ile Ala Leu Leu Ala
100 105 110

Thr Asn Gly Gly Glu Ile Gly Asp Tyr Glu Gly Val Asn Gln Ser Lys
115 120 125

Lys Ala Ala Leu Pro Leu Phe Ala Ile Asn Thr Thr Ala Gly Thr Ala
130 135 140

Ser Glu Met Thr Arg Phe Thr Ile Ile Ser Asn Glu Glu Lys Lys Ile
145 150 155 160

Lys Met Ala Ile Ile Asp Asn Asn Val Thr Pro Ala Val Ala Val Asn
165 170 175

Asp Pro Ser Thr Met Phe Gly Leu Pro Pro Ala Leu Thr Ala Ala Thr
180 185 190

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Gly Leu Asp Ala Leu Thr His Cys Ile Glu Ala Tyr Val Ser Thr Ala
 195 200 205

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

Asn Glu Ser Leu Val Ala Ala Tyr Lys Asp Gly Lys Asp Lys Lys Ala
 225 230 235 240

Arg Thr Asp Met Cys Tyr Ala Glu Tyr Leu Ala Gly Met Ala Phe Asn
 245 250 255

Asn Ala Ser Leu Gly Tyr Val His Ala Leu Ala His Gln Leu Gly Gly
 260 265 270

Phe Tyr His Leu Pro His Gly Val Cys Asn Ala Val Leu Leu Pro His
 275 280 285

Val Gln Glu Ala Asn Met Gln Cys Pro Lys Ala Lys Lys Arg Leu Gly
 290 295 300

Glu Ile Ala Leu His Phe Gly Ala Ser Gln Glu Asp Pro Glu Glu Thr
 305 310 315 320

Ile Lys Ala Leu His Val Leu Asn Arg Thr Met Asn Ile Pro Arg Asn
 325 330 335

Leu Lys Glu Leu Gly Val Lys Thr Glu Asp Phe Glu Ile Leu Ala Glu
 340 345 350

His Ala Met His Asp Ala Cys His Leu Thr Asn Pro Val Gln Phe Thr
 355 360 365

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<210> 31
 <211> 1056
 <212> DNA
 <213> Saccharomyces cerevisiae

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 gttaaataatt ctggtgtttg tcatagtgac ttgcacgcgt ggcacggtga ttggccattt 180
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 tgcattgtcct gtgaatattg tgaagtaggt aatgaatctc aatgtcctta tttggatggt 360
 actggcttca cacatgatgg tacttttcaa gaatacgcaa ctgccgatgc cgttcaagct 420

33847-BUT-P-WO-2009001860

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<210> 32
 <211> 351
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 32

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

Lys Pro Asn Glu Ile Leu Val His Val Lys Tyr Ser Gly Val Cys His
 35 40 45

Ser Asp Leu His Ala Trp His Gly Asp Trp Pro Phe Gln Leu Lys Phe
 50 55 60

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

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

Leu Asn Gly Thr Cys Met Ser Cys Glu Tyr Cys Glu Val Gly Asn Glu
 100 105 110

Ser Gln Cys Pro Tyr Leu Asp Gly Thr Gly Phe Thr His Asp Gly Thr
 115 120 125

Phe Gln Glu Tyr Ala Thr Ala Asp Ala Val Gln Ala Ala His Ile Pro
 130 135 140

Pro Asn Val Asn Leu Ala Glu Val Ala Pro Ile Leu Cys Ala Gly Ile

145 150 155 160

Thr Val Tyr Lys Ala Leu Lys Arg Ala Asn Val Ile Pro Gly Gln Trp
165 170 175

Val Thr Ile Ser Gly Ala Cys Gly Gly Leu Gly Ser Leu Ala Ile Gln
180 185 190

Tyr Ala Leu Ala Met Gly Tyr Arg Val Ile Gly Ile Asp Gly Gly Asn
195 200 205

Ala Lys Arg Lys Leu Phe Glu Gln Leu Gly Gly Glu Ile Phe Ile Asp
210 215 220

Phe Thr Glu Glu Lys Asp Ile Val Gly Ala Ile Ile Lys Ala Thr Asn
225 230 235 240

Gly Gly Ser His Gly Val Ile Asn Val Ser Val Ser Glu Ala Ala Ile
245 250 255

Glu Ala Ser Thr Arg Tyr Cys Arg Pro Asn Gly Thr Val Val Leu Val
260 265 270

Gly Met Pro Ala His Ala Tyr Cys Asn Ser Asp Val Phe Asn Gln Val
275 280 285

Val Lys Ser Ile Ser Ile Val Gly Ser Cys Val Gly Asn Arg Ala Asp
290 295 300

Thr Arg Glu Ala Leu Asp Phe Phe Ala Arg Gly Leu Ile Lys Ser Pro
305 310 315 320

Ile His Leu Ala Gly Leu Ser Asp Val Pro Glu Ile Phe Ala Lys Met
325 330 335

Glu Lys Gly Glu Ile Val Gly Arg Tyr Val Val Glu Thr Ser Lys
340 345 350

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<210> 33
<211> 1083
<212> DNA
<213> Saccharomyces cerevisiae
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[illegible]

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tag	1083

<210> 34
 <211> 360
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 34

Met Ser Tyr Pro Glu Lys Phe Glu Gly Ile Ala Ile Gln Ser His Glu
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Asp Trp Lys Asn Pro Lys Lys Thr Lys Tyr Asp Pro Lys Pro Phe Tyr
 20 25 30

Asp His Asp Ile Asp Ile Lys Ile Glu Ala Cys Gly Val Cys Gly Ser
 35 40 45

Asp Ile His Cys Ala Ala Gly His Trp Gly Asn Met Lys Met Pro Leu
 50 55 60

Val Val Gly His Glu Ile Val Gly Lys Val Val Lys Leu Gly Pro Lys
 65 70 75 80

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

Val Phe Ser Cys Leu Glu Cys Asp Arg Cys Lys Asn Asp Asn Glu Pro
 100 105 110

Tyr Cys Thr Lys Phe Val Thr Thr Tyr Ser Gln Pro Tyr Glu Asp Gly
 115 120 125

Tyr Val Ser Gln Gly Gly Tyr Ala Asn Tyr Val Arg Val His Glu His
 Seite 44

130

135

140

Phe Val Val Pro Ile Pro Glu Asn Ile Pro Ser His Leu Ala Ala Pro
145 150 155 160

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

Cys Gly Pro Gly Lys Lys Val Gly Ile Val Gly Leu Gly Gly Ile Gly
180 185 190

Ser Met Gly Thr Leu Ile Ser Lys Ala Met Gly Ala Glu Thr Tyr Val
195 200 205

Ile Ser Arg Ser Ser Arg Lys Arg Glu Asp Ala Met Lys Met Gly Ala
210 215 220

Asp His Tyr Ile Ala Thr Leu Glu Glu Gly Asp Trp Gly Glu Lys Tyr
225 230 235 240

Phe Asp Thr Phe Asp Leu Ile Val Val Cys Ala Ser Ser Leu Thr Asp
245 250 255

Ile Asp Phe Asn Ile Met Pro Lys Ala Met Lys Val Gly Gly Arg Ile
260 265 270

Val Ser Ile Ser Ile Pro Glu Gln His Glu Met Leu Ser Leu Lys Pro
275 280 285

Tyr Gly Leu Lys Ala Val Ser Ile Ser Tyr Ser Ala Leu Gly Ser Ile
290 295 300

Lys Glu Leu Asn Gln Leu Leu Lys Leu Val Ser Glu Lys Asp Ile Lys
305 310 315 320

Ile Trp Val Glu Thr Leu Pro Val Gly Glu Ala Gly Val His Glu Ala
325 330 335

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340 345 350

Gly Tyr Asp Lys Glu Phe Ser Asp
355 360

<210> 35

<211> 1086

<212> DNA

<213> *Saccharomyces cerevisiae*

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cctaaattag tgagttttga cccaaaaccc tttggcgatc atgacgttga tgttgaaatt

120

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<210> 36
<211> 361
<212> PRT
<213> Saccharomyces cerevisiae

<400> 36

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Asp Trp Lys His Pro Lys Leu Val Ser Phe Asp Pro Lys Pro Phe Gly
20 25 30

Asp His Asp Val Asp Val Glu Ile Glu Ala Cys Gly Ile Cys Gly Ser
35 40 45

Asp Phe His Ile Ala Val Gly Asn Trp Gly Pro Val Pro Glu Asn Gln
50 55 60

Ile Leu Gly His Glu Ile Ile Gly Arg Val Val Lys Val Gly Ser Lys
65 70 75 80

Cys His Thr Gly Val Lys Ile Gly Asp Arg Val Gly Val Gly Ala Gln
85 90 95

Ala Leu Ala Cys Phe Glu Cys Glu Arg Cys Lys Ser Asp Asn Glu Gln

100

105

110

Tyr Cys Thr Asn Asp His Val Leu Thr Met Trp Thr Pro Tyr Lys Asp
 115 120 125

Gly Tyr Ile Ser Gln Gly Gly Phe Ala Ser His Val Arg Leu His Glu
 130 135 140

His Phe Ala Ile Gln Ile Pro Glu Asn Ile Pro Ser Pro Leu Ala Ala
 145 150 155 160

Pro Leu Leu Cys Gly Gly Ile Thr Val Phe Ser Pro Leu Leu Arg Asn
 165 170 175

Gly Cys Gly Pro Gly Lys Arg Val Gly Ile Val Gly Ile Gly Gly Ile
 180 185 190

Gly His Met Gly Ile Leu Leu Ala Lys Ala Met Gly Ala Glu Val Tyr
 195 200 205

Ala Phe Ser Arg Gly His Ser Lys Arg Glu Asp Ser Met Lys Leu Gly
 210 215 220

Ala Asp His Tyr Ile Ala Met Leu Glu Asp Lys Gly Trp Thr Glu Gln
 225 230 235 240

Tyr Ser Asn Ala Leu Asp Leu Leu Val Val Cys Ser Ser Ser Leu Ser
 245 250 255

Lys Val Asn Phe Asp Ser Ile Val Lys Ile Met Lys Ile Gly Gly Ser
 260 265 270

Ile Val Ser Ile Ala Ala Pro Glu Val Asn Glu Lys Leu Val Leu Lys
 275 280 285

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

Arg Lys Glu Ile Glu Gln Leu Leu Lys Leu Val Ser Glu Lys Asn Val
 305 310 315 320

Lys Ile Trp Val Glu Lys Leu Pro Ile Ser Glu Glu Gly Val Ser His
 325 330 335

Ala Phe Thr Arg Met Glu Ser Gly Asp Val Lys Tyr Arg Phe Thr Leu
 340 345 350

Val Asp Tyr Asp Lys Lys Phe His Lys
 355 360

<210> 37

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<211> 1161
 <212> DNA
 <213> *Saccharomyces cerevisiae*

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 ccagaaggac ttttcccttg cgttctgggc cacgaaggag ccggtatcgt agaactctgta 240
 ggcgatgatg tcataacagt taagcctggt gatcatgtta ttgctttgta cactgctgag 300
 tgtggcaa at gtaagttctg tacttccggt aaaaccaact tatgtggtgc tgttagagct 360
 actcaaggga aaggtgta at gcctgatggg accacaagat ttcataatgc gaaaggtgaa 420
 gatataacc atttcatggg ttgctctact ttttccgaat atactgtggt ggcagatgtc 480
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<210> 38
 <211> 386
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 38
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 Ala Tyr Asp Ala Lys Lys Pro Leu Ser Val Glu Glu Ile Thr Val Asp
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 Ala Pro Lys Ala His Glu Val Arg Ile Lys Ile Glu Tyr Thr Ala Val
 35 40 45
 Cys His Thr Asp Ala Tyr Thr Leu Ser Gly Ser Asp Pro Glu Gly Leu
 50 55 60

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Phe Pro Cys Val Leu Gly His Glu Gly Ala Gly Ile Val Glu Ser Val
 65 70 75 80
 Gly Asp Asp Val Ile Thr Val Lys Pro Gly Asp His Val Ile Ala Leu
 85 90 95
 Tyr Thr Ala Glu Cys Gly Lys Cys Lys Phe Cys Thr Ser Gly Lys Thr
 100 105 110
 Asn Leu Cys Gly Ala Val Arg Ala Thr Gln Gly Lys Gly Val Met Pro
 115 120 125
 Asp Gly Thr Thr Arg Phe His Asn Ala Lys Gly Glu Asp Ile Tyr His
 130 135 140
 Phe Met Gly Cys Ser Thr Phe Ser Glu Tyr Thr Val Val Ala Asp Val
 145 150 155 160
 Ser Val Val Ala Ile Asp Pro Lys Ala Pro Leu Asp Ala Ala Cys Leu
 165 170 175
 Leu Gly Cys Gly Val Thr Thr Gly Phe Gly Ala Ala Leu Lys Thr Ala
 180 185 190
 Asn Val Gln Lys Gly Asp Thr Val Ala Val Phe Gly Cys Gly Thr Val
 195 200 205
 Gly Leu Ser Val Ile Gln Gly Ala Lys Leu Arg Gly Ala Ser Lys Ile
 210 215 220
 Ile Ala Ile Asp Ile Asn Asn Lys Lys Lys Gln Tyr Cys Ser Gln Phe
 225 230 235 240
 Gly Ala Thr Asp Phe Val Asn Pro Lys Glu Asp Leu Ala Lys Asp Gln
 245 250 255
 Thr Ile Val Glu Lys Leu Ile Glu Met Thr Asp Gly Gly Leu Asp Phe
 260 265 270
 Thr Phe Asp Cys Thr Gly Asn Thr Lys Ile Met Arg Asp Ala Leu Glu
 275 280 285
 Ala Cys His Lys Gly Trp Gly Gln Ser Ile Ile Ile Gly Val Ala Ala
 290 295 300
 Ala Gly Glu Glu Ile Ser Thr Arg Pro Phe Gln Leu Val Thr Gly Arg
 305 310 315 320
 Val Trp Lys Gly Ser Ala Phe Gly Gly Ile Lys Gly Arg Ser Glu Met
 325 330 335

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Gly Gly Leu Ile Lys Asp Tyr Gln Lys Gly Ala Leu Lys Val Glu Glu
340 345 350

Phe Ile Thr His Arg Arg Pro Phe Lys Glu Ile Asn Gln Ala Phe Glu
355 360 365

Asp Leu His Asn Gly Asp Cys Leu Arg Thr Val Leu Lys Ser Asp Glu
370 375 380

Ile Lys
385

<210> 39
<211> 939
<212> DNA
<213> Saccharomyces cerevisiae

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gaagttggca gggctattaa agattccgga gtccctcgtg aggaaatfff tattactact 240
aagctttggg gtacggaaca acgtgatccg gaagctgctc taaacaagtc ttgaaaaga 300
ctaggcttgg attatgttga cctatatctg atgcattggc cagtgccttt gaaaaccgac 360
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gaatctcaa ataacaaggf ggtaccagct actaatcaaa ttgaaattca tccattgcta 600
ccacaagacg aattgattgc cttttgtaag gaaaagggtg ttgttggtga agcctactca 660
ccatttgagg gtgctaatgc tcctttacta aaagagcaag caattattga tatggctaaa 720
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<210> 40
<211> 312
<212> PRT
<213> Saccharomyces cerevisiae

<400> 40

Met Pro Ala Thr Leu Lys Asn Ser Ser Ala Thr Leu Lys Leu Asn Thr
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Gly Ala Ser Ile Pro Val Leu Gly Phe Gly Thr Trp Arg Ser Val Asp
Seite 50

Asn Asn Gly Tyr His Ser Val Ile Ala Ala Leu Lys Ala Gly Tyr Arg
35 40 45

His Ile Asp Ala Ala Ala Ile Tyr Leu Asn Glu Glu Glu Val Gly Arg
50 55 60

Ala Ile Lys Asp Ser Gly Val Pro Arg Glu Glu Ile Phe Ile Thr Thr
65 70 75 80

Lys Leu Trp Gly Thr Glu Gln Arg Asp Pro Glu Ala Ala Leu Asn Lys
85 90 95

Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Leu Tyr Leu Met His
100 105 110

Trp Pro Val Pro Leu Lys Thr Asp Arg Val Thr Asp Gly Asn Val Leu
115 120 125

Cys Ile Pro Thr Leu Glu Asp Gly Thr Val Asp Ile Asp Thr Lys Glu
130 135 140

Trp Asn Phe Ile Lys Thr Trp Glu Leu Met Gln Glu Leu Pro Lys Thr
145 150 155 160

Gly Lys Thr Lys Ala Val Gly Val Ser Asn Phe Ser Ile Asn Asn Ile
165 170 175

Lys Glu Leu Leu Glu Ser Pro Asn Asn Lys Val Val Pro Ala Thr Asn
180 185 190

Gln Ile Glu Ile His Pro Leu Leu Pro Gln Asp Glu Leu Ile Ala Phe
195 200 205

Cys Lys Glu Lys Gly Ile Val Val Glu Ala Tyr Ser Pro Phe Gly Ser
210 215 220

Ala Asn Ala Pro Leu Leu Lys Glu Gln Ala Ile Ile Asp Met Ala Lys
225 230 235 240

Lys His Gly Val Glu Pro Ala Gln Leu Ile Ile Ser Trp Ser Ile Gln
245 250 255

Arg Gly Tyr Val Val Leu Ala Lys Ser Val Asn Pro Glu Arg Ile Val
260 265 270

Ser Asn Phe Lys Ile Phe Thr Leu Pro Glu Asp Asp Phe Lys Thr Ile
275 280 285

Ser Asn Leu Ser Lys Val His Gly Thr Lys Arg Val Val Asp Met Lys
Seite 51

290

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295 300Trp Gly Ser Phe Pro Ile Phe Gln
305 310

<210> 41

<211> 999

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 41

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gctgcttaca tgggtcaagta cgattctact catggtagat acaaggggtac tgtttcccat      180
gacgacaagc acatcatcat tgatggtgct aagatcgcta cctaccaaga aagagaccca      240
gctaacttgc catgggggttc tctaaagatc gatgtcgctg ttgactccac tgggtgttttc      300
aaggaattgg acaccgctca aaagcacatt gacgctggtg ccaagaaggt tgtcatcact      360
gctccatctt cttctgctcc aatgtttggt gttggtgtta accacactaa atacactcca      420
gacaagaaga ttgtctccaa cgcttcttgt accaccaact gtttggctcc attggccaag      480
gttatcaacg atgctttcgg tattgaagaa ggtttgatga cactgttca ctccatgacc      540
gccactcaaa agactgttga tgggtccatcc cacaaggact ggagaggtgg tagaaccgct      600
tcggtgaaca ttatcccatc ctctaccggt gctgctaagg ctgtcggtaa ggtcttgcca      660
gaattgcaag gtaagttgac cggtatggct ttcagagtcc caaccgtcga tgtttccggt      720
gttgacttga ctgtcaagtt ggaaaaggaa gctacttacg accaaatcaa gaaggctgtt      780
aaggctgccg ctgaaggctc aatgaagggt gttttgggtt acaccgaaga tgccgttgtc      840
tcctctgatt tcttgggtga cactcacgct tccatcttcg atgcctccgc tggatatccaa      900
ttgtctccaa agttcgtcaa gttgatttcc tgggtacgata acgaatacgg ttactccgcc      960
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<210> 42

<211> 332

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 42

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

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Leu Arg Leu Ala Leu Gln Arg Lys Asp Ile Glu Val Val Ala Val Asn
20           25           30

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Asp Pro Phe Ile Ser Asn Asp Tyr Ala Ala Tyr Met Val Lys Tyr Asp
35           40           45

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Ser Thr His Gly Arg Tyr Lys Gly Thr Val Ser His Asp Asp Lys His

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50

55

60

Ile Ile Ile Asp Gly Val Lys Ile Ala Thr Tyr Gln Glu Arg Asp Pro
 65 70 75 80

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

Thr Gly Val Phe Lys Glu Leu Asp Thr Ala Gln Lys His Ile Asp Ala
 100 105 110

Gly Ala Lys Lys Val Val Ile Thr Ala Pro Ser Ser Ser Ala Pro Met
 115 120 125

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

Val Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu Ala Lys
 145 150 155 160

Val Ile Asn Asp Ala Phe Gly Ile Glu Glu Gly Leu Met Thr Thr Val
 165 170 175

His Ser Met Thr Ala Thr Gln Lys Thr Val Asp Gly Pro Ser His Lys
 180 185 190

Asp Trp Arg Gly Gly Arg Thr Ala Ser Gly Asn Ile Ile Pro Ser Ser
 195 200 205

Thr Gly Ala Ala Lys Ala Val Gly Lys Val Leu Pro Glu Leu Gln Gly
 210 215 220

Lys Leu Thr Gly Met Ala Phe Arg Val Pro Thr Val Asp Val Ser Val
 225 230 235 240

Val Asp Leu Thr Val Lys Leu Glu Lys Glu Ala Thr Tyr Asp Gln Ile
 245 250 255

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

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

His Ala Ser Ile Phe Asp Ala Ser Ala Gly Ile Gln Leu Ser Pro Lys
 290 295 300

Phe Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Tyr Gly Tyr Ser Ala
 305 310 315 320

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

<210> 43
 <211> 999
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 43
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 ttgcaaagaa agaacgtcga agttgttgct ttgaacgata ctttcatctc taacgactac 120
 tccgcttaca tgttcaagta cgactctact cacggtagat acgctgggtga agtttccac 180
 gatgacaagc acatcatcgt tgatgggtcac aagatcgcca ctttccaaga aagagacca 240
 gctaacttgc catgggcttc tctaaacatt gacatcgcca ttgactccac tgggtgttttc 300
 aaggaattgg aactgtctca aaagcacatt gacgctgggtg ccaagaagggt tgtcatcact 360
 gctccatctt ccaccgcccc aatgttcgtc atgggtgtta acgaagaaa atacacttct 420
 gacttgaaga ttgtttccaa cgcttcttgt accaccaact gtttggctcc attggccaag 480
 gttatcaacg atgctttcgg tattgaagaa ggtttgatga ccactgttca ctccatgacc 540
 gccacccaaa agactgttga cgggtccatcc cacaaggact ggagagggtg tagaaccgct 600
 tccggttaaca tcatcccatc ctctaccggt gctgctaagg ctgtcggtaa ggtcttgcca 660
 gaattgcaag gtaagttgac cgggtatggct ttcagagtcc caaccgtcga tgtttccgtt 720
 gttgacttga ctgtcaagtt gaacaaggaa accacctacg atgaaatcaa gaagggtgtc 780
 aaggctgccg ctgaaggtaa gttgaagggt gtcttgggtt aactgaaga cgctgttgct 840
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 ttgtctccaa agttcgtcaa gttgggttcc tggtagaca acgaatacgg ttactctacc 960
 agagttgtcg acttggttga acacgttgcc aaggcttaa 999

<210> 44
 <211> 332
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 44

Met Val Arg Val Ala Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu Val
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Met Arg Ile Ala Leu Gln Arg Lys Asn Val Glu Val Val Ala Leu Asn
 20 25 30

Asp Pro Phe Ile Ser Asn Asp Tyr Ser Ala Tyr Met Phe Lys Tyr Asp
 35 40 45

Ser Thr His Gly Arg Tyr Ala Gly Glu Val Ser His Asp Asp Lys His
 50 55 60

Ile Ile Val Asp Gly His Lys Ile Ala Thr Phe Gln Glu Arg Asp Pro

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75

65					70					75					80
Ala	Asn	Leu	Pro	Trp 85	Ala	Ser	Leu	Asn	Ile 90	Asp	Ile	Ala	Ile	Asp 95	Ser
Thr	Gly	Val	Phe 100	Lys	Glu	Leu	Asp	Thr 105	Ala	Gln	Lys	His	Ile 110	Asp	Ala
Gly	Ala	Lys 115	Lys	Val	Val	Ile	Thr 120	Ala	Pro	Ser	Ser	Thr 125	Ala	Pro	Met
Phe	Val 130	Met	Gly	Val	Asn	Glu 135	Glu	Lys	Tyr	Thr	Ser 140	Asp	Leu	Lys	Ile
Val 145	Ser	Asn	Ala	Ser	Cys 150	Thr	Thr	Asn	Cys	Leu 155	Ala	Pro	Leu	Ala	Lys 160
Val	Ile	Asn	Asp	Ala 165	Phe	Gly	Ile	Glu	Glu 170	Gly	Leu	Met	Thr	Thr 175	Val
His	Ser	Met	Thr 180	Ala	Thr	Gln	Lys	Thr 185	Val	Asp	Gly	Pro	Ser 190	His	Lys
Asp	Trp	Arg 195	Gly	Gly	Arg	Thr	Ala 200	Ser	Gly	Asn	Ile	Ile 205	Pro	Ser	Ser
Thr	Gly 210	Ala	Ala	Lys	Ala	Val 215	Gly	Lys	Val	Leu	Pro 220	Glu	Leu	Gln	Gly
Lys 225	Leu	Thr	Gly	Met	Ala 230	Phe	Arg	Val	Pro	Thr 235	Val	Asp	Val	Ser	Val 240
Val	Asp	Leu	Thr	Val 245	Lys	Leu	Asn	Lys	Glu 250	Thr	Thr	Tyr	Asp	Glu 255	Ile
Lys	Lys	Val	Val 260	Lys	Ala	Ala	Ala	Glu 265	Gly	Lys	Leu	Lys	Gly 270	Val	Leu
Gly	Tyr	Thr 275	Glu	Asp	Ala	Val	Val 280	Ser	Ser	Asp	Phe	Leu 285	Gly	Asp	Ser
Asn	Ser 290	Ser	Ile	Phe	Asp	Ala 295	Ala	Ala	Gly	Ile	Gln 300	Leu	Ser	Pro	Lys
Phe 305	Val	Lys	Leu	Val	Ser 310	Trp	Tyr	Asp	Asn	Glu 315	Tyr	Gly	Tyr	Ser	Thr 320
Arg	Val	Val	Asp	Leu 325	Val	Glu	His	Val	Ala 330	Lys	Ala				

<210> 45

<211> 999
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 45
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 gctgcttaca tgttcaagta cgactccact cacggtagat acgctggtga agtttccac 180
 gatgacaagc acatcattgt cgatggtaag aagattgcta cttaccaaga aagagaccca 240
 gctaacttgc catgggggttc ttccaacggt gacatcgcca ttgactccac tgggtgttttc 300
 aaggaattag aactgctca aaagcacatt gacgctggtg ccaagaagg tgttatcact 360
 gctccatctt ccaccgcccc aatgttcgtc atgggtgtta acgaagaaaa atacatttct 420
 gacttgaaga ttgtttccaa cgcttcttgt accaccaact gtttggctcc attggccaag 480
 gttatcaacg atgctttcgg tattgaagaa ggtttgatga ccactgtcca ctctttgact 540
 gctactcaaa agactgttga cgggccatcc cacaaggact ggagaggtgg tagaaccgct 600
 tccggttaaca tcatcccatc ctccaccggt gctgctaagg ctgtcggtaa ggtcttgcca 660
 gaattgcaag gtaagttgac cgggtatggct ttcagagtcc caaccgtcga tgtctccgtt 720
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<210> 46
 <211> 332
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 46

Met Val Arg Val Ala Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu Val
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Met Arg Ile Ala Leu Ser Arg Pro Asn Val Glu Val Val Ala Leu Asn
 20 25 30

Asp Pro Phe Ile Thr Asn Asp Tyr Ala Ala Tyr Met Phe Lys Tyr Asp
 35 40 45

Ser Thr His Gly Arg Tyr Ala Gly Glu Val Ser His Asp Asp Lys His
 50 55 60

Ile Ile Val Asp Gly Lys Lys Ile Ala Thr Tyr Gln Glu Arg Asp Pro
 65 70 75 80

Ala Asn Leu Pro Trp Gly Ser Ser Asn Val Asp Ile Ala Ile Asp Ser
 Seite 56

Thr Gly Val Phe Lys Glu Leu Asp Thr Ala Gln Lys His Ile Asp Ala
 100 105 110

Gly Ala Lys Lys Val Val Ile Thr Ala Pro Ser Ser Thr Ala Pro Met
 115 120 125

Phe Val Met Gly Val Asn Glu Glu Lys Tyr Thr Ser Asp Leu Lys Ile
 130 135 140

Val Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu Ala Lys
 145 150 155 160

Val Ile Asn Asp Ala Phe Gly Ile Glu Glu Gly Leu Met Thr Thr Val
 165 170 175

His Ser Leu Thr Ala Thr Gln Lys Thr Val Asp Gly Pro Ser His Lys
 180 185 190

Asp Trp Arg Gly Gly Arg Thr Ala Ser Gly Asn Ile Ile Pro Ser Ser
 195 200 205

Thr Gly Ala Ala Lys Ala Val Gly Lys Val Leu Pro Glu Leu Gln Gly
 210 215 220

Lys Leu Thr Gly Met Ala Phe Arg Val Pro Thr Val Asp Val Ser Val
 225 230 235 240

Val Asp Leu Thr Val Lys Leu Asn Lys Glu Thr Thr Tyr Asp Glu Ile
 245 250 255

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

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

His Ser Ser Ile Phe Asp Ala Ser Ala Gly Ile Gln Leu Ser Pro Lys
 290 295 300

Phe Val Lys Leu Val Ser Trp Tyr Asp Asn Glu Tyr Gly Tyr Ser Thr
 305 310 315 320

Arg Val Val Asp Leu Val Glu His Val Ala Lys Ala
 325 330

<210> 47

<211> 1071

<212> DNA

<213> Kluyveromyces lactis

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<400> 47

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gtcagattaa tcaataatcc atccacaaca ccagaatacg ctgcttattt gttcaaatac      180
gattctactc acggcaagta tcgtggtgaa gttgaattcg acgatgaacg tatcatcatt      240
caaaatgacc atgtttcggc tcatatccct ctatctcatt ttagggaacc agagcgtatc      300
ccatgggctt cctacaacgt cgattatgta attgactcaa ccggtgtctt caaggaagtc      360
gatacagcct ctagacataa aggtgtcaaa aaagttatca ttactgctcc atcaaagacc      420
gcgccaatgt acgtctatgg tgttaaccac gttaaataca acccattgac ggatcacgtg      480
gtctctaata cctcctgtac taccaactgt ttggctccgt tggttaaggc tttggacgat      540
gagttcggtg tcgaagaagc cttgatgaca actattcatg caactactgc ttctcaaaag      600
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aatatcattc cttcatctac tgggtgcagct aaggctgtag ggaaaatctt gcctgaactt      720
aatggtaaga tcaccgggtat gtctataaga gtccaacaa ttaatatttc cctggttgac      780
ttgacattcc gtacagcaaa gaaaacttct tacgatgaca ttatgaaggc cctagaacaa      840
agatctcgca gcgatatgaa ggggtgttttg ggtgttacca aagacgccgt tgtgtcctct      900
gacttcacat ccgattcacg ttcattctatt gttgatgcca aggccgggtat tgaattgaac      960
gaccatTTTT tcaaggctct ttcttggtat gataatgaat atgggttactc ttcaagagtg     1020
gttgatttat ccattttcat ggctcaaaag gacttcgaag ctggtgttta a                1071

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<210> 48

<211> 356

<212> PRT

<213> Kluyveromyces lactis

<400> 48

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

Ala Leu Thr His Pro Glu Val Lys Val Arg Leu Ile Asn Asn Pro Ser
35          40          45

Thr Thr Pro Glu Tyr Ala Ala Tyr Leu Phe Lys Tyr Asp Ser Thr His
50          55          60

Gly Lys Tyr Arg Gly Glu Val Glu Phe Asp Asp Glu Arg Ile Ile Ile
65          70          75          80

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

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Pro Glu Arg Ile Pro Trp Ala Ser Tyr Asn Val Asp Tyr Val Ile Asp
100 105 110

Ser Thr Gly Val Phe Lys Glu Val Asp Thr Ala Ser Arg His Lys Gly
115 120 125

Val Lys Lys Val Ile Ile Thr Ala Pro Ser Lys Thr Ala Pro Met Tyr
130 135 140

Val Tyr Gly Val Asn His Val Lys Tyr Asn Pro Leu Thr Asp His Val
145 150 155 160

Val Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu Val Lys
165 170 175

Ala Leu Asp Asp Glu Phe Gly Ile Glu Glu Ala Leu Met Thr Thr Ile
180 185 190

His Ala Thr Thr Ala Ser Gln Lys Thr Val Asp Gly Thr Ser Ser Gly
195 200 205

Gly Lys Asp Trp Arg Gly Gly Arg Ser Cys Gln Gly Asn Ile Ile Pro
210 215 220

Ser Ser Thr Gly Ala Ala Lys Ala Val Gly Lys Ile Leu Pro Glu Leu
225 230 235 240

Asn Gly Lys Ile Thr Gly Met Ser Ile Arg Val Pro Thr Ile Asn Ile
245 250 255

Ser Leu Val Asp Leu Thr Phe Arg Thr Ala Lys Lys Thr Ser Tyr Asp
260 265 270

Asp Ile Met Lys Ala Leu Glu Gln Arg Ser Arg Ser Asp Met Lys Gly
275 280 285

Val Leu Gly Val Thr Lys Asp Ala Val Val Ser Ser Asp Phe Thr Ser
290 295 300

Asp Ser Arg Ser Ser Ile Val Asp Ala Lys Ala Gly Ile Glu Leu Asn
305 310 315 320

Asp His Phe Phe Lys Val Leu Ser Trp Tyr Asp Asn Glu Tyr Gly Tyr
325 330 335

Ser Ser Arg Val Val Asp Leu Ser Ile Phe Met Ala Gln Lys Asp Phe
340 345 350

Glu Ala Gly Val
355

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<210> 49
 <211> 1023
 <212> DNA
 <213> Bacillus subtilis

<400> 49
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 ctggctcatt taataaagta tgacacaatt cacggcagat acgacaaaga gggtgtggct 180
 ggtgaagata gcctgatcgt aaatggaaag aaagtgcttt tgtaaacag ccgtgatcca 240
 aaacagctgc cttggcggga atatgatatt gacatagtcg tcgaagcaac aggggaagttt 300
 aatgctaaag ataaagcgat gggccatata gaagcaggtg caaaaaaagt gatattgacc 360
 gctccgggaa aaaatgaaga cgttaccatt gtgatggcg taaatgagga ccaattcgac 420
 gctgagcgcc atgtcattat ttcaaatgcg tcatgcacga caaattgcct tgcgcctgtt 480
 gtaaaagtgc tggatgaaga gtttggcatt gagagcggtc tgatgactac agttcatgcg 540
 tatacgaatg accaaaaaaaa tattgataac ccgcacaaag atttgcgccg ggcgcgggct 600
 tgcggtgaat ccatcattcc aacaacaaca ggagcggcaa aggcgctttc gcttgtgctg 660
 ccgcatctga aaggaaaaact tcacggcctc gccttgctg tccctgttcc gaacgtctca 720
 ttggttgatc tcgttggtga tctgaaaacg gatgttacgg ctgaagaagt aaacgaggca 780
 tttaaacgcg ctgccaaaac gtcgatgtac ggtgtacttg attactcaga tgaaccgctc 840
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 gtaatggaag acaggaaaagt aaagggtgctg gcgtgggtatg acaacgaatg gggctactcc 960
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 taa 1023

<210> 50
 <211> 340
 <212> PRT
 <213> Bacillus subtilis

<400> 50

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Val Phe Arg Lys Ala Met Leu Asp Asp Gln Ile Gln Val Val Ala Ile
 20 25 30

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

Thr Ile His Gly Arg Tyr Asp Lys Glu Val Val Ala Gly Glu Asp Ser
 50 55 60

Leu Ile Val Asn Gly Lys Lys Val Leu Leu Asn Ser Arg Asp Pro
 Seite 60

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65				70				75				80			
Lys	Gln	Leu	Pro	Trp ₈₅	Arg	Glu	Tyr	Asp	Ile ₉₀	Asp	Ile	Val	Val	Glu ₉₅	Ala
Thr	Gly	Lys	Phe ₁₀₀	Asn	Ala	Lys	Asp	Lys ₁₀₅	Ala	Met	Gly	His	Ile ₁₁₀	Glu	Ala
Gly	Ala	Lys ₁₁₅	Lys	Val	Ile	Leu	Thr ₁₂₀	Ala	Pro	Gly	Lys	Asn ₁₂₅	Glu	Asp	Val
Thr	Ile ₁₃₀	Val	Met	Gly	Val	Asn ₁₃₅	Glu	Asp	Gln	Phe	Asp ₁₄₀	Ala	Glu	Arg	His
Val	Ile	Ile	Ser	Asn	Ala ₁₅₀	Ser	Cys	Thr	Thr	Asn ₁₅₅	Cys	Leu	Ala	Pro	Val ₁₆₀
Val	Lys	Val	Leu	Asp ₁₆₅	Glu	Glu	Phe	Gly	Ile ₁₇₀	Glu	Ser	Gly	Leu	Met ₁₇₅	Thr
Thr	Val	His	Ala ₁₈₀	Tyr	Thr	Asn	Asp	Gln ₁₈₅	Lys	Asn	Ile	Asp	Asn ₁₉₀	Pro	His
Lys	Asp	Leu ₁₉₅	Arg	Arg	Ala	Arg	Ala ₂₀₀	Cys	Gly	Glu	Ser	Ile ₂₀₅	Ile	Pro	Thr
Thr	Thr ₂₁₀	Gly	Ala	Ala	Lys	Ala ₂₁₅	Leu	Ser	Leu	Val	Leu ₂₂₀	Pro	His	Leu	Lys
Gly ₂₂₅	Lys	Leu	His	Gly	Leu ₂₃₀	Ala	Leu	Arg	Val	Pro ₂₃₅	Val	Pro	Asn	Val	Ser ₂₄₀
Leu	Val	Asp	Leu	Val ₂₄₅	Val	Asp	Leu	Lys	Thr ₂₅₀	Asp	Val	Thr	Ala	Glu ₂₅₅	Glu
Val	Asn	Glu	Ala ₂₆₀	Phe	Lys	Arg	Ala	Ala ₂₆₅	Lys	Thr	Ser	Met	Tyr ₂₇₀	Gly	Val
Leu	Asp	Tyr ₂₇₅	Ser	Asp	Glu	Pro	Leu ₂₈₀	Val	Ser	Thr	Asp	Tyr ₂₈₅	Asn	Thr	Asn
Pro	His ₂₉₀	Ser	Ala	Val	Ile	Asp ₂₉₅	Gly	Leu	Thr	Thr	Met ₃₀₀	Val	Met	Glu	Asp
Arg ₃₀₅	Lys	Val	Lys	Val	Leu ₃₁₀	Ala	Trp	Tyr	Asp	Asn ₃₁₅	Glu	Trp	Gly	Tyr	Ser ₃₂₀
Cys	Arg	Val	Val	Asp ₃₂₅	Leu	Ile	Arg	His	Val ₃₃₀	Ala	Ala	Arg	Met	Lys ₃₃₅	His
Pro	Ser	Ala	Val												

