

SEQUENCE LISTING

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<120> METHODS OF INCREASING DIHYDROXY ACID DEHYDRATASE ACTIVITY TO
 IMPROVE PRODUCTION OF FUELS, CHEMICALS, AND AMINO ACIDS

<130> GEVO-041/09WO

<150> US 61/263,952
 <151> 2009-11-24

<150> US 61/350,209
 <151> 2010-06-01

<160> 225

<170> PatentIn version 3.5

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Gly Asn Pro Ala Ala Val Pro Ser Pro Ile Met Thr Leu Asn Leu Lys
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Ser Thr His Ser Leu Asn Ile Asp Gln His Val His Thr Ser Thr Ser
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Pro Thr Glu Thr Ile Gly His Ile His His Val Glu Lys Leu Asn Gln
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Asn Asn Leu Ile His Leu Asp Pro Val Pro Asn Phe Glu Asp Lys Ser
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Asp Ile Lys Pro Trp Leu Gln Lys Ile Phe Tyr Pro Gln Gly Ile Glu
115 120 125

Leu Val Ile Glu Arg Ser Asp Ala Phe Lys Val Val Phe Lys Cys Lys
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Lys Gly Gln Asp His Glu Asp Glu Lys Ser Lys Ile Asn Asp Asp Glu
165 170 175

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

Thr Ser Pro Asp Gln Thr Ser Ser Ile Lys Pro Lys Lys Lys Arg Cys
195 200 205

Val Ser Arg Phe Asn Asn Cys Pro Phe Arg Val Arg Ala Thr Tyr Ser
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Leu Lys Arg Lys Arg Trp Ser Ile Val Val Met Asp Asn Asn His Ser
225 230 235 240

His Gln Leu Lys Phe Asn Pro Asp Ser Glu Glu Tyr Lys Lys Phe Lys
245 250 255

Glu Lys Leu Arg Lys Asp Asn Asp Val Asp Ala Ile Lys Lys Phe Asp
260 265 270

Glu Leu Glu Tyr Arg Thr Leu Ala Asn Leu Pro Ile Pro Thr Ala Thr
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Ile Pro Cys Asp Cys Gly Leu Thr Asn Glu Ile Gln Ser Phe Asn Val
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Val Leu Pro Thr Asn Ser Asn Val Thr Ser Ser Ala Ser Ser Ser Thr
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Thr Pro Thr Ser Ser Gln His Ser Ser Thr Ala Phe Ser Gly Tyr Ile
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Phe Lys Leu Asn Thr Val Thr Asn Leu Asn Glu Ile Asp Phe Thr Asn
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Ile Phe Thr Lys Ser Pro His Pro His Ser Gly Ser Thr His Pro Arg
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Gln Val Phe Asp Gln Leu Asp Asp Cys Ser Ser Ile Leu Phe Ser Pro
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Val His Ser Pro Tyr Leu Asn Ser Glu Ala Asp Phe Ser Gln Ile Leu

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Phe Tyr Pro Gln Gly Ile Asp Ile Val Ile Glu Arg Ser Asp Ser Ser
65 70 75 80

Lys Val Thr Phe Lys Cys Arg Ser Val Arg Ser Lys Val Gly Leu Asn
85 90 95

Pro Lys Ser Lys Gly Ser Ser Ser Arg Ser His Ala Cys Pro Phe Arg
100 105 110

Ile Arg Ala Ala Tyr Ser Val Arg Leu Gln Lys Trp Asn Val Val Val
115 120 125

Met Asn Asn Ile His Ser His Glu Leu Arg Phe Asp Leu Ile Thr Lys
130 135 140

Thr Asp Asp Tyr Lys Lys Phe Lys Glu Asn Leu Arg Gln Lys Asn Asp
145 150 155 160

Glu Lys Ala Ile Lys Thr Phe Asp Glu Leu Glu Tyr Lys Ala Ser Leu
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Asn Leu Pro Leu Val Thr Pro Ile Ile Ser Cys Asp Cys Gly Leu Thr
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Lys Glu Ile Glu Ala Phe Asn Asn Ile Phe Leu Pro Leu Ser Asn Pro
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Ser Lys Ile Lys Ser Arg Gln Met Asp Asn Ser Lys Pro Arg Pro Arg
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Leu Lys Thr Lys Leu Asp Ala Asp Leu His Asp Thr Gly Phe Leu Asp
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Asn Phe Lys Thr Arg Asn Ser Cys Val Lys Ile Glu Lys Glu Asp Ser
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Leu Thr Asn Leu Asn Glu Ile Asp Phe Thr Asn Met Phe Cys Asn Asp
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Asn Phe Ile Gln Asn Tyr Asn Gln Gly Leu Met Glu Leu Leu Thr Glu
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Asp Thr Asp Ile Ala Thr Asn Leu Gly Lys Glu Arg Asn Glu Asn Phe
370 375 380

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Gly	Ile	Glu	Ile	Val	Ile	Glu	Arg	Ser	Asp	Ser	Leu	Lys	Val	Val	Phe
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Glu Glu Glu Arg Leu Arg Gln Glu Ala Leu Ala Arg Glu His Glu Met
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Lys Arg Lys Ser Met Gly Asn Lys Arg Cys Val Ser Arg Tyr Asn His
85 90 95

Cys Pro Phe Arg Val Arg Ala Thr Tyr Ser Leu Lys Arg Lys Lys Trp
100 105 110

Ser Val Val Val Leu Asn Asn Thr His Thr His Pro Leu Lys Phe Asn
115 120 125

Pro Leu Ser Glu Glu Tyr Lys Lys Phe Lys Glu Lys Leu Arg Ala Asp
130 135 140

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

Gln His Asn Leu Pro Leu Pro Thr Ser Ile Ile Pro Cys Asp Cys Gly
165 170 175

Leu Thr Asn Glu Val Lys Ser Phe Asp Val Val Leu Pro Lys Thr Met
180 185 190

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

Val Leu Glu Glu Asp Glu Asn Cys Thr Phe Leu Thr Asn Leu Lys Lys
210 215 220

Ser Ser Ala Ile Ser Lys Asn Lys Gly Val Lys Arg Leu Lys Pro Lys
225 230 235 240

His Ser Leu Ser Gly Asn Thr Glu Thr Leu Arg Lys Asn Leu Leu Trp
245 250 255

Lys Ser Asn Gln Ile Tyr Tyr Ser Glu Thr Ala Val Asn Ser Pro Met
260 265 270

Leu Asp Ser Ser Pro Asn Leu Phe Gly Asn Gln Leu Ser Leu Ser Thr
275 280 285

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

Asn Ala Ile Thr Asn Leu Asp Glu Ile Asp Phe Thr Asn Ile Phe Ala
 340 345 350

Arg Ser Thr Asn Asn Asn His Lys His Pro Tyr Asn Ser Thr Ala Ile
 355 360 365

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

Ala Tyr Asp Gly Leu Asp Asp Cys Trp Ser Ile Tyr Met Ser Pro Asn
 385 390 395 400

Thr Thr His Asp Asp Thr Pro Val Asp Ile Ser Pro Ala Ser Ser Lys
 405 410 415

Leu His Asn Lys Met Pro Arg Ile Pro Glu Gln Arg Ser Asp Ser Leu
 420 425 430

Gln Pro Asn Val Arg Phe Asn Asp Thr Ala Leu Lys His Glu Ser Leu
 435 440 445

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

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

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

Ser Gly Asn Ser Ile Ile Ser Cys Asp Cys Gly Leu Thr Lys Glu Ile
180 185 190

Lys Thr Ile Asn Asn Val Tyr Leu Pro Leu Asn Ala Thr Gln Leu Gln
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Asp Glu Ile Asp Val Ser Lys Ile Leu Glu Cys Gln Asn Lys Lys Gln
210 215 220

Lys Asn Lys Gln Lys Val Met Lys Lys Arg Lys Ser Glu Lys Asn Glu
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Leu Ala Asn Ile Lys Lys Glu Glu Pro Ser Cys Ser Ser Ala Leu Ile
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His Asp Lys Gly Phe Glu Ile Thr Gln Asp Asp Leu Ile Gln Cys Gly
 260 265 270

Ile Asn Asp Ile Asn Asp Tyr Asp Cys Asp Lys Tyr Tyr Thr Glu Leu
 275 280 285

Leu Asn Lys Glu Ser Tyr Ala Asp Ala Ser Tyr Cys Asn Ile Ala Asp
 290 295 300

Phe Ser Asn Met Asn Glu Ile Asp Phe Thr Gly Met Phe Asn Lys Ser
 305 310 315 320

Lys Pro Ala Gln Pro Ser Leu Thr Lys Gly Asp Asp Leu Phe Ser Ser
 325 330 335

Ile Ala Asn Asp Asn Phe Phe Ser Tyr Glu Glu Asn Ile Lys Asp Thr
 340 345 350

Thr Leu Val Glu Pro Glu Leu Leu Met Ala Pro Val Gln Asp Ile Asn
 355 360 365

Glu Asn Asn Ile Asp Asp Ile Phe Lys Met Ser Thr Asn Thr Ser Ser
 370 375 380

Thr Pro Ile Ser Pro Ser Thr Asp Pro Ser Thr Asp Ile Asp Gln Lys
 385 390 395 400

Ile Pro Asp Pro Leu Glu Phe Glu Asn Val Asn Tyr Leu Asp Lys Tyr
 405 410 415

Val Asp Leu Ser Thr Val Met Ile Asn Asp Pro Ala Lys Glu Thr Tyr
 420 425 430

Asp Ser Leu Phe Ser
 435

<210> 9

<211> 1677

<212> DNA

<213> Zygosaccharomyces rouxii

<400> 9

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gcattagcag aagatcaaaa caaatattatt catttagatc cggtagctga ttttagagac	180
aaggcagaaa ttaaaccatg gttacagaaa atcttttacc cacaggggat agaaattgtg	240
attgaaagat cagataatat taaagtcatt ttcaaatgta aagccgcgaa aagaggtaaa	300
aatacgaagc ccaggcgaaa tgaagtcaca actacaagtt caatgagtgc aagctcttca	360
agtgttacta gtccaaatac aggattaagt tcagcagcag gtaaaaagaa aagatcagta	420
tcgagattca atacatgtcc atttagaata cgtgcaactt tttcattaaa gagaaggaaa	480
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caatttgatg aactagaata taaatcaaga tctaattttac cgattgaatc ttcattgata	660
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gcatcttcgc cagcatcttc aacgatggca actcaaccgc cacaacaaca acaacagcaa	1080
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aacactcaac aagatcatgg atcggatctt ttgcaaccat cacaatcaag tcctccacaa	1260
tttttagata ccaatcatga aacggctagt agaagagatg aatttccacc acttttattt	1320
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gatgatgaga ttttagcgcc agcaaggctt gcctcgttat ggccacagca acaagaaacg	1560
tcttcatcaa gtccactgcg tagggtggtt aatgctgtcg attctcaatc gccttgtaat	1620

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1677

<210> 10

<211> 558

<212> PRT

<213> Zygosaccharomyces rouxii

<400> 10

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20 25 30

Ile Gln Ala Asn Glu Leu Pro Lys Ala Leu Ala Glu Asp Gln Asn Lys
35 40 45

Phe Ile His Leu Asp Pro Val Pro Asp Phe Arg Asp Lys Ala Glu Ile
50 55 60

Lys Pro Trp Leu Gln Lys Ile Phe Tyr Pro Gln Gly Ile Glu Ile Val
65 70 75 80

Ile Glu Arg Ser Asp Asn Ile Lys Val Ile Phe Lys Cys Lys Ala Ala
85 90 95

Lys Arg Gly Lys Asn Thr Lys Pro Arg Arg Asn Glu Val Thr Thr Thr
100 105 110

Ser Ser Met Ser Ala Ser Ser Ser Ser Val Thr Ser Pro Asn Thr Gly
115 120 125

Leu Ser Ser Ala Ala Gly Lys Lys Lys Arg Ser Val Ser Arg Phe Asn
130 135 140

Thr Cys Pro Phe Arg Ile Arg Ala Thr Phe Ser Leu Lys Arg Arg Lys
145 150 155 160

Trp Asn Ile Val Val Val Asn Asn Ser His Ser His Glu Leu Lys Phe
165 170 175

Asp Pro Asp Ser Asp Glu Tyr Arg Lys Phe Lys Glu Lys Leu Arg Glu
180 185 190

Asp Asn Asp Trp Asp Ala Val Lys Gln Phe Asp Glu Leu Glu Tyr Lys

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

Asp Glu Phe Pro Pro Leu Leu Phe Ser Pro Leu Asp Ala Ala Ala Asn
 435 440 445

Glu Leu Met Thr Pro Thr Asp Asp Met Ser Val Ser Pro Ser His Thr
 450 455 460

Ser Asn Ser Gln Asn Asn Ser Ser Gln Arg Trp Pro Thr Gly Ile Ser
 465 470 475 480

Ile His Asp Gln His Gln His Gln His Gln His Gln Pro Ile Leu Arg
 485 490 495

Gln Tyr Phe Asn Asp Asp Glu Ile Leu Ala Pro Ala Arg Leu Ala Ser
 500 505 510

Leu Trp Pro Gln Gln Gln Glu Thr Ser Ser Ser Ser Pro Leu Arg Arg
 515 520 525

Val Val Asn Ala Val Asp Ser Gln Ser Pro Cys Asn Glu Asn Asp Tyr
 530 535 540

Ala Val Asp Asp Leu Leu Trp Lys Met Asn Phe Glu Asn Ala
 545 550 555

<210> 11
 <211> 1359
 <212> DNA
 <213> Ashbya gossypii

<400> 11
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 gggcacaacg tggagggcag cggggcgcg cagcagcccct actcggaagc gagctacaat 180
 aacgtgctga gcgaccaggc catcgagcgg atccggcggc agcagaacca gaacaagctg 240
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<210> 12
 <211> 452
 <212> PRT
 <213> Ashbya gossypii

<400> 12

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Ser Pro Ser Ala Trp Ser Val Ser Glu Thr Ala Gly Asp Val Pro Ser
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Gly Ala Ser Ala Thr Thr Ala Ser Gly His Asn Val Glu Gly Ser Gly
 35 40 45

Ala Arg Ser Ser Pro Tyr Ser Glu Ala Ser Tyr Asn Asn Val Leu Ser
 50 55 60

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

Ile His Leu Glu Pro Ile Pro Asp Phe Lys Asp Lys Asn Asp Ile Lys
 85 90 95

Pro Trp Leu Gln Lys Ile Phe Tyr Pro Gln Gly Ile Glu Ile Val Ile
 100 105 110

Glu Arg Ser Asp Lys Ile Lys Val Val Phe Lys Cys Lys Ala Ser Lys
115 120 125

Arg Thr Lys Ser Gly Ser Ala Pro Gly Ser Gln Ala Gly Ala Ala Glu
130 135 140

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

Thr Ala Ser Gln Leu Arg Lys Lys Lys Arg Ala Val Ser Pro Tyr Asn
165 170 175

Thr Cys Pro Phe Arg Val Arg Ala Ala Tyr Ser Leu Lys Arg Lys Arg
180 185 190

Trp Ser Ile Val Val Val Asn Asn Gly His Ser His Pro Leu Lys Phe
195 200 205

Asn Pro Asp Ser Ala Glu Tyr Arg Lys Phe Lys Asn Asn Leu Arg Gln
210 215 220

Glu Cys Asp Trp Asp Ala Val Lys Lys Phe Asp Glu Leu Glu Tyr Arg
225 230 235 240

Ser Lys Phe Asn Leu Pro Thr Glu Pro Thr Pro Ile Pro Cys Asp Cys
245 250 255

Gly Leu Thr Gln Glu Ile Glu Ser Phe Asn Val Ile Leu Pro Ser Thr
260 265 270

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

Ser Lys Pro Arg Cys Arg Lys Thr Leu Gln Arg Asp Arg Cys Ser Gln
290 295 300

Leu Arg Arg Gln Ser Thr Gln Ser Lys Leu Thr His Glu Leu His Thr
305 310 315 320

Ala Leu Ser Pro Thr Leu Gly Ser Ser Ala Asp Thr Leu Gly Ser Pro
325 330 335

Val Arg Tyr Ala Ala Gln Asp Ala Glu Val Asp Phe Thr Glu Val Phe

340 345 350
 Leu Arg Ser Leu Pro Pro Ala Lys Pro Leu His Ser Ala Arg Ala Pro
 355 360 365
 Asp Ala Ala Arg Asp Ser Trp His Ala Leu Glu Gln Leu Leu Asp Asp
 370 375 380
 Pro Ala Asp Ala Pro Pro Arg Thr Pro Leu Pro Ser Ala Ser Ala Asp
 385 390 395 400
 Cys Val Asn Pro Leu Leu His Phe Ala Gln Arg Pro Ala Asp Asp Pro
 405 410 415
 Val Asp Ser Leu Ala Tyr Glu Leu Asn Ala Leu Ser Ala Met Asp Ser
 420 425 430
 Pro Phe Ala Arg Pro Ala Pro Asp Ala Gln Phe Leu Trp Glu Asp Pro
 435 440 445
 Lys Tyr Phe Pro
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<210> 13
 <211> 2472
 <212> DNA
 <213> Kluyveromyces lactis

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 cccatcggtt ctggactgtc ccatacaccg gcggctcacc atgttggctc gaatttatcc 180
 tcgagtaata atagcgaagt ctcttataac aatgcgttga gtgaaaacgc gatagaagct 240
 cttcggagac agcaagacca gaataaattg attcatttgg atccgatccc tgacttcaaa 300
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ggtacttcaa ccaataataa tgaccattct aatgctaata cttcatccgt taataactaat	1800
aataaccatc ttcattcaaca acataatact agtcatgcta atgcatgat accttcgcat	1860
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gaaattaaca actttgacgt atgtgctaata gaccctcaat gtgggtgggtcc tctcattgggt	1980
actgctactg gtattcatgg actcaatata gatcgttcaa acatggagat cgctaattgggt	2040
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cgccgccacc agcatcagat gcaaaatcaa cagcaacagc aatgcaaca gcaacagcaa	2280
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gagattgaag agctcgttgc gaattcggag tacaattatc acctacagtt taataatgat	2400
cttgaccaac cgcagcaagc tacgcataat ccacaaatgc tttgggatga acctcacggc	2460

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2472

<210> 14
<211> 823
<212> PRT
<213> Kluyveromyces lactis

<400> 14

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Pro Leu His Asn Pro Asp Leu Trp Gln Pro Ser Pro Ser Phe Asp Asn
20 25 30

Met Met Ala Ser Pro Lys Thr Ser Pro Ile Gly Ser Gly Leu Ser His
35 40 45

Thr Pro Ala Ala His His Val Gly Ser Asn Leu Ser Ser Ser Asn Asn
50 55 60

Ser Glu Val Ser Tyr Asn Asn Ala Leu Ser Glu Asn Ala Ile Glu Ala
65 70 75 80

Leu Arg Arg Gln Gln Asp Gln Asn Lys Leu Ile His Leu Asp Pro Ile
85 90 95

Pro Asp Phe Lys Asp Lys Ser Glu Val Lys Pro Trp Leu Gln Lys Ile
100 105 110

Phe Tyr Pro Gln Gly Ile Glu Ile Val Ile Glu Arg Ser Asp Ser Met
115 120 125

Lys Ile Val Phe Lys Cys Lys Ala Val Lys Lys Asn Arg Asn Thr Ser
130 135 140

Ser Ile Ser Gly Cys Gly His Ser His Gly Val Gly Ser Asp Ser Cys
145 150 155 160

Asn Thr Asn Gly Lys Asn Ser Thr Lys Gly Asn Gly Ser Asn Asp Asn
165 170 175

Lys Cys Arg Lys Lys Gly Ile Gly Lys Gly Phe Ala Glu Cys Asp Gly
180 185 190

Leu Glu Thr Glu Thr Glu Asn Gly Asn Asn Ser Asn Ser Thr Val Gly
195 200 205

Gly Gly Asn Gly Ser Asn Asp Thr Asp Lys Lys Lys Arg Ala Ile Gly
210 215 220

Pro Tyr Asn Ser Cys Pro Phe Arg Val Arg Ala Thr Phe Ser Leu Lys
225 230 235 240

Arg Lys Lys Trp Asn Ile Val Val Val Asn Asn Val His Thr His Pro
245 250 255

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

Leu Lys Glu Ser Gly Asp Leu Glu Thr Val Lys Lys Phe Asp Glu Leu
275 280 285

Glu Tyr Arg Thr Arg Phe Asn Leu Pro Ile Asp Leu Ser Pro Ile Pro
290 295 300

Cys Asp Cys Gly Leu Thr Gln Glu Ile Gln Ser Phe Asn Ile Val Leu
305 310 315 320

Pro Thr Thr Asn Ile Ile Val Pro Gly Ser Arg Asn Thr Ser Met Asp
325 330 335

Ala Asn Thr Val Thr Lys Pro Lys Lys Thr Gly Lys Lys Ala Val Lys
340 345 350

Ser Lys Thr Thr Lys Gln Leu Arg Arg Lys Ser Thr Lys Lys Lys Leu
355 360 365

Gln Gln Asp Ile Glu Ser Asn Ser Ala Asn Thr Ser Arg Thr Ala Thr
370 375 380

Pro Leu Ser Thr Val Gln Asn Ser Leu Asn Leu Gln Phe Asp Ser Gln
385 390 395 400

Ser Asn Val Ser Val Ala Pro Ser Val Thr Ser Asn Leu Asn Ser Asn
405 410 415

Leu Ala Leu Thr Pro Gln Glu Asn Ile Tyr Ser Thr Asp Phe Leu Pro
420 425 430

Asn Thr Ala Ser Ser Gln Gln Met Asp Ser Pro Asn Phe Ser Asn Phe
435 440 445

Asn Ser Asn Tyr Phe Asn Val Gln Asn Glu Ile Asp Phe Thr Glu Phe
450 455 460

Phe Ser Lys Pro Leu Pro His Phe Lys Asn Asn Arg His Asp Val Val
465 470 475 480

Thr Gly Gln Gly Met Ile Pro Leu Thr Phe Ser Gln Lys His Gln Thr
485 490 495

Ser Ser Gln Ser Ala Gln His Thr Pro His Gln Asn Ile Asn Ser Asn
500 505 510

Leu Met Tyr His Asn Ala Gly Ser Ala Ser Ser Thr His Ser Ser Pro
515 520 525

Asn Met Ser Ile Met Thr Ser Val Lys Thr Pro Ile Thr Thr Ala Thr
530 535 540

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

Tyr Ser Ser Asn Leu Ala Lys Glu Pro Ile Gln Asp Phe Ile Asp Met
565 570 575

Asn Gln Ile Phe Gly Thr Ser Thr Asn Asn Asn Asp His Ser Asn Ala
580 585 590

Asn Thr Ser Ser Val Asn Thr Asn Asn Asn His Leu His Gln Gln His
595 600 605

Asn Thr Ser His Ala Asn Ala Met Ile Pro Ser His Ser Leu Asn Phe
610 615 620

Gln His Ser Asn Leu Ser Pro Val Asn Gln Asn Ile Ser Ala Val Cys
625 630 635 640

Glu Ile Asn Asn Phe Asp Val Cys Ala Asn Asp Pro Gln Cys Gly Gly
645 650 655

Pro Leu Ile Gly Thr Ala Thr Gly Ile His Gly Leu Asn Ile Asp Arg
660 665 670

Ser Asn Met Glu Ile Ala Asn Gly Ile Ser Gln Ser Asn Asp Ala Thr
675 680 685

Gly Tyr Met Asp Pro Leu His Thr Lys Pro Asp Tyr Asp Ala Gln Ser
690 695 700

Gln Glu Tyr Ile Ser Asn Val Leu Asn Ser Asp Phe Asn Glu Leu Arg
705 710 715 720

Leu Ser Gln Ser Gln His Asn Gln Gly Glu Gln His His Gln Gln His
725 730 735

Met Gln Gln Gln Arg Arg His Gln His Gln Met Gln Asn Gln Gln Gln
740 745 750

Gln Gln Met Gln Gln Gln Gln Gln Gln Gln Gln Leu His Asp Gln His
755 760 765

Asn Pro Leu His Glu Ile Leu Pro Leu Lys Glu Glu Glu Ile Glu Glu
770 775 780

Leu Val Ala Asn Ser Glu Tyr Asn Tyr His Leu Gln Phe Asn Asn Asp
785 790 795 800

Leu Asp Gln Pro Gln Gln Ala Thr His Asn Pro Gln Met Leu Trp Asp
805 810 815

Glu Pro His Gly Phe Phe Gln
820

<210> 15
<211> 2100
<212> DNA
<213> Vanderwaltozyma polyspora

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acttatattc atctagatcc aataccagat tttcaggata cctctgaagt caagccctgg 180
ttacaaaaaa ttttctatcc acaaggtgtg gagctcgtta tcgaaagatc ggataataca 240
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acaacaacaa ctactaataa taataacaat gatgatgaaa atgatgaaaa tagcgaaaat 360

aaagagacta atagcaacga cgataaaaaat agtaatgtta taaatgatgg atatttagat	420
aaaccaaaga aaaagagagt agtatcgaga tttaatacct gtccattccg tataagagca	480
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gatttatcgt tcaatcccga ttcaatagag tataagaaat ttaaagaaag attaagatta	600
aataatgatg tcgaagcaat aaaaaaattc gatgaattgg aatataaagt acgatcaaat	660
ctacctctga gcccttcggt agtggtttgt gattgtgggt taacaagtga aattcaatca	720
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aaaaatttag aaacaaattt caaccaacag tctgtaaatg ttaaaaaacc aaaaaaattg	840
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accactaccc aaaatttttt aactaatcgc aatgcaaatt ctcaccctca gccaatccc	960
tcattctcac caataacttc aaataatatt cattcaaata tgcattccta taatcatagt	1020
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<210> 16
 <211> 699
 <212> PRT
 <213> Vanderwaltozyma polyspora

<400> 16

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Asn Lys Asn Pro Lys Pro Ser Asp Thr Tyr Ile His Leu Asp Pro Ile
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Pro Asp Phe Gln Asp Thr Ser Glu Val Lys Pro Trp Leu Gln Lys Ile
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Phe Tyr Pro Gln Gly Val Glu Leu Val Ile Glu Arg Ser Asp Asn Thr
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Lys Val Val Phe Lys Cys Lys Ala Ala Lys Arg Gly Lys Gly Ser Arg
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Leu Pro Ser Lys Thr Thr Thr Thr Thr Asn Asn Asn Asn Asn Asp Asp
 100 105 110

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

Thr Tyr Ser Met Lys Arg Gly Lys Trp Asn Ile Val Ile Leu Asn Asn
 165 170 175

Lys His Ser His Asp Leu Ser Phe Asn Pro Asp Ser Ile Glu Tyr Lys
 180 185 190

Lys Phe Lys Glu Arg Leu Arg Leu Asn Asn Asp Val Glu Ala Ile Lys
 195 200 205

Lys Phe Asp Glu Leu Glu Tyr Lys Val Arg Ser Asn Leu Pro Leu Ser
 210 215 220

Pro Ser Leu Val Val Cys Asp Cys Gly Leu Thr Ser Glu Ile Gln Ser
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Phe Asp Val Val Leu Pro Thr Asn Asp Ser Leu Asn Thr Asn Ile Val
 245 250 255

Asp Leu Ser Asn Lys Asn Leu Glu Thr Asn Phe Asn Gln Gln Ser Val
 260 265 270

Asn Val Lys Lys Pro Lys Lys Leu Lys Asn Val Lys Ser Lys Ala Thr
 275 280 285

Asn Leu Asn Ile His Gln Glu Asn Leu Leu Lys Lys Thr Thr Thr Gln
 290 295 300

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

Ser Ser Ser Pro Ile Thr Ser Asn Asn Ile His Ser Asn Met His Ser
 325 330 335

Tyr Asn His Ser His Ser His Ser His Ser His Ser His Ser His Thr
 340 345 350

His Met Asn Gly His Thr His Thr His Asn His Thr Thr Pro Pro Val
 355 360 365

Glu Ser Leu Asp Leu Leu Gln Pro Asp Thr Phe Asn Ser Leu Thr Phe
 370 375 380

Ser Lys Leu Thr Thr Asp Leu Asp Glu Ile Asp Phe Thr Asp Ile Phe
 385 390 395 400

Asn Lys Pro Leu Tyr Asn Lys Asn His Asn His His His His His His
 405 410 415

His His His Asn Phe Glu Asp Asn Asn Asn Tyr Asn Glu Tyr Asn Asp
 420 425 430

Asn Asp Ile Asn Ser His Ser Ser Leu Tyr Ser Pro Ile Thr Asn Gly
 435 440 445

Gly Thr Pro Lys Met Leu Glu Ser Asp Thr Ile Ser Pro Asn Pro Asp
450 455 460

Leu Phe Pro Ser Gln Tyr Glu Leu Gln His Asn Tyr Ser Tyr Ser Asn
465 470 475 480

Asn Gln Ile Ser Ser Pro Leu Lys Asp Ser Pro Ser His Tyr Ser Asn
485 490 495

Met Asp Phe Thr His Ser Tyr Leu Ser Thr Asn Asn Asn Tyr Lys Lys
500 505 510

Tyr Ser Ile Thr Leu Cys Glu Asn Asn Asn Ser Asn Ile Cys Tyr Asn
515 520 525

Asp Glu Cys Ile Lys Leu His Asp Ile Gln Pro Ile Lys Asn Glu Phe
530 535 540

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

Tyr Asp Pro Met His Leu Ile Gln Lys Phe Met Asn Thr Ser Asn Asp
565 570 575

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

Asn Glu Leu Asp Leu Thr Ser Val Pro Leu Thr Phe Asp Ser Glu Gly
595 600 605

Asn His Ile Thr Leu Asp Asn Ile Ser Ser Ser Gln Pro Lys Arg Lys
610 615 620

Gln Asn Glu Ser Gly Asn Ser Asn Leu Ser Asp Leu Ser Thr Leu Ile
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Pro Asn Asn Gln Glu Ala Phe Pro Gln Val Ile Ser Asp Ile Asp Ile
645 650 655

Thr Asn Tyr Asn Phe Glu Ser Ile Asn Thr Thr Asn Lys Ala Ile Asn
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Gly Asn Thr Asn Thr Ser Ile Gln Asp Asp Lys Gly Ser Leu Ser Pro

675

680

685

Ser Ile Trp Glu Asn Thr Phe Asp Asp Ile Leu
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<210> 17

<211> 1563

<212> DNA

<213> *Lachancea thermotolerans*

<400> 17

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aagccgtggc ttcagaagat tttctatccc caaggatcgc agattgtgat cgagcgttct      360
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<210> 18
<211> 520
<212> PRT
<213> *Lachancea thermotolerans*

<400> 18

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35 40 45

Pro Asp Phe Thr Asn Gly Thr Pro Ser Trp Asn Asp Thr Ala Ser Leu
50 55 60

Asn Asn Met Leu Ser Glu Asn Ala Leu Glu Ser Ile Asn Arg Gln Arg
65 70 75 80

Ser Gln Asn Lys Leu Ile His Leu Asp Pro Ile Pro Asp Phe Gln Asp
85 90 95

Arg Asn Glu Ile Lys Pro Trp Leu Gln Lys Ile Phe Tyr Pro Gln Gly
100 105 110

Ile Glu Ile Val Ile Glu Arg Ser Asp Asn Ile Lys Val Val Phe Lys
115 120 125

Cys Lys Ala Ser Lys Arg Gly Arg Ala Ser Arg Lys Gln Ala Gly Cys
130 135 140

Gly Ser Leu Pro Glu Glu Lys Glu Asn Pro Glu Ser Pro Leu Ala Val
145 150 155 160

Lys Arg Val Gln Gln Ala Asn Lys Lys Lys Arg Ser Val Ser Pro Tyr
165 170 175

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

Lys Trp Asn Ile Val Val Met Asn Asn Gly His Ser His Pro Leu Lys
195 200 205

Phe Asn Ala Asp Ser Asp Asp Tyr Lys Lys Phe Lys Asn Tyr Leu Arg
210 215 220

Glu Asn Glu Asp Trp Asp Ala Val Lys Lys Phe Asp Glu Leu Glu Cys
225 230 235 240

Arg Thr Arg Phe Asn Leu Pro Thr Gln Pro Gln Pro Ile Pro Cys Asp
245 250 255

Cys Gly Leu Thr Gln Glu Ile Glu Ser Phe Asn Ile Val Leu Pro Thr
260 265 270

Ser Asp Ser Leu Ala Asn Ser Thr Asp Lys Thr Val Ser Lys Pro Arg
275 280 285

His Lys Ser Thr Arg Lys Gly Asn Lys Gln Met Ala Thr Ala Leu Ser
290 295 300

Arg Asn Ser Thr Pro Leu Gly Phe Leu Asp Lys Ser Pro Ser Gln Ser
305 310 315 320

Ala Arg Ser Gly Gln Glu Pro Gln Arg Ile Lys Gln Glu Ser Thr Gly
325 330 335

Ala Pro Gln Glu Pro His Ser Gly Met Thr Gly Leu Ser Pro Met Gln
340 345 350

Asn Phe Asp Thr Ser Met Ser Gly Trp Asp Pro Asn Thr Leu Thr Ser
355 360 365

Gln Ser Glu Glu Ile Asp Phe Thr Asp Leu Phe Leu Arg Pro Leu Pro
370 375 380

Arg Thr Lys Gln Asp Pro Ile Phe Glu Lys Pro Gln Thr Leu Asn Ser
385 390 395 400

Pro Gly Arg Asp Gln Pro Trp Asn Ala Ser Lys Asn Phe Met Asp Asp
405 410 415

Leu Gln Phe Gln Leu Ala Pro Val Cys Glu Pro Ser His Thr Ser Asn
420 425 430

Ala His Cys Ile Leu Pro Ser Ser Thr Glu Ala His Met Asn Cys Asp
435 440 445

Ala Met Asp Ala Gly Ser Gln His Glu Phe Pro His His Arg Val Gln
450 455 460

Gln Gln Asp Pro Ser Met Leu His Ser Ser Pro Ala Asn Gly Met Leu
465 470 475 480

Ser Ser Asp Leu Gly Asn Met His Leu Thr Gly Gln Gln Met Gln Val
485 490 495

Pro His Pro Asp Pro Gly Leu Pro Trp Glu Pro Gln His Ser Asn Asp
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Pro His Gly Tyr Ser Asn Asp Phe
515 520

<210> 19
<211> 1818
<212> DNA
<213> Debaromyces hanseii

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<210> 20
 <211> 605
 <212> PRT
 <213> Debaromyces hanseii

<400> 20

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

Phe Lys Ile Arg Ala Asn Tyr Ser Ile Arg Asn His Val Trp Thr Leu
 85 90 95

Val Val Met Asn Glu Asn His Asp His Glu Leu Asp Asn Phe Gly Leu
 100 105 110

Met Gln Gln Ser Lys Leu Ala Tyr Leu Phe Asn His His Lys Thr Asn
 115 120 125

Glu Ser Gly Leu Leu Ser Ser Gly Ser Asp Asp Ser Thr Ser Ala Ala
 130 135 140

Leu Thr Asn Pro Ser Lys Ser Asn Thr Ser Ser Asp Val Phe Ser Ser
 145 150 155 160

Phe Ile Pro Ser Ser Thr Glu Met Val Ser Pro Asn Glu Ala His Asp
 165 170 175

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

Ser Lys Asp Asn Ser Asp Ser Glu Lys Met Leu Asp Thr Tyr Glu Glu
 195 200 205

Gln Lys Ser Lys Lys Arg Lys Val Pro Lys Gly His Asn Val Lys Arg
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Arg Lys Thr Lys Arg Glu Thr Ile Ser Val His Asp Glu Asp Gln Glu
 225 230 235 240

Ser Arg Gln Asp Lys Ser Ser Lys Glu Val Val Gly Asp Leu Arg Glu
 245 250 255

Gln Val Asn Leu Leu Ile Ser Asn Thr Ile Ile Asn Asn Gln Asn Phe
 260 265 270

Thr Asp Lys Glu Lys Ser Met Met Ile Lys Ser Phe Phe Ser Arg Phe
 275 280 285

Ile Lys Asp Tyr Lys Gly Ile Ile Asn Thr Val Ala Asn Gln Gln Lys
 290 295 300

Met Val Leu Asn Asn Trp Phe Asn Thr Pro Asn Pro Ala Gln Thr Asn
 305 310 315 320

Leu His Ser His Ala Asn Thr Asn Leu Ile Pro Leu Ser Pro Leu Leu
 325 330 335

Asn Asp Thr Asp Thr Asp Tyr Thr Ser Ala Thr Pro Asn Asn Ser Asn
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Asn Gln Ser Ile Asp Asn Leu Thr His Leu Pro Asn Met Ser Leu Gly
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Ser Ser Leu Ile Thr Asn Val Gly Ala Ala Cys Asn Ser Thr Gly Pro
 370 375 380

Ser Asn Ser Asn Ala Asn Asn Asn Tyr Asn Asn Phe Ile Val Pro Pro
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Gln Met Gln Leu Ser Gln Ile Gln Asn Gln Asn Gln Gln Leu Pro Ser
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Phe Asn Thr Ile Gln Asn Gln Leu Pro Leu Ser Pro Asn Ser Leu Ala
 420 425 430

Asn Asn Ser Thr Ala Ser Leu Phe Val Asn Asn Phe Asn Thr Asn Leu
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Asn Ser Asn Thr Ser Ser Leu Ile Pro Pro Ile Asn Asn Ser Asn Thr
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Asn Thr Thr Leu Asn Pro Ser His Leu Leu Lys Ser Ser Asn Lys Asn
 465 470 475 480

Asn Val Phe Asn Asn Asn Met Asn Ser Thr Ala Ser Ser Asn Leu Leu
 485 490 495

Ser Arg Asn Glu Phe Lys Gln Asn Ser Ser Leu Asn Pro Ile Asn Asn
 500 505 510

Asn Ile Ala Ser Ser Asn Thr Ile Ser Leu Asn Thr Asn Gln Asn Ser
 515 520 525

Gly Ser Ile Ser Asn Ser Asn Thr Ser Asn Asn Tyr Thr Val Asn Tyr
530 535 540

Gly Gly Leu Ser Ser Pro Asn Asn Asn Ile Ile Asn Pro Asn Ile Gln
545 550 555 560

Asn Asn Ser Thr Asn Gly Ala Phe Tyr Asn Lys Glu Met Gln Ser Gly
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Asn Thr Ser Asn Asn Pro Gln Asn Ser Thr Thr Ser Asn Thr Ser Gly
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Ala Leu Asn His Ile Ala Ser Leu Asn Asp Asn Gly Trp
595 600 605

<210> 21
<211> 2082
<212> DNA
<213> Saccharomyces bayanus

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<210> 22
<211> 693
<212> PRT
<213> Saccharomyces bayanus

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<400> 22

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Ser Thr Asp Asn Asn Thr Ala Ser Phe Val Tyr Pro Leu Pro Lys Ala
20           25           30

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Thr Gly Glu Phe Val Asn Asn His Asn Glu Asn His Arg Asp Val Asp
35           40           45

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Pro 50 Pro Ala Val Pro Ser 55 Ser Met Val Ser Leu Asn 60 Phe Lys Asp Pro
 Ser 65 Ser Pro Asn Gly Asp 70 Phe His Ile His 75 Thr Ser Ala Ser Pro Thr 80
 Glu Ser Ala Glu His 85 Gly His Gln Ser 90 Glu Lys Leu Asn Gln Asn 95
 Leu Val His 100 Leu Asp Pro Val Pro 105 Asn Phe Lys Asp Lys Ala Asp Ile
 Lys Pro Trp 115 Leu Gln Lys Ile Phe Tyr Pro Gln Gly Ile Glu Leu Val 125
 Ile Glu Arg Ser Asp Thr 130 Phe Lys Val Val Phe Lys 140 Cys Lys Ala Ala
 Lys Arg Gly Arg Asn Thr 150 Arg Arg Lys Arg Lys 155 Asp Lys Ser Asn Glu 160
 Gln Asp Gln Glu Glu Asp Lys Leu Gln Val Asn Asp Asp Glu Phe Glu 175
 Asn Thr Ser 180 Ser Ser Asn Phe Ile Ala Ser Ser Asn Gly Ala Arg Ser 190
 Ser Pro Glu Leu Thr Ser Ser Gly Lys Pro Lys Lys Lys Arg Cys Val 205
 Ser Arg Phe Asn Asn Cys Pro Phe Arg Val Arg Ala Thr Tyr Ser Leu 220
 Lys Arg Lys Arg Trp Ser Ile Val Val Met Asn Ser Asn His Ser His 240
 Pro Leu Lys Phe Asn Pro Asp Ser Glu Glu Tyr Lys Lys Phe Lys Glu 255
 Lys Leu Arg Lys Asp Asn Asp Leu Asp Ala Ile Lys Lys Phe Asp Glu 270
 Leu Glu Tyr Arg Thr Leu Ala Asn Leu Pro Ile Pro Thr Ala Thr Ile 285

Pro Cys Asp Cys Gly Leu Thr Asn Glu Ile Gln Ser Phe Asn Val Val
 290 295 300

Leu Pro Thr Asn Ser Lys Ser Ser Ser Ser Ala Ser Ser Ser Ser Val
 305 310 315 320

Ser Ser Val Ser Leu Asp Pro Ser Ser Ala Ser Lys Arg Pro Cys Leu
 325 330 335

Pro Pro Val Asn Asn Ile Gly Asn Ile Asn Thr Asn Asn Ile Arg Lys
 340 345 350

Pro Arg Ser Gln Ser Lys Asn Lys Asp Thr Leu Leu Lys Arg Thr Thr
 355 360 365

Met Gln Asn Phe Leu Thr Thr Lys Ser Arg Leu His Lys Thr Gly Thr
 370 375 380

Pro Thr Ser Ser Gln His Ser Ser Thr Ala Phe Ser Gly Tyr Ile Asp
 385 390 395 400

Asp Pro Phe Asn Leu Asn Glu Ile Leu Pro Leu Pro Thr Ser Asp Phe
 405 410 415

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

Phe Thr Lys Pro Ser His Pro His Ser Gly Thr Thr His Pro Arg Gln
 435 440 445

Val Phe Asp Gln Leu Asp Asp Cys Ser Ser Ile Leu Phe Ser Pro Leu
 450 455 460

Thr Thr Asn Thr Asn Asn Glu Phe Glu Val Glu Ser Asp Asp Phe Val
 465 470 475 480

His Ser Pro Tyr Leu Asn Ser Glu Gly Asp Phe Ser Gln Ile Leu Asn
 485 490 495

Asn Ala Ser Pro Ala His His Ile Pro Asp His Thr His Leu Glu Asn
 500 505 510

Gln Asp Ile Ile Asp Arg Phe Ala Asn Ser Ser Gln Glu Gln Asn Glu
 515 520 525

Tyr Ile Leu Gln Tyr Leu Thr His Phe Asp Ala Ala Asn Asn Ala Ala
530 535 540

Asn Thr Ser Asn Asp Ile Ser His Ser Leu Asn Ile His His Asn Ile
545 550 555 560

Thr Asp Leu Ser Asn Ser Leu Leu Lys Gln Glu Thr Leu Ile Asp Asn
565 570 575

Pro Ser Thr Arg Ile Phe Asp Glu Leu Lys Phe Ile Gln His Asn Pro
580 585 590

His Gly Ala His His Pro Val Glu Phe Gln His Glu Asn His Asn His
595 600 605

Leu Met Ser Asn Glu Pro Gln Ile Arg His Gln Gln Tyr Gly Pro Gln
610 615 620

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln His Glu Tyr Pro His
625 630 635 640

Ser His Asp His His Asp His His His Asn Gln His Glu Glu Val Arg
645 650 655

Lys Glu Val Gln Ala His Glu Thr Leu Glu Ile Met Gly Asn Thr Leu
660 665 670

Leu Glu Glu Phe Asn Asp Ile Lys Met Val Asn Gly Glu Leu Lys Tyr
675 680 685

Val Lys Arg Glu Asp
690

<210> 23
<211> 2013
<212> DNA
<213> Saccharomyces castelli

<400> 23
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acatcagtgg gaaaccactg ctcgccatcc atcctcaaga accatccgga tgcacccgca 180
actgctgccc ccaatacaga taagatacaa ttgaatctaa tgttccccag taatcaaaca 240

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gcaccaccgc	cagcacaac	agaggataac	tcggtcacat	tcgcaccaga	taatattcag	360
atcgcatgga	atcaagacca	aaataccttg	attcatttgg	atccagtgcc	caattttaac	420
gataaggcag	atattaaacc	ttggttacag	aagatattct	acccgcaagg	tattgaaatc	480
gtcattgaaa	gatcggataa	tacaaaagta	atcttttaaat	gtaaagctgc	aaagaaggga	540
agaagttcca	ataaggataa	gaatcaagct	tctgcctcgg	atcccaccgt	gacaacgccg	600
aatgttaatc	atgtcttggt	gaagaagaag	aagaaaagat	ccgtttctag	gttcaatatt	660
tgtcccttta	gaattagagc	aacgtattca	ttaaagagga	agaagtggaa	tatcgtcgtc	720
ataaataaca	cacatttctca	tccattgaaa	tttaaccocgg	attctgagga	gtataagaag	780
tttaaattga	aattgaggga	agacggtgat	ttggaagcca	ttaaaaaatt	tgatgaattg	840
gaatataaga	caaggaaaaa	tctgcccatt	caatcatcta	tgatcccctg	tgattgtggg	900
ttaactaacg	aaattcaaag	ttttaacata	gtcttacctt	cgggaagaac	tgccgctaatt	960
agtaatgata	ccgcaacagc	aacatctagt	cgtccgatta	aaaaattggt	aagtgcaaac	1020
ttaattttcaa	caagcaatgg	tggcaacaac	aataacgtgc	aaaaaccaag	aactagggtta	1080
aatgataaga	gaaataagga	aaatcttttg	aaaaagacaa	ccacaacaaa	tttcttaact	1140
aataacggca	cagcaccagc	cataccgact	aatagggtta	acagcctggg	ggaaaattca	1200
aattcaatga	cagatttctt	agatgaccca	tttaattcct	ccatgaatat	tcccatgaac	1260
gattttgcac	catttaattt	ggaagcagta	actaatctta	atgaaattga	ttttaccgat	1320
atttttcaata	aaccaacaac	tttacaacaa	gatgatggac	cattttcaac	acttaacgaa	1380
atgcatattc	acgaccaaca	aacaccatat	gctgcagata	tgtctatttt	ttcatcatta	1440
gatactgcca	gtttaacaag	attccaatct	ccaatgcatg	atgtgaatga	ttcaccacta	1500
cttcgaaatc	catccaacac	aacaaactca	gaaatgttag	attatatgtc	aaatcaacat	1560
acaacgcagg	aaaacaacgt	gatacccaat	aatggtaata	acaataacaa	cactacattg	1620
gcaaacgaac	tggtatgttt	caaaatgggtg	gatgggtgaat	tgaaaattat	agaagatgat	1680
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caattttggc	aaaataatat	taccaacaac	gactcgataa	acattacatc	atccatgaat	1860
cagataactg	acaatacaac	aaacactaat	tcaaacatac	aatccatcaa	tatgcaactc	1920
atagagttga	ataatacttc	gaaaaagtac	gatgaccaca	acaacaacaa	caataacaac	1980

atcaacagcc ataatcataa taatagtaat tag

2013

<210> 24

<211> 670

<212> PRT

<213> Saccharomyces castelli

<400> 24

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

Ser Pro Ser Ser Ser Ser Ser Ser Thr Ser Val Gly Asn His Cys Ser
35 40 45

Pro Ser Ile Leu Lys Asn His Pro Asp Ala Ser Ala Thr Ala Ala Pro
50 55 60

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

Tyr Ser Leu Val Met Gly Pro Glu Thr Lys Gln Pro Arg Thr Ser Lys
85 90 95

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

Thr Phe Ala Pro Asp Asn Ile Gln Ile Ala Leu Asn Gln Asp Gln Asn
115 120 125

Thr Leu Ile His Leu Asp Pro Val Pro Asn Phe Asn Asp Lys Ala Asp
130 135 140

Ile Lys Pro Trp Leu Gln Lys Ile Phe Tyr Pro Gln Gly Ile Glu Ile
145 150 155 160

Val Ile Glu Arg Ser Asp Asn Thr Lys Val Ile Phe Lys Cys Lys Ala
165 170 175

Ala Lys Lys Gly Arg Ser Ser Asn Lys Asp Lys Asn Gln Ala Ser Ala
180 185 190

Ser Asp Pro Thr Val Thr Thr Pro Asn Val Asn His Val Leu Leu Lys

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

Leu Asn Glu Ile Asp Phe Thr Asp Ile Phe Asn Lys Pro Thr Thr Leu
435 440 445

Gln Gln Asp Asp Gly Pro Phe Ser Thr Leu Asn Glu Met His Ile His
450 455 460

Asp Gln Gln Thr Pro Tyr Ala Ala Asp Met Ser Ile Phe Ser Ser Leu
465 470 475 480

Asp Thr Ala Ser Leu Thr Arg Phe Gln Ser Pro Met His Asp Val Asn
485 490 495

Asp Ser Pro Leu Leu Arg Asn Pro Ser Asn Thr Thr Asn Ser Glu Met
500 505 510

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

Pro Asn Asn Gly Asn Asn Asn Asn Asn Thr Thr Leu Ala Asn Glu Leu
530 535 540

Asp Val Phe Lys Met Val Asp Gly Glu Leu Lys Ile Ile Glu Asp Asp
545 550 555 560

Asn Ala Leu Leu Lys Ile Asn Ser Thr Thr Gly Arg His Asp Asn Pro
565 570 575

Glu Met Thr Asn Thr Ser Asn Glu His Asn Pro Tyr Met Phe His Ala
580 585 590

Ser Pro Ala Val Gln Ala Glu Gly Gln Phe Trp Gln Asn Asn Ile Thr
595 600 605

Asn Asn Asp Ser Ile Asn Ile Thr Ser Ser Met Asn Gln Ile Thr Asp
610 615 620

Asn Thr Thr Asn Thr Asn Ser Asn Ile Gln Ser Ile Asn Met Gln Leu
625 630 635 640

Ile Glu Leu Asn Asn Thr Ser Lys Lys Tyr Asp Asp His Asn Asn Asn
645 650 655

Asn Asn Asn Asn Ile Asn Ser His Asn His Asn Asn Ser Asn
660 665 670

<210> 25
 <211> 1557
 <212> DNA
 <213> Kluyveromyces waltii

<400> 25
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 acgagtaata cggaagcag cggcaccgat ataacgaacg gcacacctgg atggggcgag 180
 acagtgaatc tcgaaaacct aatgagcgaa aaagcgctgg agtccatcgg catgcaacgc 240
 tcccagaaca agctgattca cttggacccg ataccgaact tccaggaccg caacgaaata 300
 aagccgtggc ttcaaaagat cttctaccca caaggtatcg aaatagtgat tgagcgttct 360
 gacaatatca aggttgTTTT caaatgcaag gcctcaaggc gaggcaagac atcccggagg 420
 cgaaatggat acgggtcccat tgcggaagaa aaggagaacc cggaaaacc tctggcggta 480
 caaagggtag agcagcaatc gtgcaagaag aagagatctg tttcaccata caacacatgc 540
 ccgttcaggg tgcgagcgac ttactcgctc aagcggaaga agtggaaacat tgttgtgatg 600
 aacaatggac actcgacccc gcttaaattt aatgccgaca gtgatgacta caaaaagttt 660
 aaaaattatt tgcgagagca cgaagactgg gagggcgtca aaaaattcga tgagttagag 720
 tgcagaacac gtttcaattt accaactgag cccagccta taccgtgtga ctgtgggctg 780
 actcaggaga ttgaaagttt caatattgta ctccctacgt ccgattccat ggccaactca 840
 actgataaaa cggtaaagtaa gccgcgtcat aagtcgtcgc gaaagagcaa tagccacatt 900
 gccacggcct tgagccgaca tccgacacca ctagaggctc taggtagatc ttcaccacaa 960
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 gacgcattctc tgtcaacatg ggaacctaac gcccttccta atcaatcaga ggagattgac 1140
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 tggaaccacc aacacagtga cgaccctcat gaatatagta atgatttttt gccttaa 1557

<210> 26
 <211> 518
 <212> PRT
 <213> Kluyveromyces waltii

<400> 26

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

Val Asp Thr Ile Gly Thr Gly Val Thr Ser Asn Thr Glu Ser Ser Gly
 35 40 45

Thr Asp Ile Thr Asn Gly Thr Pro Gly Trp Gly Glu Thr Val Asn Leu
 50 55 60

Glu Asn Leu Met Ser Glu Lys Ala Leu Glu Ser Ile Gly Met Gln Arg
 65 70 75 80

Ser Gln Asn Lys Leu Ile His Leu Asp Pro Ile Pro Asn Phe Gln Asp
 85 90 95

Arg Asn Glu Ile Lys Pro Trp Leu Gln Lys Ile Phe Tyr Pro Gln Gly
 100 105 110

Ile Glu Ile Val Ile Glu Arg Ser Asp Asn Ile Lys Val Val Phe Lys
 115 120 125

Cys Lys Ala Ser Arg Arg Gly Lys Thr Ser Arg Arg Arg Asn Gly Tyr
 130 135 140

Gly Pro Ile Ala Glu Glu Lys Glu Asn Pro Glu Asn Pro Leu Ala Val
 145 150 155 160

Gln Arg Val Gln Gln Gln Ser Cys Lys Lys Lys Arg Ser Val Ser Pro
 165 170 175

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

Lys Lys Trp Asn Ile Val Val Met Asn Asn Gly His Ser His Pro Leu
 195 200 205

Lys Phe Asn Ala Asp Ser Asp Asp Tyr Lys Lys Phe Lys Asn Tyr Leu
 210 215 220

Arg Glu His Glu Asp Trp Glu Ala Val Lys Lys Phe Asp Glu Leu Glu
 225 230 235 240

Cys Arg Thr Arg Phe Asn Leu Pro Thr Glu Pro Gln Pro Ile Pro Cys
 245 250 255

Asp Cys Gly Leu Thr Gln Glu Ile Glu Ser Phe Asn Ile Val Leu Pro
 260 265 270

Thr Ser Asp Ser Met Ala Asn Ser Thr Asp Lys Thr Val Ser Lys Pro
 275 280 285

Arg His Lys Ser Ser Arg Lys Ser Asn Ser His Ile Ala Thr Ala Leu
 290 295 300

Ser Arg His Pro Thr Pro Leu Glu Val Leu Gly Arg Ser Ser Pro Gln
 305 310 315 320

Leu Ala Gln Ala Gly Thr Glu Pro Gln Ser Ile Lys Val Glu Thr Pro
 325 330 335

Thr His Asn Ser Glu Ser Asn Val Met Gly Met Gln Ser Val Gln Ala
 340 345 350

Phe Asp Ala Ser Leu Ser Ala Leu Asp Ala Ser Leu Ser Thr Trp Glu
 355 360 365

Pro Asn Ala Leu Pro Asn Gln Ser Glu Glu Ile Asp Phe Thr Asp Leu
 370 375 380

Phe Leu Asn Pro Leu Thr Arg Met Lys His Glu Pro Met Thr Gly Ser
 385 390 395 400

Ser Arg Glu Leu Pro Trp Thr Ala Thr Thr Lys Gln Phe Met Asp Glu
 405 410 415

Phe Gln Phe Pro Leu Ser Pro Ala Pro Val Cys Glu Ile Asn His Thr
 420 425 430

Asp His Cys Asn Cys Leu Met Pro Ser Ser Thr Asp Gly Leu Gly Arg
 435 440 445

Asp Ser Pro His Asp Phe His Gln Arg Ile Gln Gln Gln Gly Arg Met
 450 455 460

Glu Ser Arg Ser Ser Pro Ala Gly Ala Val Leu Thr Ala Asp Leu Asn
 465 470 475 480

Asn Leu His Leu Thr Gly Gln Gln His Met Gln Thr Ser Asn Leu Asp
 485 490 495

Gln Gly Val Ala Trp Asn His Gln His Ser Asp Asp Pro His Glu Tyr
 500 505 510

Ser Asn Asp Phe Leu Pro
 515

<210> 27
 <211> 1911
 <212> DNA
 <213> *Saccharomyces kluyveri*

<400> 27
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 aaccaggctt gcacgccgac tgggcttaca atcagcagca acgaaacaac gatgagcaat 180
 gccagctata accatgcctt gagtgaaaac gctatagagt cggtaaagcg ccaacaaaat 240
 cagaacaagc tcatccactt ggaccctatc cctgatttta atgacaaaaa cgagattaaa 300
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 aatatcaaga ttattttcaa atgcaaagca tcgaaaagag gtaagaaaac cagaaagtct 420
 gccttctgcg gccagatga tcctgggaac gaagatgaaa agagcctgct tgtacagagt 480
 ctgacgaata gtaataacaa cagcacctcg tcatccaata gcacaaagaa aaaaagatcg 540
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 aagtggaata tcgtcgtaat aaacaatggc cattctcatc ctttgaaatt taacccgga 660
 agtgaagact ataagaaatt caaaaacaag ctgaggggaag atggcgattg ggatgctgta 720
 aagaaatttg acgagttgga gtatagaaca aagtttaact taccactga accgacgcct 780
 atatcttggt attgtgggct gactcaagag atagaaagtt tcaatgtcat ttaccaagt 840
 gtaaacgccc aactcccttc tctcccctca caaatgcat gtactgctaa ttcaaccgac 900
 aagaccgtgg ccaaacccaa aaaaaatctt gcaaagaaga gcaggaagtc tattactgcc 960

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ctgacacacg acatacaaag caataagagt acatctacaa cgagaactac tacaccaatg 1080
aacgcatccc tacagaaccc ctttacaagt acgagtttta ttgacggaaa cgaaatcgat 1140
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caatgggtcat taaataatct ggtatcttca ccggttacac aaacagtgca tccccaaaggc 1320
ccgatagact ttatgatggt taatcagcac caatcaattt caccagacct ccaaagccca 1380
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gatagaacaa gcgtttcagt gacgactacc ccaatgtgtg aagtaaataa tagccatact 1620
tgtcaaagcg attgcatgga attaaaatcc accaacgcag taaatgcaca gcacaatttg 1680
tctcacaact taacacaggt cgtcgatact caaaatcaag cccaagatca aaacactttg 1740
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gttgtagaag aagaaagaag tactgtggag ccagagaatc tgacgaaaaa tacgagcgat 1860
caacagtcca atttatttcc atgggatgga acacagggct tctttggtta a 1911

<210> 28
<211> 636
<212> PRT
<213> Saccharomyces kluyveri

<400> 28

Met Asn His Phe Val Asp Asn Ser Pro Met Asp Pro Leu Pro Asn Asp
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Ile Trp Glu Gln Ser Pro Ser Leu Glu Ser Met Leu Met Ser Pro Ser
20 25 30

Val Ser Ser Ser Ser Thr Thr Asn Asn Gln Ala Cys Thr Pro Thr Gly
35 40 45

Leu Thr Ile Ser Ser Asn Glu Thr Thr Met Ser Asn Ala Ser Tyr Asn
50 55 60

His Ala Leu Ser Glu Asn Ala Ile Glu Ser Val Lys Arg Gln Gln Asn
65 70 75 80

Gln Asn Lys Leu Ile His Leu Asp Pro Ile Pro Asp Phe Asn Asp Lys
85 90 95

Asn Glu Ile Lys Pro Trp Leu Gln Lys Ile Phe Tyr Pro Gln Gly Ile
100 105 110

Glu Ile Val Ile Glu Arg Ser Asp Asn Ile Lys Ile Ile Phe Lys Cys
115 120 125

Lys Ala Ser Lys Arg Gly Lys Lys Thr Arg Lys Ser Ala Phe Cys Gly
130 135 140

Pro Asp Asp Pro Gly Asn Glu Asp Glu Lys Ser Leu Leu Val Gln Ser
145 150 155 160

Leu Thr Asn Ser Asn Asn Asn Ser Thr Ser Ser Ser Asn Ser Thr Lys
165 170 175

Lys Lys Arg Ser Val Ser Pro Tyr Asn Thr Cys Pro Phe Arg Ile Arg
180 185 190

Ala Thr Phe Ser Leu Lys Arg Gln Lys Trp Asn Ile Val Val Ile Asn
195 200 205

Asn Gly His Ser His Pro Leu Lys Phe Asn Pro Glu Ser Glu Asp Tyr
210 215 220

Lys Lys Phe Lys Asn Lys Leu Arg Glu Asp Gly Asp Trp Asp Ala Val
225 230 235 240

Lys Lys Phe Asp Glu Leu Glu Tyr Arg Thr Lys Phe Asn Leu Pro Thr
245 250 255

Glu Pro Thr Pro Ile Ser Cys Asp Cys Gly Leu Thr Gln Glu Ile Glu
260 265 270

Ser Phe Asn Val Ile Leu Pro Ser Val Asn Ala Gln Leu Pro Ser Leu
275 280 285

Pro Ser Gln Asn Ala Cys Thr Ala Asn Ser Thr Asp Lys Thr Val Ala
290 295 300

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

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

Cys Met Glu Leu Lys Ser Thr Asn Ala Val Asn Ala Gln His Asn Leu
545 550 555 560

Ser His Asn Leu Thr Gln Val Val Asp Thr Gln Asn Gln Ala Gln Asp
565 570 575

Gln Asn Thr Leu Ile Gly Ser Val Leu Asn Thr Glu Leu Ser Asn Met
580 585 590

Arg Ile Ile Asp Gly Gln Leu His Val Val Glu Glu Glu Arg Ser Thr
595 600 605

Val Glu Pro Glu Asn Leu Thr Lys Asn Thr Ser Asp Gln Gln Ser Asn
610 615 620

Leu Phe Pro Trp Asp Gly Thr Gln Gly Phe Phe Gly
625 630 635

<210> 29
<211> 2310
<212> DNA
<213> Kluyveromyces marxianus

<400> 29
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aagcaacagg accagaacaa gttgatccac ttggacccga ttcctgactt caaggacaag 300
agcgaggtga agccgtggct ccagaagata ttttatccgc aggggatcga gattgtgatt 360
gagcgggtcgg acagcatgaa gattgtgttc aagtgcagg ctgtgaagaa ggcgaggagc 420
gggggttgcgg ctgcggcggc cgcggcgtct tccgggttctg gggtagcggg gagttccggc 480
cacttcctag ggtgtgcgta cgtgggcatg aacacgaatc cgatgttgaa taagggttcg 540
agtaagaaga aggatggcag cggtaataat gccaggtgca aggacgagaa gtgcggcggc 600
gatgggtcgt gtgaaaatag cggcgctaac gtcgacgcta atgctgcgga aaatgcta 660
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tgtcccttca gattgagagc tacttttctg ttgaaaagga agaagtggaa catcgtggtg 780
attaacaacg tgcacacca cccgctacgg ttcaatcccg acagcgagga ctacaaaaaa 840
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gaatacagaa ctaaatecgaa cctgcctatc gatttgagcc ctatcccatg tgactgtggt	960
ctaacacagg aaatccagtc ctttaatatc gtccttccaa caacaaacat tatagcatca	1020
accagcagag ctggttcttc tgatgcaaac actgtgtcaa agccaaagaa gtgtaaaaac	1080
tctttgaaga agaaatcaaa aaaattgagg ctaaagaata caaaacaaaa gttgcaacag	1140
gatatcgaaa gcaacagcgc tcatacttcc gctacaggaa cgccattagg aaatgtacca	1200
aatacactga acctccaatt tgacgtcaac atggacttgg gtgtacagtc cacttctgga	1260
tcaaatatga attcaagcgt ggtattaacc cctcaagaaa acatatattc gcatgatttc	1320
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catttcaaaa acaatcagca acctgtaccc caatcacagg atgctattcc actctcgttt	1500
tctcataaac catcaaacag tggatttccg gacacccatc attctcaggc ccaaggcagg	1560
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tatgatgtct gtgcaaatga ctttggacaa tgtggcggtg tcggcgctgg tgtcgaaacc	1980
aattcacata gtaatactaa cagtattact ttgacgacta gttctatggg taatgggtatc	2040
aactcgagcg tccatggtta tgatattcca attaaaacag agttaacttc aaaccacag	2100
gagtatatct ctaatgtact gaatacggat tttaacgaac ttaaactttc ccaagatgaa	2160
caacatcagc aacaaggtgg catgaacaac ctcggttctc aatcaaatta caactaccag	2220
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<210> 30
 <211> 769
 <212> PRT
 <213> Kluyveromyces marxianus

<400> 30

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Asp Pro Leu Asp Pro Leu Ser Asn Ala Glu Phe Trp His Ala Ser Pro
20 25 30

Ser Phe Glu Met Met Asn Ser Pro Lys Val Ser Pro Ala Ser Thr Val
35 40 45

Met Thr His Thr Pro Ser Val Gly Gly Gln Gln Ser Ser Asn Ser Glu
50 55 60

Val Ser Tyr Asn Asn Val Leu Ser Glu Asn Ala Ile Glu Ala Leu Gln
65 70 75 80

Lys Gln Gln Asp Gln Asn Lys Leu Ile His Leu Asp Pro Ile Pro Asp
85 90 95

Phe Lys Asp Lys Ser Glu Val Lys Pro Trp Leu Gln Lys Ile Phe Tyr
100 105 110

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

Val Phe Lys Cys Lys Ala Val Lys Lys Ala Arg Ser Gly Val Ala Ala
130 135 140

Ala Ala Ala Ala Ala Ser Ser Gly Ser Gly Val Ala Gly Ser Ser Gly
145 150 155 160

His Phe Leu Gly Cys Ala Tyr Val Gly Met Asn Thr Asn Pro Met Leu
165 170 175

Asn Lys Gly Ser Ser Lys Lys Lys Asp Gly Ser Gly Asn Asn Ala Arg
180 185 190

Cys Lys Asp Glu Lys Cys Gly Gly Asp Gly Ser Cys Glu Asn Ser Gly
195 200 205

Ala Asn Val Asp Ala Asn Ala Ala Glu Asn Ala Asn Ala Ser Asn Ser
210 215 220

Thr Thr Ser Thr Gly Lys Lys Lys Arg Val Thr Gly Pro Tyr Asn Ser
225 230 235 240

Cys Pro Phe Arg Val Arg Ala Thr Phe Ser Leu Lys Arg Lys Lys Trp

					245						250					255
Asn	Ile	Val	Val	Ile	Asn	Asn	Val	His	Thr	His	Pro	Leu	Arg	Phe	Asn	
			260					265					270			
Pro	Asp	Ser	Glu	Asp	Tyr	Lys	Lys	Phe	Lys	Lys	Gly	Leu	Tyr	Asp	Ser	
		275					280					285				
Gly	Asp	Ile	Glu	Thr	Val	Lys	Lys	Phe	Asp	Glu	Leu	Glu	Tyr	Arg	Thr	
	290					295					300					
Lys	Ser	Asn	Leu	Pro	Ile	Asp	Leu	Ser	Pro	Ile	Pro	Cys	Asp	Cys	Gly	
305					310					315					320	
Leu	Thr	Gln	Glu	Ile	Gln	Ser	Phe	Asn	Ile	Val	Leu	Pro	Thr	Thr	Asn	
				325					330					335		
Ile	Ile	Ala	Ser	Thr	Ser	Arg	Ala	Gly	Ser	Ser	Asp	Ala	Asn	Thr	Val	
			340					345					350			
Ser	Lys	Pro	Lys	Lys	Cys	Lys	Asn	Ser	Leu	Lys	Lys	Lys	Ser	Lys	Lys	
		355					360					365				
Leu	Arg	Leu	Lys	Asn	Thr	Lys	Gln	Lys	Leu	Gln	Gln	Asp	Ile	Glu	Ser	
	370					375					380					
Asn	Ser	Ala	His	Thr	Ser	Ala	Thr	Gly	Thr	Pro	Leu	Gly	Asn	Val	Pro	
385					390					395					400	
Asn	Thr	Leu	Asn	Leu	Gln	Phe	Asp	Val	Asn	Met	Asp	Leu	Gly	Val	Gln	
			405						410					415		
Ser	Thr	Ser	Gly	Ser	Asn	Met	Asn	Ser	Ser	Val	Val	Leu	Thr	Pro	Gln	
			420					425					430			
Glu	Asn	Ile	Tyr	Ser	His	Asp	Phe	Phe	Pro	Asn	Thr	Ala	Ser	Ser	Gln	
		435					440					445				
Arg	Asn	Asp	Ser	Pro	Asn	Phe	Ser	Asn	Leu	Asn	Pro	Ser	Tyr	Phe	Asn	
	450					455					460					
Thr	Glu	Asn	Glu	Ile	Asp	Phe	Thr	Glu	Leu	Phe	Ser	Lys	Pro	Leu	Pro	
465					470					475					480	

His Phe Lys Asn Asn Gln Gln Pro Val Pro Gln Ser Gln Asp Ala Ile
485 490 495

Pro Leu Ser Phe Ser His Lys Pro Ser Asn Ser Gly Ile Pro Asp Thr
500 505 510

His His Ser Gln Ala Gln Gly Arg His Met Leu Tyr Gln Asn Val Asp
515 520 525

Ser Thr Pro Ser Thr His Ser Ser Pro Ser Met Asn Val Met Thr Thr
530 535 540

Gly Lys Asn Ser Met Thr Ile Thr Pro Ala Leu Asn Thr Ala Thr Ala
545 550 555 560

Ala Thr Gly Pro Thr Gln Ser Ser Val Pro Leu Tyr Ser Ser Asp Ile
565 570 575

Ser Lys Glu Gln Ile Gln Asp Phe Val Asp Met Asn Gln Ile Phe Gly
580 585 590

Thr Ser Glu Tyr Ser Lys Asp Arg Asn Ser Asn Ser Asn Thr Pro Asn
595 600 605

Ser Val Ile Pro Gly Arg Ser Leu Asn Phe Gln His Ser Arg Leu Pro
610 615 620

Thr Ser Asn Gln His Gln Asn Gln Ser Ala Ile Cys Glu Ile Asn Asn
625 630 635 640

Tyr Asp Val Cys Ala Asn Asp Phe Gly Gln Cys Gly Gly Val Gly Ala
645 650 655

Gly Val Glu Thr Asn Ser His Ser Asn Thr Asn Ser Ile Thr Leu Thr
660 665 670

Thr Ser Ser Met Gly Asn Gly Ile Asn Ser Ser Val His Gly Tyr Asp
675 680 685

Ile Pro Ile Lys Thr Glu Leu Thr Ser Asn Pro Gln Glu Tyr Ile Ser
690 695 700

Asn Val Leu Asn Thr Asp Phe Asn Glu Leu Lys Leu Ser Gln Asp Glu
705 710 715 720

Gln His Gln Gln Gln Gly Gly Met Asn Asn Leu Gly Ser Gln Ser Asn
725 730 735

Tyr Asn Tyr Gln Leu Met Phe Asp Glu Glu Leu Asn Gln Pro Gln Gln
740 745 750

Thr Thr His Asn Pro His Thr Leu Trp Glu Glu Pro His Gly Phe Leu
755 760 765

Gln

<210> 31
<211> 1494
<212> DNA
<213> Issatchenkia orientalis

<400> 31
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cctgataggg gaatgtatac aacttcgtat tgtcccatca aggataccat tatgatgcac 180
aagtcgtcat cacaagcgtc atcacaagcg tcatcacaag cgtcatcaca agtgccatca 240
caagtgccat cacaagcgtc atcacaagct tcatcacaag cgtcctcctc gtgttgctcc 300
acaaattcgg ctccctgctc ccctacttca ccattgattc tatcgagtga ggggagagaa 360
aataaggtag attgttccaa cagcatgaca aagttgaagt tggaaaatcg ccatttcacc 420
aacaaggcag acattaagcc atggttacag agaaacctgg cctccatggg gatccatatt 480
gtaattgaga gatcagatga tacaagatt gtcttcaa at gcaagtattc ggacaagaag 540
ccactggaga aaaataactg caaatcccat gagagagcag ctaggcagcg gaaaaagaag 600
gtttgcccct ttagaatcag ggccaactat tccattcgat ccaaactg gacattggtt 660
atagtcaatg attctcataa tcaccctatt tccagtttgg acgtcaatat agctgatatt 720
aagtccaaat tgtcgataat tgaccagaaa aaatcaa atc atcgggttac taagccgaaa 780
agtttgaaac ataaagacca tttgccagta cctcgagcct ttgccattga cccctcaa at 840
gctttatcgt caacttctct gacttgcaaa ccttatcata atagtctcat acctccaata 900
ttaaatgaaa atacacatgc aaagggttaa ctccctccca tctcattgcc agataactca 960
ttgaataacc aagttagaca aattgaagat actttgaaaa ccttccaaca gggttggtaat 1020
ataccaatg tttcaaaaga aaaaatctta aaggatgtct ggtgcgtctt gaataaatca 1080

atcaatgaaa tcaccgactc caattcaggg agctttcctc taccattacc cctaccgtta 1140
ccacaccaaa aaatgggcag agtatctcaa agacaatctt tccaattggt caataactaat 1200
aacaacattg agaataatgt tattaatggc aatctcgaaa atagcaacac tagcagccga 1260
agcagcagca acagtatcaa cgacatcaac gacatcaacg acatcaacga catcaacttg 1320
gctagtaata acatgtactt gaataactat gctaaaagca atacctttac atctccacat 1380
ttcaagcttc caagatacca attttcaa at gcatctcttg gaccactgat aaaatctgcc 1440
catgatcgaa acatcagttt gccaaagtatc cgaaacctag actcaggcgc ctag 1494

<210> 32

<211> 497

<212> PRT

<213> Issatchenkia orientalis

<400> 32

Met Thr His Ser Asp Ser Gly Leu His Lys Asn Pro Ser Met Arg Cys
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Glu Ala Ser Pro Ser Asn Phe Gly Ser Glu Phe Glu Asp Gly Met Ser
20 25 30

His Gly Val Gln Ser Cys Asp Ala Pro Asp Arg Gly Met Tyr Thr Thr
35 40 45

Ser Tyr Cys Pro Ile Lys Asp Thr Ile Met Met His Lys Ser Ser Ser
50 55 60

Gln Ala Ser Ser Gln Ala Ser Ser Gln Ala Ser Ser Gln Val Pro Ser
65 70 75 80

Gln Val Pro Ser Gln Ala Ser Ser Gln Ala Ser Ser Gln Ala Ser Ser
85 90 95

Ser Cys Cys Ser Thr Asn Ser Ala Pro Cys Ser Pro Thr Ser Pro Leu
100 105 110

Ile Leu Ser Ser Glu Gly Arg Glu Asn Lys Val His Cys Ser Asn Ser
115 120 125

Met Thr Lys Leu Lys Leu Glu Asn Arg His Phe Thr Asn Lys Ala Asp
130 135 140

Ile Lys Pro Trp Leu Gln Arg Asn Leu Ala Ser Met Gly Ile His Ile

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

Met Gly Arg Val Ser Gln Arg Gln Ser Phe Gln Leu Phe Asn Thr Asn
385 390 395 400

Asn Asn Ile Glu Asn Asn Val Ile Asn Gly Asn Leu Glu Asn Ser Asn
405 410 415

Thr Ser Ser Arg Ser Ser Ser Asn Ser Ile Asn Asp Ile Asn Asp Ile
420 425 430

Asn Asp Ile Asn Asp Ile Asn Leu Ala Ser Asn Asn Met Tyr Leu Asn
435 440 445

Asn Tyr Ala Lys Ser Asn Thr Phe Thr Ser Pro His Phe Lys Leu Pro
450 455 460

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

His Asp Arg Asn Ile Ser Leu Pro Ser Ile Arg Asn Leu Asp Ser Gly
485 490 495

Ala

<210> 33
<211> 1434
<212> DNA
<213> Issatchenkia orientalis

<400> 33
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cctgataggg gaatgtatac aacttcgtat tgtcccatca aggataccat tatgatgcac 180
aagtcgtcat cacaagcgtc atcacaagct tcatcacaag cgtcctcctc gtgttgctcc 240
acaaattcgg ctccctgctc ccctacttca ccattgattc tatcgagtga ggggagagaa 300
aataaggtag attgttccaa cagcatgaca aagttgaagt tggaaaatcg ccatttcacc 360
aacaaggcag acattaagcc atggttacag agaaacctgg cctccatggg gatccatatt 420
gtaattgaga gatcagatga tacaagatt gtcttcaa at gcaagtattc ggacaagaag 480
ccactggaga aaaataactg caaatcccat gagagagcag ctaggcagcg gaaaaagaag 540
gtttgcccct ttagaatcag ggccaactat tccattcgat ccaaactg gacattggtt 600
atagtcaatg attctcataa tcaccctatt tccagtttgg acgtcaatat agctgatatt 660

aagtcctaat tgtcgataat tgaccagaaa aaatcaaata atcgggttac taagccgaaa 720
agtttgaaac ataaagacca tttgccagta cctcgagcct ttgccattga cccctcaaata 780
gctttatcgt caacttctct gacttgcaaa ccttatcata atagtctcat acctccaata 840
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ataccaatg tttcaaaaga aaaaatctta aaggatgtct ggtgcgtctt gaataaatca 1020
atcaatgaaa tcaccgactc caattcaggg agctttcctc taccattacc cctaccgtta 1080
ccacacaaaa aaatgggcag agtatctcaa agacaatctt tccaattggt caataactat 1140
aacaacattg agaataatgt tattaatggc aatctcgaaa atagcaacac tagcagccga 1200
agcagcagca acagtatcaa cgacatcaac gacatcaacg acatcaacga catcaacttg 1260
gctagtaata acatgtactt gaataactat gctaaaagca atacctttac atctccacat 1320
ttcaagcttc caagatacca attttcaaata gcatctcttg gaccactgat aaaatctgcc 1380
catgatcgaa acatcagttt gccaaagtatc cgaaacctag actcaggcgc ctag 1434

<210> 34
<211> 477
<212> PRT
<213> Issatchenkia orientalis

<400> 34

Met Thr His Ser Asp Ser Gly Leu His Lys Asn Pro Ser Met Arg Cys
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Glu Ala Ser Pro Ser Asn Phe Gly Ser Glu Phe Glu Asp Gly Met Ser
20 25 30

His Gly Val Gln Ser Cys Asp Ala Pro Asp Arg Gly Met Tyr Thr Thr
35 40 45

Ser Tyr Cys Pro Ile Lys Asp Thr Ile Met Met His Lys Ser Ser Ser
50 55 60

Gln Ala Ser Ser Gln Ala Ser Ser Gln Ala Ser Ser Ser Cys Cys Ser
65 70 75 80

Thr Asn Ser Ala Pro Cys Ser Pro Thr Ser Pro Leu Ile Leu Ser Ser
85 90 95

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

Lys Leu Glu Asn Arg His Phe Thr Asn Lys Ala Asp Ile Lys Pro Trp
115 120 125

Leu Gln Arg Asn Leu Ala Ser Met Gly Ile His Ile Val Ile Glu Arg
130 135 140

Ser Asp Asp Thr Lys Ile Val Phe Lys Cys Lys Tyr Ser Asp Lys Lys
145 150 155 160

Pro Leu Glu Lys Asn Asn Cys Lys Ser His Glu Arg Ala Ala Arg Gln
165 170 175

Arg Lys Lys Lys Val Cys Pro Phe Arg Ile Arg Ala Asn Tyr Ser Ile
180 185 190

Arg Ser Lys His Trp Thr Leu Val Ile Val Asn Asp Ser His Asn His
195 200 205

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

Ser Ile Ile Asp Gln Lys Lys Ser Asn His Arg Val Thr Lys Pro Lys
225 230 235 240

Ser Leu Lys His Lys Asp His Leu Pro Val Pro Arg Ala Phe Ala Ile
245 250 255

Asp Pro Ser Asn Ala Leu Ser Ser Thr Ser Leu Thr Cys Lys Pro Tyr
260 265 270

His Asn Ser Leu Ile Pro Pro Ile Leu Asn Glu Asn Thr His Ala Lys
275 280 285

Val Lys Leu Pro Pro Ile Ser Leu Pro Asp Asn Ser Leu Asn Asn Gln
290 295 300

Val Arg Gln Ile Glu Asp Thr Leu Lys Thr Phe Gln Gln Val Gly Asn
305 310 315 320

Ile Pro Asn Val Ser Lys Glu Lys Ile Leu Lys Asp Val Trp Cys Val
325 330 335

Leu Asn Lys Ser Ile Asn Glu Ile Thr Asp Ser Asn Ser Gly Ser Phe
 340 345 350

Pro Leu Pro Leu Pro Leu Pro Leu Pro His Gln Lys Met Gly Arg Val
 355 360 365

Ser Gln Arg Gln Ser Phe Gln Leu Phe Asn Thr Asn Asn Asn Ile Glu
 370 375 380

Asn Asn Val Ile Asn Gly Asn Leu Glu Asn Ser Asn Thr Ser Ser Arg
 385 390 395 400

Ser Ser Ser Asn Ser Ile Asn Asp Ile Asn Asp Ile Asn Asp Ile Asn
 405 410 415

Asp Ile Asn Leu Ala Ser Asn Asn Met Tyr Leu Asn Asn Tyr Ala Lys
 420 425 430

Ser Asn Thr Phe Thr Ser Pro His Phe Lys Leu Pro Arg Tyr Gln Phe
 435 440 445

Ser Asn Ala Ser Leu Gly Pro Leu Ile Lys Ser Ala His Asp Arg Asn
 450 455 460

Ile Ser Leu Pro Ser Ile Arg Asn Leu Asp Ser Gly Ala
 465 470 475

<210> 35
 <211> 1203
 <212> DNA
 <213> Saccharomyces bayanus

<400> 35
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 gaaatcaaac catggttaca aaagatcttt tatccccagg gaatagatat agtcattgaa 180
 aggtcagatt ctggcaaagt cactttttaa tgtagatcag tacgatccaa cgggaggctg 240
 aatcctgaat ccaaaggcac ctcttcaagg tcgcatgcat gtccatttag aatcagagcc 300
 gccttctctg tacggttaca gaagtggaat gtggttgtca tgaataatat acatgcgcac 360
 gagctgaggt ttgatctaata cactaaaaca gatgactata aaaaatttaa agaaaccctt 420
 cgccagaaac atgacgaaaa ggcaatcaaa acctttgatg aactagaata caaggccagc 480

ctaaacttac cgctcgtgac accgattatc tcctgtgact gtggtctgac caaagaaatt	540
gaagctttca ataatatata tcttccgata tcaaactcctt ctttgacgtc taaaaaaagt	600
atactcaagg ctaataaaaa ttctgtgtct aaggtaaaac ctaaacaacc ggaaaattca	660
aagcctgggc tgaggttgaa aacacaatta gattcaactc tgaatgcaac cagatttttg	720
gatgacatca aagtacaaag cgctcttgta tcgacaggaa gtgccgagtc actaatgaac	780
ttgaacgaaa tcgacttcac caatatgttt aataacgata gtgctattcc aaatcccaat	840
caaggactga tggatttctc agtggatccc attgcaggac cttcctcttc ttctctattt	900
ccttcaacgc ccaccgagcc tttttcacia aacaacgtgc cactagctat ttcggagtca	960
ataacatctt cttctccaaa tttcatggaa atgaagactt cttatgaaga tgaaatcatg	1020
gagcttttca aagataataa aagcaatgca ccaacttctg atacggatat caatacagat	1080
ttaggtaagg gcataagcga tagttttggc atgttaaact ataattacga agcattgctt	1140
cactttaatg atgacgaatt tagtgaattg aagtctatcg atccggcatt gatatcaaag	1200
taa	1203

<210> 36
 <211> 400
 <212> PRT
 <213> Saccharomyces bayanus

<400> 36

Met	Ser	Lys	Thr	Gly	Lys	Met	Arg	Leu	Thr	Ala	Ser	Pro	Asp	Asn	Leu
1				5					10					15	

Ala	Ser	Met	Met	Ser	Arg	Asp	Gln	Asn	Lys	Leu	Ile	His	Leu	Asp	Pro
			20					25					30		

Val	Pro	Phe	Phe	Lys	Asp	Arg	His	Glu	Ile	Lys	Pro	Trp	Leu	Gln	Lys
		35					40					45			

Ile	Phe	Tyr	Pro	Gln	Gly	Ile	Asp	Ile	Val	Ile	Glu	Arg	Ser	Asp	Ser
	50					55					60				

Gly	Lys	Val	Thr	Phe	Lys	Cys	Arg	Ser	Val	Arg	Ser	Asn	Gly	Arg	Leu
65					70				75						80

Asn	Pro	Glu	Ser	Lys	Gly	Thr	Ser	Ser	Arg	Ser	His	Ala	Cys	Pro	Phe
				85					90					95	

Arg	Ile	Arg	Ala	Ala	Phe	Ser	Val	Arg	Leu	Gln	Lys	Trp	Asn	Val	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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

Asp Glu Ile Met Glu Leu Phe Lys Asp Asn Lys Ser Asn Ala Pro Thr
 340 345 350

Ser Asp Thr Asp Ile Asn Thr Asp Leu Gly Lys Gly Ile Ser Asp Ser
 355 360 365

Phe Gly Met Leu Asn Tyr Asn Tyr Glu Ala Leu Leu His Phe Asn Asp
 370 375 380

Asp Glu Phe Ser Glu Leu Lys Ser Ile Asp Pro Ala Leu Ile Ser Lys
 385 390 395 400

<210> 37
 <211> 2205
 <212> DNA
 <213> Saccharomyces castelli

<400> 37
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 tcgacctcca tggtcggttaa tactgctaaa actggaacaa ctccaatgtt tggttctaca 180
 gggactgcga ataaggggtgc tttcacaggg ttgtgtacag cctcatctac attcggtagt 240
 atggcaaacg catcaacctc aaataccgat ggaaagacag gcactacagg atttagcttt 300
 ggcaacgcag ctaacgcaaa acctggggct gaaactgcaa ccaatgactc aaataaacca 360
 aatacctttg cacttgga aa ttcttcacg ccagcttccg gtactctctt tggcaataaa 420
 tctggatcaa ccgccacacc aatgtttaac atgggaggtg caacatctgc tgataagatt 480
 tctaaccag cctccacctt ttcgtttgga gcttctgaca agaaggatga ttcgaagcct 540
 ggattttcat ttaatcaaaa tacgggaggg aaccaaccaa gcaccacaga aacaaataaa 600
 ccagcattct ctttgagagc aacaagtgat ggaaaagatt ctgctgctaa gccaaacttg 660
 agtttttgaa cagctccagg cacaaacgat tctacaaaac cattctcttt tggacaagc 720
 actggagcta aagaatcaac atcgacacct gcttttactc tgggaggagc taaagaggca 780
 cccaacacaa ctcttcatt ttcattagga agcgctagta acgacaaaaa ctctgcttcg 840
 aagcctgggt ttacacttgg tgcaaccctt gggactcaaa cagataaaaa caaactgaa 900
 aaaaaacccg ctttagttt tgcttcact cctacagagg atactaccaa aagtgcgtca 960
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 aaatctacag aagataaatc aaccaatgaa agctctacaa caaaaccaac ctttctttc 1080
 ggggcaaaac ctgaagttaa agagactaca gatactaagt catccacagt tactatgcca 1140

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gcattttctt ttggagagaa accgagggag ggtaccggtat atgcaccaac tttttcatta 1200
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<210> 38
<211> 734
<212> PRT
<213> Saccharomyces castelli

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<400> 38

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Met Asn Gly Asp Asn Lys Gly Thr Ser Gly Ser Ser Pro Phe Gly Asn
1           5           10           15

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Phe Ser Glu Ser Ala Phe Asn Ser Gly Ala Asn Gln Thr Ala Thr Ala
          20           25           30

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Gly Gln Asp Thr Lys Asn Lys Pro Ser Thr Ser Met Phe Gly Asn Thr
          35           40           45

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Ala Lys Thr Gly Thr Thr Pro Met Phe Gly Ser Thr Gly Thr Ala Asn
          50           55           60

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Lys Gly Ala Phe Thr Gly Phe Gly Thr Ala Ser Ser Thr Phe Gly Ser
65 70 75 80

Met Ala Asn Ala Ser Thr Ser Asn Thr Asp Gly Lys Thr Gly Thr Thr
85 90 95

Gly Phe Ser Phe Gly Asn Ala Ala Asn Ala Lys Pro Gly Ala Glu Thr
100 105 110

Ala Thr Asn Asp Ser Asn Lys Pro Asn Thr Phe Ala Leu Gly Asn Ser
115 120 125

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

Ala Thr Pro Met Phe Asn Met Gly Gly Ala Thr Ser Ala Asp Lys Ile
145 150 155 160

Ser Asn Pro Ala Ser Thr Phe Ser Phe Gly Ala Ser Asp Lys Lys Asp
165 170 175

Asp Ser Lys Pro Gly Phe Ser Phe Asn Gln Asn Thr Gly Gly Asn Gln
180 185 190

Pro Ser Thr Thr Glu Thr Asn Lys Pro Ala Phe Ser Phe Gly Ala Thr
195 200 205

Ser Asp Gly Lys Asp Ser Ala Ala Lys Pro Thr Leu Ser Phe Gly Thr
210 215 220

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

Thr Gly Ala Lys Glu Ser Thr Ser Thr Pro Ala Phe Thr Leu Gly Gly
245 250 255

Ala Lys Glu Ala Pro Asn Thr Thr Pro Ser Phe Ser Leu Gly Ser Ala
260 265 270

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

Thr Leu Gly Thr Gln Thr Asp Lys Asn Asn Thr Glu Thr Lys Pro Ala

290	295	300
Phe Ser Phe Ala Ser Thr Pro Thr Glu Asp Thr Thr Lys Ser Ala Ser 305 310 315 320		
Ser Ile Ser Leu Pro Ser Asn Asn Gly Asp Thr Ala Lys Pro Ala Phe 325 330 335		
Ser Phe Ser Ser Lys Ser Thr Glu Asp Lys Ser Thr Asn Glu Ser Ser 340 345 350		
Thr Thr Lys Pro Thr Leu Ser Phe Gly Ala Lys Pro Glu Val Lys Glu 355 360 365		
Thr Thr Asp Thr Lys Ser Ser Thr Val Thr Met Pro Ala Phe Ser Phe 370 375 380		
Gly Glu Lys Pro Arg Glu Gly Thr Gly Asn Ala Pro Thr Phe Ser Leu 385 390 395 400		
Gly Lys Lys Pro Glu Glu Gln Asp Lys Ala Ala Ala Ala Pro Ser Phe 405 410 415		
Ser Leu Gly Lys Lys Ser Asp Glu Asn Gly Ser Ala Thr Pro Ala Pro 420 425 430		
Ala Phe Ser Phe Gly Lys Lys Pro Glu Glu Lys Ala Asn Ala Thr Ser 435 440 445		
Ala Pro Thr Phe Ser Leu Ala Lys Lys Ala Asp Glu Lys Asp Ser Thr 450 455 460		
Thr Ala Ala Pro Ala Phe Ser Phe Gly Lys Lys Ser Glu Glu Lys Asp 465 470 475 480		
Ser Ala Ala Lys Asp Thr Ser Thr Lys Thr Gly Phe Ser Phe Gly Asn 485 490 495		
Lys Ala Asp Glu Lys Lys Pro Glu Gly Thr Thr Leu Lys Lys Glu Asp 500 505 510		
Ile Lys Ser Asn Val Ser Glu Lys Thr Phe Glu Asn Ser Thr Lys Thr 515 520 525		

Gly Gly Leu Asp Thr Lys Pro Val Glu Leu Lys Pro Val Ser Leu Asp
530 535 540

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

Lys Ala Ala Val His Phe Asp Glu Tyr Ser Lys Lys Ile Asn Ser Trp
565 570 575

Asp Gln Met Leu Val Lys Gly Gly Glu Gln Val Ser Gln Leu Tyr Ser
580 585 590

Asp Thr Leu Ala Thr Glu Gln Thr Gln Asn Arg Ile Asp Gln Ser Leu
595 600 605

Gln Tyr Ile Glu Arg Gln Gln Asp Glu Leu Glu Ile Phe Leu Asp Asn
610 615 620

Tyr Glu Arg Lys Ala Asp Thr Leu Leu Ser Asp Ile Leu Ser Thr Thr
625 630 635 640

Ala Val Asn Thr Ala Ser Asn Asn Asp Gln Lys Arg Gln Gln Ala Tyr
645 650 655

His Thr Ala Glu Thr Leu Asp Glu Asn Leu Ser Ala Leu Ser Ser Asn
660 665 670

Leu Ser Ser Leu Ile Asn Glu Ile Asn Asp Val Ser Asn Ser Phe Asn
675 680 685

Lys Ala Thr Ser Ile Asn Leu Gly Asn Lys Asp Glu Asn Ser Gln Leu
690 695 700

Met Lys Leu Leu Asn Ser His Leu Asp Ala Leu Lys Ser Leu Asp Asp
705 710 715 720

Asn Ser Ser Leu Leu Glu Gln Lys Ile Lys Ser Phe Ser Lys
725 730

<210> 39

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> 2Fe-2S cluster protein motif

<220>
 <221> MISC_FEATURE
 <222> (2)..(5)
 <223> Xaa may be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (7)..(8)
 <223> Xaa may be any amino acid

<220>
 <221> MISC_FEATURE
 <222> (10)..(39)
 <223> Xaa may be any amino acid

<400> 39

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1				5					10						15	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25					30			

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys
		35					40

<210> 40
 <211> 1716
 <212> DNA
 <213> Bacillus subtilis

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	atcgacgccg tgtttgatgc attacaagac aaggggtccag aaattattgt tgctagacat	180
	gagcaaaatg ccgcatttat ggcgcaagct gtaggtaggc ttacaggtaa acctgggtgtt	240
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	gaggtacaag acgtaaagaa tatacctgaa gctgtgacaa acgcatttcg tatagcttct	480
	gctggtcagg ctgggtgccg gtttggttct tttcctcaag acgttggtcaa tgaagtgacc	540
	aataactaaa acgttagagc gggtgcagcc cctaaactag gtccagccgc agacgacgca	600
	attagcgctg caattgctaa aattcagacg gcgaaactac cagtagtcct tgtcggtatg	660

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cctttcgttg agacttacca agcagcaggt actttatcta gagatttaga ggatcagtat      780
tttggaaagga taggtctatt tagaaaccaa ccaggagatt tactattaga acaagctgat      840
gttgtactta ctatcggtta tgatcctata gagtatgacc caaagttttg gaacataaat      900
ggggatagaa caattataca tctagacgag ataatcgccg acatcgatca cgcttatcaa      960
ccagatttag aactaatcgg agatatcccg tcaacaatca atcatattga acatgatgct     1020
gtaaagggtg agttcgtga acgtgagcag aaaatcttat ctgatctaaa gcaatatatg     1080
catgaggggtg aacaagttcc agcagactgg aaatctgacc gtgcacatcc tttggaaatc     1140
gttaaggaac taagaaatgc ggtcgtgat catgtgactg ttacatgtga tatcggttca     1200
catgcaatth ggatgtcacg ttatttttagg agctacgaac cattaactth aatgatattc     1260
aacgggatgc aaactctggg gggtgcactt ccttgggcta ttggcgctag tttagttaag     1320
cccggtgaga aggtgggtatc ggtatcaggt gatgggtggct ttctgttttc ggctatggaa     1380
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agtccagatc agttagctga tgtgttgaga caagggatga atgccgaggg accggtaatc     1620
atagatgtgc cagttgacta ctcagacaat attaatthgg cttctgataa acttcctaaa     1680
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<210> 41
<211> 571
<212> PRT
<213> Bacillus subtilis

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<400> 41

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Met Leu Thr Lys Ala Thr Lys Glu Gln Lys Ser Leu Val Lys Asn Arg
1           5           10          15

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Gly Ala Glu Leu Val Val Asp Cys Leu Val Glu Gln Gly Val Thr His
20           25          30

```

```

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

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Gln Asp Lys Gly Pro Glu Ile Ile Val Ala Arg His Glu Gln Asn Ala
50           55          60

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Ala Phe Met Ala Gln Ala Val Gly Arg Leu Thr Gly Lys Pro Gly Val
65 70 75 80

Val Leu Val Thr Ser Gly Pro Gly Ala Ser Asn Leu Ala Thr Gly Leu
85 90 95

Leu Thr Ala Asn Thr Glu Gly Asp Pro Val Val Ala Leu Ala Gly Asn
100 105 110

Val Ile Arg Ala Asp Arg Leu Lys Arg Thr His Gln Ser Leu Asp Asn
115 120 125

Ala Ala Leu Phe Gln Pro Ile Thr Lys Tyr Ser Val Glu Val Gln Asp
130 135 140

Val Lys Asn Ile Pro Glu Ala Val Thr Asn Ala Phe Arg Ile Ala Ser
145 150 155 160

Ala Gly Gln Ala Gly Ala Ala Phe Val Ser Phe Pro Gln Asp Val Val
165 170 175

Asn Glu Val Thr Asn Thr Lys Asn Val Arg Ala Val Ala Ala Pro Lys
180 185 190

Leu Gly Pro Ala Ala Asp Asp Ala Ile Ser Ala Ala Ile Ala Lys Ile
195 200 205

Gln Thr Ala Lys Leu Pro Val Val Leu Val Gly Met Lys Gly Gly Arg
210 215 220

Pro Glu Ala Ile Lys Ala Val Arg Lys Leu Leu Lys Lys Val Gln Leu
225 230 235 240

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

Glu Asp Gln Tyr Phe Gly Arg Ile Gly Leu Phe Arg Asn Gln Pro Gly
260 265 270

Asp Leu Leu Leu Glu Gln Ala Asp Val Val Leu Thr Ile Gly Tyr Asp
275 280 285

Pro Ile Glu Tyr Asp Pro Lys Phe Trp Asn Ile Asn Gly Asp Arg Thr
290 295 300

Ile Ile His Leu Asp Glu Ile Ile Ala Asp Ile Asp His Ala Tyr Gln
 305 310 315 320

Pro Asp Leu Glu Leu Ile Gly Asp Ile Pro Ser Thr Ile Asn His Ile
 325 330 335

Glu His Asp Ala Val Lys Val Glu Phe Ala Glu Arg Glu Gln Lys Ile
 340 345 350

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

Asp Trp Lys Ser Asp Arg Ala His Pro Leu Glu Ile Val Lys Glu Leu
 370 375 380

Arg Asn Ala Val Asp Asp His Val Thr Val Thr Cys Asp Ile Gly Ser
 385 390 395 400

His Ala Ile Trp Met Ser Arg Tyr Phe Arg Ser Tyr Glu Pro Leu Thr
 405 410 415

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

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

Ser Gly Asp Gly Gly Phe Leu Phe Ser Ala Met Glu Leu Glu Thr Ala
 450 455 460

Val Arg Leu Lys Ala Pro Ile Val His Ile Val Trp Asn Asp Ser Thr
 465 470 475 480

Tyr Asp Met Val Ala Phe Gln Gln Leu Lys Lys Tyr Asn Arg Thr Ser
 485 490 495

Ala Val Asp Phe Gly Asn Ile Asp Ile Val Lys Tyr Ala Glu Ser Phe
 500 505 510

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

Leu Arg Gln Gly Met Asn Ala Glu Gly Pro Val Ile Ile Asp Val Pro

530

535

540

Val Asp Tyr Ser Asp Asn Ile Asn Leu Ala Ser Asp Lys Leu Pro Lys
 545 550 555 560

Glu Phe Gly Glu Leu Met Lys Thr Lys Ala Leu
 565 570

<210> 42

<211> 1476

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence for E. coli ilvCQ110V

<400> 42

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gtaattgttg gctgcggtgc tcaggggtcta aaccaagggt taaacatgag agattcagggt    180
ctggatatatt cgtatgcatt gaggaaagag gcaattgcag aaaagagggc ctccctggcgt    240
aaagcgacgg aaaatggggtt caaagttggt acttacgaag aactgatccc tcaggcagat    300
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gagcagatca gaaaagatat aacagtcgta atggttgcac caaagtgcc aggtacggaa    480
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aatgacccca aaggtgaagg tatggcaatt gcgaaggcat gggcagccgc aaccggagggt    600
catagagcgg gtgtgttaga gagttctttc gtagctgagg tcaagagtga cttaatgggt    660
gaacaaacca ttctgtgcgg aatgttgacg gcaggggtctt tactatgctt tgataaattg    720
gtcgaagagg gtacagatcc tgcctatgct gaaaagttga tacaatttgg ttgggagaca    780
atcaccgagg cacttaaaca aggtggcata acattgatga tggatagact ttcaaattccg    840
gccaaagctaa gagcctacgc cttatctgag caactaaaag agatcatggc accattattc    900
caaaagcaca tggacgatat tatctccggt gagttttcct caggaatgat ggcagattgg    960
gcaaacgatg ataaaaagtt attgacgtgg agagaagaaa ccggcaagac ggcattcgag   1020
acagccccac aatacgaagg taaaattggt gaacaagaat actttgataa gggagtattg   1080
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cctggtgatt tggggaaggc tattccggaa ggagcgggtg acaatggcca actgagagac 1380
gtaaatgaag ctattcgttc acatgctata gaacagggtg gtaaaaagct gagaggatat 1440
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<210> 43

<211> 493

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence for E. coli ilvCQ110V

<400> 43

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Leu Gly Lys Cys Arg Phe Met Gly Arg Asp Glu Phe Ala Asp Gly Ala
20 25 30

Ser Tyr Leu Gln Gly Lys Lys Val Val Ile Val Gly Cys Gly Ala Gln
35 40 45

Gly Leu Asn Gln Gly Leu Asn Met Arg Asp Ser Gly Leu Asp Ile Ser
50 55 60

Tyr Ala Leu Arg Lys Glu Ala Ile Ala Glu Lys Arg Ala Ser Trp Arg
65 70 75 80

Lys Ala Thr Glu Asn Gly Phe Lys Val Gly Thr Tyr Glu Glu Leu Ile
85 90 95

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

Asp Val Val Arg Thr Val Gln Pro Leu Met Lys Asp Gly Ala Ala Leu
115 120 125

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

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

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

Ser Ala Tyr Tyr Glu Ser Leu His Glu Leu Pro Leu Ile Ala Asn Thr
385 390 395 400

Ile Ala Arg Lys Arg Leu Tyr Glu Met Asn Val Val Ile Ser Asp Thr
405 410 415

Ala Glu Tyr Gly Asn Tyr Leu Phe Ser Tyr Ala Cys Val Pro Leu Leu
420 425 430

Lys Pro Phe Met Ala Glu Leu Gln Pro Gly Asp Leu Gly Lys Ala Ile
435 440 445

Pro Glu Gly Ala Val Asp Asn Gly Gln Leu Arg Asp Val Asn Glu Ala
450 455 460

Ile Arg Ser His Ala Ile Glu Gln Val Gly Lys Lys Leu Arg Gly Tyr
465 470 475 480

Met Thr Asp Met Lys Arg Ile Ala Val Ala Gly Leu Glu
485 490

<210> 44
<211> 1476
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence for E. coli ilvC coScP2D1-A1

<400> 44
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agatttatgg gaagggacga gtttgctgat ggtgcttctt atctgcaagg aaagaaagta 120
gtaattgttg gctgcggtgc tcaggggtcta aaccaagggt taaacatgag agattcaggt 180
ctggatattt cgtatgcatt gaggaagag tctattgcag aaaaggatgc cgattggcgt 240
aaagcgacgg aaaatgggtt caaagttggt acttacgaag aactgatccc tcaggcagat 300
ttagtgatta acctaacacc agataagggt cactcagacg tagtaagaac agttcaaccg 360
ctgatgaagg atggggcagc tttaggttac tctcatggct ttaatatcgt tgaagtgggc 420
gagcagatca gaaaaggat aacagtcgta atgggtgcgc caaagtgcc aggtacggaa 480
gtcagagagg agtacaagag ggggttttgggt gtacctacat tgatcgccgt acatcctgaa 540
aatgacccca aacgtgaagg tatggcaata gcgaaggcat gggcagccgc aaccggagggt 600
catagagcgg gtgtgttaga gagttctttc gtagctgagg tcaagagtga cttaatgggt 660


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gaacaaacca ttctgtgcgg aatgttgacg gcaggggtctt tactatgctt tgataaattg      720
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atcaccgagg cacttaaaca aggtggcata acattgatga tggatagact ttcaaattccg      840
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caaaagcaca tggacgatat tatctccggt gagttttcct caggaatgat ggcagattgg      960
gcaaacgatg ataaaaagtt attgacgtgg agagaagaaa ccggcaagac ggcattcgag     1020
acagccccac aatacgaagg taaaattggt gaacaagaat actttgataa gggagtattg     1080
atgatagcta tgggtgaaggc aggggtagaa cttgcattcg aaactatggt tgactccggt     1140
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cctggtgatt tggggaaggc tattccggaa ggagcggttg acaatggcca actgagagac     1380
gtaaatgaag ctattcgttc gcatgctata gaacaggtgg gtaaaaagct gagaggatat     1440
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<210> 45

<211> 491

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence for E coli IlvCP2D1-A1

<400> 45

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Met Ala Asn Tyr Phe Asn Thr Leu Asn Leu Arg Gln Gln Leu Ala Gln
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Leu Gly Lys Cys Arg Phe Met Gly Arg Asp Glu Phe Ala Asp Gly Ala
20          25          30

```

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Ser Tyr Leu Gln Gly Lys Lys Val Val Ile Val Gly Cys Gly Ala Gln
35          40          45

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```

Gly Leu Asn Gln Gly Leu Asn Met Arg Asp Ser Gly Leu Asp Ile Ser
50          55          60

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```

Tyr Ala Leu Arg Lys Glu Ser Ile Ala Glu Lys Asp Ala Asp Trp Arg
65          70          75          80

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Lys Ala Thr Glu Asn Gly Phe Lys Val Gly Thr Tyr Glu Glu Leu Ile
85 90 95

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

Asp Val Val Arg Thr Val Gln Pro Leu Met Lys Asp Gly Ala Ala Leu
115 120 125

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

Lys Gly Ile Thr Val Val Met Val Ala Pro Lys Cys Pro Gly Thr Glu
145 150 155 160

Val Arg Glu Glu Tyr Lys Arg Gly Phe Gly Val Pro Thr Leu Ile Ala
165 170 175

Val His Pro Glu Asn Asp Pro Lys Arg Glu Gly Met Ala Ile Ala Lys
180 185 190

Ala Trp Ala Ala Ala Thr Gly Gly His Arg Ala Gly Val Leu Glu Ser
195 200 205

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

Leu Cys Gly Met Leu Gln Ala Gly Ser Leu Leu Cys Phe Asp Lys Leu
225 230 235 240

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

Gly Trp Glu Thr Ile Thr Glu Ala Leu Lys Gln Gly Gly Ile Thr Leu
260 265 270

Met Met Asp Arg Leu Ser Asn Pro Ala Lys Leu Arg Ala Tyr Ala Leu
275 280 285

Ser Glu Gln Leu Lys Glu Ile Met Ala Pro Leu Phe Gln Lys His Met
290 295 300

Asp Asp Ile Ile Ser Gly Glu Phe Ser Ser Gly Met Met Ala Asp Trp
305 310 315 320

Ala Asn Asp Asp Lys Lys Leu Leu Thr Trp Arg Glu Glu Thr Gly Lys
 325 330 335

Thr Ala Phe Glu Thr Ala Pro Gln Tyr Glu Gly Lys Ile Gly Glu Gln
 340 345 350

Glu Tyr Phe Asp Lys Gly Val Leu Met Ile Ala Met Val Lys Ala Gly
 355 360 365

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

Ser Ala Tyr Tyr Glu Ser Leu His Glu Leu Pro Leu Ile Ala Asn Thr
 385 390 395 400

Ile Ala Arg Lys Arg Leu Tyr Glu Met Asn Val Val Ile Ser Asp Thr
 405 410 415

Ala Glu Tyr Gly Asn Tyr Leu Phe Ser Tyr Ala Cys Val Pro Leu Leu
 420 425 430

Glu Pro Phe Met Ala Glu Leu Gln Pro Gly Asp Leu Gly Lys Ala Ile
 435 440 445

Pro Glu Gly Ala Val Asp Asn Gly Gln Leu Arg Asp Val Asn Glu Ala
 450 455 460

Ile Arg Ser His Ala Ile Glu Gln Val Gly Lys Lys Leu Arg Gly Tyr
 465 470 475 480

Met Thr Asp Met Lys Arg Ile Ala Val Ala Gly
 485 490

<210> 46
 <211> 1647
 <212> DNA
 <213> Lactococcus lactis

<400> 46
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 atgaaatggg tgggtaacgc taacgaactg aacgcaagct acatggcaga tggttatgca 180
 cgtaccaaga aagccgcggc atttctgacc actttcggtg ttggcgaact gagcgccgctc 240

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acgagcaaag	ttcagaacga	aggtaaattc	gtccaccaca	ctctggctga	cggcgatttc	360
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aacgctactg	tggaaatcga	ccgcgttctg	tctgcgctgc	tgaaagaacg	caaaccagtt	480
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gacaaaaagc	aagaagattt	cgtaccatct	aacgcactgc	tgtcccagga	tcgcctgtgg	1080
caggccgtgg	agaacctgac	ccagagcaat	gaaaccatcg	tggcggaaca	aggtagcagc	1140
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tctcgtcata	tgctgttcat	cggtagcggg	tccctgcagc	tgaccgtaca	ggaactgggt	1320
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<210> 47
 <211> 548
 <212> PRT
 <213> Lactococcus lactis

 <400> 47

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20 25 30

Asp Gln Ile Ile Ser His Lys Asp Met Lys Trp Val Gly Asn Ala Asn
35 40 45

Glu Leu Asn Ala Ser Tyr Met Ala Asp Gly Tyr Ala Arg Thr Lys Lys
50 55 60

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

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

Val Gly Ser Pro Thr Ser Lys Val Gln Asn Glu Gly Lys Phe Val His
100 105 110

His Thr Leu Ala Asp Gly Asp Phe Lys His Phe Met Lys Met His Glu
115 120 125

Pro Val Thr Ala Ala Arg Thr Leu Leu Thr Ala Glu Asn Ala Thr Val
130 135 140

Glu Ile Asp Arg Val Leu Ser Ala Leu Leu Lys Glu Arg Lys Pro Val
145 150 155 160

Tyr Ile Asn Leu Pro Val Asp Val Ala Ala Ala Lys Ala Glu Lys Pro
165 170 175

Ser Leu Pro Leu Lys Lys Glu Asn Ser Thr Ser Asn Thr Ser Asp Gln
180 185 190

Glu Ile Leu Asn Lys Ile Gln Glu Ser Leu Lys Asn Ala Lys Lys Pro
195 200 205

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

Val Thr Gln Phe Ile Ser Lys Thr Lys Leu Pro Ile Thr Thr Leu Asn
225 230 235 240

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

Tyr Asn Gly Thr Leu Ser Glu Pro Asn Leu Lys Glu Phe Val Glu Ser
260 265 270

Ala Asp Phe Ile Leu Met Leu Gly Val Lys Leu Thr Asp Ser Ser Thr
275 280 285

Gly Ala Phe Thr His His Leu Asn Glu Asn Lys Met Ile Ser Leu Asn
290 295 300

Ile Asp Glu Gly Lys Ile Phe Asn Glu Arg Ile Gln Asn Phe Asp Phe
305 310 315 320

Glu Ser Leu Ile Ser Ser Leu Leu Asp Leu Ser Glu Ile Glu Tyr Lys
325 330 335

Gly Lys Tyr Ile Asp Lys Lys Gln Glu Asp Phe Val Pro Ser Asn Ala
340 345 350

Leu Leu Ser Gln Asp Arg Leu Trp Gln Ala Val Glu Asn Leu Thr Gln
355 360 365

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

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

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

Ala Asp Lys Glu Ser Arg His Leu Leu Phe Ile Gly Asp Gly Ser Leu
420 425 430

Gln Leu Thr Val Gln Glu Leu Gly Leu Ala Ile Arg Glu Lys Ile Asn
435 440 445

Pro Ile Cys Phe Ile Ile Asn Asn Asp Gly Tyr Thr Val Glu Arg Glu
450 455 460

Ile His Gly Pro Asn Gln Ser Tyr Asn Asp Ile Pro Met Trp Asn Tyr
465 470 475 480

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

485

490

495

Lys Ile Val Arg Thr Glu Asn Glu Phe Val Ser Val Met Lys Glu Ala
500 505 510

Gln Ala Asp Pro Asn Arg Met Tyr Trp Ile Glu Leu Ile Leu Ala Lys
515 520 525

Glu Gly Ala Pro Lys Val Leu Lys Lys Met Gly Lys Leu Phe Ala Glu
530 535 540

Gln Asn Lys Ser
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<210> 48

<211> 1713

<212> DNA

<213> Lactococcus lactis

<400> 48

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gacgaagatt tcaagaaagc tcaagtgggt atagtgtcga tggactggga tggaaatcca	180
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gaaacactag gtatgtcatt gccgtattct tcttcgaacc ctgcagtatc tcaagaaaaa	720
caagaagaat gtgatgagat tggattagcc attaagaatc ttttgaaaaa agacatcaag	780
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gggggtagta ctaatgctgt cttgcatatt attgcaatgg ctaacgcgat aggtgtcgaa	900
ataactcagg atgacttcca aagaattagt gacattactc cagtactagg tgatttttaa	960
ccttcaggta aatatatgat ggaagatttg cataaaattg gaggcttgcc agcagtgctt	1020

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cagaagccaa ctccgaaagc caccagggga gttttggcaa aattcgctaa attaaccgct      1680
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<210> 49
<211> 570
<212> PRT
<213> Lactococcus lactis

<400> 49

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Tyr Ser Lys Thr Leu Thr Gln Asp Pro Thr Gln Pro Ala Thr Gln Ala
          20          25          30

```

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Met Tyr Tyr Gly Ile Gly Phe Lys Asp Glu Asp Phe Lys Lys Ala Gln
          35          40          45

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Val Gly Ile Val Ser Met Asp Trp Asp Gly Asn Pro Cys Asn Met His
          50          55          60

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```

Leu Gly Thr Leu Gly Ser Lys Ile Lys Ser Ser Val Asn Gln Thr Asp
65          70          75          80

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```

Gly Leu Ile Gly Leu Gln Phe His Thr Ile Gly Val Ser Asp Gly Ile
          85          90          95

```

```

Ala Asn Gly Lys Leu Gly Met Arg Tyr Ser Leu Val Ser Arg Glu Val
          100          105          110

```


Ile Ala Asp Ser Ile Glu Thr Asn Ala Gly Ala Glu Tyr Tyr Asp Ala
115 120 125

Ile Val Ala Ile Pro Gly Cys Asp Lys Asn Met Pro Gly Ser Ile Ile
130 135 140

Gly Met Ala Arg Leu Asn Arg Pro Ser Ile Met Val Tyr Gly Gly Thr
145 150 155 160

Ile Glu His Gly Glu Tyr Lys Gly Glu Lys Leu Asn Ile Val Ser Ala
165 170 175

Phe Glu Ser Leu Gly Gln Lys Ile Thr Gly Asn Ile Ser Asp Glu Asp
180 185 190

Tyr His Gly Val Ile Cys Asn Ala Ile Pro Gly Gln Gly Ala Cys Gly
195 200 205

Gly Met Tyr Thr Ala Asn Thr Leu Ala Ala Ala Ile Glu Thr Leu Gly
210 215 220

Met Ser Leu Pro Tyr Ser Ser Ser Asn Pro Ala Val Ser Gln Glu Lys
225 230 235 240

Gln Glu Glu Cys Asp Glu Ile Gly Leu Ala Ile Lys Asn Leu Leu Glu
245 250 255

Lys Asp Ile Lys Pro Ser Asp Ile Met Thr Lys Glu Ala Phe Glu Asn
260 265 270

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

His Ile Ile Ala Met Ala Asn Ala Ile Gly Val Glu Ile Thr Gln Asp
290 295 300

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

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

Pro Ala Val Leu Lys Tyr Leu Leu Lys Glu Gly Lys Leu His Gly Asp
340 345 350

Cys Leu Thr Val Thr Gly Lys Thr Leu Ala Glu Asn Val Glu Thr Ala
355 360 365

Leu Asp Leu Asp Phe Asp Ser Gln Asp Ile Met Arg Pro Leu Lys Asn
370 375 380

Pro Ile Lys Ala Thr Gly His Leu Gln Ile Leu Tyr Gly Asn Leu Ala
385 390 395 400

Gln Gly Gly Ser Val Ala Lys Ile Ser Gly Lys Glu Gly Glu Phe Phe
405 410 415

Lys Gly Thr Ala Arg Val Phe Asp Gly Glu Gln His Phe Ile Asp Gly
420 425 430

Ile Glu Ser Gly Arg Leu His Ala Gly Asp Val Ala Val Ile Arg Asn
435 440 445

Ile Gly Pro Val Gly Gly Pro Gly Met Pro Glu Met Leu Lys Pro Thr
450 455 460

Ser Ala Leu Ile Gly Ala Gly Leu Gly Lys Ser Cys Ala Leu Ile Thr
465 470 475 480

Asp Gly Arg Phe Ser Gly Gly Thr His Gly Phe Val Val Gly His Ile
485 490 495

Val Pro Glu Ala Val Glu Gly Gly Leu Ile Gly Leu Val Glu Asp Asp
500 505 510

Asp Ile Ile Glu Ile Asp Ala Val Asn Asn Ser Ile Ser Leu Lys Val
515 520 525

Ser Asp Glu Glu Ile Ala Lys Arg Arg Ala Asn Tyr Gln Lys Pro Thr
530 535 540

Pro Lys Ala Thr Arg Gly Val Leu Ala Lys Phe Ala Lys Leu Thr Arg
545 550 555 560

Pro Ala Ser Glu Gly Cys Val Thr Asp Leu
565 570

<210> 50

<211> 1701

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence for *Saccharomyces cerevisiae* ILV3deltaN

<400> 50

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cctatcgggt tggtcagaga cggcgatgag attatcattg atgctgataa taacaagatt     1560
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<210> 51
 <211> 566
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Amino acid sequence for *Saccharomyces cerevisiae* ILV3deltaN

<400> 51

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 20 25 30

Asp Phe Lys Lys Pro Gln Val Gly Val Gly Ser Cys Trp Trp Ser Gly
 35 40 45

Asn Pro Cys Asn Met His Leu Leu Asp Leu Asn Asn Arg Cys Ser Gln
 50 55 60

Ser Ile Glu Lys Ala Gly Leu Lys Ala Met Gln Phe Asn Thr Ile Gly
 65 70 75 80

Val Ser Asp Gly Ile Ser Met Gly Thr Lys Gly Met Arg Tyr Ser Leu
 85 90 95

Gln Ser Arg Glu Ile Ile Ala Asp Ser Phe Glu Thr Ile Met Met Ala
 100 105 110

Gln His Tyr Asp Ala Asn Ile Ala Ile Pro Ser Cys Asp Lys Asn Met
 115 120 125

Pro Gly Val Met Met Ala Met Gly Arg His Asn Arg Pro Ser Ile Met
 130 135 140

Val Tyr Gly Gly Thr Ile Leu Pro Gly His Pro Thr Cys Gly Ser Ser
 145 150 155 160

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

				165						170					175
Glu	Tyr	Ile	Ser	Lys	Gln	Phe	Thr	Glu	Glu	Glu	Arg	Glu	Asp	Val	Val
			180					185					190		
Glu	His	Ala	Cys	Pro	Gly	Pro	Gly	Ser	Cys	Gly	Gly	Met	Tyr	Thr	Ala
		195					200					205			
Asn	Thr	Met	Ala	Ser	Ala	Ala	Glu	Val	Leu	Gly	Leu	Thr	Ile	Pro	Asn
	210					215					220				
Ser	Ser	Ser	Phe	Pro	Ala	Val	Ser	Lys	Glu	Lys	Leu	Ala	Glu	Cys	Asp
225					230					235					240
Asn	Ile	Gly	Glu	Tyr	Ile	Lys	Lys	Thr	Met	Glu	Leu	Gly	Ile	Leu	Pro
				245					250					255	
Arg	Asp	Ile	Leu	Thr	Lys	Glu	Ala	Phe	Glu	Asn	Ala	Ile	Thr	Tyr	Val
			260					265					270		
Val	Ala	Thr	Gly	Gly	Ser	Thr	Asn	Ala	Val	Leu	His	Leu	Val	Ala	Val
		275					280					285			
Ala	His	Ser	Ala	Gly	Val	Lys	Leu	Ser	Pro	Asp	Asp	Phe	Gln	Arg	Ile
	290					295					300				
Ser	Asp	Thr	Thr	Pro	Leu	Ile	Gly	Asp	Phe	Lys	Pro	Ser	Gly	Lys	Tyr
305					310					315					320
Val	Met	Ala	Asp	Leu	Ile	Asn	Val	Gly	Gly	Thr	Gln	Ser	Val	Ile	Lys
				325					330					335	
Tyr	Leu	Tyr	Glu	Asn	Asn	Met	Leu	His	Gly	Asn	Thr	Met	Thr	Val	Thr
			340					345					350		
Gly	Asp	Thr	Leu	Ala	Glu	Arg	Ala	Lys	Lys	Ala	Pro	Ser	Leu	Pro	Glu
		355					360					365			
Gly	Gln	Glu	Ile	Ile	Lys	Pro	Leu	Ser	His	Pro	Ile	Lys	Ala	Asn	Gly
	370					375					380				
His	Leu	Gln	Ile	Leu	Tyr	Gly	Ser	Leu	Ala	Pro	Gly	Gly	Ala	Val	Gly
385					390					395					400

Lys Ile Thr Gly Lys Glu Gly Thr Tyr Phe Lys Gly Arg Ala Arg Val
405 410 415

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

Lys Lys Gly Glu Lys Thr Val Val Val Ile Arg Tyr Glu Gly Pro Arg
435 440 445

Gly Ala Pro Gly Met Pro Glu Met Leu Lys Pro Ser Ser Ala Leu Met
450 455 460

Gly Tyr Gly Leu Gly Lys Asp Val Ala Leu Leu Thr Asp Gly Arg Phe
465 470 475 480

Ser Gly Gly Ser His Gly Phe Leu Ile Gly His Ile Val Pro Glu Ala
485 490 495

Ala Glu Gly Gly Pro Ile Gly Leu Val Arg Asp Gly Asp Glu Ile Ile
500 505 510

Ile Asp Ala Asp Asn Asn Lys Ile Asp Leu Leu Val Ser Asp Lys Glu
515 520 525

Met Ala Gln Arg Lys Gln Ser Trp Val Ala Pro Pro Pro Arg Tyr Thr
530 535 540

Arg Gly Thr Leu Ser Lys Tyr Ala Lys Leu Val Ser Asn Ala Ser Asn
545 550 555 560

Gly Cys Val Leu Asp Ala
565

<210> 52
<211> 1716
<212> DNA
<213> Streptococcus mutans

<400> 52
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aagcctatcg tgggtgtgat ttctacatgg gctgagaaca cgccttgcaa tatccatctt 180
cacgatttcg gtaaaactggc aaaggttgga gtgaaggaag ccggtgcgtg gccagtccag 240
ttcgggacaa taactgtgtc agatggcatc gccatgggta ctcaaggatat gaggttttcc 300

ttgacatcaa gagatatcat cgctgattct atagaggcag ccatgggtgg acataatgcc	360
gatgctttttg tagctatagg tggttgtgac aaaaacatgc caggctcagt cattgctatg	420
gccaatatgg atattccagc gatttttcgct tatgggtggga ctattgctcc aggggaatttg	480
gacggtaaag atatcgacct tgtcagcggtt ttcgaggggtg ttggccattg gaatcatgga	540
gacatgacca aggaagaggt taaagcgctg gaatgtaacg cttgtcctgg tcctgggtgga	600
tgcggtggaa tgtataaccgc caacacaatg gcaactgcta ttgaagtact aggccctttct	660
ctacctgggt cttcaagtca tccagcagaa tctgctgaga aaaaggccga tattgaagag	720
gctggacgtg cagtagtaaa gatgttgaa atggggttga agccaagtga tatactgact	780
cgtgaggcgt tcgaagatgc aattacagtc actatggcct taggcggatc aaccaactct	840
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tttcaagatt tgtacaaggt cggaggcggt ccagctgtta tgaaatacct cctcaaaaac	1020
ggcttcttac atgggtgatag aatcacatgt acaggcaaaa cagtagccga aaacttaag	1080
gcattcgatg atctcactcc tgggtcaaaaa gttatcatgc cactggaaaa tccaaagaga	1140
gaagatggac cactgataat cttacacggg aacttggtc ctgatgggtgc cgtagcaaag	1200
gtttccggtg ttaagggttag gagacacgtc ggtccagcaa aagttttcaa ctctgaggag	1260
gaagcaatcg aagctgtgct caacgatgat atagttgatg gcgacgttgt agtggttcga	1320
ttcgttggac caaaagggtg gcctgggatg cctgaaatgc tatctctgtc cagtatgatt	1380
gtaggaaagg gtcagggcga aaaagtagca ttgttaactg atggaagatt ctctggcgga	1440
acatacgggt tagtcgtcgg ccacatcgcc ccagaagccc aagacggagg cccaatcgca	1500
tacttgcaaa ccggcgatat tgtgacgata gatcaagata caaaggaact acactttgac	1560
attagcgatg aggagcttaa gcatagacag gaaaccatcg aattgccacc attgtactca	1620
agaggaatac tagggaagta cgcgcatatc gttagttcag cctccagagg ggctgttact	1680
gactttttgga agccagagga gacaggcaaa aagtaa	1716

<210> 53
 <211> 571
 <212> PRT
 <213> Streptococcus mutans

<400> 53

Met	Thr	Asp	Lys	Lys	Thr	Leu	Lys	Asp	Leu	Arg	Asn	Arg	Ser	Ser	Val
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Tyr Asp Ser Met Val Lys Ser Pro Asn Arg Ala Met Leu Arg Ala Thr
20 25 30

Gly Met Gln Asp Glu Asp Phe Glu Lys Pro Ile Val Gly Val Ile Ser
35 40 45

Thr Trp Ala Glu Asn Thr Pro Cys Asn Ile His Leu His Asp Phe Gly
50 55 60

Lys Leu Ala Lys Val Gly Val Lys Glu Ala Gly Ala Trp Pro Val Gln
65 70 75 80

Phe Gly Thr Ile Thr Val Ser Asp Gly Ile Ala Met Gly Thr Gln Gly
85 90 95

Met Arg Phe Ser Leu Thr Ser Arg Asp Ile Ile Ala Asp Ser Ile Glu
100 105 110

Ala Ala Met Gly Gly His Asn Ala Asp Ala Phe Val Ala Ile Gly Gly
115 120 125

Cys Asp Lys Asn Met Pro Gly Ser Val Ile Ala Met Ala Asn Met Asp
130 135 140

Ile Pro Ala Ile Phe Ala Tyr Gly Gly Thr Ile Ala Pro Gly Asn Leu
145 150 155 160

Asp Gly Lys Asp Ile Asp Leu Val Ser Val Phe Glu Gly Val Gly His
165 170 175

Trp Asn His Gly Asp Met Thr Lys Glu Glu Val Lys Ala Leu Glu Cys
180 185 190

Asn Ala Cys Pro Gly Pro Gly Gly Cys Gly Gly Met Tyr Thr Ala Asn
195 200 205

Thr Met Ala Thr Ala Ile Glu Val Leu Gly Leu Ser Leu Pro Gly Ser
210 215 220

Ser Ser His Pro Ala Glu Ser Ala Glu Lys Lys Ala Asp Ile Glu Glu
225 230 235 240

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

97

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

Gly Pro Ile Ala Tyr Leu Gln Thr Gly Asp Ile Val Thr Ile Asp Gln
500 505 510

Asp Thr Lys Glu Leu His Phe Asp Ile Ser Asp Glu Glu Leu Lys His
515 520 525

Arg Gln Glu Thr Ile Glu Leu Pro Pro Leu Tyr Ser Arg Gly Ile Leu
530 535 540

Gly Lys Tyr Ala His Ile Val Ser Ser Ala Ser Arg Gly Ala Val Thr
545 550 555 560

Asp Phe Trp Lys Pro Glu Glu Thr Gly Lys Lys
565 570

<210> 54
<211> 1923
<212> DNA
<213> Neurospora crassa

<400> 54
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tcaacaacca ccacaactac aaatgataac agtgaaagga atctaccaa ggaaggcgaa 120
tacattcaat ggaggacact tccagcgggc aatccagatc agttgaacag atggagtcac 180
ttcctgactc gtgagcatga gtttccaggc gctcaggcaa tgttgtagcg tgcgggtgta 240
cctaacaaag atatgatgaa aaaggctcct catgttgagg tgcgtactgt ttggtgggaa 300
ggtaacccat gtaataactca tctgcttgat ctaggtcaaa aagtcaaaaa ggctgttgaa 360
agagagaaga tgtagcttg gcaattcaac acaattggcg ttagtgacgg aataacaatg 420
gggtggtgaag gcatgaggtc ctctttgcag agcagagaga tcatagcaga ttctatagag 480
actgtgacat gtgcacaaca ccatgatgcc aatatctcaa ttccagggtg cgacaaaaac 540
atgccaggcg tcatcatggc agctgcaaga cacaacagac cattcggtat gatctacgga 600
ggtacaatga gaggcgggtc ttccgaatta cttgatagac ctatcaatat cgtaacttgt 660
tacgaggcct caggggccta tacttatggg agacttaagc cagcctgtcc aaactccact 720
gctaccccat ctgacgtgat ggacgatata gaacaacacg cctgtccagg ggctggagct 780
tgtggaggga tgtacaccgc gaatactatg gcaaccgcca tagaagctat ggggtctgaca 840
gcaccagggt catcctcctt tccagccagc tcaccagaaa agttcagaga gtgcgaaaaa 900

gccgcggaat acattaagat atgcatggaa aaagatattc gtccaagaga cttactaaca 960
 aaggcttcct tcgagaatgc tctcgtcttg acaatgattc taggtgggtc aaccaacggt 1020
 gttttacatt acttagccat ggccaactcc gccgatgtcg atctaactct tgatgatatc 1080
 aatagagtca gtgctaagac tcctttcctc gctgatatgg ctccatctgg tagatactat 1140
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 ggctatatcg atggaacaat tccaacaata acaggaaaat ctttggctga aaacgtgtca 1260
 gattggccat ctttagaccc tgatcaaaag attatccgtc ctttggataa tcctatcaaa 1320
 tcacaagggtc acattagagt gctgtatggt aactttctctc ctggtggggc tgttgccaag 1380
 atcacgggta aggaaggtct tagttttact ggtaaggcaa gatgctttaa caaagagttt 1440
 gaattggatg ctgcgctgaa aaactctgaa atcacgctcg aacaaggaaa tcaagttcta 1500
 attgtaaggt atgaaggccc taagggcgga ccaggcatgc cagaacaatt gaaagcatct 1560
 gccgctatca tgggcgctgg tttgacgaac gtagcttttag tcacggatgg gcgatactct 1620
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 aggaaaaagg gatggaaagc acctaagatg aagccaacaa gaggagccct ggccaaatac 1860
 gcaagacttg ttggtgacgc atcacatgga gcagttacag acttaggagg agatgcttac 1920
 taa 1923

<210> 55
 <211> 640
 <212> PRT
 <213> *Neurospora crassa*

<400> 55

Met Ala Ser Asn Gln Asp Asn Lys Ala Val Ala Pro Asp Ala Ala Ala
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Pro Ala Gly Gln Ser Thr Thr Thr Thr Thr Thr Asn Asp Asn Ser Glu
 20 25 30

Arg Asn Leu Pro Lys Glu Gly Glu Tyr Ile Gln Trp Arg Thr Leu Pro
 35 40 45

Ala Gly Asn Pro Asp Gln Leu Asn Arg Trp Ser His Phe Leu Thr Arg
 50 55 60

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

Pro Asn Lys Asp Met Met Lys Lys Ala Pro His Val Gly Ile Ala Thr
85 90 95

Val Trp Trp Glu Gly Asn Pro Cys Asn Thr His Leu Leu Asp Leu Gly
100 105 110

Gln Lys Val Lys Lys Ala Val Glu Arg Glu Lys Met Leu Ala Trp Gln
115 120 125

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

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

Thr Val Thr Cys Ala Gln His His Asp Ala Asn Ile Ser Ile Pro Gly
165 170 175

Cys Asp Lys Asn Met Pro Gly Val Ile Met Ala Ala Ala Arg His Asn
180 185 190

Arg Pro Phe Val Met Ile Tyr Gly Gly Thr Met Arg Gly Gly His Ser
195 200 205

Glu Leu Leu Asp Arg Pro Ile Asn Ile Val Thr Cys Tyr Glu Ala Ser
210 215 220

Gly Ala Tyr Thr Tyr Gly Arg Leu Lys Pro Ala Cys Pro Asn Ser Thr
225 230 235 240

Ala Thr Pro Ser Asp Val Met Asp Asp Ile Glu Gln His Ala Cys Pro
245 250 255

Gly Ala Gly Ala Cys Gly Gly Met Tyr Thr Ala Asn Thr Met Ala Thr
260 265 270

Ala Ile Glu Ala Met Gly Leu Thr Ala Pro Gly Ser Ser Ser Phe Pro
275 280 285

Ala Ser Ser Pro Glu Lys Phe Arg Glu Cys Glu Lys Ala Ala Glu Tyr

290	295	300
Ile Lys Ile Cys Met 305	Glu Lys Asp Ile Arg 310	Pro Arg Asp Leu Leu Thr 315 320
Lys Ala Ser Phe 325	Glu Asn Ala Leu Val 330	Leu Thr Met Ile Leu Gly Gly 335
Ser Thr Asn Gly Val 340	Leu His Tyr Leu Ala Met 345	Ala Asn Ser Ala Asp 350
Val Asp Leu Thr Leu 355	Asp Ile Asn Arg Val Ser 360	Ala Lys Thr Pro 365
Phe Leu Ala Asp Met 370	Ala Pro Ser Gly Arg Tyr 375	Tyr Met Glu Asp Leu 380
Tyr Lys Val Gly Gly 385	Thr Pro Ala Val Leu Lys 390 395	Met Leu Ile Ala Ala 400
Gly Tyr Ile Asp Gly 405	Thr Ile Pro Thr Ile Thr 410	Gly Lys Ser Leu Ala 415
Glu Asn Val Ser Asp 420	Trp Pro Ser Leu Asp 425	Pro Asp Gln Lys Ile Ile 430
Arg Pro Leu Asp Asn 435	Pro Ile Lys Ser Gln Gly 440	His Ile Arg Val Leu 445
Tyr Gly Asn Phe Ser 450	Pro Gly Gly Ala Val Ala 455	Lys Ile Thr Gly Lys 460
Glu Gly Leu Ser Phe 465	Thr Gly Lys Ala Arg 470	Cys Phe Asn Lys Glu Phe 475 480
Glu Leu Asp Ala Ala 485	Leu Lys Asn Ser Glu 490	Ile Thr Leu Glu Gln Gly 495
Asn Gln Val Leu Ile 500	Val Arg Tyr Glu Gly 505	Pro Lys Gly Gly Pro Gly 510
Met Pro Glu Gln Leu 515	Lys Ala Ser Ala Ala 520	Ile Met Gly Ala Gly Leu 525

Thr Asn Val Ala Leu Val Thr Asp Gly Arg Tyr Ser Gly Ala Ser His
530 535 540

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

Ile Ala Leu Val Lys Asp Gly Asp Leu Ile Thr Ile Asp Ala Val Arg
565 570 575

Asn Arg Ile Asp Val Val Lys Thr Val Glu Gly Val Glu Gly Glu Glu
580 585 590

Glu Ile Ala Lys Val Leu Glu Glu Arg Lys Lys Gly Trp Lys Ala Pro
595 600 605

Lys Met Lys Pro Thr Arg Gly Ala Leu Ala Lys Tyr Ala Arg Leu Val
610 615 620

Gly Asp Ala Ser His Gly Ala Val Thr Asp Leu Gly Gly Asp Ala Tyr
625 630 635 640

<210> 56
<211> 771
<212> DNA
<213> Drosophila melanogaster

<400> 56
atgtcgttta ctttgaccaa caagaacgtg attttcgttg ccggtctggg aggcattggt 60
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attgagaacc cggtcgccat tgccgagctg aaggcaatca atccaaaggt gaccgtcacc 180
ttctaccctt atgatgtgac cgtgcccatt gccgagacca ccaagctgct gaagaccatc 240
ttcgcccagc tgaagaccgt cgatgtcctg atcaacggag ctggtatcct ggacgatcac 300
cagatcgagc gcaccattgc cgtcaactac actggcctgg tcaacaccac gacggccatt 360
ctggacttct gggacaagcg caagggcggg cccgggtgga tcatctgcaa cattggatcc 420
gtcactggat tcaatgccat ctaccaggtg cccgtctact ccggcaccaa ggccgccgtg 480
gtcaacttca ccagctccct ggcgaaactg gccccatta ccggcgtgac ggcttacact 540
gtgaaccccc gcatcaccgc caccaccctg gtgcacacgt tcaactcctg gttggatgtt 600
gagcctcagg ttgccgagaa gtcctgggt catcccaccc agcctcgtt ggccctgcgc 660
gagaacttcg tcaaggctat cgagctgaac cagaacggag ccatctggaa actggacttg 720
ggcacccctg aggccatcca gtggaccaag cactgggact ccggcatcta a 771

<210> 57
 <211> 256
 <212> PRT
 <213> Drosophila melanogaster

<400> 57

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

Lys Asn Leu Val Ile Leu Asp Arg Ile Glu Asn Pro Ala Ala Ile Ala
 35 40 45

Glu Leu Lys Ala Ile Asn Pro Lys Val Thr Val Thr Phe Tyr Pro Tyr
 50 55 60

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

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

Leu Asp Asp His Gln Ile Glu Arg Thr Ile Ala Val Asn Tyr Thr Gly
 100 105 110

Leu Val Asn Thr Thr Thr Ala Ile Leu Asp Phe Trp Asp Lys Arg Lys
 115 120 125

Gly Gly Pro Gly Gly Ile Ile Cys Asn Ile Gly Ser Val Thr Gly Phe
 130 135 140

Asn Ala Ile Tyr Gln Val Pro Val Tyr Ser Gly Thr Lys Ala Ala Val
 145 150 155 160

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

Thr Ala Tyr Thr Val Asn Pro Gly Ile Thr Arg Thr Thr Leu Val His
 180 185 190

Thr Phe Asn Ser Trp Leu Asp Val Glu Pro Gln Val Ala Glu Lys Leu
 195 200 205

Leu Ala His Pro Thr Gln Pro Ser Leu Ala Cys Ala Glu Asn Phe Val
 210 215 220

Lys Ala Ile Glu Leu Asn Gln Asn Gly Ala Ile Trp Lys Leu Asp Leu
 225 230 235 240

Gly Thr Leu Glu Ala Ile Gln Trp Thr Lys His Trp Asp Ser Gly Ile
 245 250 255

<210> 58
 <211> 1023
 <212> DNA
 <213> Lactococcus lactis

<400> 58
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 accgatttgc acgttgcagc aggtgattat ggcaacaaaag cagggactgt tcttggtcat 180
 gaaggaattg gaattgtcaa agaaattgga gctgatgtaa gctcgcttca agttgggtgat 240
 cggggtttcag tggcttgggt ctttgaagga tgtgggtcact gtgaatactg tgtatctgggt 300
 aatgaaactt tttgtcgaga agttaaaaaat gcaggatatt cagttgatgg cggaatggct 360
 gaagaagcaa ttgttgttgc cgattatgct gtcaaagttc ctgacggact tgaccaat 420
 gaagctagct caattacttg tgctggagta acaacttaca aagcaatcaa agtatcagga 480
 gtaaaacctg gtgattggca agtaatTTTT ggtgctggag gacttggaaa tttagcaatt 540
 caatatgcta aaaatgtttt tggagcaaaa gtaattgctg ttgatattaa tcaagataaa 600
 ttaaatttag ctaaaaaaat tggagctgat gtgattatca attctgggtga tgtaaatacca 660
 gttgatgaaa ttaaaaaaat aactggcggc ttaggggtgc aaagtgcaat agtttgtgct 720
 gttgcaagga ttgcttttga acaagcggtt gcttctttga aacatatggg caaaatggtt 780
 gctgtggcac ttcccaatac tgagatgact ttatcagttc caacagttgt ttttgacgga 840
 gtggaggttg caggttcact tgtcgggaaca agacttgact tggcagaagc ttttcaattt 900
 ggagcagaag gtaaggtaaa accaattggt gcgacacgca aactggaaga aatcaatgat 960
 attattgatg aaatgaaggc aggaaaaatt gaaggccgaa tggtcattga ttttactaaa 1020
 taa 1023

<210> 59
 <211> 340

<212> PRT

<213> Lactococcus lactis

<400> 59

Met Lys Ala Ala Val Val Arg His Asn Pro Asp Gly Tyr Ala Asp Leu
1 5 10 15

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

Met Glu Tyr Cys Gly Val Cys His Thr Asp Leu His Val Ala Ala Gly
35 40 45

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

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

Arg Val Ser Val Ala Trp Phe Phe Glu Gly Cys Gly His Cys Glu Tyr
85 90 95

Cys Val Ser Gly Asn Glu Thr Phe Cys Arg Glu Val Lys Asn Ala Gly
100 105 110

Tyr Ser Val Asp Gly Gly Met Ala Glu Glu Ala Ile Val Val Ala Asp
115 120 125

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

Ile Thr Cys Ala Gly Val Thr Thr Tyr Lys Ala Ile Lys Val Ser Gly
145 150 155 160

Val Lys Pro Gly Asp Trp Gln Val Ile Phe Gly Ala Gly Gly Leu Gly
165 170 175

Asn Leu Ala Ile Gln Tyr Ala Lys Asn Val Phe Gly Ala Lys Val Ile
180 185 190

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

Ala Asp Val Ile Ile Asn Ser Gly Asp Val Asn Pro Val Asp Glu Ile
210 215 220

Lys Lys Ile Thr Gly Gly Leu Gly Val Gln Ser Ala Ile Val Cys Ala
 225 230 235 240

Val Ala Arg Ile Ala Phe Glu Gln Ala Val Ala Ser Leu Lys Pro Met
 245 250 255

Gly Lys Met Val Ala Val Ala Leu Pro Asn Thr Glu Met Thr Leu Ser
 260 265 270

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

Gly Thr Arg Leu Asp Leu Ala Glu Ala Phe Gln Phe Gly Ala Glu Gly
 290 295 300

Lys Val Lys Pro Ile Val Ala Thr Arg Lys Leu Glu Glu Ile Asn Asp
 305 310 315 320

Ile Ile Asp Glu Met Lys Ala Gly Lys Ile Glu Gly Arg Met Val Ile
 325 330 335

Asp Phe Thr Lys
 340

<210> 60
 <211> 1023
 <212> DNA
 <213> Lactococcus lactis

<400> 60
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 accgatttgc acgttgcagc aggtgat ttt ggcaacaaag cagggactgt tcttggtcat 180
 gaaggaattg gaattgtcaa agaaattgga gctgatgtaa gctcgcttca agttggtgat 240
 cggggtttcag tggcttggtt ctttgaagga tgtgggtcact gtgaatactg tgtatctggt 300
 aatgaaactt tttgtcgaga agttaaaaat gcaggatatt cagttgatgg cggaatggct 360
 gaagaagcaa ttgttggtgc cgattatgct gtcaaagttc ctgacggact tgacccaatt 420
 gaagctagct caattacttg tgctggagta acaacttaca aagcaatcaa agtatcagga 480
 gtaaaacctg gtgattggca agtaat tttt ggtgctggag gacttggaat ttagcaatt 540
 caatatgcta aaaatgtttt tggagcaaaa gtaattgctg ttgatattaa tcaagataaa 600

ttaaatttag ctaaaaaaat tggagctgat gtgactatca attctgggtga tgtaaatacca	660
gttgatgaaa ttaaaaaaat aactggcggc ttaggggtgc aaagtgcaat agtttgtgct	720
gttgcaagga ttgcttttga acaagcgggt gcttctttga aacctatggg caaaatgggt	780
gctgtggcag ttcccaatac tgagatgact ttatcagttc caacagttgt ttttgacgga	840
gtggaggttg caggttcact tgtcgggaaca agacttgact tggcagaagc ttttcaattt	900
ggagcagaag gtaaggtaaa accaattggt gcgacacgca aactggaaga aatcaatgat	960
attattgatg aaatgaaggc aggaaaaatt gaaggccgaa tggtcattga ttttactaaa	1020
taa	1023

<210> 61
 <211> 340
 <212> PRT
 <213> Lactococcus lactis

 <400> 61

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

Met	Glu	Tyr	Cys	Gly	Val	Cys	His	Thr	Asp	Leu	His	Val	Ala	Ala	Gly
		35					40					45			

Asp	Phe	Gly	Asn	Lys	Ala	Gly	Thr	Val	Leu	Gly	His	Glu	Gly	Ile	Gly
	50					55					60				

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

Arg	Val	Ser	Val	Ala	Trp	Phe	Phe	Glu	Gly	Cys	Gly	His	Cys	Glu	Tyr
				85					90					95	

Cys	Val	Ser	Gly	Asn	Glu	Thr	Phe	Cys	Arg	Glu	Val	Lys	Asn	Ala	Gly
			100					105					110		

Tyr	Ser	Val	Asp	Gly	Gly	Met	Ala	Glu	Glu	Ala	Ile	Val	Val	Ala	Asp
		115					120					125			

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

Asn Leu Ala Ile Gln Tyr Ala Lys Asn Val Phe Gly Ala Lys Val Ile
 180 185 190

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

Ala Asp Val Thr Ile Asn Ser Gly Asp Val Asn Pro Val Asp Glu Ile
 210 215 220

Lys Lys Ile Thr Gly Gly Leu Gly Val Gln Ser Ala Ile Val Cys Ala
 225 230 235 240

Val Ala Arg Ile Ala Phe Glu Gln Ala Val Ala Ser Leu Lys Pro Met
 245 250 255

Gly Lys Met Val Ala Val Ala Val Pro Asn Thr Glu Met Thr Leu Ser
 260 265 270

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

Gly Thr Arg Leu Asp Leu Ala Glu Ala Phe Gln Phe Gly Ala Glu Gly
 290 295 300

Lys Val Lys Pro Ile Val Ala Thr Arg Lys Leu Glu Glu Ile Asn Asp
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Asp Phe Thr Lys
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<223> Saccharomyces cerevisiae AFT1-1UP Integration Construct

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tattacctat tatcctcttt tcggtgtcat tgacaaacct cttagcgaca gaaactccct	360
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<220>
 <223> AFT1UP Forward Primer

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<210> 65
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 <223> pEN02 Reverse Primer

<400> 65
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<210> 66
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<220>
 <223> AFT1term Reverse Primer

<400> 66
 ctgatcttag caccgatata tg 22

<210> 67
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<220>
 <223> AFT1UpfullF Primer

<400> 67
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<210> 68
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<213> Artificial Sequence
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 <223> AFT1UPsequence1 Primer
 <400> 68
 ggagtgatag acgacgattc 20

<210> 69
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 <223> AFT1UPsequence2 Primer
 <400> 69
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<210> 70
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 <223> AFT2UP Forward Primer
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<210> 71
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 <223> AFT2term Reverse Primer
 <400> 71
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<210> 72
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 <212> DNA
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 <223> AFT2UP full Forward
 <400> 72
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<210> 73
 <211> 23

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 <400> 73
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<210> 74
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 <223> AFT2UP sequence 2

 <400> 74
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<210> 75
 <211> 22
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 <220>
 <223> Primer 2649

 <400> 75
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<210> 76
 <211> 25
 <212> DNA
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 <220>
 <223> Primer 2650

 <400> 76
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<210> 77
 <211> 23
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 <220>
 <223> Primer 2962

 <400> 77
 acgccaacat cttcgcaaca ctc 23

<210> 78

<211> 21
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 <220>
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<210> 79
 <211> 25
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 <400> 79
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<210> 80
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 <400> 81
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<210> 84
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<210> 85
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 <400> 85
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<210> 86
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 <223> Primer 2979

 <400> 86
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<210> 87
 <211> 615
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 <213> *Saccharomyces cerevisiae*

<400> 88

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Val	Tyr	Thr	Lys	Thr	Val	Thr	Gln	Asp	Ala	Thr	Phe	Val	Trp	Gly	Gly
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Ala	Asp	Glu	Gly	Ser	Gly	Ser	Ser	Ile	Thr	Thr	Thr	Ile	Thr	Ala	Thr
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Lys	Asn	Gly	His	Val	Tyr	Thr	Lys	Thr	Val	Thr	Gln	Asp	Ala	Thr	Phe
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Thr Thr Ala Glu Thr Ser Ser Ser Ala Thr Ser Ser Ser Thr Ala Glu
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<210> 89
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 <213> *Saccharomyces cerevisiae*

<400> 89
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 tctactgtcg ctgcaacgtc tgctgccgct gaaacatctg ttgccgctga aacatctatt 240
 gttgagcctt ccacttctgc tcagggcacc tctgctgatg aagggctctgg ttcgagtata 300
 accaccacta ttacagccac caaaaatgga catgtctaca caaagaccgt caccaggat 360
 gctactttcg tatggactgg agagggtgaa cgtgctcctg cctcaactgt tgctactgtc 420
 gaaacatctg ttgccgctga aacatctgtt gctgaacctt ctacctctgc tcagggcacc 480
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<210> 90
<211> 528
<212> PRT
<213> *Saccharomyces cerevisiae*
<400> 90

Met Lys Leu Ser Ser Ala Phe Val Leu Ser Ala Ile Thr Val Ala Ala
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Leu Gly Glu Ser Ile Thr Thr Thr Ile Thr Ala Thr Lys Asn Gly His
20 25 30

Val Tyr Thr Lys Thr Val Thr Gln Asp Ala Thr Phe Val Trp Ala Gly
35 40 45

Glu Gly Ala Ala Val Thr Ser Ala Val Thr Glu Ala Ser Thr Val Ala
50 55 60

Ala Thr Ser Ala Ala Ala Glu Thr Ser Val Ala Ala Glu Thr Ser Ile
65 70 75 80

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

Gly Ser Ser Ile Thr Thr Thr Ile Thr Ala Thr Lys Asn Gly His Val
100 105 110

Tyr Thr Lys Thr Val Thr Gln Asp Ala Thr Phe Val Trp Thr Gly Glu
115 120 125

Gly Glu Arg Ala Pro Ala Ser Thr Val Ala Thr Val Glu Thr Ser Val
130 135 140

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

Ser Ala Asp Glu Gly Ser Gly Ser Ser Ile Thr Thr Thr Ile Thr Ala
165 170 175

Thr Lys Asn Gly His Val Tyr Thr Lys Thr Val Thr Gln Asp Ala Thr
180 185 190

Phe Val Trp Thr Gly Glu Gly Glu Arg Ala Pro Val Ser Thr Val Ala
195 200 205

Thr Val Glu Thr Ala Ala Ser Pro Val Thr Ser Val Ala Glu Pro Ser
210 215 220

Ala Ser Thr Asp Glu Gly Ser Gly Ser Ser Ile Thr Thr Thr Ile Thr
225 230 235 240

Ala Thr Lys Asn Gly His Val Tyr Thr Lys Thr Val Thr Gln Asp Ala
245 250 255

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

Ala Thr Ser Ser Ile Ser Ala Ile Glu Ile Pro Ser Thr Thr Glu Ala
275 280 285

Ser Ile Val Glu Ala Ser Ser Ala Val Glu Thr Ser Ser Ala Ala Glu
290 295 300

Thr Ser Ser Ala Val Glu Thr Ser Ser Ala Val Glu Thr Ser Ser Ala
305 310 315 320

Val Glu Thr Ser Ser Ala Ala Glu Thr Ser Ser Ala Ala Glu Thr Ser
325 330 335

Ser Ala Val Glu Thr Ser Ser Ala Val Glu Ile Ser Ser Ala Val Glu
340 345 350

Thr Ser Ala Val Glu Thr Ser Ser Ser Ser Thr Ile Glu Thr Thr
355 360 365

Ser Val Lys Ser Leu Ser Pro Thr Gln Thr Ser Leu Ser Ser Ser Val
 370 375 380

Gln Ala Ser Ser Pro Ile Glu Thr Ser Ser Ala Ala Lys Thr Ser Ser
 385 390 395 400

Val Val Pro Thr Phe Ser Ser Thr Thr Thr Glu Asn Ser Ser Asn Ser
 405 410 415

Lys Ser Thr Ser Ala Val Val Ala Ser Thr Thr Thr Ser Ser Glu Ser
 420 425 430

Ser Ala Thr Ile Val Thr Pro Thr Arg Ile Gly Gln Ala Tyr Thr Glu
 435 440 445

Ser Ser Ser Arg Asp Ala Gln Ser Val Arg Thr His Glu Ser Asn Asn
 450 455 460

Trp Ser Ser Ser Ser Ser Ala Ser Thr Lys Met Val Ser Ser Ile Thr
 465 470 475 480

Arg Val Gln Thr Thr Thr Ala Gly Ile Phe Thr Asn Gly Lys Ser Ser
 485 490 495

Thr Thr Pro Gln Ile Val Asn Tyr Thr Gly Ala Ala Asp Ser Ile Ala
 500 505 510

Ala Gly Thr Gly Leu Met Gly Ala Ala Leu Ala Ala Val Ile Phe Leu
 515 520 525

<210> 91
 <211> 1911
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 91
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 aagagccgtc ccgtgatcac ctgtaatggc cagttcccat ggccagatat aacggtcaac 180
 aaaggtgacc gtgtgcagat ttacttgacc aacggaatga acaacaccaa tacttctatg 240
 catttccacg gtctcttcca aaacggaacc gcctctatgg acggtgtgcc cttcttgacg 300
 caatgtccaa ttgcgccagg cagtactatg ctttacaatt tcacggtgga ctacaatgta 360

ggcacctact ggtaccattc acacacggac ggtcaatatg aagacgggat gaaaggtctt	420
ttcatcatca aggatgatag cttcccctac gattacgatg aggaactttc tttatcgctt	480
agtgagtggg accacgactt ggtcacggac ttgacgaagt cgttcatgag tgtttataat	540
ccgacaggtg ctgagcccat cccacagaac ttgattgtta acaacacgat gaatctgaca	600
tgggaagtcc agcccgatac gacgtatctt ttgagaattg tcaacgtggg tgggttcgtt	660
tcgcagtact tttggatcga ggaccacgaa atgaccgtgg tcgaaatcga cggtatcact	720
accgagaaga acgtaacgga tatgctttac atcactgtcg ctgagagata tacagtcctg	780
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atgttggatg tcattccaag tgattttacag ctgaatgcaa cctcttatat ggtctacaac	900
aaaaccgctg cgctgccac acaaaattac gtggattcaa ttgataactt cttggacgat	960
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gttgacgttg ttatggataa cttgaaaaac ggtgtgaatt acgccttctt caataatata	1080
acctatactg caccaaaagt tcctactttg atgaccgttt tgtcttcagg tgatcaagca	1140
aacaactccg aaatctacgg ttcaaacacg cacactttca tcctagagaa ggatgaaatc	1200
gtggagattg tgctaaataa ccaggacaca ggtacccatc ctttccattt acatggtcac	1260
gctttccaaa ccatccagag agatcgtaca tatgatgatg ccctaggtga agttcctcac	1320
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tacgttagac cacaatccaa tttcgtcatc aggttttaaag ccgataaccc aggtgtttgg	1440
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gatccttttg gtatccaaga tgctcattct caacaactca gtgaaaacca cttagaagtt	1560
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gatttaactg gtgaaaatgt tcagcatgcc ttcatctcta ccggttttac caaaaaaggt	1680
attattgcca tgacattctc ctgctttgcc ggtattcttg gtattatcac aattgcaatt	1740
tatggtatga tggatatgga agatgcgacc gaaaagggtta ttcgagactt gcacgtggac	1800
cctgaagtct tgctaaatga ggttgatgaa aatgaagagc gtcaggtaaa cgaagatcgt	1860
cattccactg aaaagcatca atttttaact aaagccaaac ggttcttcta a	1911

<210> 92
 <211> 635
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 92

Met Thr Asn Ala Leu Leu Ser Ile Ala Val Leu Leu Phe Ser Met Leu
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Ser Leu Ala Gln Ala Glu Thr His Thr Phe Asn Trp Thr Thr Gly Trp
20 25 30

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

Asn Gly Gln Phe Pro Trp Pro Asp Ile Thr Val Asn Lys Gly Asp Arg
50 55 60

Val Gln Ile Tyr Leu Thr Asn Gly Met Asn Asn Thr Asn Thr Ser Met
65 70 75 80

His Phe His Gly Leu Phe Gln Asn Gly Thr Ala Ser Met Asp Gly Val
85 90 95

Pro Phe Leu Thr Gln Cys Pro Ile Ala Pro Gly Ser Thr Met Leu Tyr
100 105 110

Asn Phe Thr Val Asp Tyr Asn Val Gly Thr Tyr Trp Tyr His Ser His
115 120 125

Thr Asp Gly Gln Tyr Glu Asp Gly Met Lys Gly Leu Phe Ile Ile Lys
130 135 140

Asp Asp Ser Phe Pro Tyr Asp Tyr Asp Glu Glu Leu Ser Leu Ser Leu
145 150 155 160

Ser Glu Trp Tyr His Asp Leu Val Thr Asp Leu Thr Lys Ser Phe Met
165 170 175

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

Val Asn Asn Thr Met Asn Leu Thr Trp Glu Val Gln Pro Asp Thr Thr
195 200 205

Tyr Leu Leu Arg Ile Val Asn Val Gly Gly Phe Val Ser Gln Tyr Phe
210 215 220

Trp Ile Glu Asp His Glu Met Thr Val Val Glu Ile Asp Gly Ile Thr
225 230 235 240

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

Tyr Thr Val Leu Val His Thr Lys Asn Asp Thr Asp Lys Asn Phe Ala
260 265 270

Ile Met Gln Lys Phe Asp Asp Thr Met Leu Asp Val Ile Pro Ser Asp
275 280 285

Leu Gln Leu Asn Ala Thr Ser Tyr Met Val Tyr Asn Lys Thr Ala Ala
290 295 300

Leu Pro Thr Gln Asn Tyr Val Asp Ser Ile Asp Asn Phe Leu Asp Asp
305 310 315 320

Phe Tyr Leu Gln Pro Tyr Glu Lys Glu Ala Ile Tyr Gly Glu Pro Asp
325 330 335

His Val Ile Thr Val Asp Val Val Met Asp Asn Leu Lys Asn Gly Val
340 345 350

Asn Tyr Ala Phe Phe Asn Asn Ile Thr Tyr Thr Ala Pro Lys Val Pro
355 360 365

Thr Leu Met Thr Val Leu Ser Ser Gly Asp Gln Ala Asn Asn Ser Glu
370 375 380

Ile Tyr Gly Ser Asn Thr His Thr Phe Ile Leu Glu Lys Asp Glu Ile
385 390 395 400

Val Glu Ile Val Leu Asn Asn Gln Asp Thr Gly Thr His Pro Phe His
405 410 415

Leu His Gly His Ala Phe Gln Thr Ile Gln Arg Asp Arg Thr Tyr Asp
420 425 430

Asp Ala Leu Gly Glu Val Pro His Ser Phe Asp Pro Asp Asn His Pro
435 440 445

Ala Phe Pro Glu Tyr Pro Met Arg Arg Asp Thr Leu Tyr Val Arg Pro
450 455 460

Gln Ser Asn Phe Val Ile Arg Phe Lys Ala Asp Asn Pro Gly Val Trp

gcgtcaaatt atttgagagc acctgagaaa agtgataaaa aaaccgtggt tagtcaaccg	360
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aacctaattgc gctctcaatg gtgcgcttgg ggtctcgtct tcttctgggt ggctgtgctt	480
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tatttatgga agcgtctacc atttaatttt acaactcgag gcaagggctc cgctcgatta	660
atttttgtta ttttgactat attatctctc agttttggtc ataataatga acttccacac	720
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acaaattcag atgagagtac aaaaggtttt gatgataaag aagaaagcga aatcactgtt	1860
gaatgtctca ataaaagacc tgatttgaaa gaactagtgc gctcggaaat aaaactctca	1920
gaactagaga ataataatat taccttttat tcctgcgggc cagcaacgtt taacgacgat	1980
tttagaaatg cagtgggtcca aggtatagac tcttccttga agattgacgt tgaactagaa	2040
gaagaaagtt ttacatggta a	2061

<210> 94
 <211> 686
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 94

Met Val Arg Thr Arg Val Leu Phe Cys Leu Phe Ile Ser Phe Phe Ala
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Thr Val Gln Ser Ser Ala Thr Leu Ile Ser Thr Ser Cys Ile Ser Gln
 20 25 30

Ala Ala Leu Tyr Gln Phe Gly Cys Ser Ser Lys Ser Lys Ser Cys Tyr
 35 40 45

Cys Lys Asn Ile Asn Trp Leu Gly Ser Val Thr Ala Cys Ala Tyr Glu
 50 55 60

Asn Ser Lys Ser Asn Lys Thr Leu Asp Ser Ala Leu Met Lys Leu Ala
 65 70 75 80

Ser Gln Cys Ser Ser Ile Lys Val Tyr Thr Leu Glu Asp Met Lys Asn
 85 90 95

Ile Tyr Leu Asn Ala Ser Asn Tyr Leu Arg Ala Pro Glu Lys Ser Asp
 100 105 110

Lys Lys Thr Val Val Ser Gln Pro Leu Met Ala Asn Glu Thr Ala Tyr
 115 120 125

His Tyr Tyr Tyr Glu Glu Asn Tyr Gly Ile His Leu Asn Leu Met Arg
 130 135 140

Ser Gln Trp Cys Ala Trp Gly Leu Val Phe Phe Trp Val Ala Val Leu
 145 150 155 160

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

Ile Met Ala Asn Ser Val Lys Lys Ser Leu Ile Tyr Pro Ser Val Tyr
 180 185 190

Lys Asp Tyr Asn Glu Arg Thr Phe Tyr Leu Trp Lys Arg Leu Pro Phe
 195 200 205

Asn Phe Thr Thr Arg Gly Lys Gly Leu Val Val Leu Ile Phe Val Ile
210 215 220

Leu Thr Ile Leu Ser Leu Ser Phe Gly His Asn Ile Lys Leu Pro His
225 230 235 240

Pro Tyr Asp Arg Pro Arg Trp Arg Arg Ser Met Ala Phe Val Ser Arg
245 250 255

Arg Ala Asp Leu Met Ala Ile Ala Leu Phe Pro Val Val Tyr Leu Phe
260 265 270

Gly Ile Arg Asn Asn Pro Phe Ile Pro Ile Thr Gly Leu Ser Phe Ser
275 280 285

Thr Phe Asn Phe Tyr His Lys Trp Ser Ala Tyr Val Cys Phe Met Leu
290 295 300

Ala Val Val His Ser Ile Val Met Thr Ala Ser Gly Val Lys Arg Gly
305 310 315 320

Val Phe Gln Ser Leu Val Arg Lys Phe Tyr Phe Arg Trp Gly Ile Val
325 330 335

Ala Thr Ile Leu Met Ser Ile Ile Ile Phe Gln Ser Glu Lys Val Phe
340 345 350

Arg Asn Arg Gly Tyr Glu Ile Phe Leu Leu Ile His Lys Ala Met Asn
355 360 365

Ile Met Phe Ile Ile Ala Met Tyr Tyr His Cys His Thr Leu Gly Trp
370 375 380

Met Gly Trp Ile Trp Ser Met Ala Gly Ile Leu Cys Phe Asp Arg Phe
385 390 395 400

Cys Arg Ile Val Arg Ile Ile Met Asn Gly Gly Leu Lys Thr Ala Thr
405 410 415

Leu Ser Thr Thr Asp Asp Ser Asn Val Ile Lys Ile Ser Val Lys Lys
420 425 430

Pro Lys Phe Phe Lys Tyr Gln Val Gly Ala Phe Ala Tyr Met Tyr Phe

435																	
Leu	Ser	Pro	Lys	Ser	Ala	Trp	Phe	Tyr	Ser	Phe	Gln	Ser	His	Pro	Phe		
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Thr	Val	Leu	Ser	Glu	Arg	His	Arg	Asp	Pro	Asn	Asn	Pro	Asp	Gln	Leu		
465					470					475					480		
Thr	Met	Tyr	Val	Lys	Ala	Asn	Lys	Gly	Ile	Thr	Arg	Val	Leu	Leu	Ser		
				485					490					495			
Lys	Val	Leu	Ser	Ala	Pro	Asn	His	Thr	Val	Asp	Cys	Lys	Ile	Phe	Leu		
			500					505					510				
Glu	Gly	Pro	Tyr	Gly	Val	Thr	Val	Pro	His	Ile	Ala	Lys	Leu	Lys	Arg		
		515					520					525					
Asn	Leu	Val	Gly	Val	Ala	Ala	Gly	Leu	Gly	Val	Ala	Ala	Ile	Tyr	Pro		
530						535					540						
His	Phe	Val	Glu	Cys	Leu	Arg	Leu	Pro	Ser	Thr	Asp	Gln	Leu	Gln	His		
545					550					555					560		
Lys	Phe	Tyr	Trp	Ile	Val	Asn	Asp	Leu	Ser	His	Leu	Lys	Trp	Phe	Glu		
				565					570					575			
Asn	Glu	Leu	Gln	Trp	Leu	Lys	Glu	Lys	Ser	Cys	Glu	Val	Ser	Val	Ile		
			580					585					590				
Tyr	Thr	Gly	Ser	Ser	Val	Glu	Asp	Thr	Asn	Ser	Asp	Glu	Ser	Thr	Lys		
		595					600					605					
Gly	Phe	Asp	Asp	Lys	Glu	Glu	Ser	Glu	Ile	Thr	Val	Glu	Cys	Leu	Asn		
	610					615					620						
Lys	Arg	Pro	Asp	Leu	Lys	Glu	Leu	Val	Arg	Ser	Glu	Ile	Lys	Leu	Ser		
625					630					635					640		
Glu	Leu	Glu	Asn	Asn	Asn	Ile	Thr	Phe	Tyr	Ser	Cys	Gly	Pro	Ala	Thr		
			645						650					655			
Phe	Asn	Asp	Asp	Phe	Arg	Asn	Ala	Val	Val	Gln	Gly	Ile	Asp	Ser	Ser		
			660					665					670				

Leu Lys Ile Asp Val Glu Leu Glu Glu Glu Ser Phe Thr Trp
675 680 685

<210> 95
<211> 1215
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 95
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cgggcgctgt accgtaaatt aaggattcag gtttgggtcg gtgtgttact cgggttcac 180
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gaagctgttg tgttcggtgc cgggtgcagg attaccacac agggctcgca cgcctctgct 540
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cttgccagtg gtggtgatgc ttccgaaggc ggtgatggta atgggtctta taacatcaga 780
aaggccgttt accatgtcaa ttgttgcaac ccagaactgg acaatgggtg ggatatcttc 840
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atcaacttca atgaagatgg tgagatcaat gtgcaagaga actacgaact tcccgagcaa 1140
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gccgactctc ttgga 1215

<210> 96
<211> 404
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 96

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

Leu Ala Ser Gly Gly Asp Ala Ser Glu Gly Gly Asp Gly Asn Gly Ser
245 250 255

Tyr Asn Ile Arg Lys Ala Val Tyr His Val Asn Cys Cys Asn Pro Glu
260 265 270

Leu Asp Asn Gly Trp Asp Ile Phe Asn Ala Leu Leu Gly Trp Gln Asn
275 280 285

Thr Gly Tyr Leu Ser Ser Met Leu Cys Tyr Asn Ile Tyr Trp Leu Val
290 295 300

Leu Ile Ile Val Leu Ser Leu Met Ile Phe Glu Glu Arg Arg Gly His
305 310 315 320

Leu Pro Phe Thr Lys Asn Leu Gln Leu Lys His Leu Asn Pro Gly Tyr
325 330 335

Trp Ile Lys Asn Lys Lys Lys Gln Glu Leu Thr Glu Glu Gln Lys Arg
340 345 350

Gln Leu Phe Ala Lys Met Glu Asn Ile Asn Phe Asn Glu Asp Gly Glu
355 360 365

Ile Asn Val Gln Glu Asn Tyr Glu Leu Pro Glu Gln Thr Thr Ser His
370 375 380

Ser Ser Ser Gln Asn Val Ala Thr Asp Lys Glu Val Leu His Val Lys
385 390 395 400

Ala Asp Ser Leu

<210> 97

<211> 462

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 97

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<210> 98
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 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 98

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

Glu Lys Ser Thr Thr Lys Thr Leu Thr Leu Thr Asn Gly Ser Gly Ser
 85 90 95

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

Thr Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ala Ser Ser
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Ser Gly Ala Ala Pro Ala Ala Phe Gln Gly Ala Ser Val Gly Ala Leu
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Ala Leu Gly Leu Ile Ser Tyr Leu Leu
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<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 99

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<211> 439

<212> PRT

<213> *Saccharomyces cerevisiae*

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Ser Leu Ala Leu Ile Ala Asp Ser Phe His Met Leu Asn Asp Ile Ile
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Ser Leu Val Val Ala Leu Trp Ala Val Asn Val Ala Lys Asn Arg Asn
50 55 60

Pro Asp Ser Thr Tyr Thr Tyr Gly Trp Lys Arg Ala Glu Ile Leu Gly
65 70 75 80

Ala Leu Ile Asn Ala Val Phe Leu Ile Ala Leu Cys Val Ser Ile Leu
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Ile Glu Ala Leu Gln Arg Ile Ile Ala Pro Pro Val Ile Glu Asn Pro
100 105 110

Lys Phe Val Leu Tyr Val Gly Val Ala Gly Leu Ile Ser Asn Thr Val
115 120 125

Gly Leu Phe Leu Phe His Asp Asn Asp Gln Glu His Gly His Gly His
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Gly His Ser His Gly Gly Ile Phe Ala Asp His Glu Met His Met Pro
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Ser Ser His Thr His Thr His Ala His Val Asp Gly Ile Glu Asn Thr
165 170 175

Thr Pro Met Asp Ser Thr Asp Asn Ile Ser Glu Ile Met Pro Asn Ala
180 185 190

Ile Val Asp Ser Phe Met Asn Glu Asn Thr Arg Leu Leu Thr Pro Glu
195 200 205

Asn Ala Ser Lys Thr Pro Ser Tyr Ser Thr Ser Ser His Thr Ile Ala
210 215 220

Ser Gly Gly Asn Tyr Thr Glu His Asn Lys Arg Lys Arg Ser Leu Asn
225 230 235 240

Met His Gly Val Phe Leu His Val Leu Gly Asp Ala Leu Gly Asn Ile
245 250 255

Gly Val Met Leu Ser Ala Phe Phe Ile Trp Lys Thr Asp Tyr Ser Trp
 260 265 270

Lys Tyr Tyr Thr Asp Pro Leu Val Ser Leu Ile Ile Thr Gly Ile Ile
 275 280 285

Phe Ser Ser Ala Leu Pro Leu Ser Cys Lys Ala Ser Lys Ile Leu Leu
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Gln Ala Thr Pro Ser Thr Leu Ser Gly Asp Gln Val Glu Gly Asp Leu
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Leu Lys Ile Pro Gly Ile Ile Ala Ile His Asp Phe His Ile Trp Asn
 325 330 335

Leu Thr Glu Ser Ile Phe Ile Ala Ser Leu His Ile Gln Leu Asp Ile
 340 345 350

Ser Pro Glu Gln Phe Thr Asp Leu Ala Lys Ile Val Arg Ser Lys Leu
 355 360 365

His Arg Tyr Gly Ile His Ser Ala Thr Leu Gln Pro Glu Phe Ile Thr
 370 375 380

Arg Glu Val Thr Ser Thr Glu Arg Ala Gly Asp Ser Gln Gly Asp His
 385 390 395 400

Leu Gln Asn Asp Pro Leu Ser Leu Arg Pro Lys Thr Tyr Gly Thr Gly
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Ile Ser Gly Ser Thr Cys Leu Ile Asp Asp Ala Ala Asn Cys Asn Thr
 420 425 430

Ala Asp Cys Leu Glu Asp His
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<210> 101
 <211> 1203
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 <213> *Saccharomyces cerevisiae*

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cgtgctcaaa gacctggtac catgatcatc acggaaggta cgtttatttc ccctcaagcc      240
ggcggctatg acaacgcccc tgggatttgg tctgatgagc aggtcgctga gtggaagaat      300
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tgggcatcct tcccagacgt attggcaaga gacgggttac gctatgactg tgcacatgac      420
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<210> 102
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<213> Saccharomyces cerevisiae

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<400> 102

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20           25           30

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Val Met Pro Pro Leu Thr Arg Met Arg Ala Thr His Pro Gly Asn Ile
35           40           45

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

Gly Gly Tyr Asp Asn Ala Pro Gly Ile Trp Ser Asp Glu Gln Val Ala
85 90 95

Glu Trp Lys Asn Ile Phe Leu Ala Ile His Asp Cys Gln Ser Phe Ala
100 105 110

Trp Val Gln Leu Trp Ser Leu Gly Trp Ala Ser Phe Pro Asp Val Leu
115 120 125

Ala Arg Asp Gly Leu Arg Tyr Asp Cys Ala Ser Asp Arg Val Tyr Met
130 135 140

Asn Ala Thr Leu Gln Glu Lys Ala Lys Asp Ala Asn Asn Leu Glu His
145 150 155 160

Ser Leu Thr Lys Asp Asp Ile Lys Gln Tyr Ile Lys Asp Tyr Ile His
165 170 175

Ala Ala Lys Asn Ser Ile Ala Ala Gly Ala Asp Gly Val Glu Ile His
180 185 190

Ser Ala Asn Gly Tyr Leu Leu Asn Gln Phe Leu Asp Pro His Ser Asn
195 200 205

Lys Arg Thr Asp Glu Tyr Gly Gly Thr Ile Glu Asn Arg Ala Arg Phe
210 215 220

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

Val Gly Leu Arg Leu Ser Pro Tyr Gly Thr Phe Asn Ser Met Ser Gly
245 250 255

Gly Ala Glu Pro Gly Ile Ile Ala Gln Tyr Ser Tyr Val Leu Gly Glu
260 265 270

Leu Glu Lys Arg Ala Lys Ala Gly Lys Arg Leu Ala Phe Val His Leu
275 280 285

Val Glu Pro Arg Val Thr Asp Pro Ser Leu Val Glu Gly Glu Gly Glu
290 295 300

Tyr Ser Glu Gly Thr Asn Asp Phe Ala Tyr Ser Ile Trp Lys Gly Pro
305 310 315 320

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

Gln Val Lys Asp Pro Arg Thr Leu Ile Gly Tyr Gly Arg Phe Phe Ile
340 345 350

Ser Asn Pro Asp Leu Val Tyr Arg Leu Glu Glu Gly Leu Pro Leu Asn
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Lys Tyr Asp Arg Ser Thr Phe Tyr Thr Met Ser Ala Glu Gly Tyr Thr
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Asp Tyr Pro Thr Tyr Glu Glu Ala Val Asp Leu Gly Trp Asn Lys Asn
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<210> 103

<211> 858

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 103

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agtgaaatat cttcggcagt ttcattctct ccaccaaaaa atacaaacgc tattcaaccg	240
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 <213> *Saccharomyces cerevisiae*

<400> 104

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			20					25					30		

Tyr	Gln	Tyr	Gln	Ile	Asn	Ile	Arg	Glu	Leu	Glu	Glu	Tyr	Tyr	Asn	Lys
	35						40					45			

Thr	Ile	Leu	Asn	Glu	Asp	Asn	Ile	Gln	Glu	Thr	Ser	Ser	Glu	Ile	Ser
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Ser	Ala	Val	Ser	Phe	Ser	Pro	Pro	Lys	Asn	Thr	Asn	Ala	Ile	Gln	Pro
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Gly	Leu	Leu	Tyr	Asp	Pro	Gln	Leu	Met	Asn	Pro	Phe	Leu	Pro	Ser	Ala
				85					90					95	

His	Leu	Asn	Ser	Thr	Ala	Pro	Thr	Thr	Phe	Lys	Lys	Lys	Leu	Glu	Val
			100					105					110		

Gln	Ile	Asn	Pro	Asp	Tyr	Val	Pro	Lys	Ser	Ser	Gln	Leu	Pro	Leu	Thr
		115					120					125			

Ser	Gln	Asn	Leu	Gln	Gln	Leu	Ser	Gln	Gln	Lys	Pro	Lys	Asn	Asp	Ala
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Ser	Phe	Ser	Ser	Glu	Lys	Glu	Ser	Ser	Ala	Gln	Pro	Lys	Val	Lys	Ser
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Gln	Val	Gln	Glu	Thr	Pro	Lys	Gln	Leu	Tyr	Lys	Thr	Glu	Leu	Cys	Glu
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Ser	Phe	Thr	Leu	Lys	Gly	Ser	Cys	Pro	Tyr	Gly	Ser	Lys	Cys	Gln	Phe
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Arg Thr Lys Pro Cys Val Asn Trp Glu Lys Leu Gly Tyr Cys Pro Tyr			
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Gly Arg Arg Cys Cys Phe Lys His Gly Asp Asp Asn Asp Ile Ala Val			
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Tyr Val Lys Ala Gly Thr Tyr Cys Asn Val Ser Ser Thr Ser Lys Gln			
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<210> 106
 <211> 1592
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 106

Met Gly Thr Asp Pro Leu Ile Ile Arg Asn Asn Gly Ser Phe Trp Glu
 1 5 10 15

Val Asp Asp Phe Thr Arg Leu Gly Arg Thr Gln Leu Leu Ser Tyr Tyr
 20 25 30

Leu Pro Leu Ala Ile Ile Ala Ser Ile Gly Ile Phe Ala Leu Cys Arg
 35 40 45

Ser Gly Leu Ser Arg Tyr Val Arg Ser Ala Glu Cys Asp Leu Val Asn
 50 55 60

Glu Tyr Leu Phe Gly Ala Gln Glu Glu Arg Lys Glu Asp Asn Ser Ile
 65 70 75 80

Glu Arg Leu Leu Arg Asn Ser Asn Thr Gln Ala Asn Tyr Val Asn Val
 85 90 95

Lys Lys Gln Gly Arg Ile Leu Lys Leu Arg His Phe Asp Ile Thr Thr
 100 105 110

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

Ser Arg Pro Ser Thr Ser Asp His Leu Arg Lys Ser Ser Glu Ile Val
 130 135 140

Leu Met Ser Leu Gln Ile Ile Gly Leu Ser Phe Leu Arg Val Thr Lys
145 150 155 160

Ile Asn Ile Glu Leu Thr Asn Arg Asp Val Thr Thr Leu Leu Leu Phe
165 170 175

Trp Leu Ile Leu Leu Ser Leu Ser Ile Leu Arg Val Tyr Lys Arg Ser
180 185 190

Thr Asn Leu Trp Ala Ile Cys Phe Thr Ala His Thr Thr Ile Trp Ile
195 200 205

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

Val Pro Ser Gln Ile Phe Tyr Ile Phe Glu Phe Val Ile Thr Ser Thr
225 230 235 240

Leu Gln Pro Ile Lys Leu Thr Ser Pro Ile Lys Asp Asn Ser Ser Ile
245 250 255

Ile Tyr Val Arg Asp Asp His Thr Ser Pro Ser Arg Glu His Ile Ser
260 265 270

Ser Ile Leu Ser Cys Ile Thr Trp Ser Trp Ile Thr Asn Phe Ile Trp
275 280 285

Glu Ala Gln Lys Asn Thr Ile Lys Leu Lys Asp Ile Trp Gly Leu Ser
290 295 300

Met Glu Asp Tyr Ser Ile Phe Ile Leu Lys Gly Phe Thr Arg Arg Asn
305 310 315 320

Lys His Ile Asn Asn Leu Thr Leu Ala Leu Phe Glu Ser Phe Lys Thr
325 330 335

Tyr Leu Leu Ile Gly Met Leu Trp Val Leu Val Asn Ser Ile Val Asn
340 345 350

Leu Leu Pro Thr Ile Leu Met Lys Arg Phe Leu Glu Ile Val Asp Asn
355 360 365

Pro Asn Arg Ser Ser Ser Cys Met Asn Leu Ala Trp Leu Tyr Ile Ile
370 375 380

Gly Met Phe Ile Cys Arg Leu Thr Leu Ala Ile Cys Asn Ser Gln Gly
385 390 395 400

Gln Phe Val Ser Asp Lys Ile Cys Leu Arg Ile Arg Ala Ile Leu Ile
405 410 415

Gly Glu Ile Tyr Ala Lys Gly Leu Arg Arg Arg Leu Phe Thr Ser Pro
420 425 430

Lys Thr Ser Ser Asp Ser Asp Ser Ile Ser Ala Asn Leu Gly Thr Ile
435 440 445

Ile Asn Leu Ile Ser Ile Asp Ser Phe Lys Val Ser Glu Leu Ala Asn
450 455 460

Tyr Leu Tyr Val Thr Val Gln Ala Val Ile Met Ile Ile Val Val Val
465 470 475 480

Gly Leu Leu Phe Asn Phe Leu Gly Val Ser Ala Phe Ala Gly Ile Ser
485 490 495

Ile Ile Leu Val Met Phe Pro Leu Asn Phe Leu Leu Ala Asn Leu Leu
500 505 510

Gly Lys Phe Gln Lys Gln Thr Leu Lys Cys Thr Asp Gln Arg Ile Ser
515 520 525

Lys Leu Asn Glu Cys Leu Gln Asn Ile Arg Ile Val Lys Tyr Phe Ala
530 535 540

Trp Glu Arg Asn Ile Ile Asn Glu Ile Lys Ser Ile Arg Gln Lys Glu
545 550 555 560

Leu Arg Ser Leu Leu Lys Lys Ser Leu Val Trp Ser Val Thr Ser Phe
565 570 575

Leu Trp Phe Val Thr Pro Thr Leu Val Thr Gly Val Thr Phe Ala Ile
580 585 590

Cys Thr Phe Val Gln His Glu Asp Leu Asn Ala Pro Leu Ala Phe Thr
595 600 605

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

610	615	620
Asn Met Leu Ser Phe 625	Ile Asn Gln Ser Lys 630	Val Ser Leu Lys Arg Ile 635 640
Ser Asp Phe Leu Arg 645	Met Asp Asp Thr Glu Lys Tyr Asn Gln Leu Thr 650 655	
Ile Ser Pro Asp Lys Asn Lys Ile Glu Phe Lys Asn Ala Thr Leu Thr 660 665 670		
Trp Asn Glu Asn Asp Ser Asp Met Asn Ala Phe Lys Leu Cys Gly Leu 675 680 685		
Asn Ile Lys Phe Gln Ile Gly Lys Leu Asn Leu Ile Leu Gly Ser Thr 690 695 700		
Gly Ser Gly Lys Ser Ala Leu Leu Leu Gly Leu Leu Gly Glu Leu Asn 705 710 715 720		
Leu Ile Ser Gly Ser Ile Ile Val Pro Ser Leu Glu Pro Lys His Asp 725 730 735		
Leu Ile Pro Asp Cys Glu Gly Leu Thr Asn Ser Phe Ala Tyr Cys Ser 740 745 750		
Gln Ser Ala Trp Leu Leu Asn Asp Thr Val Lys Asn Asn Ile Ile Phe 755 760 765		
Asp Asn Phe Tyr Asn Glu Asp Arg Tyr Asn Lys Val Ile Asp Ala Cys 770 775 780		
Gly Leu Lys Arg Asp Leu Glu Ile Leu Pro Ala Gly Asp Leu Thr Glu 785 790 795 800		
Ile Gly Glu Lys Gly Ile Thr Leu Ser Gly Gly Gln Lys Gln Arg Ile 805 810 815		
Ser Leu Ala Arg Ala Val Tyr Ser Ser Ala Lys His Val Leu Leu Asp 820 825 830		
Asp Cys Leu Ser Ala Val Asp Ser His Thr Ala Val Trp Ile Tyr Glu 835 840 845		

Asn Cys Ile Thr Gly Pro Leu Met Lys Asn Arg Thr Cys Ile Leu Val
 850 855 860

Thr His Asn Val Ser Leu Thr Leu Arg Asn Ala His Phe Ala Ile Val
 865 870 875 880

Leu Glu Asn Gly Lys Val Lys Asn Gln Gly Thr Ile Thr Glu Leu Gln
 885 890 895

Ser Lys Gly Leu Phe Lys Glu Lys Tyr Val Gln Leu Ser Ser Arg Asp
 900 905 910

Ser Ile Asn Glu Lys Asn Ala Asn Arg Leu Lys Ala Pro Arg Lys Asn
 915 920 925

Asp Ser Gln Lys Ile Glu Pro Val Thr Glu Asn Ile Asn Phe Asp Ala
 930 935 940

Asn Phe Val Asn Asp Gly Gln Leu Ile Glu Glu Glu Glu Lys Ser Asn
 945 950 955 960

Gly Ala Ile Ser Pro Asp Val Tyr Lys Trp Tyr Leu Lys Phe Phe Gly
 965 970 975

Gly Phe Lys Ala Leu Thr Ala Leu Phe Ala Leu Tyr Ile Thr Ala Gln
 980 985 990

Ile Leu Phe Ile Ser Gln Ser Trp Trp Ile Arg His Trp Val Asn Asp
 995 1000 1005

Thr Asn Val Arg Ile Asn Ala Pro Gly Phe Ala Met Asp Thr Leu
 1010 1015 1020

Pro Leu Lys Gly Met Thr Asp Ser Ser Lys Asn Lys His Asn Ala
 1025 1030 1035

Phe Tyr Tyr Leu Thr Val Tyr Phe Leu Ile Gly Ile Ile Gln Ala
 1040 1045 1050

Met Leu Gly Gly Phe Lys Thr Met Met Thr Phe Leu Ser Gly Met
 1055 1060 1065

Arg Ala Ser Arg Lys Ile Phe Asn Asn Leu Leu Asp Leu Val Leu
 1070 1075 1080

His	Ala	Gln	Ile	Arg	Phe	Phe	Asp	Val	Thr	Pro	Val	Gly	Arg	Ile
1085						1090					1095			
Met	Asn	Arg	Phe	Ser	Lys	Asp	Ile	Glu	Gly	Val	Asp	Gln	Glu	Leu
1100						1105					1110			
Ile	Pro	Tyr	Leu	Glu	Val	Thr	Ile	Phe	Cys	Leu	Ile	Gln	Cys	Ala
1115						1120					1125			
Ser	Ile	Ile	Phe	Leu	Ile	Thr	Val	Ile	Thr	Pro	Arg	Phe	Leu	Thr
1130						1135					1140			
Val	Ala	Val	Ile	Val	Phe	Val	Leu	Tyr	Phe	Phe	Val	Gly	Lys	Trp
1145						1150					1155			
Tyr	Leu	Thr	Ala	Ser	Arg	Glu	Leu	Lys	Arg	Leu	Asp	Ser	Ile	Thr
1160						1165					1170			
Lys	Ser	Pro	Ile	Phe	Gln	His	Phe	Ser	Glu	Thr	Leu	Val	Gly	Val
1175						1180					1185			
Cys	Thr	Ile	Arg	Ala	Phe	Gly	Asp	Glu	Arg	Arg	Phe	Ile	Leu	Glu
1190						1195					1200			
Asn	Met	Asn	Lys	Ile	Asp	Gln	Asn	Asn	Arg	Ala	Phe	Phe	Tyr	Leu
1205						1210					1215			
Ser	Val	Thr	Val	Lys	Trp	Phe	Ser	Phe	Arg	Val	Asp	Met	Ile	Gly
1220						1225					1230			
Ala	Phe	Ile	Val	Leu	Ala	Ser	Gly	Ser	Phe	Ile	Leu	Leu	Asn	Ile
1235						1240					1245			
Ala	Asn	Ile	Asp	Ser	Gly	Leu	Ala	Gly	Ile	Ser	Leu	Thr	Tyr	Ala
1250						1255					1260			
Ile	Leu	Phe	Thr	Asp	Gly	Ala	Leu	Trp	Leu	Val	Arg	Leu	Tyr	Ser
1265						1270					1275			
Thr	Phe	Glu	Met	Asn	Met	Asn	Ser	Val	Glu	Arg	Leu	Lys	Glu	Tyr
1280						1285					1290			
Ser	Ser	Ile	Glu	Gln	Glu	Asn	Tyr	Leu	Gly	His	Asp	Glu	Gly	Arg
1295						1300					1305			

Ile Leu Leu Leu Asn Glu Pro Ser Trp Pro Lys Asp Gly Glu Ile
1310 1315 1320

Glu Ile Glu Asn Leu Ser Leu Arg Tyr Ala Pro Asn Leu Pro Pro
1325 1330 1335

Val Ile Arg Asn Val Ser Phe Lys Val Asp Pro Gln Ser Lys Ile
1340 1345 1350

Gly Ile Val Gly Arg Thr Gly Ala Gly Lys Ser Thr Ile Ile Thr
1355 1360 1365

Ala Leu Phe Arg Leu Leu Glu Pro Ile Thr Gly Cys Ile Lys Ile
1370 1375 1380

Asp Gly Gln Asp Ile Ser Lys Ile Asp Leu Val Thr Leu Arg Arg
1385 1390 1395

Ser Ile Thr Ile Ile Pro Gln Asp Pro Ile Leu Phe Ala Gly Thr
1400 1405 1410

Ile Lys Ser Asn Val Asp Pro Tyr Asp Glu Tyr Asp Glu Lys Lys
1415 1420 1425

Ile Phe Lys Ala Leu Ser Gln Val Asn Leu Ile Ser Ser His Glu
1430 1435 1440

Phe Glu Glu Val Leu Asn Ser Glu Glu Arg Phe Asn Ser Thr His
1445 1450 1455

Asn Lys Phe Leu Asn Leu His Thr Glu Ile Ala Glu Gly Gly Leu
1460 1465 1470

Asn Leu Ser Gln Gly Glu Arg Gln Leu Leu Phe Ile Ala Arg Ser
1475 1480 1485

Leu Leu Arg Glu Pro Lys Ile Ile Leu Leu Asp Glu Ala Thr Ser
1490 1495 1500

Ser Ile Asp Tyr Asp Ser Asp His Leu Ile Gln Gly Ile Ile Arg
1505 1510 1515

Ser Glu Phe Asn Lys Ser Thr Ile Leu Thr Ile Ala His Arg Leu

1520	1525	1530
Arg Ser Val Ile Asp Tyr Asp Arg Ile Ile Val Met Asp Ala Gly		
1535	1540	1545
Glu Val Lys Glu Tyr Asp Arg Pro Ser Glu Leu Leu Lys Asp Glu		
1550	1555	1560
Arg Gly Ile Phe Tyr Ser Met Cys Arg Asp Ser Gly Gly Leu Glu		
1565	1570	1575
Leu Leu Lys Gln Ile Ala Lys Gln Ser Ser Lys Met Met Lys		
1580	1585	1590

<210> 107
 <211> 1917
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 107
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 caggttgaga tcattaaata tctaacaagc ggtggggttcg ctcaagtata ttccgcgtta 120
 atcaaccac ctgaccaca ttctaattca agcggttgcg gcttaaaaag agtcattggt 180
 ccagacaaac ctagtctaaa cactttaaga gctgaagtag atgctatgag gttgctgaaa 240
 aacaataggt atgttgatc ttacattgat tctcatgcag ctaaggcaat gttacataat 300
 gggttcgtatg aagtattcgt cttaatggaa tattgtgaaa gaggtggtct cattgatttt 360
 atgaacacaa ggctacaaaa caggcttcat gaatttgaaa ttttgcaa atagagccaa 420
 gttactcaag gagttgccgc tatgcatgct ttgcaacctc cgtaattca ccgtgatata 480
 aagatagaaa atgttcttat ctgagccaat aatgagtaca agctttgtga ctttggttct 540
 gtatgcggtta ttataaggcc tcctaggaat tcacaagagc tatcatatgt tcagcaagac 600
 attttgaaaa acacaactgc acagtaccgg tcgccagaga tgattgatac atttcgcggt 660
 ctgccgatag atgaaaagtc ggatatatgg gcgctgggta ttttctata taagctttgc 720
 tattacacaa caccgtttga aaaggcggt gatcttgcca tattaagcgg aaagtttgaa 780
 tttccattgt atccgaacta cagtgaacag ttgaaaggct taatacgtga tatattggtt 840
 caagatccgc gccataggcc taacgtttat caactactga agaggatatc aattatgcaa 900
 aatgttccgt gtccaataaa tgacatacaa gtgggttcagg cgcccagtag ccatttgaat 960
 ttgaccgaac ttcacagct ttcggcaaca caaatattc taagcttgaa ctctcccaca 1020

accatggaaa atacgatgcc gaacgctaca tttcaaata gcatggctga taatactaca 1080
 acagcacaaa tgcatacctaa tagaaaacca tcacaaatag catatgacgc tagcttcagt 1140
 aattccgcca aaggtttctca accactttttt gacaaatcac agaataatgta ccacgcattg 1200
 gatcctccac ttgttgaacc gctagcgagt agtggtttcaa ataatagaaa cgaactcaag 1260
 gcaaattccg caaccaagtt aaagcaggca attgtctctg aagcacatac ttttaggcag 1320
 aataattcaa tagactttcc actacaaaac ataatacccc agtacgaaga ttcttcttcc 1380
 tcttcagatg aatcttattc tggagacgta gatgaattaa agaaaactcg atctctaggt 1440
 tcttattcca cagcggttaa cataaaaaaa aaccaatccg taaaggaatc tcttacttca 1500
 tcaagcctac caggcactag cttcacccca acgtctacaa aggtaaattt gaaacacgaa 1560
 aattcacctt ttaagtcgac attcgttaat acgattgata attccaaaga cgatcttaac 1620
 aaaccatctt atgaagattt ggacgtatct aagcagaatt tgaagaactc cattcaacag 1680
 cgtatgatcg ataaactcaa ctcttctgag gagtcattca acgctaggaa aatgtccaag 1740
 gtcaagctgc atgagaaagg ggagatagat aagccaacaa tgctgaaatc aagtggcccc 1800
 atttcaaaag acaaaaaaac aaaacctacc ccaccaccta agccttcaca tttaaagcct 1860
 aaacctcctc caaaaccact gctcctcgcg ggacgaaagt tctccttgga taagtga 1917

<210> 108
 <211> 638
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 108

Met Asn Gln Pro Gln Ile Gly Thr Tyr Asn Val Gly Thr Gln Leu Thr
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Val Gly Ser His Gln Val Glu Ile Ile Lys Tyr Leu Thr Ser Gly Gly
 20 25 30

Phe Ala Gln Val Tyr Ser Ala Leu Ile Asn Pro Pro Asp Pro His Ser
 35 40 45

Asn Ser Ser Val Ala Cys Leu Lys Arg Val Ile Val Pro Asp Lys Pro
 50 55 60

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

Asn Asn Arg Tyr Val Val Ser Tyr Ile Asp Ser His Ala Ala Lys Ala

95

Pro Ile Asn Asp Ile Gln Val Val Gln Ala Pro Ser Ser His Leu Asn
305 310 315 320

Leu Thr Glu Leu His Gln Leu Ser Ala Thr Gln Asn Ile Leu Ser Leu
325 330 335

Asn Ser Pro Thr Thr Met Glu Asn Thr Met Pro Asn Ala Thr Phe Gln
340 345 350

Ile Ser Met Ala Asp Asn Thr Thr Thr Ala Gln Met His Pro Asn Arg
355 360 365

Lys Pro Ser Gln Ile Ala Tyr Asp Ala Ser Phe Ser Asn Ser Ala Lys
370 375 380

Gly Ser Gln Pro Leu Phe Asp Lys Ser Gln Asn Met Tyr His Ala Leu
385 390 395 400

Asp Pro Pro Leu Val Glu Pro Leu Ala Ser Ser Val Ser Asn Asn Asp
405 410 415

Asn Glu Leu Lys Ala Asn Ser Ala Thr Lys Leu Lys Gln Ala Ile Val
420 425 430

Ser Glu Ala His Thr Phe Arg Gln Asn Asn Ser Ile Asp Phe Pro Leu
435 440 445

Gln Asn Ile Ile Pro Gln Tyr Glu Asp Ser Ser Ser Ser Ser Asp Glu
450 455 460

Ser Tyr Ser Gly Asp Val Asp Glu Leu Lys Lys Thr Arg Ser Leu Gly
465 470 475 480

Ser Tyr Ser Thr Arg Gly Asn Ile Lys Lys Asn Gln Ser Val Lys Glu
485 490 495

Ser Leu Thr Ser Ser Ser Leu Pro Gly Thr Ser Phe Thr Pro Thr Ser
500 505 510

Thr Lys Val Asn Leu Lys His Glu Asn Ser Pro Phe Lys Ser Thr Phe
515 520 525

Val Asn Thr Ile Asp Asn Ser Lys Asp Asp Leu Asn Lys Pro Ser Tyr
530 535 540

Glu Asp Leu Asp Val Ser Lys Gln Asn Leu Lys Asn Ser Ile Gln Gln
545 550 555 560

Arg Met Ile Asp Lys Leu Asn Ser Ser Glu Glu Ser Phe Asn Ala Arg
565 570 575

Lys Met Ser Lys Val Lys Leu His Glu Lys Gly Glu Ile Asp Lys Pro
580 585 590

Thr Met Leu Lys Ser Ser Gly Pro Ile Ser Lys Asp Lys Lys Thr Lys
595 600 605

Pro Thr Pro Pro Pro Lys Pro Ser His Leu Lys Pro Lys Pro Pro Pro
610 615 620

Lys Pro Leu Leu Leu Ala Gly Arg Lys Leu Ser Leu Asp Lys
625 630 635

<210> 109
<211> 1686
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 109
atgaacagag taggggcagt gttcctatth gtatatgaaa gaaatthttt tttgtctatt 60
gttccagatc gtcacaggac ggaaataaga atgtctagtt cagaaaggtc agaagtcaag 120
tttgacaagc actttaattg gtgggtcccta ttaggtatcg cgthctcatt aagttgctca 180
tggttcggta tctcagcgtc gatggccgtt ggtattgcca gtggagggcc actgcttatt 240
atctatgggt tgataattgc tgctthtttc agtctcatgt gtggtatatc tctgggagat 300
tttgctgcta tcttgccaaa cagcagcgtt ggttcatttt gggttcttaa aatgttgga 360
caagaatcag tcaatttgaa aaccctgag tacgaggacc cttctgacga tgatgaagaa 420
gtgttcctcg agaattattg tcaaactttc aacgtggaag tttcttctaa atttcaaaag 480
gtttcttcca tggttgtagg gttgctgaac tatttcggtg ccattthttac taccgcaagt 540
atctgctcat ctttgtcaat gagctgtatc ggtattcata agttgttgca tccggactac 600
gagttaaagc actggcatgt ttttgtgggt tacgagtgtg tcaatgccgt tttgacactt 660
ttcaacattt attcaactcc gttgccctat atctctcagt ttgggctcta tacgtctcta 720
ttgtctttcg ccatgacttt cattatttgt attgtttcaa gatctgacaa caccgtagac 780
ccatggccca aagcttctaa tatatttggg agctttgata atcaaacagg ctggaattcg 840
tctggaatgg cgthtggtgt cggtttggtc aatccgatct gggcatttgt tggcattgac 900
tctgctacgc acatgattga tgaagtgggt tatagtaagt cacgtthctt agttcccaaa 960

gttattatca ctaccatcat tgtgggcttt gtaactagtt ttatttattg cgttgggtttg 1020
 tttttctgca tcaactgacca aacggcagtc gttgagtcta ttttacctat cgtagaaaata 1080
 ttttaccagg ccactggtaa taggaatctc agtgtcttcc tgcaatgtat gtgtatcaca 1140
 acagggttttg tttcaggcat tgcaagtgga acctggcaaa gtcgaatcct ccaatcattc 1200
 gggaaaagtt acgcaccatt ttataaagag ggttccttgg gaaacaaatc cttgaagaag 1260
 ctagcagtgt tgacacctgg gtttaagtct ccattatatg cccatttttt gtcacaaaata 1320
 tgtgtaacga taattggctg tatatttatg ggatctagta ccgctttcaa cgcaattatc 1380
 actgcatgca tcaccctggt actaatgtcg tacgcagttc cttcttttat attcctgttc 1440
 gttattaaaa aggaaaaatt cattcataga atcgagagtg acgtaaattg tgtcagcagg 1500
 cctaaccgtc gtcgtatgtc tatgattcct catattatat gtattctatg gaccttgttc 1560
 tgccctggat ttttatcttt cccatataca ctaccgggta ctgcaggaaa catgaattac 1620
 acctcagtag tgtatgcagt agttttctgc attatcagca tcgttggttt ccctacatgc 1680
 atctaa 1686

<210> 110
 <211> 561
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 110

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

Phe Leu Ser Ile Val Pro Asp Arg His Arg Thr Glu Ile Arg Met Ser
 20 25 30

Ser Ser Glu Arg Ser Glu Val Lys Phe Asp Lys His Phe Asn Trp Trp
 35 40 45

Ser Leu Leu Gly Ile Ala Phe Ser Leu Ser Cys Ser Trp Val Gly Ile
 50 55 60

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

Ile Tyr Gly Leu Ile Ile Ala Ala Phe Phe Ser Leu Met Cys Gly Ile
 85 90 95

Ser Leu Gly Asp Phe Ala Ala Ile Leu Pro Asn Ser Ser Gly Gly Ser

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

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

Ser Ile Leu Pro Ile Val Glu Ile Phe Tyr Gln Ala Thr Gly Asn Arg
355 360 365

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

Ser Gly Ile Ala Ser Gly Thr Trp Gln Ser Arg Ile Leu Gln Ser Phe
385 390 395 400

Gly Lys Ser Tyr Ala Pro Phe Tyr Lys Glu Gly Ser Leu Gly Asn Lys
405 410 415

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

Tyr Ala His Phe Leu Ser Gln Ile Cys Val Thr Ile Ile Gly Cys Ile
435 440 445

Phe Met Gly Ser Ser Thr Ala Phe Asn Ala Ile Ile Thr Ala Cys Ile
450 455 460

Thr Leu Leu Leu Met Ser Tyr Ala Val Pro Ser Phe Ile Phe Leu Phe
465 470 475 480

Val Ile Lys Lys Glu Lys Phe Ile His Arg Ile Glu Ser Asp Val Asn
485 490 495

Cys Val Ser Arg Pro Asn Arg Arg Arg Met Ser Met Ile Pro His Ile
500 505 510

Ile Cys Ile Leu Trp Thr Leu Phe Cys Leu Val Phe Leu Ser Phe Pro
515 520 525

Tyr Thr Leu Pro Val Thr Ala Gly Asn Met Asn Tyr Thr Ser Val Val
530 535 540

Tyr Ala Val Val Phe Cys Ile Ile Ser Ile Val Val Phe Pro Thr Cys
545 550 555 560

Ile

<210> 111
 <211> 621
 <212> DNA
 <213> *Saccharomyces cerevisiae*

 <400> 111
 atgagtttcc taaacatttt tacttttttc agcgtccttg tgtctggtgc aacagccgtc 60
 agatttgatt tgactaacgt cacttgtaat aacctacatg gacctactg tggtaacctac 120
 gttatggaag tcgttggcca aaatggtaca tttttgggtc aatctacggt tgctggtgcc 180
 gacgttttaa ctgaaagcgc tggtgacgct tgggcaagat atttgggcca ggaaacaaga 240
 ttcctcccaa agttgactac tattgctagc aatgatacga agaacttttc tccactaatc 300
 ttcaccacca atatctacac ttgtaaccct caatccattg gtgatgctat ggttcctttt 360
 gctaacactg ttactggtga aattgaatac aactcctggg cagacaccgc tgataatgct 420
 tccttcataa ccggttttagc taaccaattg ttttaactcta ctcagtatgg cgttcaagtt 480
 gcttcctggt acccaaactt tgcttctggt attttgagca cccaactgt gaacattttc 540
 gctgcgaatg agacattacc agattattgt accgccatcc agttgaaggc cgtttggtcca 600
 ccagacgctg gttttgcttg a 621

<210> 112
 <211> 206
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 112

Met Ser Phe Leu Asn Ile Phe Thr Phe Phe Ser Val Leu Val Ser Val
1 5 10 15

Ala Thr Ala Val Arg Phe Asp Leu Thr Asn Val Thr Cys Asn Asn Leu
20 25 30

His Gly Pro His Cys Gly Thr Tyr Val Met Glu Val Val Gly Gln Asn
35 40 45

Gly Thr Phe Leu Gly Gln Ser Thr Phe Ala Gly Ala Asp Val Leu Thr
50 55 60

Glu Ser Ala Gly Asp Ala Trp Ala Arg Tyr Leu Gly Gln Glu Thr Arg
65 70 75 80

Phe Leu Pro Lys Leu Thr Thr Ile Ala Ser Asn Asp Thr Lys Asn Phe
85 90 95

Ser Pro Leu Ile Phe Thr Thr Asn Ile Tyr Thr Cys Asn Pro Gln Ser
 100 105 110

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

Glu Tyr Asn Ser Trp Ala Asp Thr Ala Asp Asn Ala Ser Phe Ile Thr
 130 135 140

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

Ala Ser Cys Tyr Pro Asn Phe Ala Ser Val Ile Leu Ser Thr Pro Thr
 165 170 175

Val Asn Ile Phe Ala Ala Asn Glu Thr Leu Pro Asp Tyr Cys Thr Ala
 180 185 190

Ile Gln Leu Lys Ala Val Cys Pro Pro Asp Ala Gly Phe Ala
 195 200 205

<210> 113
 <211> 372
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 113
 atgaatatta attattatta ttgttataaa tctatatgct cgtggatttt tttaaataaa 60
 ttagacttac ctgttattta caagacttct tcgtttgaca ttagtccggc ctgtgattct 120
 atgtcttgct cacctgcaat agcccgcgta gaaaaaagcc ttgaccaaaa attcccaatc 180
 gaaaatttgg acttgaaatc tgaaatccca tgtgattcaa tatccggtgg agtccacttc 240
 ttcaacatca atgaacttag aacgacactg accgagctga atgccatcgc taaaccggcg 300
 agcattggag gaagagttat gcccgaagga atgagcacac ccatagcaat cggaatcatg 360
 aatatattat ag 372

<210> 114
 <211> 123
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 114

Met Asn Ile Asn Tyr Tyr Tyr Cys Tyr Lys Ser Ile Cys Ser Trp Ile

1	5	10	15
Phe	Leu	Asn	Lys
	20		25
Leu	Asp	Leu	Pro
			30
Ile	Tyr	Lys	Thr
			35
Asp	Ile	Ser	Pro
	35		40
Ala	Cys	Asp	Ser
			45
Met	Ser	Cys	Ser
			50
Val	Glu	Lys	Ser
			55
Leu	Asp	Gln	Lys
			60
Phe	Pro	Ile	Glu
			65
Asn	Leu	Asp	
			70
Leu	Lys	Ser	Glu
			75
Ile	Pro	Cys	Asp
			80
Ser	Ile	Ser	Gly
			85
Gly	Gly	Val	His
			90
Phe	Asn	Ile	Asn
			95
Ala	Ile		
			100
Ala	Lys	Pro	Ala
			105
Ser	Ile	Gly	Gly
			110
Arg	Val	Met	Pro
			115
Gln	Gly	Met	Ser
			120
Thr	Pro	Ile	Ala
			125
Ile	Gly	Ile	Met
			130
Asn	Ile	Leu	
			135

<210> 115
 <211> 1305
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 115	
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aaatcccagt gggttttcat ctgtttggct attttaatcg ttattgcaag atttgctccg	120
aattttgcaa gagacggagg gttaattaaa ggccaatata gtattgggta cggctgcgtc	180
gcctggattt ttctccaaag tggcctggga atgaaatcaa ggtcactaat ggcaaatatg	240
ttaaattgga gagctcatgc cactattctg gttctgagtt tccttattac ctcgccata	300
gtatatggat tttgttgccg ggtaaaggct gctaattgatc cgaaaataga tgactgggta	360
cttatcggtc taattttgac tgccacttgt ccaacaaccg tggcttcaaa cgttatcatg	420
actacgaatg caggtggaaa tagccttttg tgcgtttgtg aagtattcat tggaaatttg	480
ttgggtgcgt ttattacacc tgcattgggt caaatgttta ctaaccgcgc accatttgca	540
tacggcaacc ctgccactgg aaatggcatt ggtgcgcttt atggccgtgt tatgaaacag	600
gttgggtctct ctgtattcgt acccttggtt gtgggtcagg ttattcaaaa ttgctttccg	660

aagggtactg cttattacct gggctttttg aaaaaatacc atattaaaat tggatcttac 720
atgcttttat tgattatggt tagttcattc tcaactgcct tttatcagga tgcgtttact 780
agcggttctc atgtttgcat catatttctc tgctttttta atttgggaat ttatatattc 840
ttcacgggtc tgtcatactt atgtgcaagg ccatgggttca tcctcaagct tttccctcat 900
gaaccaatag agggcaaatc tacaagattg taccgctatt cgtataatat ctttaggcct 960
ttttattatt caaaggaaga tgcgatttgc attatgtttt gtggcccggc taaaactgca 1020
gcactgggtg tatcactaat tacttcacaa tacggcgata aaaaagaaca cctgggtaag 1080
ttgttggttc ccttggtttt atatcaagtt gagcaagtca tgacggcaaa tttctttgta 1140
agcttggttca aaagatggat acaaaaggac gctcaagcag acggaagcga gtcattctgt 1200
gcaaatgaga atgaggaagt tgatttggaa aagatcatat caattggaac tggtgaaaaat 1260
caatccgttc tgtcgaacaa cgtcccatat acacaaccaa ggtga 1305

<210> 116
<211> 434
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 116

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

Thr Glu Phe Leu Lys Ser Gln Trp Phe Phe Ile Cys Leu Ala Ile Leu
20 25 30

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

Ile Lys Gly Gln Tyr Ser Ile Gly Tyr Gly Cys Val Ala Trp Ile Phe
50 55 60

Leu Gln Ser Gly Leu Gly Met Lys Ser Arg Ser Leu Met Ala Asn Met
65 70 75 80

Leu Asn Trp Arg Ala His Ala Thr Ile Leu Val Leu Ser Phe Leu Ile
85 90 95

Thr Ser Ser Ile Val Tyr Gly Phe Cys Cys Ala Val Lys Ala Ala Asn
100 105 110

Asp Pro Lys Ile Asp Asp Trp Val Leu Ile Gly Leu Ile Leu Thr Ala

Asp Lys Lys Glu His Leu Gly Lys Leu Leu Val Pro Leu Val Leu Tyr
 355 360 365

Gln Val Glu Gln Val Met Thr Ala Asn Phe Phe Val Ser Leu Phe Lys
 370 375 380

Arg Trp Ile Gln Lys Asp Ala Gln Ala Asp Gly Ser Glu Ser Ser Cys
 385 390 395 400

Ala Asn Glu Asn Glu Glu Val Asp Leu Glu Lys Ile Ile Ser Ile Gly
 405 410 415

Thr Gly Glu Asn Gln Ser Val Leu Ser Asn Asn Val Pro Tyr Thr Gln
 420 425 430

Pro Arg

<210> 117
 <211> 2136
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 117
 atgcattgga cgtccatctt gagcgctatt ttgcttttct gcctgtcagg agcaagagca 60
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 aggatttttc aaaaagttac ttgggagtat accagcaagt ctaagcggtc atcaccagta 180
 tgttcttacg aaccagcggt tcaatcaatg ctgtattgta tctatgaaac gttggatgaa 240
 aaaggttatt cgaataaaac cttagaaaaa acatttagta ccatcaaaaa aaactgtgca 300
 agttatagtg atgctcttca gaacatgact aattctgagt tttatgacgt tctaaacaac 360
 ggaacgaggc atatgacgcc ctatgtcaaa ggcagtgcaa acctaacata tccagttgaa 420
 atggatacac agttaagaaa agcctactat catgcattgc atggtttcta tgctaactta 480
 gatgtcggaa acatatatgg tggcattata tgtgcttatt ttgtcgctat catggctttt 540
 gcaggcggtc ttcatcgcat gaattacact ccctttaaaa ctgttctatt gaagcaaaag 600
 cttgtgggat atgtaagggg atacctcact ctacctacca ttggaagcaa acatgcgtca 660
 gatttctctt attttagaat attcacagga tatttaccta caagattaga gggatatcatt 720
 attcttggat atctcgtgct tcataccggt tttttggcat acggttatga atacgatcct 780
 gaaaatataa tattcaagtc tcgtagagtt caagttgctc gatatgtggc agacagaagt 840
 ggtgtactcg cattcgcaca ctttccatta atagttcttt tcgcgggaag aaacaacttt 900

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ctcgagtata tttctggggt taaatatact tccttcatta tgtttcacaa atgggttgga      960
agaatgatgt ttttggatgc tatgattcat ggctctgcat atactagtta tacggtagcg      1020
aataaaactt gggcaacaag taaaaaccga ttatatattggc aattcggggt ggcagcactt      1080
tgtttagctg gcacaatggt tttcttttcc tttgcagtat tcaggaagta tttttatgaa      1140
gcctttcttt ttcttcatat cgtccttggt gcaatgttct tttatgcatg ttgggagcat      1200
gttggttagtt taagtggcat tgagtggata tacactgcta ttgcgatttg gatcgttgac      1260
cggattatta gaattatcaa agcttcttat tttgggtttcc ccaaagcttc cctacaacta      1320
atcgggggatg atctcattcg tttaacagtt aaaaaaccgg caaggccatg gagggccaaa      1380
cctgggcaat atgttttcgt ttcgttttta catccactgt acttctggca gtcacatcca      1440
tttactgttt tggattcagt aagcaagaat ggtgaactgg ttattatcct gaaagaaaaa      1500
aagggagtaa caagacttgt caaaaagtat gtgtgtcgca atggaggtaa gacatctatg      1560
agactagcta tagaagggtcc atatggttct tcatctccgg tcaataatta caataatgta      1620
ttgttactca ctggagggtac cggtttgctt ggacctattg cacatgcaat taaacttgga      1680
aagacgtcag cggctgctgg aaaacaatct gtaaaattag tgattgcagt tagaggattc      1740
gacgtactcg aggcttataa gccggagttg atgtgttttag aaaatctgaa tgtacagctt      1800
cacatctaca acacaatgga agtcccatca ttaacccta gtgatagttt agatatattct      1860
caacaggatg agaaggctga tgaaaaaggc actgttggtg caactacttt agaaaagtct      1920
gccaatccac ttggttttga tgggtgtgtt ttccattgcg ggcgaccaa tggttaaggaa      1980
cttctacatg aagcggctga attgagtggc tcattatctg tggtttgctg tggacctcct      2040
atttttgttg acaaagtgag gaatgaaacc gcaaaaatag ttttagataa gtctgcaaaa      2100
gccattgagt actttgaaga gtatcaatgc tgggtga      2136

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<210> 118
<211> 711
<212> PRT
<213> Saccharomyces cerevisiae

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<400> 118
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Met His Trp Thr Ser Ile Leu Ser Ala Ile Leu Leu Phe Cys Leu Ser
1           5           10           15

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Gly Ala Arg Ala Ser Pro Ala Lys Thr Val Ile Arg Asn Lys Val Pro
          20           25           30

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Leu Leu Val Thr Asn Ala Cys Thr Arg Ile Phe Gln Lys Val Thr Trp
35 40 45

Glu Tyr Thr Ser Lys Ser Lys Arg Ser Ser Pro Val Cys Ser Tyr Glu
50 55 60

Pro Ala Phe Gln Ser Met Leu Tyr Cys Ile Tyr Glu Thr Leu Asp Glu
65 70 75 80

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

Lys Asn Cys Ala Ser Tyr Ser Asp Ala Leu Gln Asn Met Thr Asn Ser
100 105 110

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

Val Lys Gly Ser Ala Asn Leu Thr Tyr Pro Val Glu Met Asp Thr Gln
130 135 140

Leu Arg Lys Ala Tyr Tyr His Ala Leu His Gly Phe Tyr Ala Asn Leu
145 150 155 160

Asp Val Gly Asn Ile Tyr Gly Gly Ile Ile Cys Ala Tyr Phe Val Ala
165 170 175

Ile Met Ala Phe Ala Gly Val Leu His Cys Met Asn Tyr Thr Pro Phe
180 185 190

Lys Thr Val Leu Leu Lys Gln Lys Leu Val Gly Tyr Val Arg Gly Tyr
195 200 205

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

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

Ile Leu Gly Tyr Leu Val Leu His Thr Val Phe Leu Ala Tyr Gly Tyr
245 250 255

Glu Tyr Asp Pro Glu Asn Ile Ile Phe Lys Ser Arg Arg Val Gln Val
260 265 270

Ala Arg Tyr Val Ala Asp Arg Ser Gly Val Leu Ala Phe Ala His Phe
275 280 285

Pro Leu Ile Val Leu Phe Ala Gly Arg Asn Asn Phe Leu Glu Tyr Ile
290 295 300

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

Arg Met Met Phe Leu Asp Ala Met Ile His Gly Ser Ala Tyr Thr Ser
325 330 335

Tyr Thr Val Ala Asn Lys Thr Trp Ala Thr Ser Lys Asn Arg Leu Tyr
340 345 350

Trp Gln Phe Gly Val Ala Ala Leu Cys Leu Ala Gly Thr Met Val Phe
355 360 365

Phe Ser Phe Ala Val Phe Arg Lys Tyr Phe Tyr Glu Ala Phe Leu Phe
370 375 380

Leu His Ile Val Leu Gly Ala Met Phe Phe Tyr Ala Cys Trp Glu His
385 390 395 400

Val Val Ser Leu Ser Gly Ile Glu Trp Ile Tyr Thr Ala Ile Ala Ile
405 410 415

Trp Ile Val Asp Arg Ile Ile Arg Ile Ile Lys Ala Ser Tyr Phe Gly
420 425 430

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

Thr Val Lys Lys Pro Ala Arg Pro Trp Arg Ala Lys Pro Gly Gln Tyr
450 455 460

Val Phe Val Ser Phe Leu His Pro Leu Tyr Phe Trp Gln Ser His Pro
465 470 475 480

Phe Thr Val Leu Asp Ser Val Ser Lys Asn Gly Glu Leu Val Ile Ile
485 490 495

Leu Lys Glu Lys Lys Gly Val Thr Arg Leu Val Lys Lys Tyr Val Cys
500 505 510

Arg Asn Gly Gly Lys Thr Ser Met Arg Leu Ala Ile Glu Gly Pro Tyr
515 520 525

Gly Ser Ser Ser Pro Val Asn Asn Tyr Asn Asn Val Leu Leu Leu Thr
530 535 540

Gly Gly Thr Gly Leu Pro Gly Pro Ile Ala His Ala Ile Lys Leu Gly
545 550 555 560

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

Val Arg Gly Phe Asp Val Leu Glu Ala Tyr Lys Pro Glu Leu Met Cys
580 585 590

Leu Glu Asn Leu Asn Val Gln Leu His Ile Tyr Asn Thr Met Glu Val
595 600 605

Pro Ser Leu Thr Pro Ser Asp Ser Leu Asp Ile Ser Gln Gln Asp Glu
610 615 620

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

Ala Asn Pro Leu Gly Phe Asp Gly Val Val Phe His Cys Gly Arg Pro
645 650 655

Asn Val Lys Glu Leu Leu His Glu Ala Ala Glu Leu Ser Gly Ser Leu
660 665 670

Ser Val Val Cys Cys Gly Pro Pro Ile Phe Val Asp Lys Val Arg Asn
675 680 685

Glu Thr Ala Lys Ile Val Leu Asp Lys Ser Ala Lys Ala Ile Glu Tyr
690 695 700

Phe Glu Glu Tyr Gln Cys Trp
705 710

<210> 119
<211> 1884
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 119

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cctcagttat	ctgaaaaata	caatgccttg	agacagaaca	ggagcctaata	tatccagcag	180
actgaaatca	ttggctctgc	ttacaataaa	tggtacttac	aagcgatttt	acttttgagt	240
gctttcatat	gtggctacgg	ttatggactg	gacggtaaca	tccgttatat	ttacactggg	300
tacgccacat	catcctatag	tgagcattct	ctgctgtcta	caatcaacgt	cattaatgct	360
gtgggtcagt	ccgcttcgca	aatcatatac	gctagggtgt	ctgatgtgtt	tggtagacta	420
taccttttca	ttagtgtgt	catcctatat	gttgtgggta	caattattca	atcacaagct	480
tatgatgttc	aaagatacgc	tgacagtgcc	atcttctaca	atgctggcta	tgtgggtgta	540
atccttattc	ttttgattat	cctatccgat	ttttcatctt	taaagtggag	actgctgtat	600
caatttgtcc	cgacttggcc	ttttatcatc	aacacatgga	ttgctggtaa	tatcacttcc	660
agagccaatc	ctgttgtcaa	ctggctcttg	gatgtaggta	tgtgggcttt	catctttccc	720
ctatcatgtg	ttccaatcgt	tttgtgtatg	ttgcacatgc	aatggagggc	cagaaagact	780
cctgaatggc	acgctttgaa	gggccagaag	tcctattatc	aagaacatgg	ttttathtaag	840
atcttaaagc	aattattttg	gatgttagat	gtcgttgggt	tccttttgat	gggttgttcc	900
ctagggttga	tcttgggtcc	actgaccttg	gctgggtggg	tcaaaactac	ctggaatgat	960
tcaagattga	tcggccccct	tgttcttggc	tttgttttga	tccttatctt	atggatttgg	1020
gaatatcgat	tcgctagaga	tccaattctt	ccatataggc	tggtcaaaga	tagggctgta	1080
tggtcttcta	tggttatttc	tttcctgatt	gattttatct	actatatggc	cgctgattat	1140
ttgtacacgg	ttatgattgt	tgccgtcaat	gaatccgtta	aatctgcaac	cagaattgcc	1200
acattatctt	catttgtctc	tactgtggcc	tctccatttt	tcgctttact	tgtacaaga	1260
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ttattgtacc	actttagagg	tggaagtcag	tcccattcag	gtattattgg	tgcattatgt	1380
gtctgggggt	tgggcactac	tttgttctac	taccagttta	ccgtctctgt	acaatctgcc	1440
gtctctcatg	aaaacatggc	gacagttaca	gctttaaact	ataccctcta	tagaattggg	1500
tctgctgtcg	gttccgcagt	ttccggtgcc	atttggactc	agactttgta	caaacaaatt	1560
ttgaagagaa	tggtgatgt	tgctctagcc	acaactgcct	acgaatctcc	atatactttc	1620
attgaaacct	atacttgggg	tacccacaa	aggaatgcct	taatgaacgc	ttacaaatac	1680
gttcaaagat	tggaactat	cgtggcttta	gtattttgtg	ttcattaat	tgcattctcc	1740

ttatgtctaa gggatcctaa attgactgat actgttgctg tggaatacat cgaggatggc 1800
 gaatatgtcg acacgaaaga caatgatcca attttggatt ggtttgaaaa acttccatca 1860
 aaattcactt ttaaacggga ataa 1884

<210> 120
 <211> 627
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 120

Met Glu Ser Val His Ser Arg Asp Pro Val Lys Glu Glu Lys Lys His
 1 5 10 15

Val Phe Met Gly Met Glu His Glu Leu Asn Pro Glu Thr His Asn Asp
 20 25 30

Ser Asn Ser Asp Ser Tyr Gly Leu Pro Gln Leu Ser Glu Lys Tyr Asn
 35 40 45

Ala Leu Arg Gln Asn Arg Ser Leu Ile Ile Gln Gln Thr Glu Ile Ile
 50 55 60

Gly Ser Ala Tyr Asn Lys Trp Tyr Leu Gln Ala Ile Leu Leu Leu Ser
 65 70 75 80

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

Ile Tyr Thr Gly Tyr Ala Thr Ser Ser Tyr Ser Glu His Ser Leu Leu
 100 105 110

Ser Thr Ile Asn Val Ile Asn Ala Val Val Ser Ala Ala Ser Gln Ile
 115 120 125

Ile Tyr Ala Arg Leu Ser Asp Val Phe Gly Arg Leu Tyr Leu Phe Ile
 130 135 140

Ser Ala Val Ile Leu Tyr Val Val Gly Thr Ile Ile Gln Ser Gln Ala
 145 150 155 160

Tyr Asp Val Gln Arg Tyr Ala Ala Gly Ala Ile Phe Tyr Asn Ala Gly
 165 170 175

Tyr Val Gly Val Ile Leu Ile Leu Leu Ile Ile Leu Ser Asp Phe Ser

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

Leu Val Thr Arg Cys Thr Arg Leu Lys Pro Phe Ile Met Phe Gly Cys
420 425 430

Ala Leu Trp Met Val Ala Met Gly Leu Leu Tyr His Phe Arg Gly Gly
435 440 445

Ser Gln Ser His Ser Gly Ile Ile Gly Ala Leu Cys Val Trp Gly Val
450 455 460

Gly Thr Thr Leu Phe Thr Tyr Pro Val Thr Val Ser Val Gln Ser Ala
465 470 475 480

Val Ser His Glu Asn Met Ala Thr Val Thr Ala Leu Asn Tyr Thr Leu
485 490 495

Tyr Arg Ile Gly Ser Ala Val Gly Ser Ala Val Ser Gly Ala Ile Trp
500 505 510

Thr Gln Thr Leu Tyr Lys Gln Ile Leu Lys Arg Met Gly Asp Val Ala
515 520 525

Leu Ala Thr Thr Ala Tyr Glu Ser Pro Tyr Thr Phe Ile Glu Thr Tyr
530 535 540

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

Val Gln Arg Leu Glu Thr Ile Val Ala Leu Val Phe Cys Val Pro Leu
565 570 575

Ile Ala Phe Ser Leu Cys Leu Arg Asp Pro Lys Leu Thr Asp Thr Val
580 585 590

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

Asp Pro Ile Leu Asp Trp Phe Glu Lys Leu Pro Ser Lys Phe Thr Phe
610 615 620

Lys Arg Glu
625

<210> 121
<211> 222
<212> DNA

<213> Saccharomyces cerevisiae

<400> 121

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gcagtcaata aagttttgac gaaattagaa ccagacgttt ccaaaataga tatatccctt      120
gaaaagcaat tagtagatgt atatactaca cttccttacg attttatttt agaaaagatt      180
aagaaaaccg gaaaggaagt tagatctggc aaacaattgt ga                          222
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<210> 122

<211> 73

<212> PRT

<213> Saccharomyces cerevisiae

<400> 122

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

```
Val Ser Lys Ile Asp Ile Ser Leu Glu Lys Gln Leu Val Asp Val Tyr
          35          40          45
```

```
Thr Thr Leu Pro Tyr Asp Phe Ile Leu Glu Lys Ile Lys Lys Thr Gly
          50          55          60
```

```
Lys Glu Val Arg Ser Gly Lys Gln Leu
65          70
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<210> 123

<211> 1821

<212> DNA

<213> Saccharomyces cerevisiae

<400> 123

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gctgtcaaca aggtcttgtc tgactacagc tctttcacag cttttggagt tacgtttagt      180
tactcaaga ccgccctact ggtggctctg tttttgcagg gttactgtac tggactcgga      240
gggcagattt cgcaatcaat acaaacctat gccgctaaca gttttggaaa gcattctcaa      300
gtaggatcga tcaataccgt caaatcaata gtagcctctg ttgtcgcagt gccatacgca      360
cgtatatctg atcggtttgg acgtatagaa tgctggattht ttgcgcttgt gctctatact      420
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attggagaaa	ttatttctgc	tgctactcca	acgttttccg	gactttttgc	aggtattggt	480
atacaacagt	tcggttattc	tggatttcgt	cttcttgcta	cagcactgac	tggtgatctg	540
tctggattga	gagatcgta	atttgcgatg	aacatatttc	tgattcccgt	gattataaac	600
acatgggtaa	gtggaaatat	tgtagctca	gttgctggta	atgttgacc	atataaatgg	660
cgttggggct	atggaatttt	ttgcatcatt	gtgccatct	ccacccta	attggtcctt	720
ccctatgtgt	atgctcagta	catttcctgg	cgcagcggta	agttaccacc	attaaaattg	780
aaagaaaaag	gacagaccct	gcgtcaaacg	ctctggaaat	ttgcggatga	cataaactta	840
attggagtca	ttcttttcac	tgctttctta	gttttagtat	tattacctct	cacaatagct	900
ggtaggagcca	cctccaaatg	gagagaggg	cacattattg	caatgattgt	ggttggtagc	960
tgcttagggt	ttatctttct	aatttgggaa	ttaaaatttg	ctaagaatcc	atttatccca	1020
cgagtatatc	taggtgatcc	aaccatctac	gttgcatctg	taatggaatt	tgtatggcgt	1080
ctaggtttgc	agattgagtt	agagtatttg	gtcacctgt	taatggtagc	attcggagaa	1140
tcaacattaa	gtgcgcagcg	gatagctcag	ctttacaatt	ttctacagtc	atgcactaat	1200
attgttgtcg	gcattatgct	gcatttctat	cctcatccga	aagtctttgt	agtcgctggg	1260
tcgcttcttg	gtgtcatcgg	aatgggtctt	ttgtacaaat	acagggtggt	atatgacggg	1320
atttcgggtc	ttattggcgc	tgagattgtg	gtcgggtatg	ctgggtggtat	gatacgtttt	1380
cctatgtgga	cgctagtga	cgcttcaacc	accacaatg	agatggcaac	tgtcactggg	1440
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tggactcagc	gtctggcaaa	ggagttgata	cagcgactcg	gctctagttt	agggatggca	1560
atctacaaat	caccactcaa	ttatctaaaa	aaatacccta	ttggatcaga	ggttcgtggt	1620
cagatgatag	aatcctattc	gaagattcaa	cgcttattga	taattgtgtc	catttcgttt	1680
gcggctttca	atgctgttct	ctgttttttc	ttgcgtggct	ttactgtaaa	caagaagcaa	1740
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cgtcgtgtaa	ttggatattg	a				1821

<210> 124
 <211> 606
 <212> PRT
 <213> *Saccharomyces cerevisiae*

 <400> 124

Met	Leu	Glu	Thr	Asp	His	Ser	Arg	Asn	Asp	Asn	Leu	Asp	Asp	Lys	Ser
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Thr Val Cys Tyr Ser Glu Lys Thr Asp Ser Asn Val Glu Lys Ser Thr
20 25 30

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

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

Ala Leu Leu Val Ala Leu Phe Leu Gln Gly Tyr Cys Thr Gly Leu Gly
65 70 75 80

Gly Gln Ile Ser Gln Ser Ile Gln Thr Tyr Ala Ala Asn Ser Phe Gly
85 90 95

Lys His Ser Gln Val Gly Ser Ile Asn Thr Val Lys Ser Ile Val Ala
100 105 110

Ser Val Val Ala Val Pro Tyr Ala Arg Ile Ser Asp Arg Phe Gly Arg
115 120 125

Ile Glu Cys Trp Ile Phe Ala Leu Val Leu Tyr Thr Ile Gly Glu Ile
130 135 140

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

Ile Gln Gln Phe Gly Tyr Ser Gly Phe Arg Leu Leu Ala Thr Ala Leu
165 170 175

Thr Gly Asp Leu Ser Gly Leu Arg Asp Arg Thr Phe Ala Met Asn Ile
180 185 190

Phe Leu Ile Pro Val Ile Ile Asn Thr Trp Val Ser Gly Asn Ile Val
195 200 205

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

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

Pro Tyr Val Tyr Ala Gln Tyr Ile Ser Trp Arg Ser Gly Lys Leu Pro
245 250 255

Pro Leu Lys Leu Lys Glu Lys Gly Gln Thr Leu Arg Gln Thr Leu Trp
260 265 270

Lys Phe Ala Asp Asp Ile Asn Leu Ile Gly Val Ile Leu Phe Thr Ala
275 280 285

Phe Leu Val Leu Val Leu Leu Pro Leu Thr Ile Ala Gly Gly Ala Thr
290 295 300

Ser Lys Trp Arg Glu Gly His Ile Ile Ala Met Ile Val Val Gly Gly
305 310 315 320

Cys Leu Gly Phe Ile Phe Leu Ile Trp Glu Leu Lys Phe Ala Lys Asn
325 330 335

Pro Phe Ile Pro Arg Val Tyr Leu Gly Asp Pro Thr Ile Tyr Val Ala
340 345 350

Leu Leu Met Glu Phe Val Trp Arg Leu Gly Leu Gln Ile Glu Leu Glu
355 360 365

Tyr Leu Val Thr Val Leu Met Val Ala Phe Gly Glu Ser Thr Leu Ser
370 375 380

Ala Gln Arg Ile Ala Gln Leu Tyr Asn Phe Leu Gln Ser Cys Thr Asn
385 390 395 400

Ile Val Val Gly Ile Met Leu His Phe Tyr Pro His Pro Lys Val Phe
405 410 415

Val Val Ala Gly Ser Leu Leu Gly Val Ile Gly Met Gly Leu Leu Tyr
420 425 430

Lys Tyr Arg Val Val Tyr Asp Gly Ile Ser Gly Leu Ile Gly Ala Glu
435 440 445

Ile Val Val Gly Ile Ala Gly Gly Met Ile Arg Phe Pro Met Trp Thr
450 455 460

Leu Val His Ala Ser Thr Thr His Asn Glu Met Ala Thr Val Thr Gly
465 470 475 480

Leu Leu Met Ser Val Tyr Gln Ile Gly Asp Ala Val Gly Ala Ser Ile

485	490	495	
Ala Gly Ala Ile Trp Thr Gln Arg Leu Ala Lys Glu Leu Ile Gln Arg			
500	505	510	
Leu Gly Ser Ser Leu Gly Met Ala Ile Tyr Lys Ser Pro Leu Asn Tyr			
515	520	525	
Leu Lys Lys Tyr Pro Ile Gly Ser Glu Val Arg Val Gln Met Ile Glu			
530	535	540	
Ser Tyr Ser Lys Ile Gln Arg Leu Leu Ile Ile Val Ser Ile Ser Phe			
545	550	555	560
Ala Ala Phe Asn Ala Val Leu Cys Phe Phe Leu Arg Gly Phe Thr Val			
565	570	575	
Asn Lys Lys Gln Ser Leu Ser Ala Glu Glu Arg Glu Lys Glu Lys Leu			
580	585	590	
Lys Ile Lys Gln Gln Ser Trp Leu Arg Arg Val Ile Gly Tyr			
595	600	605	
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<212>	DNA		
<213>	<i>Saccharomyces cerevisiae</i>		
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tctccagcac cttcttacat tgaattgata gatccaggtg tgcataacat cgagatttac			180
gcagaaatgt acaaccgccc gatctaccgt gtcgcattat tcttctcact tttcctcatt			240
gcctatgctt acggattaga tggtaatatc cgttacactt tccaggcgta cgcgacttcg			300
tcgtactccc agcactcgct gctatcgacc gtcaactgta ttaagacggt tattgcggct			360
gtaggccaga tcttctttgc cagattatca gatatcttcg gcagattttc cattatgatt			420
gtcagtatca ttttttatag catggggacc atcattgagt cgcaagcggt gaatattaca			480
agatttgcag ttggtggttg tttttaccaa ttgggtctta ccggtattat tctaattttg			540
gaagttattg cttctgactt ttccaacttg aactggaggt tgtagcctt attcattcca			600
gctttaccat ttatcatcaa cacctggatt agcgggaacg taacaagtgc catagatgct			660

aattggaaat ggggtattgg tatgtgggct tttatactgc cgctagcttg tattccgctt	720
ggaatttgta tggtgcacat gaggtattta gcaagaaagc atgctaaaga tagattgaag	780
cccaggttcg aagcgctaaa caaattgaag tggaagtcct tttgtataga catcgcatth	840
tggaaattgg atatcattgg aatgttatta attactgtat ttttcgggtg tgtattgggt	900
ccattcacct tagcgggtgg tttgaaagag gaatggaaaa ctgcgcatat tattgtccct	960
gaagtcattg gttgggttgt agtgttacca ctgtacatgc tatgggaaat aaagtactcg	1020
agacatccat tgacaccttg ggacttgatt caagatagag gtatcttttt cgctctactc	1080
atcgcattht ttatcaattt taactgggtat atgcaagggtg attacatgta tactgtacta	1140
gtcgttgacg ttcattgaatc cataaagtcc gctacaagaa ttacctcctt gtattcattt	1200
gtttctgtta tcgttggtac aatcctcggg ttcatactga tttaaagttag aaggactaag	1260
ccttttatta tatttggcat ttcttggttg atcgtctcat ttgggttgct ggtccattac	1320
cgtggtgact ccggtgctca ttccggtatc attggctctt tgtgtctatt aggtttcggg	1380
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agaatggcgg tagtaacctc attatacctt gccacttata atattgggtc tgcatttggt	1500
agttctgtta gcggagctgt ctggactaat atcctacca aagaaatttc aaaaagaatt	1560
tccgatccaa ccttagctgc acaagcgtac ggttctccat ttacattcat tacaacttat	1620
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ttatgtatca taggtttggt attctgcttt cctttgttag gttgcgcatt catgttgaga	1740
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acaagcagta aagataggaa agattaa	1887

<210> 126
 <211> 628
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 126

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Val	Val	Val	Pro	Glu	Met	Leu	Glu	Lys	Glu	Val	Gly	Ala	Lys	Val	Asp
			20					25					30		

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

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

Ser Phe Cys Ile Asp Ile Ala Phe Trp Lys Leu Asp Ile Ile Gly Met
275 280 285

Leu Leu Ile Thr Val Phe Phe Gly Cys Val Leu Val Pro Phe Thr Leu
290 295 300

Ala Gly Gly Leu Lys Glu Glu Trp Lys Thr Ala His Ile Ile Val Pro
305 310 315 320

Glu Val Ile Gly Trp Val Val Val Leu Pro Leu Tyr Met Leu Trp Glu
325 330 335

Ile Lys Tyr Ser Arg His Pro Leu Thr Pro Trp Asp Leu Ile Gln Asp
340 345 350

Arg Gly Ile Phe Phe Ala Leu Leu Ile Ala Phe Phe Ile Asn Phe Asn
355 360 365

Trp Tyr Met Gln Gly Asp Tyr Met Tyr Thr Val Leu Val Val Ala Val
370 375 380

His Glu Ser Ile Lys Ser Ala Thr Arg Ile Thr Ser Leu Tyr Ser Phe
385 390 395 400

Val Ser Val Ile Val Gly Thr Ile Leu Gly Phe Ile Leu Ile Lys Val
405 410 415

Arg Arg Thr Lys Pro Phe Ile Ile Phe Gly Ile Ser Cys Trp Ile Val
420 425 430

Ser Phe Gly Leu Leu Val His Tyr Arg Gly Asp Ser Gly Ala His Ser
435 440 445

Gly Ile Ile Gly Ser Leu Cys Leu Leu Gly Phe Gly Ala Gly Ser Phe
450 455 460

Thr Tyr Val Thr Gln Ala Ser Ile Gln Ala Ser Ala Lys Thr His Ala
465 470 475 480

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

Ser Ala Phe Gly Ser Ser Val Ser Gly Ala Val Trp Thr Asn Ile Leu
500 505 510

Pro Lys Glu Ile Ser Lys Arg Ile Ser Asp Pro Thr Leu Ala Ala Gln
515 520 525

Ala Tyr Gly Ser Pro Phe Thr Phe Ile Thr Thr Tyr Thr Trp Gly Thr
530 535 540

Pro Glu Arg Ile Ala Leu Val Met Ser Tyr Arg Tyr Val Gln Lys Ile
545 550 555 560

Leu Cys Ile Ile Gly Leu Val Phe Cys Phe Pro Leu Leu Gly Cys Ala
565 570 575

Phe Met Leu Arg Asn His Lys Leu Thr Asp Ser Ile Ala Leu Glu Gly
580 585 590

Asn Asp His Leu Glu Ser Lys Asn Thr Phe Glu Ile Glu Glu Lys Glu
595 600 605

Glu Ser Phe Leu Lys Asn Lys Phe Phe Thr His Phe Thr Ser Ser Lys
610 615 620

Asp Arg Lys Asp
625

<210> 127
<211> 1914
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 127
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atgaaagata aattaaaggg aacaaaatca ttgattattc gtaagtctga gctaattggct 180
aaaaagtatg atacttggca attaaaagct atattcctgt tttctgcatt catttgcact 240
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tcacaggtga tctttggagg gttatcagat atctttggaa ggctaacggt gtttcttgta 420
tccattgtac ttacattgt gggtaacaata attcaatctc aagcatatga tgtccagagg 480
tatgctgctg gagctgtctt ttattatgtg ggacttgctg gtgttatgct acaggttgtt 540
ttgatgttgt ctgataattc ttcattaaaa tggaggctat ttacacatt gataccttca 600

tgccctcga ttatcactac gtgggtctca ggtagtgtag tggaggcagc aaacccgtta	660
gagaactggc cgtggaatat tgctatgtgg gcgttcattt tccctctatg ctgtatccca	720
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gtaccactca ctcttgctgg tggcgtctct acaaattgga gaaattcaaa gattatcggg	960
ccctttgtgc ttggctttgt cctgggtcca ggcttcatat attgggaaag tcgacttgct	1020
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attatgtttt ttatctgctt tgtatatcaa atggctgctg ggtatctcta caccattcta	1140
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gtgactgctg ttgttgctcc atttctgggg ctcatcgta cgagatcatc tagattgaag	1260
tcgtatatatta tttttggtgg ctcaactttat ttcattacta tgggactatt ttaccgctac	1320
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agttgtttat tcgattatcc tacaattggt tctattcagt cggtaacatc ccatgagaat	1440
atggctactg tcacagcatt aaactataca gttttcagaa taggtggagc agttgcagct	1500
gccatttccg gtgccatatg gacgcagtca ttgtacccta aattattgca ctacatggga	1560
gacgctgacc tggctacagc agcatatggc tcaccactaa cttttattct ttccaatccc	1620
tggggacttc cagttaggtc tgcgatgggt gaagcttaca gacacgttca aaaatacgaa	1680
gttattgttg cgcttgattt ttcagcgcct atgttccttc taacattctg cgtaagagat	1740
cctcggttga ctgaagattt tgcccaaaag ttacctgaca gagaatatgt ccaaaccaag	1800
gaagatgatc ctatcaatga ctggatcgcg aaacgttttg caaaggcctt aggaggtcat	1860
aagaaagatt taaaaaacc caacaggata tgtgttcgaa aaaatgatct ctga	1914

<210> 128
 <211> 637
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 128

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

Asp Asp Ser Ser Pro Arg Asp Glu Met Lys Asp Lys Leu Lys Gly Thr
35 40 45

Lys Ser Leu Ile Ile Arg Lys Ser Glu Leu Met Ala Lys Lys Tyr Asp
50 55 60

Thr Trp Gln Leu Lys Ala Ile Phe Leu Phe Ser Ala Phe Ile Cys Thr
65 70 75 80

Phe Ala Tyr Gly Leu Asp Ser Ser Ile Arg Gly Thr Tyr Met Thr Tyr
85 90 95

Ala Met Asn Ser Tyr Ser Ala His Ser Leu Ile Ser Thr Val Ser Val
100 105 110

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

Ser Asp Ile Phe Gly Arg Leu Thr Leu Phe Leu Val Ser Ile Val Leu
130 135 140

Tyr Ile Val Gly Thr Ile Ile Gln Ser Gln Ala Tyr Asp Val Gln Arg
145 150 155 160

Tyr Ala Ala Gly Ala Val Phe Tyr Tyr Val Gly Leu Val Gly Val Met
165 170 175

Leu Gln Val Val Leu Met Leu Ser Asp Asn Ser Ser Leu Lys Trp Arg
180 185 190

Leu Phe Tyr Thr Leu Ile Pro Ser Trp Pro Ser Ile Ile Thr Thr Trp
195 200 205

Val Ser Gly Ser Val Val Glu Ala Ala Asn Pro Leu Glu Asn Trp Ser
210 215 220

Trp Asn Ile Ala Met Trp Ala Phe Ile Phe Pro Leu Cys Cys Ile Pro
225 230 235 240

Leu Ile Leu Cys Met Leu His Met Arg Trp Lys Val Arg Asn Asp Val
245 250 255

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

Leu Val Gln Met Leu Val Gln Leu Phe Trp Lys Leu Asp Val Val Gly
275 280 285

Val Leu Leu Phe Thr Ala Gly Val Gly Cys Ile Leu Val Pro Leu Thr
290 295 300

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

Pro Phe Val Leu Gly Phe Val Leu Val Pro Gly Phe Ile Tyr Trp Glu
325 330 335

Ser Arg Leu Ala Leu Val Pro Phe Ala Pro Phe Lys Leu Leu Lys Asp
340 345 350

Arg Gly Val Trp Ala Pro Leu Gly Ile Met Phe Phe Ile Cys Phe Val
355 360 365

Tyr Gln Met Ala Ala Gly Tyr Leu Tyr Thr Ile Leu Val Val Ala Val
370 375 380

Asp Glu Ser Ala Ser Ser Ala Thr Arg Ile Ile Asn Leu Tyr Ser Phe
385 390 395 400

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

Ser Arg Leu Lys Ser Tyr Ile Ile Phe Gly Gly Ser Leu Tyr Phe Ile
420 425 430

Thr Met Gly Leu Phe Tyr Arg Tyr Arg Ser Gly Gln Asp Ala Asp Gly
435 440 445

Gly Ile Ile Ala Gly Met Val Ile Trp Gly Leu Ser Ser Cys Leu Phe
450 455 460

Asp Tyr Pro Thr Ile Val Ser Ile Gln Ser Val Thr Ser His Glu Asn
465 470 475 480

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

Ala Val Ala Ala Ala Ile Ser Gly Ala Ile Trp Thr Gln Ser Leu Tyr

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Pro Lys Leu Leu His Tyr Met Gly Asp Ala Asp Leu Ala Thr Ala Ala			
515	520	525	
Tyr Gly Ser Pro Leu Thr Phe Ile Leu Ser Asn Pro Trp Gly Thr Pro			
530	535	540	
Val Arg Ser Ala Met Val Glu Ala Tyr Arg His Val Gln Lys Tyr Glu			
545	550	555	560
Val Ile Val Ala Leu Val Phe Ser Ala Pro Met Phe Leu Leu Thr Phe			
565	570	575	
Cys Val Arg Asp Pro Arg Leu Thr Glu Asp Phe Ala Gln Lys Leu Pro			
580	585	590	
Asp Arg Glu Tyr Val Gln Thr Lys Glu Asp Asp Pro Ile Asn Asp Trp			
595	600	605	
Ile Ala Lys Arg Phe Ala Lys Ala Leu Gly Gly His Lys Lys Asp Leu			
610	615	620	
Gln Asn Pro Asn Arg Ile Cys Val Arg Lys Asn Asp Leu			
625	630	635	
<210> 129			
<211> 3201			
<212> DNA			
<213> Saccharomyces cerevisiae			
<400> 129			
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ggtgccaatt caaaggacta tacggagcat ttgccggatg ctgtagattt tgaagatgaa			180
gatgaacttg ctgatgacga tgacgatttg ccagaagaat ctgatgctaa tttgcatcca			240
gctatgatga ctatggg'gcg gtatgatgat gtaaacgaga acggtgccgt actcggatc			300
gactcaaata gtttgaatat gcaactgcct gaaattaatg gtgatttgtc tcaacagttt			360
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<211> 1066
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 130

Met Val Lys Gln Gln Gly Ser Gly Lys Thr Asn Leu Ala Asn Glu Asp
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20 25 30

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

Glu His Leu Pro Asp Ala Val Asp Phe Glu Asp Glu Asp Glu Leu Ala
50 55 60

Asp Asp Asp Asp Asp Leu Pro Glu Glu Ser Asp Ala Asn Leu His Pro
65 70 75 80

Ala Met Met Thr Met Gly Ala Tyr Asp Asp Val Asn Glu Asn Gly Ala
85 90 95

Val Leu Gly Ile Asp Ser Asn Ser Leu Asn Met Gln Leu Pro Glu Ile
100 105 110

Asn Gly Asp Leu Ser Gln Gln Phe Ile Leu Glu Asp Asp Gly Gly Thr
115 120 125

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

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

Ile Gly His Ser Gln Leu Ser Ile Gly Gly Val Asn Gly Asn Asp Met
165 170 175

Ser Ile Asn Gly Gly Phe Ile Met Glu Pro Asp Met Ser Asp Gly Lys
180 185 190

His Lys Lys Ala Thr Lys Leu Asp Leu Ile Asn His Glu Lys Tyr Leu
195 200 205

Leu Lys Lys Tyr Phe Pro Asp Phe Glu Lys Gly Lys Ile Leu Lys Trp
210 215 220

Asn Lys Leu Ile Tyr Arg Arg Ser Val Pro Tyr His Trp His Ser Glu
225 230 235 240

Ile Ser Arg Val Lys Lys Pro Phe Met Pro Leu Asn Leu Lys Phe Lys
245 250 255

Val Gln Gln Asp Asp Lys Arg Leu Phe Asn Ser Arg Thr Ile Ser Tyr
260 265 270

Val Ala Pro Ile Tyr Gln Gly Lys Asn Asn Leu Leu Gln Ser Asn Ser
275 280 285

Ser Ala Ser Arg Arg Gly Leu Ile His Val Ser Ile Asp Glu Leu Phe
290 295 300

Pro Ile Lys Glu Gln Gln Lys Lys Arg Lys Ile Ile His Asp Glu Lys
305 310 315 320

Thr Ile Ser Glu Asp Leu Leu Ile Ala Thr Asp Asp Trp Asp Gln Glu
325 330 335

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

Ser Met Thr Pro Asn Leu Lys Phe Ser Gly Gly Tyr Lys Leu Lys Ser
355 360 365

Leu Ile Glu Asp Val Ala Glu Asp Trp Gln Trp Asp Glu Asp Met Ile
370 375 380

Ile Asp Ala Lys Leu Lys Glu Ser Lys His Ala Glu Leu Asn Met Asn
385 390 395 400

Asp Glu Lys Leu Leu Leu Met Ile Glu Lys Thr Asn Asn Leu Ala Gln
405 410 415

Gln Lys Gln Gln Leu Asp Ser Ser Asn Leu Ile Leu Pro Leu Asn Glu
420 425 430

Thr Ile Leu Gln Gln Lys Phe Asn Leu Ser Asn Asp Asp Lys Tyr Gln
435 440 445

Ile Leu Lys Lys Thr His Gln Thr Lys Val Arg Ser Thr Ile Ser Asn
450 455 460

Leu Asn Ile Gln His Ser Gln Pro Ala Ile Asn Leu Gln Ser Pro Phe
465 470 475 480

Tyr Lys Val Ala Val Pro Arg Tyr Gln Leu Arg His Phe His Arg Glu
485 490 495

Asn Phe Gly Ser His Ile Arg Pro Gly Thr Lys Ile Val Phe Ser Lys
500 505 510

Leu Lys Ala Arg Lys Arg Lys Arg Asp Lys Gly Lys Asp Val Lys Glu
515 520 525

Ser Phe Ser Thr Ser Gln Asp Leu Thr Ile Gly Asp Thr Ala Pro Val
530 535 540

Tyr Leu Met Glu Tyr Ser Glu Gln Thr Pro Val Ala Leu Ser Lys Phe
545 550 555 560

Gly Met Ala Asn Lys Leu Ile Asn Tyr Tyr Arg Lys Ala Asn Glu Gln
565 570 575

Asp Thr Leu Arg Pro Lys Leu Pro Val Gly Glu Thr His Val Leu Gly
580 585 590

Val Gln Asp Lys Ser Pro Phe Trp Asn Phe Gly Phe Val Glu Pro Gly
595 600 605

His Ile Val Pro Thr Leu Tyr Asn Asn Met Ile Arg Ala Pro Val Phe
610 615 620

Lys His Asp Ile Ser Gly Thr Asp Phe Leu Leu Thr Lys Ser Ser Gly
625 630 635 640

Phe Gly Ile Ser Asn Arg Phe Tyr Leu Arg Asn Ile Asn His Leu Phe
645 650 655

Thr Val Gly Gln Thr Phe Pro Val Glu Glu Ile Pro Gly Pro Asn Ser
660 665 670

Arg Lys Val Thr Ser Met Lys Ala Thr Arg Leu Lys Met Ile Ile Tyr
675 680 685

Arg Ile Leu Asn His Asn His Ser Lys Ala Ile Ser Ile Asp Pro Ile
690 695 700

Ala Lys His Phe Pro Asp Gln Asp Tyr Gly Gln Asn Arg Gln Lys Val
705 710 715 720

Lys Glu Phe Met Lys Tyr Gln Arg Asp Gly Pro Glu Lys Gly Leu Trp
725 730 735

Arg Leu Lys Asp Asp Glu Lys Leu Leu Asp Asn Glu Ala Val Lys Ser
740 745 750

Leu Ile Thr Pro Glu Gln Ile Ser Gln Val Glu Ser Met Ser Gln Gly
755 760 765

Leu Gln Phe Gln Glu Asp Asn Glu Ala Tyr Asn Phe Asp Ser Lys Leu
770 775 780

Lys Ser Leu Glu Glu Asn Leu Leu Pro Trp Asn Ile Thr Lys Asn Phe

785		790		795		800
Ile Asn Ser Thr Gln Met Arg Ala Met Ile Gln Ile His Gly Val Gly	805	810	815			
Asp Pro Thr Gly Cys Gly Glu Gly Phe Ser Phe Leu Lys Thr Ser Met	820	825	830			
Lys Gly Gly Phe Val Lys Ser Gly Ser Pro Ser Ser Asn Asn Asn Ser	835	840	845			
Ser Asn Lys Lys Gly Thr Asn Thr His Ser Tyr Asn Val Ala Gln Gln	850	855	860			
Gln Lys Ala Tyr Asp Glu Glu Ile Ala Lys Thr Trp Tyr Thr His Thr	865	870	875			880
Lys Ser Leu Ser Ile Ser Asn Pro Phe Glu Glu Met Thr Asn Pro Asp	885	890	895			
Glu Ile Asn Gln Thr Asn Lys His Val Lys Thr Asp Arg Asp Asp Lys	900	905	910			
Lys Ile Leu Lys Ile Val Arg Lys Lys Arg Asp Glu Asn Gly Ile Ile	915	920	925			
Gln Arg Gln Thr Ile Phe Ile Arg Asp Pro Arg Val Ile Gln Gly Tyr	930	935	940			
Ile Lys Ile Lys Glu Gln Asp Lys Glu Asp Val Asn Lys Leu Leu Glu	945	950	955			960
Glu Asp Thr Ser Lys Ile Asn Asn Leu Glu Glu Leu Glu Lys Gln Lys	965	970	975			
Lys Leu Leu Gln Leu Glu Leu Ala Asn Leu Glu Lys Ser Gln Gln Arg	980	985	990			
Arg Ala Ala Arg Gln Asn Ser Lys Arg Asn Gly Gly Ala Thr Arg Thr	995	1000	1005			
Glu Asn Ser Val Asp Asn Gly Ser Asp Leu Ala Gly Val Thr Asp	1010	1015	1020			

Gly Lys Ala Ala Arg Asn Lys Gly Lys Asn Thr Thr Arg Arg Cys
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Ala Thr Cys Gly Gln Ile Gly His Ile Arg Thr Asn Lys Ser Cys
 1040 1045 1050

Pro Met Tyr Ser Ser Lys Asp Asn Pro Ala Ser Pro Lys
 1055 1060 1065

<210> 131
 <211> 2085
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 131
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<210> 132
<211> 694
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 132

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

Ile Ala Ile Asp Ala Cys Ala Lys Glu Leu Glu Ser His Lys Phe Asp
35 40 45

Thr Asp Val Lys Gly Arg His Ala Thr Leu Cys Thr Tyr Glu Pro Ala
50 55 60

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

Lys Ser Lys Lys Ile Phe Glu Lys Thr Phe Ser Lys Ile Asn Gln Tyr
85 90 95

Cys His Asp Tyr His Lys Asp Glu Val Val Ser Asn Glu Glu Tyr Tyr
100 105 110

Arg Ile Phe Ala Asn Ala Ser Leu Phe Ile Arg Pro Leu Asp Glu Val
115 120 125

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

Arg Trp Val Trp Ala Tyr Phe Gly Pro Leu Asp Asn Ile Asp Lys Gly
145 150 155 160

Asn Val Tyr Gly Val Thr Ile Cys Leu Tyr Trp Ile Gly Val Leu Phe
165 170 175

Ile Ala Ala Val Tyr His Phe Leu Asn Phe Ser Arg Leu Lys Gln Thr
180 185 190

Val Phe Lys Asn Lys Val Ser Ala Phe Leu Arg Gly His Tyr Val Leu
195 200 205

Pro Ala Leu Val His Asn His Ala Met Ser Val Gly Arg Trp Phe Phe
210 215 220

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

Val Leu Leu His Gly Phe Leu Leu Ser Ser Tyr Asn Phe Asp His Asn
245 250 255

Glu Leu Leu Ser Asp Arg Arg Ser Gln Val Leu Ile Phe Leu Ser Asp
260 265 270

Arg Ala Gly Ile Leu Ala Phe Ala His Phe Pro Leu Ile Val Leu Phe
275 280 285

Gly Gly Lys Asn Ser Thr Met Thr Trp Leu Thr Gly Ile Arg Tyr Thr
290 295 300

Ala Phe Ile Thr Tyr His Lys Trp Leu Gly Arg Phe Met Leu Val Asp
305 310 315 320

Cys Thr Ile His Ala Ile Gly Tyr Thr Tyr His Ala Tyr Ile Glu Asn

Asp Ser His Gln Met Ile Lys Phe Val Trp Ser Val Arg Asn Leu Asp
565 570 575

Leu Leu Glu Val Tyr Arg Lys Glu Ile Met Val Leu Lys Glu Leu Asn
580 585 590

Ile Asp Thr Lys Ile Tyr Phe Thr Gly Glu Arg Lys Asp Glu Ser Asn
595 600 605

Thr Glu Glu Gly Ala Ile Ala Asn Met Ser Thr Glu Gly Arg Leu Leu
610 615 620

Thr Thr Ser Lys Ser Ala Glu Met Ile Thr Asp Phe Gly Arg Pro Asn
625 630 635 640

Ile Asp Glu Ile Ile Glu Glu Ala Val Ser Gly Ala Lys Ser Leu Leu
645 650 655

Val Thr Cys Cys Gly Ser Glu Gly Phe Val Asp Lys Thr Arg Glu Leu
660 665 670

Thr Ala Lys Arg Val Leu Glu His Gly Asp Lys Trp Ile Glu Tyr Val
675 680 685

Glu Glu Phe Gln Asn Trp
690

<210> 133
<211> 2139
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 133
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tcctatataa atactctgaa gtggtcattt gatagctccg tcgtaccggg tttctatttct 180
accatatgct cttattcacc agcgtttgat acttggtcac tttgtatctt caattcgctt 240
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acatccattc gattcgatcg tgagacaaga tctagatgga tacgagcttt tcatgcgcat 480
gcctataatt tagatatcag cagtgtttat ggtgcatatt taacttacta cttcgtcata 540

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catattttgc	aatcttttaa	tggtaaatta	caactccgag	tggccattga	gggaccttat	1620
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gaaaacgcaa	taaaaagtac	gccgcctgga	gattcattag	cggtcgtgtg	ctgcggccct	2040
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<210> 134
 <211> 712
 <212> PRT

<213> Saccharomyces cerevisiae

<400> 134

Met His Arg Thr Leu Leu Phe Leu Thr Trp Leu Ile Ser Leu Thr Lys
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Ala Phe Asn Ile Lys Leu Pro His Thr Glu Lys Lys Asp His Leu Glu
20 25 30

Ser Asn Ala Val Leu Ala Cys Ala Ser Tyr Ile Asn Thr Leu Lys Trp
35 40 45

Ser Phe Asp Ser Ser Val Val Pro Gly Phe Tyr Ser Thr Ile Cys Ser
50 55 60

Tyr Ser Pro Ala Phe Asp Thr Trp Ser Leu Cys Ile Phe Asn Ser Leu
65 70 75 80

Thr Asp Gln Ile Ile Pro Met Asp Asn Thr Ser Phe Glu Glu Ser Leu
85 90 95

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

Ile Ser Leu Glu Gln Tyr Tyr Ser Ser Leu Asn Asn Ala Ser Ser His
115 120 125

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

Val Asp Arg Glu Thr Arg Ser Arg Trp Ile Arg Ala Phe His Ala His
145 150 155 160

Ala Tyr Asn Leu Asp Ile Ser Ser Val Tyr Gly Ala Tyr Leu Thr Tyr
165 170 175

Tyr Phe Val Ile Val Gly Ile Ile Ala Val Phe Phe His Met Ser His
180 185 190

Tyr Asn Gly Leu Asn Arg Ala Leu Phe Ala Ser Arg Phe Val Asn Tyr
195 200 205

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

Asn His Phe Lys Phe Leu Asn Val Glu Val Phe Thr Gly Leu Met Pro
 225 230 235 240

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

Ile Phe Leu Ser Ile Ser Tyr Ile Ile Asp Pro Tyr Asn Leu Ile Phe
 260 265 270

Asn Ser His Leu Ser Gln Phe Thr Arg Leu Leu Ala Asp Arg Ser Gly
 275 280 285

Ile Leu Ala Phe Thr Gln Phe Pro Leu Ile Ile Ile Phe Thr Ala Arg
 290 295 300

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

Ser Phe His Lys Trp Ile Gly Arg Ile Met Val Leu Asn Ala Thr Ile
 325 330 335

His Ser Leu Ser Tyr Ser Leu Phe Ala Ile Ile Asn His Ala Phe Lys
 340 345 350

Ile Ser Asn Lys Gln Leu Tyr Trp Lys Phe Gly Ile Ala Ser Ile Thr
 355 360 365

Val Leu Cys Val Leu Leu Val Leu Ser Leu Gly Ile Val Arg Lys Arg
 370 375 380

His Tyr Glu Phe Phe Leu Tyr Thr His Ile Ile Leu Ala Leu Leu Phe
 385 390 395 400

Phe Tyr Cys Cys Trp Gln His Val Lys Ile Phe Asn Gly Trp Lys Glu
 405 410 415

Trp Ile Val Val Ser Leu Leu Ile Trp Gly Leu Glu Lys Leu Phe Arg
 420 425 430

Ile Trp Asn Ile Leu Gln Phe Arg Phe Pro Lys Ala Thr Leu Ile Asn
 435 440 445

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

Pro Lys Tyr Asn Arg Arg Trp His Ser Lys Pro Gly Gln Tyr Cys Phe
465 470 475 480

Ile Tyr Phe Leu His Pro Leu Val Phe Trp Gln Cys His Pro Phe Thr
485 490 495

Ile Ile Asp Glu Gly Glu Lys Cys Val Leu Val Ile Lys Pro Lys Ser
500 505 510

Gly Leu Thr Arg Phe Ile Tyr Asn His Ile Leu Gln Ser Leu Asn Gly
515 520 525

Lys Leu Gln Leu Arg Val Ala Ile Glu Gly Pro Tyr Gly Pro Ser Asn
530 535 540

Leu His Leu Asp Lys Phe Asp His Leu Leu Leu Leu Ser Gly Gly Thr
545 550 555 560

Gly Leu Pro Gly Pro Leu Asp His Ala Ile Lys Leu Ser Arg Asn Pro
565 570 575

Asp Lys Pro Lys Ser Ile Asp Leu Ile Met Ala Ile Lys Asn Pro Ser
580 585 590

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

Ser His Val Asn Val Gln Val Tyr Leu Thr Gln Lys Thr Ala Val Thr
610 615 620

Lys Ala Ala Asn Ala Arg Asp Gln Leu Ile His Phe Asp Asp Ile Met
625 630 635 640

Thr Glu Leu Thr Ser Phe Ala His Ile Gly Asn Ala Arg Pro Asn Phe
645 650 655

Ser Asn Val Ile Glu Asn Ala Ile Lys Ser Thr Pro Pro Gly Asp Ser
660 665 670

Leu Ala Val Val Cys Cys Gly Pro Pro Val Leu Val Asp Asp Val Arg
675 680 685

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

690

695

700

Tyr Phe Glu Glu Tyr Gln Cys Trp
705 710

<210> 135

<211> 2136

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 135

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<210> 136
 <211> 711
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 136

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Gly Ala Ser Ala Ser Pro Ala Lys Thr Lys Met Tyr Gly Lys Leu Pro
 20 25 30

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

Glu Tyr Ser Ser Asp Asp Leu Tyr Ser Ser Pro Ala Cys Thr Tyr Glu
 50 55 60

Pro Ala Leu Gln Ser Met Leu Tyr Cys Ile Tyr Glu Ser Leu Asn Glu
 65 70 75 80

Lys Gly Tyr Ser Asn Arg Thr Phe Glu Lys Thr Phe Ala Ala Ile Lys
 85 90 95

Glu Asp Cys Ala Tyr Tyr Thr Asp Asn Leu Gln Asn Met Thr Asn Ala

	100		105		110												
Asp	Phe	Tyr	Asn	Met	Leu	Asn	Asn	Gly	Thr	Thr	Tyr	Ile	Ile	Gln	Tyr		
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Ser	Glu	Gly	Ser	Ala	Asn	Leu	Thr	Tyr	Pro	Ile	Glu	Met	Asp	Ala	Gln		
	130					135					140						
Val	Arg	Glu	Asn	Tyr	Tyr	Tyr	Ser	Tyr	His	Gly	Phe	Tyr	Ala	Asn	Tyr		
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Asp	Ile	Gly	His	Thr	Tyr	Gly	Gly	Ile	Ile	Cys	Ala	Tyr	Phe	Val	Gly		
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Val	Met	Ile	Leu	Ala	Ser	Ile	Leu	His	Tyr	Leu	Ser	Tyr	Thr	Pro	Phe		
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Lys	Thr	Ala	Leu	Phe	Lys	Gln	Arg	Leu	Val	Arg	Tyr	Val	Arg	Arg	Tyr		
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	210					215					220						
Leu	Lys	Ile	Phe	Thr	Gly	Phe	Leu	Pro	Thr	Arg	Ser	Glu	Gly	Val	Ile		
225					230					235					240		
Ile	Leu	Gly	Tyr	Leu	Val	Leu	His	Thr	Val	Phe	Leu	Ala	Tyr	Gly	Tyr		
				245					250					255			
Gln	Tyr	Asp	Pro	Tyr	Asn	Leu	Ile	Phe	Asp	Ser	Arg	Arg	Glu	Gln	Ile		
			260					265					270				
Ala	Arg	Tyr	Val	Ala	Asp	Arg	Ser	Gly	Val	Leu	Ala	Phe	Ala	His	Phe		
		275					280					285					
Pro	Leu	Ile	Ala	Leu	Phe	Ala	Gly	Arg	Asn	Asn	Phe	Leu	Glu	Phe	Ile		
	290					295					300						
Ser	Gly	Val	Lys	Tyr	Thr	Ser	Phe	Ile	Met	Phe	His	Lys	Trp	Leu	Gly		
305					310					315					320		
Arg	Met	Met	Phe	Leu	Asp	Ala	Val	Ile	His	Gly	Ala	Ala	Tyr	Thr	Ser		
				325					330					335			

Tyr Ser Val Phe Tyr Lys Asp Trp Ala Ala Ser Lys Glu Glu Thr Tyr
340 345 350

Trp Gln Phe Gly Val Ala Ala Leu Cys Ile Val Gly Val Met Val Phe
355 360 365

Phe Ser Leu Ala Met Phe Arg Lys Phe Phe Tyr Glu Ala Phe Leu Phe
370 375 380

Leu His Ile Val Leu Gly Ala Leu Phe Phe Tyr Thr Cys Trp Glu His
385 390 395 400

Val Val Glu Leu Ser Gly Ile Glu Trp Ile Tyr Ala Ala Ile Ala Ile
405 410 415

Trp Thr Ile Asp Arg Leu Ile Arg Ile Val Arg Val Ser Tyr Phe Gly
420 425 430

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

Thr Val Lys Arg Pro Val Arg Leu Trp Lys Ala Lys Pro Gly Gln Tyr
450 455 460

Val Phe Val Ser Phe Leu His His Leu Tyr Phe Trp Gln Ser His Pro
465 470 475 480

Phe Thr Val Leu Asp Ser Ile Ile Lys Asp Gly Glu Leu Thr Ile Ile
485 490 495

Leu Lys Glu Lys Lys Gly Val Thr Lys Leu Val Lys Lys Tyr Val Cys
500 505 510

Cys Asn Gly Gly Lys Ala Ser Met Arg Leu Ala Ile Glu Gly Pro Tyr
515 520 525

Gly Ser Ser Ser Pro Val Asn Asn Tyr Asp Asn Val Leu Leu Leu Thr
530 535 540

Gly Gly Thr Gly Leu Pro Gly Pro Ile Ala His Ala Ile Lys Leu Gly
545 550 555 560

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

Val Arg Gly Phe Asn Val Leu Glu Ala Tyr Lys Pro Glu Leu Met Cys
580 585 590

Leu Glu Asp Leu Asn Val Gln Leu His Ile Tyr Asn Thr Met Glu Val
595 600 605

Pro Ala Leu Thr Pro Asn Asp Ser Leu Glu Ile Ser Gln Gln Asp Glu
610 615 620

Lys Ala Asp Gly Lys Gly Val Val Met Ala Thr Thr Leu Glu Gln Ser
625 630 635 640

Pro Asn Pro Val Glu Phe Asp Gly Thr Val Phe His His Gly Arg Pro
645 650 655

Asn Val Glu Lys Leu Leu His Glu Val Gly Asp Leu Asn Gly Ser Leu
660 665 670

Ala Val Val Cys Cys Gly Pro Pro Val Phe Val Asp Glu Val Arg Asp
675 680 685

Gln Thr Ala Asn Leu Val Leu Glu Lys Pro Ala Lys Ala Ile Glu Tyr
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Phe Glu Glu Tyr Gln Ser Trp
705 710

<210> 137
<211> 1362
<212> DNA
<213> *Saccharomyces cerevisiae*

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attgcaaggc cactgttggg gacagcacat attttgggtg tgccaccgtt agctacgtac 420
tcctcgttgg tgttatggaa cttcaaagtg accgacgagt gcaagaaaac ggaaaccggg 480

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ttgcagatat	tgagagccat	tagaagcgg	gataaaggag	acgctaacgt	gatagacggg	660
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<210> 138
 <211> 453
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 138

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			20					25					30		

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

Tyr	Met	Lys	Trp	Glu	Glu	Ile	Val	Ala	Asp	Leu	Pro	Ser	Leu	Leu	Gln
	50					55					60				

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

Leu	Asp	Glu	Thr	Ile	Leu	Gly	Asp	Val	Arg	Glu	Leu	Arg	Arg	Ala	Tyr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Asp Glu Met Lys Lys Tyr Met Pro Arg Glu His Arg Glu Phe Leu Tyr
 325 330 335

His Leu Glu Ser Val Cys Asn Ile Arg Glu Tyr Val Ser Arg Asn Ala
 340 345 350

Ser Asn Arg Ala Leu Gln Glu Ala Tyr Gly Arg Cys Ile Ser Met Leu
 355 360 365

Lys Ile Phe Arg Asp Asn His Ile Gln Ile Val Thr Lys Tyr Ile Ile
 370 375 380

Leu Pro Ser Asn Ser Lys Gln His Gly Ser Asn Lys Pro Asn Val Leu
 385 390 395 400

Ser Pro Ile Glu Pro Asn Thr Lys Ala Ser Gly Cys Leu Gly His Lys
 405 410 415

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

Phe Leu Lys Gln Cys Arg Asp Glu Thr Val Ala Thr Ala Asp Ile Lys
 435 440 445

Asn Glu Asp Lys Asn
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<210> 139
 <211> 1113
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 139
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 aatgacagtc aaagattcat ggttgatgct accaatgagc ctactatgg atacaagaga 420
 atcagtgact tatattacaa gagcgatcct caatactcgg caaggttcac cgtcccagtc 480
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ttgaactcta gtgcgttcga tgaatttgtc gacgacgatc acaagaaaac ggaccttgtt	600
cctgctcagt tgaaaacaca gatcgatgac ttcaattctt gggtttacga cagcatcaac	660
aatggtgtat acaagaccgg attcgcagag aaagcagaag ttacgaaag tgaagtcaac	720
aacgtatttg aacatttggg caaagtggag aaaatcctga gtgacaaata ttccaaattg	780
aaggccaaat acggtgaaga agatagacaa aaaatccttg gtgagttctt cactgtgggt	840
gatcaattaa cagaagctga cattagattg tatactaccg tcataagatt cgatcctgtg	900
tacgtccaac atttcaaag caattttacc tctattagag ccggatatcc atttattcat	960
ttgtgggtaa gaaatttata ctggaattat gatgccttca ggtacacaac agattttgac	1020
catatcaagt tacactacac gcgttccac acaaggatca accccttggg aattacgccc	1080
ctgggaccca agccagatat tcgtccttta taa	1113

<210> 140
 <211> 370
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 140

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Val	Ser	Ser	Phe	Arg	Glu	Thr	Ile	Ser	Lys	Gln	His	Pro	Ile	Tyr	Lys
			20					25					30		

Pro	Ala	Lys	Gly	Arg	Tyr	Trp	Leu	Tyr	Val	Ser	Leu	Ala	Cys	Pro	Trp
		35					40					45			

Ala	His	Arg	Thr	Leu	Ile	Thr	Arg	Ala	Leu	Lys	Gly	Leu	Thr	Ser	Val
	50					55					60				

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

Phe	Leu	Asp	Met	Glu	Lys	Gln	Leu	Glu	Asp	Ser	Glu	Asp	Phe	Leu	Glu
			85					90						95	

His	Trp	His	Asp	Val	Ala	Gly	Gly	Ile	Arg	Thr	Ala	Lys	Glu	Asp	Ser
			100					105					110		

Ser	Lys	Ser	Phe	Ala	Glu	Ile	Lys	Asn	Asp	Ser	Gln	Arg	Phe	Met	Val
		115					120					125			

Asp Ala Thr Asn Glu Pro His Tyr Gly Tyr Lys Arg Ile Ser Asp Leu
130 135 140

Tyr Tyr Lys Ser Asp Pro Gln Tyr Ser Ala Arg Phe Thr Val Pro Val
145 150 155 160

Leu Trp Asp Leu Glu Thr Gln Thr Ile Val Asn Asn Glu Ser Ser Glu
165 170 175

Ile Ile Arg Ile Leu Asn Ser Ser Ala Phe Asp Glu Phe Val Asp Asp
180 185 190

Asp His Lys Lys Thr Asp Leu Val Pro Ala Gln Leu Lys Thr Gln Ile
195 200 205

Asp Asp Phe Asn Ser Trp Val Tyr Asp Ser Ile Asn Asn Gly Val Tyr
210 215 220

Lys Thr Gly Phe Ala Glu Lys Ala Glu Val Tyr Glu Ser Glu Val Asn
225 230 235 240

Asn Val Phe Glu His Leu Asp Lys Val Glu Lys Ile Leu Ser Asp Lys
245 250 255

Tyr Ser Lys Leu Lys Ala Lys Tyr Gly Glu Glu Asp Arg Gln Lys Ile
260 265 270

Leu Gly Glu Phe Phe Thr Val Gly Asp Gln Leu Thr Glu Ala Asp Ile
275 280 285

Arg Leu Tyr Thr Thr Val Ile Arg Phe Asp Pro Val Tyr Val Gln His
290 295 300

Phe Lys Cys Asn Phe Thr Ser Ile Arg Ala Gly Tyr Pro Phe Ile His
305 310 315 320

Leu Trp Val Arg Asn Leu Tyr Trp Asn Tyr Asp Ala Phe Arg Tyr Thr
325 330 335

Thr Asp Phe Asp His Ile Lys Leu His Tyr Thr Arg Ser His Thr Arg
340 345 350

Ile Asn Pro Leu Gly Ile Thr Pro Leu Gly Pro Lys Pro Asp Ile Arg

355

360

365

Pro Leu
370

<210> 141
<211> 645
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 141
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<210> 142
<211> 214
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 142

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

Gly Lys Glu Val Ala Arg Pro Asn Asn Tyr Ala Gly Ala Leu Tyr Asp
50 55 60

Pro Arg Asp Glu Thr Leu Asp Asp Trp Phe Asp Asn Asp Leu Ser Leu
65 70 75 80

Phe Pro Ser Gly Phe Gly Phe Pro Arg Ser Val Ala Val Pro Val Asp
85 90 95

Ile Leu Asp His Asp Asn Asn Tyr Glu Leu Lys Val Val Val Pro Gly
100 105 110

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

Gln Ile Leu Val Ser Gly Glu Ile Pro Ser Thr Leu Asn Glu Glu Ser
130 135 140

Lys Asp Lys Val Lys Val Lys Glu Ser Ser Ser Gly Lys Phe Lys Arg
145 150 155 160

Val Ile Thr Leu Pro Asp Tyr Pro Gly Val Asp Ala Asp Asn Ile Lys
165 170 175

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

Pro Gln Lys Asp Gly Lys Asn His Val Lys Lys Ile Glu Val Ser Ser
195 200 205

Gln Glu Ser Trp Gly Asn
210

<210> 143
<211> 1230
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 143
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attgactctg aagctaagag taggaggact gccagaata gggcagctca acgagcgttc 180
cgagatagga aagaagccaa aatgaagagt ttgcaagaga gggtagagtt actagaacag 240
aaagatgcgc agaataagac taccacggac tttttactat gttctttaaa aagtttactg 300
tcggaaatta caaaatatag agctaagaat tctgatgatg aaagaatatt agccttcctc 360
gatgatctgc aagaacaaca gaaaaggga aacgaaaaag gaacaagtac agcagtttagc 420

aaggctgcaa aggaattgcc atcgcctaata tcagatgaaa acatgactgt gaacacaagt 480
atagaagtac agccgcacac tcaagagaat gagaaagtta tgtggaacat aggctcatgg 540
aacgctccca gttaaccaa ttcgtgggat tctccccccg gaaatcgaac aggtgccgtt 600
accatcggtg acgaaagtat taatggtagt gaaatgccag atttcagtct cgatcttgtc 660
tccaatgata gacagactgg tctagaagct ttagattacg acattcataa ctactttcct 720
cagcactctg aacgcctgac cgctgaaaaa atagatacgt cagcatgtca atgtgaaatt 780
gaccaaagt atcttcata cgagacagaa gatgatactt tattccccag cgtgcttccc 840
cttgctgtag ggagccagt taataatatt tgcaaccgca agtgtatcgg gaccaaacca 900
tgttcaaata aggagatcaa atgcgactta ataacaagcc acctgttgaa tcagaaatct 960
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gcaattgaac acattagcag cgccatatcg aatggaaaag cgtcttgcta ccacattctc 1080
gaagagatct cctccctacc aaaatattca tcgttggaca tagatgattt atgcagcgaa 1140
ttaataatca aggcaaatg tacagatgac tgcaaatag tagtcaaagc tcgcgactta 1200
cagagtgtc tggttagaca gctcctgtag 1230

<210> 144
<211> 409
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 144

Met Gly Asn Ile Leu Arg Lys Gly Gln Gln Ile Tyr Leu Ala Gly Asp
1 5 10 15

Met Lys Lys Gln Met Leu Leu Asn Lys Asp Gly Thr Pro Lys Arg Lys
20 25 30

Val Gly Arg Pro Gly Arg Lys Arg Ile Asp Ser Glu Ala Lys Ser Arg
35 40 45

Arg Thr Ala Gln Asn Arg Ala Ala Gln Arg Ala Phe Arg Asp Arg Lys
50 55 60

Glu Ala Lys Met Lys Ser Leu Gln Glu Arg Val Glu Leu Leu Glu Gln
65 70 75 80

Lys Asp Ala Gln Asn Lys Thr Thr Thr Asp Phe Leu Leu Cys Ser Leu
85 90 95

Lys Ser Leu Leu Ser Glu Ile Thr Lys Tyr Arg Ala Lys Asn Ser Asp
100 105 110

Asp Glu Arg Ile Leu Ala Phe Leu Asp Asp Leu Gln Glu Gln Gln Lys
115 120 125

Arg Glu Asn Glu Lys Gly Thr Ser Thr Ala Val Ser Lys Ala Ala Lys
130 135 140

Glu Leu Pro Ser Pro Asn Ser Asp Glu Asn Met Thr Val Asn Thr Ser
145 150 155 160

Ile Glu Val Gln Pro His Thr Gln Glu Asn Glu Lys Val Met Trp Asn
165 170 175

Ile Gly Ser Trp Asn Ala Pro Ser Leu Thr Asn Ser Trp Asp Ser Pro
180 185 190

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

Gly Ser Glu Met Pro Asp Phe Ser Leu Asp Leu Val Ser Asn Asp Arg
210 215 220

Gln Thr Gly Leu Glu Ala Leu Asp Tyr Asp Ile His Asn Tyr Phe Pro
225 230 235 240

Gln His Ser Glu Arg Leu Thr Ala Glu Lys Ile Asp Thr Ser Ala Cys
245 250 255

Gln Cys Glu Ile Asp Gln Lys Tyr Leu Pro Tyr Glu Thr Glu Asp Asp
260 265 270

Thr Leu Phe Pro Ser Val Leu Pro Leu Ala Val Gly Ser Gln Cys Asn
275 280 285

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

Glu Ile Lys Cys Asp Leu Ile Thr Ser His Leu Leu Asn Gln Lys Ser
305 310 315 320

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

	325		330		335										
Thr	Gln	Ser	Glu	Ala	Ile	Glu	His	Ile	Ser	Ser	Ala	Ile	Ser	Asn	Gly
	340							345					350		
Lys	Ala	Ser	Cys	Tyr	His	Ile	Leu	Glu	Glu	Ile	Ser	Ser	Leu	Pro	Lys
	355						360					365			
Tyr	Ser	Ser	Leu	Asp	Ile	Asp	Asp	Leu	Cys	Ser	Glu	Leu	Ile	Ile	Lys
	370					375					380				
Ala	Lys	Cys	Thr	Asp	Asp	Cys	Lys	Ile	Val	Val	Lys	Ala	Arg	Asp	Leu
385					390					395					400
Gln	Ser	Ala	Leu	Val	Arg	Gln	Leu	Leu							
				405											

<210> 145
 <211> 1545
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 145
 atggaggaac aacgtgaaat actggaacaa ttgaagaaaa ctctgcagat gctaactgta 60
 gagccatcta aaaataacca aatcgccaac gaagaaaagg aaaagaaaga aaatgaaaat 120
 tcgtggtgca tcctcgagca caattatgag gatattgcac aggaattcat tgatttcatt 180
 tacaagaacc ctaccactta ccatgtagta tcatttttcg cgagctgtt agataagcat 240
 aacttcaa atctgagcga gaaatccaat tggcaggact ccattggcga agatgggtgg 300
 aaattctaca ctataagaaa tggaactaac ctatctgcct ttatcctggg caaaaactgg 360
 agagccgaaa aggggtgtcg tgtcattgga tctcatgtgg acgctttgac ggtcaaattg 420
 aagcccgctt cctttaaaga cacagcgga gggttacgga gaattgctgt tgctccctat 480
 ggaggtacac tgaatgaatt gtggctagac agagacctag gtattgggtg tcgccttctt 540
 tacaagaaga agggcactaa cgaaattaaa agcgcttgg ttgattctac acccctacct 600
 gtttgtcgaa ttccttcctt ggctcccat ttcggtaa ac ctgctgaagg cccatttgat 660
 aaagaggacc aaactatccc ggtcatcggc tccccactc cggatgagga aggtaatgaa 720
 cctcccacgg atgatgaaaa gaaatcgccc ttatttggca aacactgcat ccacctgtta 780
 aggtacgttg ccaaattagc cgggtgtgga gtgtccgaat tgattcaaat ggatttagac 840
 ttattcgatg tgcaaaaggg taccattgga ggtattggta aacacttcct ttttgcacca 900

cgtctagatg acaggttggtg tagtttcgca gcaatgattg ctttgatttg ctacgctaag 960
 gatgttaata ccgaggaatc agattttattc tctactgtca ctttgtatga taatgaagaa 1020
 atcggatcgt tgacaagaca aggcgcaaaa ggtggccttggt tggagtcagt ggtggaacgc 1080
 agttcttctg cattcactaa gaaaccggtc gatttgcata cggtttgggc taattccatc 1140
 atcttgtccg cagacgtcaa ccacctctac aacccaaact ttcctgaagt ctatttgaag 1200
 aatcattttc cagtgcctaa tgtcgggaatc actttatcac tggatcctaa cggtcatatg 1260
 gccacagatg tcgtaggaac tgccctagta gaagaattag cacgccgcaa tggagacaaa 1320
 gtgcaatatt tccaaatcaa aaacaactca agatcagggtg gtactatcgg cccatcattg 1380
 gcttctcaaa caggtgctcg taccatagac ctgggaattg cacagttgtc catgcacagc 1440
 atcagagctg ctacagggtc caaggatgtc ggattaggtg ttaagttctt caacggattt 1500
 ttcaagcact ggagatcagt ctacgatgaa ttcggcgagt tgtga 1545

<210> 146
 <211> 514
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 146

Met Glu Glu Gln Arg Glu Ile Leu Glu Gln Leu Lys Lys Thr Leu Gln
 1 5 10 15

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

Lys Glu Lys Lys Glu Asn Glu Asn Ser Trp Cys Ile Leu Glu His Asn
 35 40 45

Tyr Glu Asp Ile Ala Gln Glu Phe Ile Asp Phe Ile Tyr Lys Asn Pro
 50 55 60

Thr Thr Tyr His Val Val Ser Phe Phe Ala Glu Leu Leu Asp Lys His
 65 70 75 80

Asn Phe Lys Tyr Leu Ser Glu Lys Ser Asn Trp Gln Asp Ser Ile Gly
 85 90 95

Glu Asp Gly Gly Lys Phe Tyr Thr Ile Arg Asn Gly Thr Asn Leu Ser
 100 105 110

Ala Phe Ile Leu Gly Lys Asn Trp Arg Ala Glu Lys Gly Val Gly Val

219

Leu Leu Glu Ser Val Val Glu Arg Ser Ser Ser Ala Phe Thr Lys Lys
 355 360 365

Pro Val Asp Leu His Thr Val Trp Ala Asn Ser Ile Ile Leu Ser Ala
 370 375 380

Asp Val Asn His Leu Tyr Asn Pro Asn Phe Pro Glu Val Tyr Leu Lys
 385 390 395 400

Asn His Phe Pro Val Pro Asn Val Gly Ile Thr Leu Ser Leu Asp Pro
 405 410 415

Asn Gly His Met Ala Thr Asp Val Val Gly Thr Ala Leu Val Glu Glu
 420 425 430

Leu Ala Arg Arg Asn Gly Asp Lys Val Gln Tyr Phe Gln Ile Lys Asn
 435 440 445

Asn Ser Arg Ser Gly Gly Thr Ile Gly Pro Ser Leu Ala Ser Gln Thr
 450 455 460

Gly Ala Arg Thr Ile Asp Leu Gly Ile Ala Gln Leu Ser Met His Ser
 465 470 475 480

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

Phe Asn Gly Phe Phe Lys His Trp Arg Ser Val Tyr Asp Glu Phe Gly
 500 505 510

Glu Leu

<210> 147
 <211> 636
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 147
 atgagcaccg cattcaacga ttactgcact gtttgtgatc gtctcattcc aacatctcca 60
 cagaaaacga acattaatac caggaagatc caaagggaca atgaaaccaa gagcagttta 120
 caatcaaata agttatattg ctccgaagat tgtaagctga aggattcgaa ccctcttaat 180
 gagaaattat tatcccactt gcataaaaaa tcaaaaactt ctcatcgcga taatctcact 240
 ccaccgcttt catattctaa aaattttaact gcatcaaacc tcttcgagcc gactacctca 300

ctatcttcat ctccgacatc ttcaactatc ccctttgacg agttggagaa gctagagtcc	360
ttattaattt caccattgct gctacctcag gatggtatag tcaatcctaa gcaggagtct	420
aatccttctc gtgttgacga atatgatgaa aatgaacatt atttgaactt agccgactct	480
cttagactcg attctagtta ccaattgcat tcaaaggcac atttgggtta cgaaaacaac	540
ttgccacgat caaacgatct aattgatgat catttgatct cagatcagat cattgagaat	600
aactacaacc tatggtttag actatcctcc agttaa	636

<210> 148
 <211> 211
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 148

Met	Ser	Thr	Ala	Phe	Asn	Asp	Tyr	Cys	Thr	Val	Cys	Asp	Arg	Leu	Ile
1				5					10					15	

Pro	Thr	Ser	Pro	Gln	Lys	Thr	Asn	Ile	Asn	Thr	Arg	Lys	Ile	Gln	Arg
			20					25					30		

Asp	Asn	Glu	Thr	Lys	Ser	Ser	Leu	Gln	Ser	Asn	Lys	Leu	Tyr	Cys	Ser
		35					40					45			

Glu	Asp	Cys	Lys	Leu	Lys	Asp	Ser	Asn	Pro	Leu	Asn	Glu	Lys	Leu	Leu
	50					55					60				

Ser	His	Leu	His	Lys	Lys	Ser	Lys	Thr	Ser	His	Ser	His	Asn	Leu	Thr
65					70					75					80

Pro	Pro	Leu	Ser	Tyr	Ser	Lys	Asn	Leu	Thr	Ala	Ser	Asn	Leu	Phe	Glu
				85					90					95	

Pro	Thr	Thr	Ser	Leu	Ser	Ser	Ser	Pro	Thr	Ser	Ser	Thr	Ile	Pro	Phe
			100					105					110		

Asp	Glu	Leu	Glu	Lys	Leu	Glu	Ser	Leu	Leu	Ile	Ser	Pro	Leu	Leu	Leu
		115					120					125			

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

Val	Asp	Glu	Tyr	Asp	Glu	Asn	Glu	His	Tyr	Leu	Asn	Leu	Ala	Asp	Ser
145					150					155					160

Leu Arg Leu Asp Ser Ser Tyr Gln Leu His Ser Lys Ala His Leu Gly
165 170 175

Tyr Glu Asn Asn Leu Pro Arg Ser Asn Asp Leu Ile Asp Asp His Leu
180 185 190

Ile Ser Asp Gln Ile Ile Glu Asn Asn Tyr Asn Leu Trp Phe Arg Leu
195 200 205

Ser Ser Ser
210

<210> 149
<211> 837
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 149
atgagagcac caccttcacc gagaaagtcc aaatctggtc atttttttta cctataatttt 60
cgactgtgtc aactgttcag tggccggaaa tttaaagagga ggtggcatgt ccacaaaactt 120
cacattcacc aatataatac tcgctggaac ttgagccccc tctccgaaat acacattgag 180
gacatgataa atgaaccgtc tggactatgt ccaggaagtt ccaaaaagaa accactactg 240
attgcaaggt ttcccaaggg ttgccaagaa tcaccaaggg tatatgtact gcaaaggaac 300
aatttgtctc gtttaaaatt aagcaaaaaga aaatatgccc taaggttcta tcacaatgaa 360
atttttggca ataatttaaa gagaaaagac ggaagcatcc acaaagttga acaccaacag 420
tgcgcagaaa ccgttagaaa gatcaagaaa gtcacagcaa accatgctga tgttaaaata 480
atatttcacg ataaaaatac tataagaagt gacaaattag ggggtaggag taataagatg 540
cagactaggc ctagtgttct tgaagaggat gtagaagaag aagtctcttc ggtatatatc 600
agattttgtg acgaccattc cctgagagtt aaagattatc actctttgca caggcattct 660
aaaaaatctt ctaaagaaaa acgaaataat caggagattg gaaaatctaa gttgcttggg 720
aagctttttg aagaggaaac atcgcgtaaa aacaaagggtg tagagaagaa actagatacg 780
attgtgatac agaaatttca aaattatcct attgtctcct tctctcgtgt catttaa 837

<210> 150
<211> 278
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 150

Met Arg Ala Pro Pro Ser Pro Arg Lys Ser Lys Ser Gly His Phe Phe
 1 5 10 15

Tyr Leu Tyr Phe Arg Leu Cys Gln Leu Phe Ser Gly Arg Lys Leu Lys
 20 25 30

Arg Arg Trp His Val His Lys Leu His Ile His Gln Tyr Asn Thr Arg
 35 40 45

Trp Asn Leu Ser Pro Leu Ser Glu Ile His Ile Glu Asp Met Ile Asn
 50 55 60

Glu Pro Ser Gly Leu Cys Pro Gly Ser Ser Lys Lys Lys Pro Leu Leu
 65 70 75 80

Ile Ala Arg Phe Pro Lys Gly Cys Gln Glu Ser Pro Arg Val Tyr Val
 85 90 95

Leu Gln Arg Asn Asn Leu Ser Arg Leu Lys Leu Ser Lys Arg Lys Tyr
 100 105 110

Ala Leu Arg Phe Tyr His Asn Glu Ile Phe Gly Asn Asn Leu Lys Arg
 115 120 125

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

Val Arg Lys Ile Lys Lys Val Thr Ala Asn His Ala Asp Val Lys Ile
 145 150 155 160

Ile Phe His Asp Lys Asn Thr Ile Arg Ser Asp Lys Leu Gly Gly Arg
 165 170 175

Ser Asn Lys Met Gln Thr Arg Pro Ser Val Leu Glu Glu Asp Val Glu
 180 185 190

Glu Glu Val Ser Ser Val Tyr Ile Arg Phe Cys Asp Asp His Ser Leu
 195 200 205

Arg Val Lys Asp Tyr His Ser Leu His Arg His Ser Lys Lys Ser Ser
 210 215 220

Lys Glu Lys Arg Asn Asn Gln Glu Ile Gly Lys Ser Lys Leu Leu Gly
 225 230 235 240

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

Lys Leu Asp Thr Ile Val Ile Gln Lys Phe Gln Asn Tyr Pro Ile Val
260 265 270

Ser Phe Ser Arg Val Ile
275

<210> 151
<211> 3657
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 151
atgataaaaa atggtacatg cccctattgg gaacgtgatg atctttcgga atgtgctagg 60
cgagaatata tcgagtttaa atttcctcta tttatattgt tgactggtat gatatacgcg 120
ttttgcaaag tctttcgagc cttttatcta agggggaaaa atcatacaaa tgaagcgcca 180
gaatttgaag aacaaggtaa tggaaaccac gaatatgcaa ggttctcagt tttaagacta 240
aaatctgcat gggaaagccg tagcttttgt aatgttaata atagatctac tttcgacaaa 300
ttcaaaaaat ttatagaggg tgccttcatt gttttgcagc ttactatcca cctgtatatt 360
ttatctagta tgccaatgga taacaaaaag ttctttcacc aaggttttct ggttcaaattg 420
tttctctgga ttttactgct tgttggtatt acacttcggt taatttcagc aagccagtca 480
tttcggtggg ttttagcatg taagcgtgat ttatgggctg tttcgtttta ctcatatgca 540
tccctgttta ctctttcgat tttacctctt cgttccgtct tcattggaaa gataaaagat 600
aaaattatgg tcaaatatat catttccgag actttcattg atttagcgct tttattatta 660
ttatcaacgt caagtataga aggaactagg tactcatttt tggttgaaaa tgagaacaaa 720
aagttgccac cggctcctac cgtctttggc cttcttactt tttctaggat tgatcggctt 780
at ttggaaag catacaaaca ctgccttgga aacgctgata tttgggattt ggatattaat 840
aataagtcta tagcaatttt ggcgaacttt gaaatgtctt ctaaaaaagg aaggctcctt 900
ccaaacatta tttgttattt taaggctggt ttcattctccc aattatttct ggcttttgta 960
tctagttttt tgaactttgt accctcattg ttgatgccaa gaatactatc atacgttaat 1020
gacccaaagt caaatcatg gaacttggtg tctttatacg tctcatctat gctcgtcagt 1080
aaaatcattg ccacgacttg tagaggtaa ggattgtttt taggtgaaaa ggggtactatg 1140
caactaagaa cagttttgat atccaatatc tattccaaaa ccttaagaag aacaattcta 1200

aaagactcaa	caacgtcact	tcaaaaaaat	gcgtcaacat	cctttgaaga	aaatcctgac	1260
tcttctgaag	cggaacctag	aaaaaagtct	agtaggaaag	acaactctgt	gaacaatggt	1320
atgtcaattg	acgctttcaa	ggtttctgaa	gctatgaaca	ctttttatct	ggcatgtgaa	1380
gcagttttca	tgacagttac	ggccctaata	atactatatt	ccctactggg	atgggtccgc	1440
tttgctggta	cctttgctct	tcttgccatg	attcctttga	atttttggtg	tgcaactttt	1500
tacgggaact	atcaggccga	tcaattaatc	ctaactgaca	agcgtacctc	tgggattagt	1560
gaggctctga	actcaatacg	tgtaataaag	ctactggcat	gggaaaatct	gttttatcaa	1620
aagattataa	acgtaagaga	tggggaaata	agactcctta	aaaagaaggc	aacaattttc	1680
tttttgaacc	atctcatttg	gttctttggg	cccactttgg	tctctgcaat	aacattctca	1740
gtgtttatta	aattccaaaa	tcagacactt	actcctacaa	tagcatttac	agctctttct	1800
ttatttgcaa	tattgaggac	acccatggac	caaattgctt	cgactgtcag	ccttttgata	1860
cagtctttta	tttctcttga	aagaatccag	gattatctta	atgaatcaga	aacaagaaaa	1920
tatgagattt	tggaacaaag	caatactaaa	tttggtcttg	aagatgcaag	catggaatgg	1980
gaagctgctg	aaacaagttt	taaacttaag	aacatttcta	ttgattttta	gctgaatagt	2040
ctcaacgcaa	ttataggtcc	gactgggtca	ggaaagtctt	cgctattact	tggactattg	2100
ggagaattga	accttctttc	tggaaaaata	tacgtaccta	cagttgaatc	ccgcgacgac	2160
ttagagattg	gtaaagacgg	aatgacgaat	tcaatggcat	attgttctca	aactccgtgg	2220
ttgattagtg	gaacaattaa	agataacggt	gtttttggag	aaatcttcaa	caaacaaaaa	2280
tttgatgatg	taatgaaatc	ctgttgtctt	gacaaagata	tcaaagcaat	gacagctggc	2340
ataagaacag	acgtgggtga	tggaggattt	tccttatctg	gcggacagca	gcaaaggatt	2400
gctttagcca	gagcaattta	ctcctcttcc	aggtatttga	tccttgatga	ttgcttgagt	2460
gcagtagatc	ctgaaactgc	actttatata	tatgaagagt	gtttatgcgg	cccatgatg	2520
aaaggaagga	cctgcatcat	tacgagtcac	aatatttctt	tagttacgaa	acgggctgac	2580
tggcttgtga	ttttagatcg	tggcgagggt	aaatcacagg	gtaaaccatc	ggacctcatt	2640
aaatctaata	agtttttgag	ggaaagcata	aacaatgatt	caaaaaatac	aactcacaat	2700
caaattgact	tgaaaagatc	aacaacatca	aagaaaacta	agaatggaga	tcccgaggga	2760
gggaactcgc	aagacgaagt	gtgtgctgaa	gttgaaaatt	ttgaggaaac	aaaaatggaa	2820
ggatcagtta	aattttcagc	ttacaaatgg	ttagcagact	atttcggggg	actgggagtt	2880
gtttttgttt	tcacctcgtc	ctccatcctt	attcatggaa	tcacactgtc	tcagggtctt	2940

tggctcagat actggctgga cactggatct tcagggagta agtctacctg gctttataga 3000
 atagttgagg gtcactctaa catctatttc ttactgactt atattatcat aggtcttggt 3060
 tcttcatttt taacttctgg taaagtttgg atagcaataa tttcaggtac caacgtcacc 3120
 aagaaaatat ttgcgaagct tctatccagt atcttatatg ccaagttacg ttttcataat 3180
 gtcacgcccga ctggaagaat aatgaacaga tttagcaagg atatggatat tattgatcaa 3240
 caattgatcc ctaatttcga aggactctct tatagcgctcg ttgtttgtct gtggattata 3300
 cttttaattg gatatgttac tcctcaattt ctgttatttg ctattccttt atgcgctctt 3360
 tattataaccg tatgtacggt atatcttcgt gcatctagag agttgaagag aatagataac 3420
 atcaatatct ctccaataca ccagttattc gctgaagcca tcaaaggagt aactacaatt 3480
 agagcattag cagatgagcg taggtttatc actcaatctt tggttgcaat tgacagaagt 3540
 aatgctccat ttttttatct caatatggcc accgagtgga tcacatatag agtggatata 3600
 attgggacac ttgttctttt tagttcttct gtaatgatca taatgaaggc ctcatag 3657

<210> 152
 <211> 1218
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 152

Met Ile Lys Asn Gly Thr Cys Pro Tyr Trp Glu Arg Asp Asp Leu Ser
 1 5 10 15

Glu Cys Ala Arg Arg Glu Tyr Ile Glu Phe Lys Phe Pro Leu Phe Ile
 20 25 30

Leu Leu Thr Gly Met Ile Tyr Ala Phe Cys Lys Val Phe Arg Ala Phe
 35 40 45

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

Gln Gly Asn Gly Asn His Glu Tyr Ala Arg Phe Ser Val Leu Arg Leu
 65 70 75 80

Lys Ser Ala Trp Glu Ser Arg Ser Phe Cys Asn Val Asn Asn Arg Ser
 85 90 95

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

Gln Leu Thr Ile His Leu Tyr Ile Leu Ser Ser Met Pro Met Asp Asn
115 120 125

Lys Lys Phe Phe His Gln Gly Phe Leu Val Gln Met Phe Leu Trp Ile
130 135 140

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

Phe Arg Trp Val Leu Ala Cys Lys Arg Asp Leu Trp Ala Val Ser Phe
165 170 175

Tyr Ser Tyr Ala Ser Leu Phe Thr Leu Ser Ile Leu Pro Leu Arg Ser
180 185 190

Val Phe Ile Gly Lys Ile Lys Asp Lys Ile Met Val Lys Tyr Ile Ile
195 200 205

Ser Glu Thr Phe Ile Asp Leu Ala Leu Leu Leu Leu Leu Ser Thr Ser
210 215 220

Ser Ile Glu Gly Thr Arg Tyr Ser Phe Leu Val Glu Asn Glu Asn Lys
225 230 235 240

Lys Leu Pro Pro Ala Pro Thr Val Phe Gly Leu Leu Thr Phe Ser Arg
245 250 255

Ile Asp Arg Leu Ile Trp Lys Ala Tyr Lys His Cys Leu Gly Asn Ala
260 265 270

Asp Ile Trp Asp Leu Asp Ile Asn Asn Lys Ser Ile Ala Ile Leu Ala
275 280 285

Asn Phe Glu Met Ser Ser Lys Lys Gly Arg Leu Leu Pro Asn Ile Ile
290 295 300

Cys Tyr Phe Lys Ala Val Phe Ile Ser Gln Leu Phe Leu Ala Phe Val
305 310 315 320

Ser Ser Phe Leu Asn Phe Val Pro Ser Leu Leu Met Pro Arg Ile Leu
325 330 335

Ser Tyr Val Asn Asp Pro Lys Ser Lys Ser Trp Asn Leu Val Ser Leu
340 345 350

Tyr Val Ser Ser Met Leu Val Ser Lys Ile Ile Ala Thr Thr Cys Arg
355 360 365

Gly Gln Gly Leu Phe Leu Gly Glu Lys Gly Thr Met Gln Leu Arg Thr
370 375 380

Val Leu Ile Ser Asn Ile Tyr Ser Lys Thr Leu Arg Arg Thr Ile Leu
385 390 395 400

Lys Asp Ser Thr Thr Ser Leu Gln Lys Asn Ala Ser Thr Ser Phe Glu
405 410 415

Glu Asn Pro Asp Ser Ser Glu Ala Glu Pro Arg Lys Lys Ser Ser Arg
420 425 430

Lys Asp Asn Ser Val Asn Asn Val Met Ser Ile Asp Ala Phe Lys Val
435 440 445

Ser Glu Ala Met Asn Thr Phe Tyr Leu Ala Cys Glu Ala Val Phe Met
450 455 460

Thr Val Thr Ala Leu Met Ile Leu Tyr Ser Leu Leu Gly Trp Ser Ala
465 470 475 480

Phe Ala Gly Thr Phe Ala Leu Leu Ala Met Ile Pro Leu Asn Phe Trp
485 490 495

Cys Ala Thr Phe Tyr Gly Asn Tyr Gln Ala Asp Gln Leu Ile Leu Thr
500 505 510

Asp Lys Arg Thr Ser Gly Ile Ser Glu Ala Leu Asn Ser Ile Arg Val
515 520 525

Ile Lys Leu Leu Ala Trp Glu Asn Leu Phe Tyr Gln Lys Ile Ile Asn
530 535 540

Val Arg Asp Gly Glu Ile Arg Leu Leu Lys Lys Lys Ala Thr Ile Phe
545 550 555 560

Phe Leu Asn His Leu Ile Trp Phe Phe Gly Pro Thr Leu Val Ser Ala
565 570 575

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

580		585		590											
Thr	Ile	Ala	Phe	Thr	Ala	Leu	Ser	Leu	Phe	Ala	Ile	Leu	Arg	Thr	Pro
	595						600					605			
Met	Asp	Gln	Ile	Ala	Ser	Thr	Val	Ser	Leu	Leu	Ile	Gln	Ser	Phe	Ile
	610					615					620				
Ser	Leu	Glu	Arg	Ile	Gln	Asp	Tyr	Leu	Asn	Glu	Ser	Glu	Thr	Arg	Lys
625					630					635					640
Tyr	Glu	Ile	Leu	Glu	Gln	Ser	Asn	Thr	Lys	Phe	Gly	Phe	Glu	Asp	Ala
			645						650					655	
Ser	Met	Glu	Trp	Glu	Ala	Ala	Glu	Thr	Ser	Phe	Lys	Leu	Lys	Asn	Ile
		660						665					670		
Ser	Ile	Asp	Phe	Lys	Leu	Asn	Ser	Leu	Asn	Ala	Ile	Ile	Gly	Pro	Thr
	675						680					685			
Gly	Ser	Gly	Lys	Ser	Ser	Leu	Leu	Leu	Gly	Leu	Leu	Gly	Glu	Leu	Asn
	690					695					700				
Leu	Leu	Ser	Gly	Lys	Ile	Tyr	Val	Pro	Thr	Val	Glu	Ser	Arg	Asp	Asp
705					710					715					720
Leu	Glu	Ile	Gly	Lys	Asp	Gly	Met	Thr	Asn	Ser	Met	Ala	Tyr	Cys	Ser
			725						730					735	
Gln	Thr	Pro	Trp	Leu	Ile	Ser	Gly	Thr	Ile	Lys	Asp	Asn	Val	Val	Phe
		740						745					750		
Gly	Glu	Ile	Phe	Asn	Lys	Gln	Lys	Phe	Asp	Asp	Val	Met	Lys	Ser	Cys
	755					760						765			
Cys	Leu	Asp	Lys	Asp	Ile	Lys	Ala	Met	Thr	Ala	Gly	Ile	Arg	Thr	Asp
	770					775					780				
Val	Gly	Asp	Gly	Gly	Phe	Ser	Leu	Ser	Gly	Gly	Gln	Gln	Gln	Arg	Ile
785					790					795					800
Ala	Leu	Ala	Arg	Ala	Ile	Tyr	Ser	Ser	Ser	Arg	Tyr	Leu	Ile	Leu	Asp
			805						810					815	

Asp Cys Leu Ser Ala Val Asp Pro Glu Thr Ala Leu Tyr Ile Tyr Glu
 820 825 830

Glu Cys Leu Cys Gly Pro Met Met Lys Gly Arg Thr Cys Ile Ile Thr
 835 840 845

Ser His Asn Ile Ser Leu Val Thr Lys Arg Ala Asp Trp Leu Val Ile
 850 855 860

Leu Asp Arg Gly Glu Val Lys Ser Gln Gly Lys Pro Ser Asp Leu Ile
 865 870 875 880

Lys Ser Asn Glu Phe Leu Arg Glu Ser Ile Asn Asn Asp Ser Lys Asn
 885 890 895

Thr Thr His Asn Gln Ile Asp Leu Lys Arg Ser Thr Thr Ser Lys Lys
 900 905 910

Thr Lys Asn Gly Asp Pro Glu Gly Gly Asn Ser Gln Asp Glu Val Cys
 915 920 925

Ala Glu Val Glu Asn Phe Glu Glu Thr Lys Met Glu Gly Ser Val Lys
 930 935 940

Phe Ser Ala Tyr Lys Trp Leu Ala Asp Tyr Phe Gly Gly Leu Gly Val
 945 950 955 960

Val Phe Val Phe Thr Ser Ser Ser Ile Leu Ile His Gly Ile Thr Leu
 965 970 975

Ser Gln Gly Phe Trp Leu Arg Tyr Trp Leu Asp Thr Gly Ser Ser Gly
 980 985 990

Ser Lys Ser Thr Trp Leu Tyr Arg Ile Val Glu Gly His Ser Asn Ile
 995 1000 1005

Tyr Phe Leu Leu Thr Tyr Ile Ile Ile Gly Leu Val Ser Ser Phe
 1010 1015 1020

Leu Thr Ser Gly Lys Val Trp Ile Ala Ile Ile Ser Gly Thr Asn
 1025 1030 1035

Val Thr Lys Lys Ile Phe Ala Lys Leu Leu Ser Ser Ile Leu Tyr
 1040 1045 1050

Ala Lys Leu Arg Phe His Asn Val Thr Pro Thr Gly Arg Ile Met
1055 1060 1065

Asn Arg Phe Ser Lys Asp Met Asp Ile Ile Asp Gln Gln Leu Ile
1070 1075 1080

Pro Asn Phe Glu Gly Leu Ser Tyr Ser Val Val Val Cys Leu Trp
1085 1090 1095

Ile Ile Leu Leu Ile Gly Tyr Val Thr Pro Gln Phe Leu Leu Phe
1100 1105 1110

Ala Ile Pro Leu Cys Ala Leu Tyr Tyr Thr Val Cys Thr Leu Tyr
1115 1120 1125

Leu Arg Ala Ser Arg Glu Leu Lys Arg Ile Asp Asn Ile Asn Ile
1130 1135 1140

Ser Pro Ile His Gln Leu Phe Ala Glu Ala Ile Lys Gly Val Thr
1145 1150 1155

Thr Ile Arg Ala Leu Ala Asp Glu Arg Arg Phe Ile Thr Gln Ser
1160 1165 1170

Leu Val Ala Ile Asp Arg Ser Asn Ala Pro Phe Phe Tyr Leu Asn
1175 1180 1185

Met Ala Thr Glu Trp Ile Thr Tyr Arg Val Asp Ile Ile Gly Thr
1190 1195 1200

Leu Val Leu Phe Ser Ser Ser Val Met Ile Ile Met Lys Ala Ser
1205 1210 1215

<210> 153

<211> 420

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 153

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gaaagaaacg gcactgaatg ggaatatata tttgcatcaa attcagcttg tcttgattat 120

aataataata cagctgttaa taatgatata atttcgtcac ttaattattg catcagtgat 180

gacagatatt atgaaactgc agcgatgtgt gtgggttttga aattatctca agattgctct 240

tttgatgtga ggcttcaacg aagtggaaat gggccatata agaatatctg ggatatgcct 300
 tgcggagaat tacaacaaca cattgggttac aaaaatggta tatgctataa tagtgaaaac 360
 acggtgttat cggcagtagg tgtagaacat cgatatcata aaagtgtttc tcgtctataa 420

<210> 154
 <211> 139
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 154

Met Asn Lys Leu Lys Val Ser Gln Asn Asn Tyr Leu Gln Arg Ser Asp
 1 5 10 15

Phe Tyr Lys Phe Glu Arg Asn Gly Thr Glu Trp Glu Tyr Ile Phe Ala
 20 25 30

Ser Asn Ser Ala Cys Leu Asp Tyr Asn Asn Asn Thr Ala Val Asn Asn
 35 40 45

Asp Ile Ile Ser Ser Leu Asn Tyr Cys Ile Ser Asp Asp Arg Tyr Tyr
 50 55 60

Glu Thr Ala Ala Met Cys Val Val Leu Lys Leu Ser Gln Asp Cys Ser
 65 70 75 80

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

Trp Asp Met Pro Cys Gly Glu Leu Gln Gln His Ile Gly Tyr Lys Asn
 100 105 110

Gly Ile Cys Tyr Asn Ser Glu Asn Thr Val Leu Ser Ala Val Gly Val
 115 120 125

Glu His Arg Tyr His Lys Ser Val Ser Arg Leu
 130 135

<210> 155
 <211> 1239
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 155

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 tctacttttt cagcgccaaa caccaaagtt gacactatta agggttgtat taacaagttt 120

attgaacaat ttaatgtata tgatgagcaa cacatatattt ggcaacctcc tggaaaatca	180
aacgtcagat tgctgtcaaa cgccaatgac tttggccaat tgggaaactt tttgcataag	240
aaaatcaaat gtaacatttt tattggagaa gaagcattaa ggaaatacga tttaaatatc	300
tgtggacctt atgacaaatt tgtagaaaat tctgacccta gtgttaaaaa ggttgtgaac	360
agagatgatg tcatgttgtc ggcgaaatgt ttaaacaatca tatcggaaca actctctata	420
cttgagaagt ccataagtaa ggctcaaaac caagtgttgc agtcaagtga ggttgaagga	480
aaaaaatgta ttatcttgcc ggaagataaa ccagaactca tcaagttttt ttctaaattt	540
gaaacgagtg ttcagttaca ggaggtttac gagggctata aggtatatga aaagctatta	600
caaaaatttg gtgggcaaaa aaaaagaatg gagtctttct tgaatgaaaa cacgccaatg	660
tcaggtgccg aagctatcaa gcaaataaat atatctgagg agtcaagga aaaaggggaa	720
cgtttaacaa caccaaacga tccgttatta cacgttgagg tgagtaatga ggataactcg	780
ctgcacttta tattgtacaa taaaacgaat atcataattc caggaaattg tacatttgaa	840
ttttctagcc aaatctccga ggtattcagt atcaaaatgg gaccgcatga gataggcata	900
aagggtcaga aagagctatg gttttttcca tcattacctc ctctctctc caattacaca	960
atgaaagtcg taaaccagga tggagaaaact attctggttg gtaaagtgtc tgactccaat	1020
gaaataactc taaaatctcc actagcctca ttttcgacag gcagtttcca gacaggcagt	1080
ttccacactt tgcaagatcc tactaatgtt ttccgggcag acgcgctttc ttcccctgat	1140
gaatcaagca tcatgagcac tccctttcta ggcgagacag atgaagttta taattctggc	1200
tctacattaa gtaggccatt tacttgggaa gaaatataa	1239

<210> 156
 <211> 412
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 156

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

Gln	Phe	Lys	Lys	Ser	Thr	Phe	Ser	Ala	Pro	Asn	Thr	Lys	Val	Asp	Thr
			20					25					30		

Ile	Lys	Gly	Cys	Ile	Asn	Lys	Phe	Ile	Glu	Gln	Phe	Asn	Val	Tyr	Asp
		35					40					45			

Glu Gln His Ile Phe Trp Gln Pro Pro Gly Lys Ser Asn Val Arg Leu
 50 55 60

Leu Ser Asn Ala Asn Asp Phe Gly Gln Leu Gly Asn Phe Leu His Lys
 65 70 75 80

Lys Ile Lys Cys Asn Ile Phe Ile Gly Glu Glu Ala Leu Arg Lys Tyr
 85 90 95

Asp Leu Asn Ile Cys Gly Pro Tyr Asp Lys Phe Val Glu Asn Ser Asp
 100 105 110

Pro Ser Val Lys Lys Val Val Asn Arg Asp Asp Val Met Leu Ser Arg
 115 120 125

Lys Cys Leu Asn Ile Ile Ser Glu Gln Leu Ser Ile Leu Glu Lys Ser
 130 135 140

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

Lys Lys Cys Ile Ile Leu Pro Glu Asp Lys Pro Glu Leu Ile Lys Phe
 165 170 175

Phe Ser Lys Phe Glu Thr Ser Val Gln Leu Gln Glu Val Tyr Glu Gly
 180 185 190

Tyr Lys Val Tyr Glu Lys Leu Leu Gln Lys Phe Gly Gly Gln Lys Lys
 195 200 205

Arg Met Glu Ser Phe Leu Asn Glu Asn Thr Pro Met Ser Gly Ala Glu
 210 215 220

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

Arg Leu Thr Thr Pro Asn Asp Pro Leu Leu His Val Glu Val Ser Asn
 245 250 255

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

Ile Pro Gly Asn Cys Thr Phe Glu Phe Ser Ser Gln Ile Ser Glu Val
 275 280 285

Phe Ser Ile Lys Met Gly Pro His Glu Ile Gly Ile Lys Gly Gln Lys
 290 295 300

Glu Leu Trp Phe Phe Pro Ser Leu Pro Thr Pro Leu Ser Asn Tyr Thr
 305 310 315 320

Met Lys Val Val Asn Gln Asp Gly Glu Thr Ile Leu Val Gly Lys Cys
 325 330 335

Ala Asp Ser Asn Glu Ile Thr Leu Lys Ser Pro Leu Ala Ser Phe Ser
 340 345 350

Thr Gly Ser Phe Gln Thr Gly Ser Phe His Thr Leu Gln Asp Pro Thr
 355 360 365

Asn Val Phe Arg Ala Asp Ala Leu Ser Ser Pro Asp Glu Ser Ser Ile
 370 375 380

Met Ser Thr Pro Phe Leu Gly Glu Thr Asp Glu Val Tyr Asn Ser Gly
 385 390 395 400

Ser Thr Leu Ser Arg Pro Phe Thr Trp Glu Glu Ile
 405 410

<210> 157
 <211> 1008
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 157
 atggttaatg aaaaagtga tccattcgac ttagcttcgg tttctccttt agtcttagga 60
 ggtgcaatac tgaaccagca atatacagat gagccagaat ccattccact ggaagacata 120
 atcaaatacg cattttcgca tggatatcaat gcaattgaca cttctcccta ctatggccct 180
 agtgagggttc tttatggtag ggcaactgtcc aatttaagga atgaatttcc cagagacact 240
 tattttatat gcacaaaggt tgggcgtatt ggtgcggaag agtttaacta ttctagagat 300
 ttcgtgagat ttagtggttca cagatcgtgc gaaagattac aactacata tctcgatttg 360
 gtgtacttgc acgatgtcga gtttgtcaaa tttccagaca tcttagaggc attaaaggaa 420
 ttgaggacct tgaagaacaa aggagttatc aaaaattttg gcatatcagg ctaccaatc 480
 gactttatca cctggcttgc tgagtactgc tctaccgagg aaagtgatat tgggtcattg 540
 gatgcagtat tgtcctattg taacttgaac ttacaaaaca ataagctatt gaactttcga 600

gaaagactgc tacgcaatgc taaactgaaa atggtttgca acgcatcaat cttgagcatg 660
 tcgctactaa ggtcacagga gacaagacag tttcaccctg gttctcatga attgagagaa 720
 tgcgcatctc aggctgcaa atactgtcaa gaacaaaatg tcgacttagc cgatttggcc 780
 acaagatacg cgatttcgga atgggtagga aagggacccg ttgttcttgg agtcagtagc 840
 atggaagaat tgaaacttgc tctggataat tacgaaattg tgaaatcgaa tggcaacaga 900
 ttatcttcta aggacggaca actagtagaa tatatccaaa agaataattt taaagaacat 960
 tttaatgaag agtggctctc aggtattcct catccagaaa tgatataa 1008

<210> 158
 <211> 335
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 158

Met Val Asn Glu Lys Val Asn Pro Phe Asp Leu Ala Ser Val Ser Pro
 1 5 10 15

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

Glu Ser Ile Pro Leu Glu Asp Ile Ile Lys Tyr Ala Phe Ser His Gly
 35 40 45

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

Tyr Gly Arg Ala Leu Ser Asn Leu Arg Asn Glu Phe Pro Arg Asp Thr
 65 70 75 80

Tyr Phe Ile Cys Thr Lys Val Gly Arg Ile Gly Ala Glu Glu Phe Asn
 85 90 95

Tyr Ser Arg Asp Phe Val Arg Phe Ser Val His Arg Ser Cys Glu Arg
 100 105 110

Leu His Thr Thr Tyr Leu Asp Leu Val Tyr Leu His Asp Val Glu Phe
 115 120 125

Val Lys Phe Pro Asp Ile Leu Glu Ala Leu Lys Glu Leu Arg Thr Leu
 130 135 140

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

tgtctctgtg tgaagctggg tactatcact ggctatgatt tggctgaaaa ctgtcgtcat	240
aatttgccta aaaagctaaa ctataccctt taccttttcg ctgaagtggc aatcattgct	300
actgatctgg ccgaggttgt aggcactgcc atcgctttac aaattctttt caaaatacca	360
ctaacttggg gtgtcttatt aacggtgcta gatgttttggt taattttaat gttctacaca	420
ccaaacggcc agtccttaaa aaaagttagg gttttcgaat ttggcgttgg gatttttggtc	480
attggaactt gcatttgctt tgttttgtag ctgttttaaag tttcaatccc agacaaagct	540
gaattgttta aagggttttt gccttcaa atcattttta aggaacaaca agctctttac	600
atttcattgg gtatcttagg tgccactgtg atgcctcatt cattatactt gggctcatcc	660
attgttaaac caagattgca cgattacgat ttgaagaaat acggtaagggt taatgcccgc	720
ccaagtttaa gcgctataaa atatacgta aactatgcgt acgctgaact aatcattttct	780
ttgttcttaa ttgccacctt tgttaattcc gctattttaa ttgttgtagg tgctacttta	840
tcaggccaac ctgaggcaga ggatgctgat ttgttatcta ttacaaaatt actggtccac	900
tacatatctc ctgcggcagg gttaatcttt gcattggcca tggtatgttc tggccaatct	960
gccggtatca tctgtacact tgccgggcaa atcgtttctg agggatTTTT acagtggctc	1020
ttaccacctt gggccacaag attgtgcacc agattgattg ccattgtacc atgtttattt	1080
gttactttaa ccatggggga aaaggaatt tcagatatTT tgaatttttc tcaagtggtc	1140
ttgtccttaa ttttaccaat cgtttccgct cctttaattt attttaccgc aaatagaaaag	1200
ttgatggttg ttcatgacga aaatggtgtg gtaagagcac ctgccgatgt taacgccatt	1260
gctgatgaaa ccactccatt gaactccaag cacagtaaaa tagttgattt tactaacagt	1320
cgtttgttga cctatacctc tgttttcgta tgggctttta tcgggagctt gaattgctat	1380
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<210> 160

<211> 473

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 160

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

Thr	Ser	Val	Ser	Gly	Gly	Ala	Gln	Tyr	Lys	Tyr	Thr	Leu	Leu	Phe	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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

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

Ala Asp Leu Leu Ser Ile Tyr Lys Leu Leu Val His Tyr Ile Ser Pro
290 295 300

Ala Ala Gly Leu Ile Phe Ala Leu Ala Met Leu Cys Ser Gly Gln Ser
305 310 315 320

Ala Gly Ile Ile Cys Thr Leu Ala Gly Gln Ile Val Ser Glu Gly Phe
325 330 335

Leu Gln Trp Ser Leu Pro Pro Trp Ala Thr Arg Leu Cys Thr Arg Leu
340 345 350

Ile Ala Ile Val Pro Cys Leu Phe Val Thr Leu Thr Met Gly Glu Lys
355 360 365

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

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

Leu Met Val Val His Asp Glu Asn Gly Val Val Arg Ala Pro Ala Asp
405 410 415

Val Asn Ala Ile Ala Asp Glu Thr Thr Pro Leu Asn Ser Lys His Ser
420 425 430

Lys Ile Val Asp Phe Thr Asn Ser Arg Leu Leu Thr Tyr Thr Ser Val
435 440 445

Phe Val Trp Ala Leu Ile Gly Ser Leu Asn Cys Tyr Leu Val Ile Ser
450 455 460

Tyr Leu Leu Gly Ala Asp Ile His Phe
465 470

<210> 161

<211> 915

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 161

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60

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atgtttccaa tagatgctct gaaaacccga gtgcaggctg caggattgaa taaagctgcc 180
tctacagggga tgatatctca gatatccaaa atatctacaa tggaagggtc gatggcttta 240
tggaagggtg ttcaatcggg aatactgggg gcagggcctg cgcattgcagt atatttttgt 300
acatacgagt ttgcaaagc tcgcctgata agccctgaag atatgcaaac tcatcaacca 360
atgaagaccg cactgagtgg taccattgct accattgctg cggatgcatt gatgaacccc 420
tttgacaccg ttaaacaag actacaattg gatactaatac taagagtttg gaatgttact 480
aagcaaatat atcaaaatga aggccttgca gcattttact actcctatcc cacaacattg 540
gccatgaata tcccatttgc agcgttcaat ttcattgatat atgaatctgc cagcaaattc 600
ttcaaccac aaaattccta caatccattg attcattgtc tttgcggtgg gataagtggg 660
gcaacatgtg ctgcgttaac tacaccgttg gattgcataa agactgtatt acagggttaga 720
ggcagcgaaa ctgtctccat cgaaataatg aaggatgcga acacttttgg tagagcctca 780
agagccatac tggaggttca tggttggaag gggttttggc gaggtttgaa accaaggata 840
gtggctaata taccagccac tgccatttct tggactgcat atgaatgtgc taagcatttt 900
ttaatgaaaa attga 915

<210> 162
<211> 304
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 162

Met Asn Thr Ser Glu Leu Ser Ile Ala Glu Glu Ile Asp Tyr Glu Ala
1 5 10 15

Leu Pro Ser His Ala Pro Leu His Ser Gln Leu Leu Ala Gly Ala Phe
20 25 30

Ala Gly Ile Met Glu His Ser Leu Met Phe Pro Ile Asp Ala Leu Lys
35 40 45

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

Ile Ser Gln Ile Ser Lys Ile Ser Thr Met Glu Gly Ser Met Ala Leu
65 70 75 80

Trp Lys Gly Val Gln Ser Val Ile Leu Gly Ala Gly Pro Ala His Ala
85 90 95

Val Tyr Phe Gly Thr Tyr Glu Phe Cys Lys Ala Arg Leu Ile Ser Pro
100 105 110

Glu Asp Met Gln Thr His Gln Pro Met Lys Thr Ala Leu Ser Gly Thr
115 120 125

Ile Ala Thr Ile Ala Ala Asp Ala Leu Met Asn Pro Phe Asp Thr Val
130 135 140

Lys Gln Arg Leu Gln Leu Asp Thr Asn Leu Arg Val Trp Asn Val Thr
145 150 155 160

Lys Gln Ile Tyr Gln Asn Glu Gly Phe Ala Ala Phe Tyr Tyr Ser Tyr
165 170 175

Pro Thr Thr Leu Ala Met Asn Ile Pro Phe Ala Ala Phe Asn Phe Met
180 185 190

Ile Tyr Glu Ser Ala Ser Lys Phe Phe Asn Pro Gln Asn Ser Tyr Asn
195 200 205

Pro Leu Ile His Cys Leu Cys Gly Gly Ile Ser Gly Ala Thr Cys Ala
210 215 220

Ala Leu Thr Thr Pro Leu Asp Cys Ile Lys Thr Val Leu Gln Val Arg
225 230 235 240

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

Gly Arg Ala Ser Arg Ala Ile Leu Glu Val His Gly Trp Lys Gly Phe
260 265 270

Trp Arg Gly Leu Lys Pro Arg Ile Val Ala Asn Ile Pro Ala Thr Ala
275 280 285

Ile Ser Trp Thr Ala Tyr Glu Cys Ala Lys His Phe Leu Met Lys Asn
290 295 300

<210> 163
<211> 498
<212> DNA

<213> Saccharomyces cerevisiae

<400> 163

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gccatggggg ttttgagagc gtccagcata acgaaaaggc tttatcatcc caaggtcata      120
gagcattata cacatccaag aaacgtcggc tcattagata aaaaattgcc caacgtcggc      180
actggtctag tgggtgcgcc agcgtgcggt gatgtgatga ggttgagat caaagtcaac      240
gactctactg gcgttattga agatgtcaaa ttcaaaactt ttggatgtgg ctccgccatt      300
gcctcctctt catatatgac tgaattggta caggggatga ccttggacga tgcggcaaaa      360
attaagaaca ctgaaattgc taaggagttg agcttgcccc cagtcaagtt gcattgctct      420
atgttagcgg aagatgcat caaggcagct attaaggact acaaatctaa gagaaacact      480
ccaacatgt tatcgtaa                                          498
```

<210> 164

<211> 165

<212> PRT

<213> Saccharomyces cerevisiae

<400> 164

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

```
Arg Pro Val Asn Ala Met Gly Val Leu Arg Ala Ser Ser Ile Thr Lys
          20           25           30
```

```
Arg Leu Tyr His Pro Lys Val Ile Glu His Tyr Thr His Pro Arg Asn
          35           40           45
```

```
Val Gly Ser Leu Asp Lys Lys Leu Pro Asn Val Gly Thr Gly Leu Val
          50           55           60
```

```
Gly Ala Pro Ala Cys Gly Asp Val Met Arg Leu Gln Ile Lys Val Asn
65           70           75           80
```

```
Asp Ser Thr Gly Val Ile Glu Asp Val Lys Phe Lys Thr Phe Gly Cys
          85           90           95
```

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

```
Met Thr Leu Asp Asp Ala Ala Lys Ile Lys Asn Thr Glu Ile Ala Lys
          115          120          125
```

Glu Leu Ser Leu Pro Pro Val Lys Leu His Cys Ser Met Leu Ala Glu
 130 135 140

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

Pro Thr Met Leu Ser
 165

<210> 165
 <211> 1659
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 165
 atgggtaaaa ttgcagagtt tctcgggaat ccagggtgcta ggccctgacgt tcatcataga 60
 gcacctactg ttgactgcaa acagtacgaa gaattcgggtg attctaacga ttacaaaaat 120
 gatgatgtgg tcagagtagt cagccatagc gatgagagta ctgatgacga actttgtaat 180
 gtgaatttaa cagaaacagg ggcaatcttc acgagtaaag gttttaccgg gttaagcaaa 240
 ggtttcacag ataagaccct ggatttcctg gtacgagtgg ccgggttcgca ggcgggtttt 300
 tttattgttt ggatcatcct cataatttgg gtgggttattg gtattgttta taacgcacct 360
 ttcaattggc aagttgttat gcaggacgga cagtctattc aaagttatgt ttgggacaca 420
 ctgttgatga gacaacagtt gatgagtacg catgaacaaa ttttgatctg cggtagattg 480
 aagtcgagat tggcttcctt caaaaactat ctaacaagaa gcaccccgaga ggaagaaaaa 540
 gcgactgca cagttgaagc taatgaagtc agctctgttg aaaatcatat agacccatct 600
 gccattaacg gagaactgcc tgtggaaaat tggtagcacc gtttatctaa cgtagcaagt 660
 aggtatatgg gttcaattgc agcaatgggtg atattttgga taggtatttt cgtttggatt 720
 gggtgcggtg ctatcccaaa agatgcgggc aacactccac cttacaccgg agaaactaca 780
 ggtagtaatc caagattgaa aaagttcagt gacgcttggc agatgtatat taacactgca 840
 gttgcagttt cccttctaata ttgcactact ttcttacaaa atataagggc tagacatgat 900
 tatttcacgg ggagggtttt agttgatatc tttgatatgg acgagaaaat cgactatcgt 960
 ataagaaagc attttaacga ttttgaaaca cctcaccagc ttgttactat tgaatctaaa 1020
 aaaaggtcga caggagagaa gatgattgat tggtagctg atattattgg tactgggtatt 1080
 ggtgtcctga ttgggtgtggc agtggttcgcc acatggattg gtattgggtc gccaatgaag 1140
 tgggatgata attggtgggt gattatcggc acatacacag gttaattgg gtttttggac 1200

gggtttcgttt tgagagaagt gtacttccga atcgttcaac atgaagagaa aaattattct 1260
 gatgtggcta aagaagacct tgaattattc caagaattag gtattgaatg tcccgaagaa 1320
 tttagtggta aagctcctga aattaacact attgggttaca gaacatccca atatattaat 1380
 aggatctgct caactccatg gagtggttctt gtatccgtca tcatcatcat tggtttaatt 1440
 tgtattgctt ccggtttgcg ttggagtaca acaggtcaat tgattgctaa caccgcaact 1500
 atgattatcg aagaattttt cttgctagtt ttggttgcaag cacataattg ggccgatcgt 1560
 caaagaagag tggagggttac cgctttgtac gcacgtaggc gcatacttct atcatacgta 1620
 gaaaagcggt tcccagaggt tatgatgttg gaaaaatag 1659

<210> 166
 <211> 552
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 166

Met Gly Lys Ile Ala Glu Phe Leu Gly Asn Pro Gly Ala Arg Pro Asp
 1 5 10 15

Val His His Arg Ala Pro Thr Val Asp Cys Lys Gln Tyr Glu Glu Phe
 20 25 30

Gly Asp Ser Asn Asp Tyr Lys Asn Asp Asp Val Val Arg Val Val Ser
 35 40 45

His Ser Asp Glu Ser Thr Asp Asp Glu Leu Cys Asn Val Asn Leu Thr
 50 55 60

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

Gly Phe Thr Asp Lys Thr Leu Asp Phe Leu Val Arg Val Ala Gly Ser
 85 90 95

Gln Ala Val Phe Phe Ile Val Trp Ile Ile Leu Ile Ile Trp Val Val
 100 105 110

Ile Gly Ile Val Tyr Asn Ala Pro Phe Asn Trp Gln Val Val Met Gln
 115 120 125

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

Gln Gln Leu Met Ser Thr His Glu Gln Ile Leu Ile Cys Gly Arg Leu
145 150 155 160

Lys Ser Arg Leu Ala Ser Phe Lys Asn Tyr Leu Thr Arg Ser Thr Pro
165 170 175

Glu Glu Glu Lys Ala Asp Cys Thr Val Glu Ala Asn Glu Val Ser Ser
180 185 190

Val Glu Asn His Ile Asp Pro Ser Ala Ile Asn Gly Glu Leu Pro Val
195 200 205

Glu Asn Trp Tyr Asp Arg Leu Ser Asn Val Ala Ser Arg Tyr Met Gly
210 215 220

Ser Ile Ala Ala Met Val Ile Phe Trp Ile Gly Ile Phe Val Trp Ile
225 230 235 240

Gly Cys Gly Ala Ile Pro Lys Asp Ala Gly Asn Thr Pro Pro Tyr Thr
245 250 255

Gly Glu Thr Thr Gly Ser Asn Pro Arg Leu Lys Lys Phe Ser Asp Ala
260 265 270

Trp Gln Met Tyr Ile Asn Thr Ala Val Ala Val Ser Leu Leu Ile Cys
275 280 285

Thr Thr Phe Leu Gln Asn Ile Arg Ala Arg His Asp Tyr Phe Thr Gly
290 295 300

Arg Phe Leu Val Asp Ile Phe Asp Met Asp Glu Lys Ile Asp Tyr Arg
305 310 315 320

Ile Arg Lys His Phe Asn Asp Phe Glu Thr Pro His Pro Val Val Thr
325 330 335

Ile Glu Ser Lys Lys Arg Ser Thr Gly Arg Lys Met Ile Asp Trp Tyr
340 345 350

Ala Asp Ile Ile Gly Thr Gly Ile Gly Val Leu Ile Gly Val Ala Val
355 360 365

Phe Ala Thr Trp Ile Gly Ile Gly Ser Pro Met Lys Trp Asp Asp Asn

370 375 380
 Trp Trp Leu Ile Ile Gly Thr Tyr Thr Gly Leu Ile Gly Phe Leu Asp
 385 390 395 400
 Gly Phe Val Leu Arg Glu Val Tyr Phe Arg Ile Val Gln His Glu Glu
 405 410 415
 Lys Asn Tyr Ser Asp Val Ala Lys Glu Asp Leu Glu Leu Phe Gln Glu
 420 425 430
 Leu Gly Ile Glu Cys Pro Glu Glu Phe Ser Gly Lys Ala Pro Glu Ile
 435 440 445
 Asn Thr Ile Gly Tyr Arg Thr Ser Gln Tyr Ile Asn Arg Ile Cys Ser
 450 455 460
 Thr Pro Trp Ser Val Leu Val Ser Val Ile Ile Ile Ile Gly Leu Ile
 465 470 475 480
 Cys Ile Ala Ser Gly Leu Arg Trp Ser Thr Thr Gly Gln Leu Ile Ala
 485 490 495
 Asn Thr Pro Thr Met Ile Ile Glu Glu Phe Phe Leu Leu Val Leu Leu
 500 505 510
 Gln Ala His Asn Trp Ala Asp Arg Gln Arg Arg Val Glu Val Thr Ala
 515 520 525
 Leu Tyr Ala Arg Arg Arg Ile Leu Leu Ser Tyr Val Glu Lys Arg Phe
 530 535 540
 Pro Glu Val Met Met Leu Glu Lys
 545 550

<210> 167
 <211> 1869
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 167
 atgttggttct actcgttcgt gtggtctgta ctggccgcta gtgttgcttt ggcaaagaca 60
 cataagttaa actataccgc ttcttgggta actgccaatc ctgatggatt gcatgaaaaa 120
 aggatgattg gttttaatgg cgaatggcca cttccagata tccatgttga aaaaggagat 180

cgtgttgagc tttatttgac taacggcttt caagacaata ctgctacttc tctacatttc	240
catggtccttt tccagaatac gagtttgggg aaccagcttc aaatggatgg tccttctatg	300
gtgacacaat gtcccatcgt tccgggacaa acatacctgt acaacttcac tgtcccagag	360
caggtaggaa cgttctggta ccatgcacac atgggtgccc agtacgggtga cggtatgagg	420
ggtgcattta tcatccacga tccggaggag cccttcgaat atgatcatga acgagtcac	480
actctatcgg accattatca cgaaaattat aaaacggtta ccaaagagtt tctgtcaaga	540
tataatccaa ccggtgctga acctattcct caaaatattc tttttaataa tacgatgaat	600
gtaacttttag attttacacc cggtgaaacg tatctcttca ggttcttgaa cgttgggctg	660
tttgtatccc agtatatcat tcttgaggat catgaaatga gtatagtaga ggtggacggt	720
gtttacgtaa agccaaactt tactgattcg atatatcttt ctgcggggca aagaatgagt	780
gtgttgatta aagctaaaga taaaatgcct acaagaaact acgctatgat gcaaataatg	840
gatgagacga tgcttgatgt tgtcccacct gagttacaac tcaaccaaac tatccaaatg	900
aggatatggcc actcgttgcc ggaggcacgc gcattgaaca ttgaagattg tgacttggac	960
cgcgccacga atgactttta cctagaacct ctgattgaga gagacctact tgctcactat	1020
gaccaccaaa ttgtcatgga tgtaagaatg gtcaacttgg gtgatggtgt gaagtatgca	1080
tttttcaata atatcactta cgtcacacca aagggtgccta ctttgacaac gttgcttacc	1140
tcaggaaaagc ttgcgtcaga tcctagaatt tatgggtgata atatcaatgc gcagttattg	1200
aaacataatg atatcataga ggttgttcta aacaattatg attctggcag acatccattc	1260
catttgcacg gtcataatth ccaaatagtc caaaagtcgc cagggttcca tgttgatgaa	1320
gcttatgacg aatctgagca agatgaaatg accgtccctt ataacgaatc tgcgccatta	1380
caaccgttcc ctgagaggcc gatggtgaga gatacagtgg ttcttgaacc tagtggacat	1440
gttgtcctga gatttagagc tgacaacctt ggtgtctggt atttccattg tcatgtagat	1500
tggcacttac aacaaggtht ggcttcggtc tttattgagg caccgthttt acttcaggaa	1560
agggaaaagc ttaatgagaa ctatctggat atatgcaaag ccgctgatat tccggtagtt	1620
ggtaatgctg caggtcattc gaatgattgg tttgacttaa aaggattacc aagacaacct	1680
gagccactac caaagggtt tactactgaa ggatatttgg cattgattat ttcaaccatt	1740
atcgggtgtct ggggcctata ttccattgct cagtatggta ttggcgagggt tatccctaac	1800
gatgagaagg tgtaccacac gttaaggga atcttggctg aaaatgaaat agaggthttc	1860
cgcggtctaa	1869

<210> 168
 <211> 622
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 168

Met Leu Phe Tyr Ser Phe Val Trp Ser Val Leu Ala Ala Ser Val Ala
 1 5 10 15

Leu Ala Lys Thr His Lys Leu Asn Tyr Thr Ala Ser Trp Val Thr Ala
 20 25 30

Asn Pro Asp Gly Leu His Glu Lys Arg Met Ile Gly Phe Asn Gly Glu
 35 40 45

Trp Pro Leu Pro Asp Ile His Val Glu Lys Gly Asp Arg Val Glu Leu
 50 55 60

Tyr Leu Thr Asn Gly Phe Gln Asp Asn Thr Ala Thr Ser Leu His Phe
 65 70 75 80

His Gly Leu Phe Gln Asn Thr Ser Leu Gly Asn Gln Leu Gln Met Asp
 85 90 95

Gly Pro Ser Met Val Thr Gln Cys Pro Ile Val Pro Gly Gln Thr Tyr
 100 105 110

Leu Tyr Asn Phe Thr Val Pro Glu Gln Val Gly Thr Phe Trp Tyr His
 115 120 125

Ala His Met Gly Ala Gln Tyr Gly Asp Gly Met Arg Gly Ala Phe Ile
 130 135 140

Ile His Asp Pro Glu Glu Pro Phe Glu Tyr Asp His Glu Arg Val Ile
 145 150 155 160

Thr Leu Ser Asp His Tyr His Glu Asn Tyr Lys Thr Val Thr Lys Glu
 165 170 175

Phe Leu Ser Arg Tyr Asn Pro Thr Gly Ala Glu Pro Ile Pro Gln Asn
 180 185 190

Ile Leu Phe Asn Asn Thr Met Asn Val Thr Leu Asp Phe Thr Pro Gly
 195 200 205

Glu Thr Tyr Leu Phe Arg Phe Leu Asn Val Gly Leu Phe Val Ser Gln
 210 215 220

Tyr Ile Ile Leu Glu Asp His Glu Met Ser Ile Val Glu Val Asp Gly
 225 230 235 240

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

Gln Arg Met Ser Val Leu Ile Lys Ala Lys Asp Lys Met Pro Thr Arg
 260 265 270

Asn Tyr Ala Met Met Gln Ile Met Asp Glu Thr Met Leu Asp Val Val
 275 280 285

Pro Pro Glu Leu Gln Leu Asn Gln Thr Ile Gln Met Arg Tyr Gly His
 290 295 300

Ser Leu Pro Glu Ala Arg Ala Leu Asn Ile Glu Asp Cys Asp Leu Asp
 305 310 315 320

Arg Ala Thr Asn Asp Phe Tyr Leu Glu Pro Leu Ile Glu Arg Asp Leu
 325 330 335

Leu Ala His Tyr Asp His Gln Ile Val Met Asp Val Arg Met Val Asn
 340 345 350

Leu Gly Asp Gly Val Lys Tyr Ala Phe Phe Asn Asn Ile Thr Tyr Val
 355 360 365

Thr Pro Lys Val Pro Thr Leu Thr Thr Leu Leu Thr Ser Gly Lys Leu
 370 375 380

Ala Ser Asp Pro Arg Ile Tyr Gly Asp Asn Ile Asn Ala Gln Leu Leu
 385 390 395 400

Lys His Asn Asp Ile Ile Glu Val Val Leu Asn Asn Tyr Asp Ser Gly
 405 410 415

Arg His Pro Phe His Leu His Gly His Asn Phe Gln Ile Val Gln Lys
 420 425 430

Ser Pro Gly Phe His Val Asp Glu Ala Tyr Asp Glu Ser Glu Gln Asp
 435 440 445

Glu Met Thr Val Pro Tyr Asn Glu Ser Ala Pro Leu Gln Pro Phe Pro
 450 455 460

Glu Arg Pro Met Val Arg Asp Thr Val Val Leu Glu Pro Ser Gly His
 465 470 475 480

Val Val Leu Arg Phe Arg Ala Asp Asn Pro Gly Val Trp Tyr Phe His
 485 490 495

Cys His Val Asp Trp His Leu Gln Gln Gly Leu Ala Ser Val Phe Ile
 500 505 510

Glu Ala Pro Val Leu Leu Gln Glu Arg Glu Lys Leu Asn Glu Asn Tyr
 515 520 525

Leu Asp Ile Cys Lys Ala Ala Asp Ile Pro Val Val Gly Asn Ala Ala
 530 535 540

Gly His Ser Asn Asp Trp Phe Asp Leu Lys Gly Leu Pro Arg Gln Pro
 545 550 555 560

Glu Pro Leu Pro Lys Gly Phe Thr Thr Glu Gly Tyr Leu Ala Leu Ile
 565 570 575

Ile Ser Thr Ile Ile Gly Val Trp Gly Leu Tyr Ser Ile Ala Gln Tyr
 580 585 590

Gly Ile Gly Glu Val Ile Pro Asn Asp Glu Lys Val Tyr His Thr Leu
 595 600 605

Arg Glu Ile Leu Ala Glu Asn Glu Ile Glu Val Ser Arg Gly
 610 615 620

<210> 169
 <211> 1398
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 169
 atggcggttg aggattat ttctttccag atattcttca ttttcttaag gaaatcctta 60
 gaaattgttg tcattgtttc tatcctgttg acgatcgtca aacaagatct gtctgttgag 120
 gacgacagcc cgtttgaagg aagttcctct tctgctgggc ttccaagtcc aaatacgaac 180
 acaaacgcag attcgaccac tgccttctta caagcagggc cttcagacgg taatgctatt 240

ggaacgtccg ctacggctgc taataataaa tcgaggccgc taaatgtgga ggaagaagaa 300
gaaatttacg agtactctaa tgagcttaga gaccaggacc gcgagtccga tgaacatacg 360
gctgacaacg ttaagctata tcagaaatta aaaatacaaa ttctagcggg cggcgcattt 420
ggtttgttgc tgtgtatggt aatcgggggt gcgtttgtta gtatctttta tcatattgga 480
accgacttat ggacactgag tgaacattat tatgaagggtg tcttaagtct tgtcgcgtcc 540
gttattattt ctgtcatggg gttgtttttt ttaagaatgg ggaagttaag agagaagttc 600
agagtgaat tagcttctat cattttattca aaggacaata atttgctggg aaacaaaacc 660
caaaaagggtg tgaaattcag tcaaaagtac tccttcttca tattaccatt tataacgact 720
ttgagagaag ggtagaagc tgtgtattca attggaggta tcggtattga ccaaccacta 780
tcctcgattc ccctctctat ggtccttgct actgcaatca gtacggtggt cggtattttt 840
ttcttcaggt actcaagttc tctttcactt aagatatgcc ttgtagtcgc cacctgcttc 900
ctctacttga tcgcggtcgg tttgttttcc aaagggtgat ggcaacttga attgcaagac 960
tacgtcaaca aatgtaacgg tcaagacatg agtgaagtag aaaatggacc cggttcgtac 1020
gacatatctc gttctgtttg gcatgttaat tgttgcaatg gtgaaaaaga tggagggttg 1080
atgattttta ctgccatttt tggttggacg aatagtgtca ccgtcggctc tgtaattagc 1140
tacaacgcct actggttggt attaaaatac gctttgaagc ttctaatagat agaaggaaaa 1200
tgccgatata tcccatatct acctattagc tggcaaaaaga aacgtattat gaaaagatta 1260
agcattgcca aggcacgct cgatctcaaa catcatactt ctgaactcaa ctctagcaca 1320
tcagagccag acagtcaaag acggtccaaa gatagttctg tgcccctaata aattgatagc 1380
agtggttcag caaattga 1398

<210> 170
<211> 465
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 170

Met Ala Phe Glu Asp Tyr Phe Ser Phe Gln Ile Phe Phe Ile Phe Leu
1 5 10 15

Arg Lys Ser Leu Glu Ile Val Val Ile Val Ser Ile Leu Leu Thr Ile
20 25 30

Val Lys Gln Asp Leu Ser Val Glu Asp Asp Ser Pro Phe Glu Gly Ser
35 40 45

Ser Ser Ser Ala Gly Leu Pro Ser Pro Asn Thr Asn Thr Asn Ala Asp
50 55 60

Ser Thr Thr Ala Phe Leu Gln Ala Gly Pro Ser Asp Gly Asn Ala Ile
65 70 75 80

Gly Thr Ser Ala Thr Ala Ala Asn Asn Lys Ser Arg Pro Leu Asn Val
85 90 95

Glu Glu Glu Glu Glu Ile Tyr Glu Tyr Ser Asn Glu Leu Arg Asp Gln
100 105 110

Asp Arg Glu Ser Asp Glu His Thr Ala Asp Asn Val Lys Leu Tyr Gln
115 120 125

Lys Leu Lys Ile Gln Ile Leu Ala Gly Gly Ala Phe Gly Leu Leu Leu
130 135 140

Cys Met Leu Ile Gly Gly Ala Phe Val Ser Ile Phe Tyr His Ile Gly
145 150 155 160

Thr Asp Leu Trp Thr Leu Ser Glu His Tyr Tyr Glu Gly Val Leu Ser
165 170 175

Leu Val Ala Ser Val Ile Ile Ser Val Met Gly Leu Phe Phe Leu Arg
180 185 190

Met Gly Lys Leu Arg Glu Lys Phe Arg Val Lys Leu Ala Ser Ile Ile
195 200 205

Tyr Ser Lys Asp Asn Asn Leu Leu Gly Asn Lys Thr Gln Lys Gly Val
210 215 220

Lys Phe Ser Gln Lys Tyr Ser Phe Phe Ile Leu Pro Phe Ile Thr Thr
225 230 235 240

Leu Arg Glu Gly Leu Glu Ala Val Tyr Ser Ile Gly Gly Ile Gly Ile
245 250 255

Asp Gln Pro Leu Ser Ser Ile Pro Leu Ser Met Val Leu Ala Thr Ala
260 265 270

Ile Ser Thr Val Phe Gly Ile Phe Phe Phe Arg Tyr Ser Ser Ser Leu
275 280 285

Ser Leu Lys Ile Cys Leu Val Val Ala Thr Cys Phe Leu Tyr Leu Ile
 290 295 300

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

Tyr Val Asn Lys Cys Asn Gly Gln Asp Met Ser Glu Val Glu Asn Gly
 325 330 335

Pro Gly Ser Tyr Asp Ile Ser Arg Ser Val Trp His Val Asn Cys Cys
 340 345 350

Asn Gly Glu Lys Asp Gly Gly Trp Met Ile Phe Thr Ala Ile Phe Gly
 355 360 365

Trp Thr Asn Ser Ala Thr Val Gly Ser Val Ile Ser Tyr Asn Ala Tyr
 370 375 380

Trp Leu Val Leu Lys Tyr Ala Leu Lys Leu Leu Met Ile Glu Gly Lys
 385 390 395 400

Cys Gly Tyr Ile Pro Tyr Leu Pro Ile Ser Trp Gln Lys Lys Arg Ile
 405 410 415

Met Lys Arg Leu Ser Ile Ala Lys Ala Ser Leu Asp Leu Lys His His
 420 425 430

Thr Ser Glu Leu Asn Ser Ser Thr Ser Glu Pro Asp Ser Gln Arg Arg
 435 440 445

Ser Lys Asp Ser Ser Val Pro Leu Ile Ile Asp Ser Ser Gly Ser Ala
 450 455 460

Asn
 465

<210> 171
 <211> 3015
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 171
 atgagagaag tgatacttgc tgtacatgga atgacatgca ggcctgtac taataacaatc 60
 aatacgcagt tacgagcttt aaagggtgta acaaaatgtg atattagttt agtgactaat 120

gagtgccagg	tgacatacga	taacgagggt	accgccgatt	ctattaagga	aattatagag	180
gatttgtggat	ttgactgtga	gatactaaga	gattctgaaa	ttacagccat	aagtacgaag	240
gaaggactac	tgagtgtaca	aggtatgacc	tgtgggtcct	gtgtttctac	agtcaccaaa	300
caagtggaag	gcattgaggg	tgttgaatcg	gtagtcgttt	ccttggtaac	ggaagagtgc	360
catgttattt	atgaaccgtc	caagacaacg	ctagaaaccg	ccagagaaat	gattgaagac	420
tgtggatttg	actcaaatat	tattatggat	ggcaacggga	atgcagacat	gaccgaaaaa	480
acggtgatct	tgaagtaac	taaggctttc	gaggacgaat	cccactcat	actttcttca	540
gtaagcgaaa	ggtttcaatt	tttgtagac	ctaggtgtaa	aatcgataga	aatttctgat	600
gatatgcaca	cactcaccat	aaaatactgt	tgtaacgaac	tcggcattag	agatttattg	660
aggcaccttg	agaggaccgg	atataaattc	actgtatttt	ccaatttaga	taatactacc	720
cagttaaggc	ttctctctaa	agaggacgag	ataagattct	ggaaaaaaaa	cagcataaaa	780
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acaattgttc	aggaccgcat	attcccttac	aaagaaacct	cctttgttag	aggctctgtc	900
tacagagata	ttttgggtgt	aataattggca	agctatattc	agttcagcgt	tggtttttac	960
ttttacaagg	cagcatgggc	atctttaaag	cacgggttcag	gaaccatgga	tacactagtt	1020
tgtgtttcca	ctacttgtgc	atacacattt	tctgtgtttt	ctttagttca	caatatgttc	1080
catccctcaa	gtactggcaa	actcccaagg	atcgttttcg	acacatcaat	catgatcatt	1140
tcatatatatt	ccatcgggaa	atatttgga	acttttagcta	aatcacaaac	atcaaccgca	1200
ctttctaaat	taattcagct	cactccatcg	gtgtgttcaa	ttatatctga	cgtggagcgg	1260
aatgaaacca	aggaaattcc	catagaatta	ttgcaagtga	acgatatagt	ggagattaaa	1320
ccagggatga	aaattcctgc	tgatggcatc	ataacaagag	gtgaatctga	aattgacgag	1380
tcgttaatga	caggcgaatc	cattttggtg	ccaagaaaa	ctggttttcc	ggttattgct	1440
ggttctgtta	atggacctgg	acatttctac	ttcagaacta	ctaccgttgg	ggaggaaact	1500
aaattagcaa	atattatcaa	ggtaatgaaa	gaagcacaat	tgagtaaagc	tcccatcag	1560
gggtatgcag	attatttagc	ctctattttt	gttcggggga	tcctaatttt	ggcagtattg	1620
actttcttta	tttgggtgtt	tattttaaac	atctcggcta	atcctcccgt	cgttttcacc	1680
gcaaatacta	aggctgataa	tttttttatt	tgcttacaaa	ctgctacttc	tgttgtcatc	1740
gtcgcacgcc	catgtgcatt	gggacttgcc	acgccgactg	ctataatggt	gggtacaggg	1800
gttgagagctc	agaatggtgt	cttaataaag	ggcggagaag	tattggaaaa	attcaatagt	1860

attactactt ttgtttttga taaaacaggt accttaacta caggttttat ggttgtgaaa 1920
 aagttcctta aagattcaaa ttgggttgga aacgtggatg aagacgaagt tctcgctgt 1980
 ataaaagcaa cggaatccat tagtgaccat ccagtttcga aagcaattat acgttattgt 2040
 gatggtttga actgtaataa ggcttttaaat gccgttgttt tagaaagcga atacgtgctt 2100
 ggaaagggaa tagtctcaaa gtgtcaagtt aatggaaata cttatgatat ttgtattggg 2160
 aacgagggcg tgattttgga ggatgcatta aaaaaatccg gatttattaa cagtaatgtc 2220
 gaccaaggaa acactgtatc atacgtatca gtaaacgggc atgtgtttgg cttgttcgag 2280
 attaatgatg aagttaaaca tgattcttac gcaacagttc agtatctaca aagaaatgga 2340
 tatgaaacgt atatgattac tggcgataat aactcagcag caaaaagagt cgctagagaa 2400
 gtaggtataa gcttcgaaaa tgtttacagc gatgtgtcac ccacaggcaa atgtgatctc 2460
 gtgaaaaaaaa ttcaagataa agaaggtaat aacaaggttg ctgttggttg cgatggcatt 2520
 aacgacgctc ccgctttagc actgagtgat ctaggtattg ccatttcaac aggtacggag 2580
 attgctattg aagcagctga tattgttata ctgtgcggta atgatctgaa tactaatagt 2640
 ttgagaggac tggccaacgc catcgatatt tcaactaaaa cgttcaaaag aataaagctg 2700
 aatttgttct gggcactttg ctataatata ttcattgattc cgattgctat ggggtgtgctc 2760
 attccttggg gcataactct tcctccaatg ctgcgcgggt tagcgatggc attcagctcg 2820
 gtcagtgtcg ttctaagttc attgatgttg aagaagtgga ctccaccgga tattgaatca 2880
 catgggattt cagatttcaa gtccaaattt tcgattggga atttttggtc aaggcttttt 2940
 tctacgcggg ctattgcagg tgagcaagac atagaatcac aggccggact aatgtcaaac 3000
 gaagaagtct tgtaa 3015

<210> 172
 <211> 1004
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 172

Met Arg Glu Val Ile Leu Ala Val His Gly Met Thr Cys Ser Ala Cys
 1 5 10 15

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

Cys Asp Ile Ser Leu Val Thr Asn Glu Cys Gln Val Thr Tyr Asp Asn
 35 40 45

Glu Val Thr Ala Asp Ser Ile Lys Glu Ile Ile Glu Asp Cys Gly Phe
50 55 60

Asp Cys Glu Ile Leu Arg Asp Ser Glu Ile Thr Ala Ile Ser Thr Lys
65 70 75 80

Glu Gly Leu Leu Ser Val Gln Gly Met Thr Cys Gly Ser Cys Val Ser
85 90 95

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

Val Ser Leu Val Thr Glu Glu Cys His Val Ile Tyr Glu Pro Ser Lys
115 120 125

Thr Thr Leu Glu Thr Ala Arg Glu Met Ile Glu Asp Cys Gly Phe Asp
130 135 140

Ser Asn Ile Ile Met Asp Gly Asn Gly Asn Ala Asp Met Thr Glu Lys
145 150 155 160

Thr Val Ile Leu Lys Val Thr Lys Ala Phe Glu Asp Glu Ser Pro Leu
165 170 175

Ile Leu Ser Ser Val Ser Glu Arg Phe Gln Phe Leu Leu Asp Leu Gly
180 185 190

Val Lys Ser Ile Glu Ile Ser Asp Asp Met His Thr Leu Thr Ile Lys
195 200 205

Tyr Cys Cys Asn Glu Leu Gly Ile Arg Asp Leu Leu Arg His Leu Glu
210 215 220

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

Gln Leu Arg Leu Leu Ser Lys Glu Asp Glu Ile Arg Phe Trp Lys Lys
245 250 255

Asn Ser Ile Lys Ser Thr Leu Leu Ala Ile Ile Cys Met Leu Leu Tyr
260 265 270

Met Ile Val Pro Met Met Trp Pro Thr Ile Val Gln Asp Arg Ile Phe
275 280 285

Pro Tyr Lys Glu Thr Ser Phe Val Arg Gly Leu Phe Tyr Arg Asp Ile
290 295 300

Leu Gly Val Ile Leu Ala Ser Tyr Ile Gln Phe Ser Val Gly Phe Tyr
305 310 315 320

Phe Tyr Lys Ala Ala Trp Ala Ser Leu Lys His Gly Ser Gly Thr Met
325 330 335

Asp Thr Leu Val Cys Val Ser Thr Thr Cys Ala Tyr Thr Phe Ser Val
340 345 350

Phe Ser Leu Val His Asn Met Phe His Pro Ser Ser Thr Gly Lys Leu
355 360 365

Pro Arg Ile Val Phe Asp Thr Ser Ile Met Ile Ile Ser Tyr Ile Ser
370 375 380

Ile Gly Lys Tyr Leu Glu Thr Leu Ala Lys Ser Gln Thr Ser Thr Ala
385 390 395 400

Leu Ser Lys Leu Ile Gln Leu Thr Pro Ser Val Cys Ser Ile Ile Ser
405 410 415

Asp Val Glu Arg Asn Glu Thr Lys Glu Ile Pro Ile Glu Leu Leu Gln
420 425 430

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

Gly Ile Ile Thr Arg Gly Glu Ser Glu Ile Asp Glu Ser Leu Met Thr
450 455 460

Gly Glu Ser Ile Leu Val Pro Lys Lys Thr Gly Phe Pro Val Ile Ala
465 470 475 480

Gly Ser Val Asn Gly Pro Gly His Phe Tyr Phe Arg Thr Thr Thr Val
485 490 495

Gly Glu Glu Thr Lys Leu Ala Asn Ile Ile Lys Val Met Lys Glu Ala
500 505 510

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

515		520		525
Ile Phe Val Pro Gly Ile Leu Ile Leu Ala Val Leu Thr Phe Phe Ile				
530		535		540
Trp Cys Phe Ile Leu Asn Ile Ser Ala Asn Pro Pro Val Ala Phe Thr				
545		550		555
Ala Asn Thr Lys Ala Asp Asn Phe Phe Ile Cys Leu Gln Thr Ala Thr				
	565		570	575
Ser Val Val Ile Val Ala Cys Pro Cys Ala Leu Gly Leu Ala Thr Pro				
	580		585	590
Thr Ala Ile Met Val Gly Thr Gly Val Gly Ala Gln Asn Gly Val Leu				
	595		600	605
Ile Lys Gly Gly Glu Val Leu Glu Lys Phe Asn Ser Ile Thr Thr Phe				
610		615		620
Val Phe Asp Lys Thr Gly Thr Leu Thr Thr Gly Phe Met Val Val Lys				
625		630		635
Lys Phe Leu Lys Asp Ser Asn Trp Val Gly Asn Val Asp Glu Asp Glu				
	645		650	655
Val Leu Ala Cys Ile Lys Ala Thr Glu Ser Ile Ser Asp His Pro Val				
	660		665	670
Ser Lys Ala Ile Ile Arg Tyr Cys Asp Gly Leu Asn Cys Asn Lys Ala				
	675		680	685
Leu Asn Ala Val Val Leu Glu Ser Glu Tyr Val Leu Gly Lys Gly Ile				
	690		695	700
Val Ser Lys Cys Gln Val Asn Gly Asn Thr Tyr Asp Ile Cys Ile Gly				
705		710		715
Asn Glu Ala Leu Ile Leu Glu Asp Ala Leu Lys Lys Ser Gly Phe Ile				
	725		730	735
Asn Ser Asn Val Asp Gln Gly Asn Thr Val Ser Tyr Val Ser Val Asn				
	740		745	750

Gly His Val Phe Gly Leu Phe Glu Ile Asn Asp Glu Val Lys His Asp
755 760 765

Ser Tyr Ala Thr Val Gln Tyr Leu Gln Arg Asn Gly Tyr Glu Thr Tyr
770 775 780

Met Ile Thr Gly Asp Asn Asn Ser Ala Ala Lys Arg Val Ala Arg Glu
785 790 795 800

Val Gly Ile Ser Phe Glu Asn Val Tyr Ser Asp Val Ser Pro Thr Gly
805 810 815

Lys Cys Asp Leu Val Lys Lys Ile Gln Asp Lys Glu Gly Asn Asn Lys
820 825 830

Val Ala Val Val Gly Asp Gly Ile Asn Asp Ala Pro Ala Leu Ala Leu
835 840 845

Ser Asp Leu Gly Ile Ala Ile Ser Thr Gly Thr Glu Ile Ala Ile Glu
850 855 860

Ala Ala Asp Ile Val Ile Leu Cys Gly Asn Asp Leu Asn Thr Asn Ser
865 870 875 880

Leu Arg Gly Leu Ala Asn Ala Ile Asp Ile Ser Leu Lys Thr Phe Lys
885 890 895

Arg Ile Lys Leu Asn Leu Phe Trp Ala Leu Cys Tyr Asn Ile Phe Met
900 905 910

Ile Pro Ile Ala Met Gly Val Leu Ile Pro Trp Gly Ile Thr Leu Pro
915 920 925

Pro Met Leu Ala Gly Leu Ala Met Ala Phe Ser Ser Val Ser Val Val
930 935 940

Leu Ser Ser Leu Met Leu Lys Lys Trp Thr Pro Pro Asp Ile Glu Ser
945 950 955 960

His Gly Ile Ser Asp Phe Lys Ser Lys Phe Ser Ile Gly Asn Phe Trp
965 970 975

Ser Arg Leu Phe Ser Thr Arg Ala Ile Ala Gly Glu Gln Asp Ile Glu
980 985 990

Ser Gln Ala Gly Leu Met Ser Asn Glu Glu Val Leu
 995 1000

<210> 173
 <211> 2160
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 173
 atgttggttg tacatattat atctttcctt ctgttcttcc agctttcggc cgcaaaggcc 60
 ccaccagta aaacgtctct aataaatact catgagagaa ggtcgatata ttcattgctac 120
 gttgggtttac gtaaagaaac atgggggttc aatgggtccg ctatatgtcg gtatgaacca 180
 gcaatccaat cgatgcttta ctgtctttac gaagacacgc atgagaaagg gtattcaaatt 240
 aaaacttttg agaaagggtt tgaagaaatg agacaatttt gctatacacc aaagtttttg 300
 aacatgactg atgccgagtt ttacacctca ttggataatg gaacatacta tatacaagat 360
 caacctaaag ctggcatcaa tatcacttat cctatcagac tgaacactac actaagaaaa 420
 gcatactatg atgcatacta tggttactac tataaccatg acattccgta ttatttcggg 480
 ggcatttatct gtgcatactt tgtgggtgtc atgttgcttg caggtttaatt tcgttttttg 540
 aattataccc caataaaaaa gattatgttt cagcaaaagc tagtcaatta cgtgagaggt 600
 tatactactc taccactctt ttatgaaaag catgcagagc ccttctcgta cttaaaagtg 660
 ataacaggct atcttcttac taggtttgaa acgttggtta ttttaggcta cctcactatt 720
 cataccattt tcatggccta caaatatcaa tatgatccat accacatcat atttgccgct 780
 catagagcag aagtggcaca ttttggtgag tacagaagcg gtatactttc ttttgccac 840
 ctgccactca ttgttttatt tgcgggaaga aataactttc tccaacttat ttctggcttg 900
 aagcatacct cattcattgt gttccataag tggctgggaa gaatgatgtt tcttgatgca 960
 ataattcatg ctgccggctt tacgaactat tatttgtatt ataaaaaatg gaatacgggt 1020
 agattaagag tctactggaa attcgggtatt gctaccacct gtttagcggg aatgttaatt 1080
 ttcttttcca tcgcagcatt tagaagacac tactatgaaa cgtttatggc cctccatata 1140
 gtattcgcag cactatttct ctatacttgt tgggagcatg ttactaactt cagcgggtatc 1200
 gaatggattt acgcggcaat agcaatttgg ggagttgata gaattgtacg tatcaccaga 1260
 attgcactct taggatttcc taaagcagat ctacaactgg ttggatctga tttgggtccg 1320
 gtaacgggta aaaaaccaa gaagttttgg aaggcaaac caggccaata cgttttcgtt 1380
 tccttcttgc gtccattgtg cttctggcag tcgcatccat ttacagtgat ggattcttgc 1440

gtaaacgata gagaattggt catcggttctg aaagcaaaga aaggtgtgac aaaactggta 1500
 agaaactttg ttgaacgtaa aggcggcaag gcatccatga gattagctat cgaaggccct 1560
 tatggctcca agtccaccgc ccatcgcttt gataatgtat tattgttggc aggtggctca 1620
 gggcttcccg gtccaatttc tcatgccctt gaattaggaa agacaacagc tgcaagcggc 1680
 aaaaactttg tacagttagt catagcagta agaggactag acatgctcaa cgcgtgtaag 1740
 aaagaactaa tggcattaaa gggcttgaat gttcaagttc acatttataa ttctaagcaa 1800
 gagctagctt cggctgaaaa aatttcctca aatgaagtca aaaacgggtga aacgacagca 1860
 gagaaggccc catctagtct aagcaattca gaaaaagctc cttctgaaag tgaaaataca 1920
 gaactacctc tttccctgaa tgacacgtct atctccgatt tagaatttgc cactttccat 1980
 gttggaaggc caaatgttga agaaatacta aatgaatctg ttaaccattc tggttcactt 2040
 gccgtcgtat gttgcggacc acctattttc gtcgacaccg ctagaaatca aactgccaaa 2100
 gctgttatca gaaaccatc aagaatgatt gaatacttgg aggaatacca agcctggtga 2160

<210> 174
 <211> 719
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 174

Met Leu Leu Val His Ile Ile Ser Phe Leu Leu Phe Phe Gln Leu Ser
 1 5 10 15

Ala Ala Lys Ala Pro Pro Ser Lys Thr Ser Leu Ile Asn Thr His Glu
 20 25 30

Arg Arg Ser Ile Tyr Ser Cys Tyr Val Gly Leu Arg Lys Glu Thr Trp
 35 40 45

Gly Phe Asn Gly Ser Ala Ile Cys Arg Tyr Glu Pro Ala Ile Gln Ser
 50 55 60

Met Leu Tyr Cys Leu Tyr Glu Asp Thr His Glu Lys Gly Tyr Ser Asn
 65 70 75 80

Lys Thr Leu Glu Lys Gly Phe Glu Glu Met Arg Gln Phe Cys Tyr Thr
 85 90 95

Pro Lys Phe Leu Asn Met Thr Asp Ala Glu Phe Tyr Thr Ser Leu Asp
 100 105 110

Asn Gly Thr Tyr Tyr Ile Gln Asp Gln Pro Lys Ala Gly Ile Asn Ile
115 120 125

Thr Tyr Pro Ile Arg Leu Asn Thr Thr Leu Arg Lys Ala Tyr Tyr Asp
130 135 140

Ala Tyr Tyr Gly Tyr Tyr Tyr Asn His Asp Ile Pro Tyr Tyr Phe Gly
145 150 155 160

Gly Ile Ile Cys Ala Tyr Phe Val Gly Val Met Leu Leu Ala Gly Leu
165 170 175

Ile Arg Phe Leu Asn Tyr Thr Pro Ile Lys Lys Ile Met Phe Gln Gln
180 185 190

Lys Leu Val Asn Tyr Val Arg Gly Tyr Thr Thr Leu Pro Thr Leu Tyr
195 200 205

Glu Lys His Ala Glu Pro Phe Ser Tyr Leu Lys Val Ile Thr Gly Tyr
210 215 220

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

His Thr Ile Phe Met Ala Tyr Lys Tyr Gln Tyr Asp Pro Tyr His Ile
245 250 255

Ile Phe Ala Ala His Arg Ala Glu Val Ala His Phe Val Ala Tyr Arg
260 265 270

Ser Gly Ile Leu Ser Phe Ala His Leu Pro Leu Ile Val Leu Phe Ala
275 280 285

Gly Arg Asn Asn Phe Leu Gln Leu Ile Ser Gly Leu Lys His Thr Ser
290 295 300

Phe Ile Val Phe His Lys Trp Leu Gly Arg Met Met Phe Leu Asp Ala
305 310 315 320

Ile Ile His Ala Ala Gly Phe Thr Asn Tyr Tyr Leu Tyr Tyr Lys Lys
325 330 335

Trp Asn Thr Val Arg Leu Arg Val Tyr Trp Lys Phe Gly Ile Ala Thr
340 345 350

Thr Cys Leu Ala Gly Met Leu Ile Phe Phe Ser Ile Ala Ala Phe Arg
355 360 365

Arg His Tyr Tyr Glu Thr Phe Met Ala Leu His Ile Val Phe Ala Ala
370 375 380

Leu Phe Leu Tyr Thr Cys Trp Glu His Val Thr Asn Phe Ser Gly Ile
385 390 395 400

Glu Trp Ile Tyr Ala Ala Ile Ala Ile Trp Gly Val Asp Arg Ile Val
405 410 415

Arg Ile Thr Arg Ile Ala Leu Leu Gly Phe Pro Lys Ala Asp Leu Gln
420 425 430

Leu Val Gly Ser Asp Leu Val Arg Val Thr Val Lys Lys Pro Lys Lys
435 440 445

Phe Trp Lys Ala Lys Pro Gly Gln Tyr Val Phe Val Ser Phe Leu Arg
450 455 460

Pro Leu Cys Phe Trp Gln Ser His Pro Phe Thr Val Met Asp Ser Cys
465 470 475 480

Val Asn Asp Arg Glu Leu Val Ile Val Leu Lys Ala Lys Lys Gly Val
485 490 495

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

Met Arg Leu Ala Ile Glu Gly Pro Tyr Gly Ser Lys Ser Thr Ala His
515 520 525

Arg Phe Asp Asn Val Leu Leu Leu Ala Gly Gly Ser Gly Leu Pro Gly
530 535 540

Pro Ile Ser His Ala Leu Glu Leu Gly Lys Thr Thr Ala Ala Ser Gly
545 550 555 560

Lys Asn Phe Val Gln Leu Val Ile Ala Val Arg Gly Leu Asp Met Leu
565 570 575

Asn Ala Cys Lys Lys Glu Leu Met Ala Leu Lys Gly Leu Asn Val Gln

580	585	590	
Val His Ile Tyr Asn Ser Lys Gln Glu Leu Ala Ser Ala Glu Lys Ile			
595	600	605	
Ser Ser Asn Glu Val Lys Asn Gly Glu Thr Thr Ala Glu Lys Ala Pro			
610	615	620	
Ser Ser Leu Ser Asn Ser Glu Lys Ala Pro Ser Glu Ser Glu Asn Thr			
625	630	635	640
Glu Leu Pro Leu Ser Leu Asn Asp Thr Ser Ile Ser Asp Leu Glu Phe			
645	650	655	
Ala Thr Phe His Val Gly Arg Pro Asn Val Glu Glu Ile Leu Asn Glu			
660	665	670	
Ser Val Asn His Ser Gly Ser Leu Ala Val Val Cys Cys Gly Pro Pro			
675	680	685	
Ile Phe Val Asp Thr Ala Arg Asn Gln Thr Ala Lys Ala Val Ile Arg			
690	695	700	
Asn Pro Ser Arg Met Ile Glu Tyr Leu Glu Glu Tyr Gln Ala Trp			
705	710	715	
<210>	175		
<211>	471		
<212>	DNA		
<213>	<i>Saccharomyces cerevisiae</i>		
<400>	175		
atgttcgcca gactcgctaa tcctgcccac ttcaagcctc tcacgggctc ccacataaca			60
agagctgcca aaagacttta ccatacctaag gtaattgacc actacacaaa cccaagaaac			120
gttgggtcca tggataagtc cttagctaat gtcggcacag gaatcgtggg cgcccctgcg			180
tgtggtgatg tgataaaact acaaatacag gtgaatgata aatcgggtat tatcgagaac			240
gttaagttca agaccttcgg gtgtgggtct gccatcgctt cctcctccta catgaccgag			300
ctggtacgcg gtatgtcact tgatgaggcc gttaaaatta aaaacacgga aatcgcggaag			360
gagctaagtc ttctccagt aaaactgcat tgttccatgc ttgcagaaga cgctatcaag			420
gcggcaatca aggactacaa acaaagagg aaccctccg ttttgattg a			471

<210> 176

<211> 156
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 176

Met Phe Ala Arg Leu Ala Asn Pro Ala His Phe Lys Pro Leu Thr Gly
 1 5 10 15

Ser His Ile Thr Arg Ala Ala Lys Arg Leu Tyr His Pro Lys Val Ile
 20 25 30

Asp His Tyr Thr Asn Pro Arg Asn Val Gly Ser Met Asp Lys Ser Leu
 35 40 45

Ala Asn Val Gly Thr Gly Ile Val Gly Ala Pro Ala Cys Gly Asp Val
 50 55 60

Ile Lys Leu Gln Ile Gln Val Asn Asp Lys Ser Gly Ile Ile Glu Asn
 65 70 75 80

Val Lys Phe Lys Thr Phe Gly Cys Gly Ser Ala Ile Ala Ser Ser Ser
 85 90 95

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

Ile Lys Asn Thr Glu Ile Ala Lys Glu Leu Ser Leu Pro Pro Val Lys
 115 120 125

Leu His Cys Ser Met Leu Ala Glu Asp Ala Ile Lys Ala Ala Ile Lys
 130 135 140

Asp Tyr Lys Thr Lys Arg Asn Pro Ser Val Leu His
 145 150 155

<210> 177
 <211> 954
 <212> DNA
 <213> Saccharomyces cerevisiae

<400> 177

atggaggaca gtagcaatac aatcataccc tcacccactg acgtgggggc gctagcaaac 60

agaatcaact ttcaaaccag agatgcccac aataaaatca ataccttcat gggcataaag 120

atggccatcg ccatgagaca tggctttata tacagacagg gtattctggc gtactattat 180

gtgttcgatg ccatcgagca agagatagat cgcctactga atgaccccg t aacggaggag 240

gagctgcaaa cttcgaccat tctgaagcag ttttggctcg aagatttttag aagatctacg 300
cagatctata aggacctgaa gctgctatac tcaaacacgt ttaaagcac agaatcatta 360
aacgaattcc tggctacgtt ccagaagcca ccgctactac agcagtttat caataacatc 420
cacgaaaaca tacacaagga gccatgcacc attctttctt actgtcacgt tctgtacttg 480
gcgcttttcg ccggcggcaa gctaatacga tcgaatttgt acagaagact ggggctcttc 540
cccaacttcg agaagctatc acagaaggaa ctgggtcaaaa agggcacaaa cttcttcacc 600
ttcagcgatc tgggtccac tgaagaaaca cgcttgaaat gggaatacaa gaagaactat 660
gagctggcca ccaggacgga attgaccgaa gcacaaaagt tgcagatcat tagcgtcgca 720
gaaggcattt ttgattggaa cttcaacatc gttgcagaaa ttggagagtt gaatcgtcgc 780
gagttaatgg gcaagttcag cttcaagtgt attacgtact tgtacgaaga atggatgttc 840
aacaaggatt ctgctactag aagagcactc cacacgggtca tgctgctggg gctttctatt 900
atcgcgatct gggttcttta cttcttggtta aagagttttc ttagcatagt ataa 954

<210> 178

<211> 317

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 178

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

Ala Leu Ala Asn Arg Ile Asn Phe Gln Thr Arg Asp Ala His Asn Lys
20 25 30

Ile Asn Thr Phe Met Gly Ile Lys Met Ala Ile Ala Met Arg His Gly
35 40 45

Phe Ile Tyr Arg Gln Gly Ile Leu Ala Tyr Tyr Tyr Val Phe Asp Ala
50 55 60

Ile Glu Gln Glu Ile Asp Arg Leu Leu Asn Asp Pro Val Thr Glu Glu
65 70 75 80

Glu Leu Gln Thr Ser Thr Ile Leu Lys Gln Phe Trp Leu Glu Asp Phe
85 90 95

Arg Arg Ser Thr Gln Ile Tyr Lys Asp Leu Lys Leu Leu Tyr Ser Asn
100 105 110

Thr Phe Lys Ser Thr Glu Ser Leu Asn Glu Phe Leu Ala Thr Phe Gln
115 120 125

Lys Pro Pro Leu Leu Gln Gln Phe Ile Asn Asn Ile His Glu Asn Ile
130 135 140

His Lys Glu Pro Cys Thr Ile Leu Ser Tyr Cys His Val Leu Tyr Leu
145 150 155 160

Ala Leu Phe Ala Gly Gly Lys Leu Ile Arg Ser Asn Leu Tyr Arg Arg
165 170 175

Leu Gly Leu Phe Pro Asn Phe Glu Lys Leu Ser Gln Lys Glu Leu Val
180 185 190

Lys Lys Gly Thr Asn Phe Phe Thr Phe Ser Asp Leu Gly Pro Thr Glu
195 200 205

Glu Thr Arg Leu Lys Trp Glu Tyr Lys Lys Asn Tyr Glu Leu Ala Thr
210 215 220

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

Glu Gly Ile Phe Asp Trp Asn Phe Asn Ile Val Ala Glu Ile Gly Glu
245 250 255

Leu Asn Arg Arg Glu Leu Met Gly Lys Phe Ser Phe Lys Cys Ile Thr
260 265 270

Tyr Leu Tyr Glu Glu Trp Met Phe Asn Lys Asp Ser Ala Thr Arg Arg
275 280 285

Ala Leu His Thr Val Met Leu Leu Val Leu Ser Ile Ile Ala Ile Trp
290 295 300

Val Leu Tyr Phe Leu Val Lys Ser Phe Leu Ser Ile Val
305 310 315

<210> 179
<211> 690
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 179
atggatggaa atcatagggt tactccagat tccaaagaat ttaatactgt tgtaaaaagt 60
aaagagtctt ccactggcag aaatccgtat cagactccgc ccttagagca caacggtact 120
catcatcaga caaattacag cagaaagaaa acaaatctag caattatcat atcgaatttc 180
ttgtccgaga tcagtcggcc tctttcaa at ggcaaaatca ataattctac ccacaacatt 240
ttaaaatttc taaatgaagt gcttaagaga tcgaagtgc gtaaagaaaa cgctgtgtta 300
gccactttct actttcaaaa gattcaccaa tccagagggtg tccgggatga gtcctcattg 360
cctgaattct cgcactgttc ccgcagaatt tttctctgct gtcttattct atcgcacaaa 420
tttttgaacg acaacactta ctcgatgaaa aattggcaaa ttataagtgg gctccatgca 480
aaggatctat ctctaattga aagatggtgt ctgggtaagc tgaattatga gctggccatt 540
ccatatgacg agtttttgct atgggaaacg aacactttaa tgaaagcgaa attgcgcgtc 600
ggaactcccg ccaacgctcc ggtgaagaga cccagagaat cagacaatga ttatgatgca 660
aattcttgga aacagattaa atcttggtta 690

<210> 180
<211> 229
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 180

Met Asp Gly Asn His Arg Phe Thr Pro Asp Ser Lys Glu Phe Asn Thr
1 5 10 15

Val Val Lys Ser Lys Glu Ser Ser Thr Gly Arg Asn Pro Tyr Gln Thr
20 25 30

Pro Pro Leu Glu His Asn Gly Thr His His Gln Thr Asn Tyr Ser Arg
35 40 45

Lys Lys Thr Asn Leu Ala Ile Ile Ile Ser Asn Phe Leu Ser Glu Ile
50 55 60

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

Leu Lys Phe Leu Asn Glu Val Leu Lys Arg Ser Lys Cys Ser Lys Glu
85 90 95

Asn Ala Val Leu Ala Thr Phe Tyr Phe Gln Lys Ile His Gln Ser Arg
100 105 110

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

Arg Ile Phe Leu Cys Cys Leu Ile Leu Ser His Lys Phe Leu Asn Asp
 130 135 140

Asn Thr Tyr Ser Met Lys Asn Trp Gln Ile Ile Ser Gly Leu His Ala
 145 150 155 160

Lys Asp Leu Ser Leu Met Glu Arg Trp Cys Leu Gly Lys Leu Asn Tyr
 165 170 175

Glu Leu Ala Ile Pro Tyr Asp Glu Phe Leu Leu Trp Glu Thr Asn Thr
 180 185 190

Leu Met Lys Ala Lys Leu Arg Val Gly Thr Pro Ala Asn Ala Pro Val
 195 200 205

Lys Arg Pro Arg Glu Ser Asp Asn Asp Tyr Asp Ala Asn Ser Trp Lys
 210 215 220

Gln Ile Lys Ser Cys
 225

<210> 181
 <211> 411
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 181
 atgtcctctg tggaatcttc ccccatctcg cgctatgaag acgaggtctt ccctctttcg 60
 ttttcaaacg ttgctttcga gcccctatg ctctcgcata gcccgacag atcgacttat 120
 gccgatgact tttctcaatc ttaccagcaa gaattgctaa cttttccgct atcgtaaccg 180
 attgtcgatg agtcagaatg cacgcacact aaagataaga cggacagcaa cataataacg 240
 agtactgaag acgattgcat gttcgatatg gaatttaacg gcaacgccgc cagtgcagtt 300
 gctgctgcta gtaaggaatc taactctgcc tctgggtttg cctttgcaag taacgatgcc 360
 tttgccaatg tcgcacaaca gaactacaga ctgtggttgt catcggtatg a 411

<210> 182
 <211> 136
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 182

Met Ser Ser Val Glu Ser Ser Pro Ile Ser Arg Tyr Glu Asp Glu Val
1 5 10 15

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

His Ser Pro Asp Arg Ser Thr Tyr Ala Asp Asp Phe Ser Gln Ser Tyr
35 40 45

Gln Gln Glu Leu Leu Thr Phe Pro Leu Ser Tyr Pro Ile Val Asp Glu
50 55 60

Ser Glu Cys Thr His Thr Lys Asp Lys Thr Asp Ser Asn Ile Ile Thr
65 70 75 80

Ser Thr Glu Asp Asp Cys Met Phe Asp Met Glu Phe Asn Gly Asn Ala
85 90 95

Ala Ser Ala Val Ala Ala Ala Ser Lys Glu Ser Asn Ser Ala Ser Gly
100 105 110

Phe Ala Phe Ala Ser Asn Asp Ala Phe Ala Asn Val Ala Gln Gln Asn
115 120 125

Tyr Arg Leu Trp Leu Ser Ser Val
130 135

<210> 183

<211> 900

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 183

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gtagtttatg tcgaaaacgg ccaaacacgt acaacttacg aaacactagc tcctgcttcc	180
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aaaactaccg attcaacgac cacgttgaca tcttctgaat ctacatcgca atcgttggct	360
caagctacta cgacttctac acccgctgct gcttccacca cttccacacc cgctgctacc	420

accaccactt ctcaagccgc tgctactagc tcagcatcgt cttcggatag tgacctgtca 480
gattttgcct cttctgtggt ggctgaacac aacaagaaga gagctttgca caaggacaca 540
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gattgctccg gcactttgac ccattctggc ggtccatacg gtgaaaactt ggctttgggt 660
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aatccaggct tttcaagtaa cactggccac ttactcaag tcgtttggaa gtccaccacc 780
caagttgggt gtggcatcaa aacctgtggc ggtgcatggg gtgactatgt catctgtagt 840
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<210> 184
<211> 299
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 184

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Ala Ala Val Val Thr Val Gln Gly Val Val Tyr Val Glu Asn Gly Gln
35 40 45

Thr Arg Thr Thr Tyr Glu Thr Leu Ala Pro Ala Ser Thr Ala Thr Pro
50 55 60

Thr Ser Thr Ala Thr Ala Leu Val Ala Pro Pro Val Ala Pro Ser Ser
65 70 75 80

Ala Ser Ser Asn Ser Asp Val Val Leu Ser Ala Leu Lys Asn Leu Ala
85 90 95

Ser Val Trp Gly Lys Thr Thr Asp Ser Thr Thr Thr Leu Thr Ser Ser
100 105 110

Glu Ser Thr Ser Gln Ser Leu Ala Gln Ala Thr Thr Thr Ser Thr Pro
115 120 125

Ala Ala Ala Ser Thr Thr Ser Thr Pro Ala Ala Thr Thr Thr Thr Ser
130 135 140

Gln Ala Ala Ala Thr Ser Ser Ala Ser Ser Ser Asp Ser Asp Leu Ser
145 150 155 160

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

His Lys Asp Thr Pro Ala Leu Ser Trp Ser Asp Thr Leu Ala Ser Tyr
180 185 190

Ala Gln Asp Tyr Ala Asp Asn Tyr Asp Cys Ser Gly Thr Leu Thr His
195 200 205

Ser Gly Gly Pro Tyr Gly Glu Asn Leu Ala Leu Gly Tyr Asp Gly Pro
210 215 220

Ala Ala Val Asp Ala Trp Tyr Asn Glu Ile Ser Asn Tyr Asp Phe Ser
225 230 235 240

Asn Pro Gly Phe Ser Ser Asn Thr Gly His Phe Thr Gln Val Val Trp
245 250 255

Lys Ser Thr Thr Gln Val Gly Cys Gly Ile Lys Thr Cys Gly Gly Ala
260 265 270

Trp Gly Asp Tyr Val Ile Cys Ser Tyr Asp Pro Ala Gly Asn Tyr Glu
275 280 285

Gly Glu Tyr Ala Asp Asn Val Glu Pro Leu Ala
290 295

<210> 185
<211> 939
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 185
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gctgagatct acagaacata tccagaagtt gggaaggcac ttagcctcac cgaaaaacca 240
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gcggatggac tagatttagc tttgaagaag atgggcactg actatgtcga tctatacctt 360

ttgcatagcc catttgtttc caaagaggtc aacgggttaa gtttgaggga agcctggaag	420
gacatggagc aattgtacaa atcaggtaaa gctaaaaata tcggtgtttc caactttgct	480
gtggaagact tgcaaagaat tctgaaagtt gcggaagtca agccccaagt taatcaaatt	540
gagttcagtc ctttcttgca gaatcaaaca ccagggatct acaaattttg ccaagaacat	600
gatataattgg tagaagcata ctgcgccaata ggtcccttac aaaagaaaac agcacaagat	660
gactctcaac cgtttttcga atacgtgaaa gagttatccg agaaatatat caaatctgaa	720
gcccaaatta tcctacgttg ggtgacccaa cgtggcggtgt tgacctgtaac cacctcttcc	780
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<210> 186
 <211> 312
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 186

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			20					25					30		

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

Ala	Leu	Lys	Leu	Pro	Gly	Ile	Ile	His	Ile	Asp	Ala	Ala	Glu	Ile	Tyr
	50					55					60				

Arg	Thr	Tyr	Pro	Glu	Val	Gly	Lys	Ala	Leu	Ser	Leu	Thr	Glu	Lys	Pro
65					70					75					80

Arg	Asn	Ala	Ile	Phe	Leu	Thr	Asp	Lys	Tyr	Ser	Pro	Gln	Ile	Lys	Met
			85						90					95	

Ser	Asp	Ser	Pro	Ala	Asp	Gly	Leu	Asp	Leu	Ala	Leu	Lys	Lys	Met	Gly
			100					105					110		

Thr	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Leu	His	Ser	Pro	Phe	Val	Ser	Lys
		115					120					125			

Glu Val Asn Gly Leu Ser Leu Glu Glu Ala Trp Lys Asp Met Glu Gln
 130 135 140

Leu Tyr Lys Ser Gly Lys Ala Lys Asn Ile Gly Val Ser Asn Phe Ala
 145 150 155 160

Val Glu Asp Leu Gln Arg Ile Leu Lys Val Ala Glu Val Lys Pro Gln
 165 170 175

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

Ile Tyr Lys Phe Cys Gln Glu His Asp Ile Leu Val Glu Ala Tyr Ser
 195 200 205

Pro Leu Gly Pro Leu Gln Lys Lys Thr Ala Gln Asp Asp Ser Gln Pro
 210 215 220

Phe Phe Glu Tyr Val Lys Glu Leu Ser Glu Lys Tyr Ile Lys Ser Glu
 225 230 235 240

Ala Gln Ile Ile Leu Arg Trp Val Thr Lys Arg Gly Val Leu Pro Val
 245 250 255

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

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

Leu Glu His Glu Pro Leu Arg Leu Tyr Trp Asn Lys Leu Tyr Gly Lys
 290 295 300

Tyr Asn Tyr Ala Ala Gln Lys Val
 305 310

<210> 187
 <211> 636
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 187
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caatcaaata agttatattg ctccgaagat tgtaagctga aggattcgaa ccctcttaat	180
gagaaattat tatcccactt gcataaaaaa tcaaaaactt ctcatcgca taatctcact	240
ccaccgcttt catattctaa aaattttaact gcatcaaacc tcttcgagcc gactacctca	300
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cttagactcg attctagtta ccaattgcat tcaaaggcac atttgggtta cgaaaacaac	540
ttgccacgat caaacgatct aattgatgat catttgatct cagatcagat cattgagaat	600
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<210> 188
 <211> 211
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 188

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

Asp	Asn	Glu	Thr	Lys	Ser	Ser	Leu	Gln	Ser	Asn	Lys	Leu	Tyr	Cys	Ser
		35					40					45			

Glu	Asp	Cys	Lys	Leu	Lys	Asp	Ser	Asn	Pro	Leu	Asn	Glu	Lys	Leu	Leu
	50					55					60				

Ser	His	Leu	His	Lys	Lys	Ser	Lys	Thr	Ser	His	Ser	His	Asn	Leu	Thr
65					70					75					80

Pro	Pro	Leu	Ser	Tyr	Ser	Lys	Asn	Leu	Thr	Ala	Ser	Asn	Leu	Phe	Glu
				85					90					95	

Pro	Thr	Thr	Ser	Leu	Ser	Ser	Ser	Pro	Thr	Ser	Ser	Thr	Ile	Pro	Phe
			100					105					110		

Asp	Glu	Leu	Glu	Lys	Leu	Glu	Ser	Leu	Leu	Ile	Ser	Pro	Leu	Leu	Leu
		115					120					125			

Pro	Gln	Asp	Gly	Ile	Val	Asn	Pro	Lys	Gln	Glu	Ser	Asn	Pro	Ser	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

130	135	140	
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145	150	155	160
Leu Arg Leu Asp Ser Ser Tyr Gln Leu His Ser Lys Ala His Leu Gly			
	165	170	175
Tyr Glu Asn Asn Leu Pro Arg Ser Asn Asp Leu Ile Asp Asp His Leu			
	180	185	190
Ile Ser Asp Gln Ile Ile Glu Asn Asn Tyr Asn Leu Trp Phe Arg Leu			
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aaggatgctc atcacaatac gcttctagat ctattatgca ttataattaa tagttgtagc	240
tacaaaaggt aaaagaaagt ccggggcagg caacaataga aatcggcaaa aaaaactaca	300
gaaatactaa gagcttcttc cccattcagt catcgcattt cgaaacaaga ggggaatggc	360
tctggctagg gaactaacca ccatcgctg actctatgca ctaaccacgt gactacatat	420
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gaccgtggaa attgccaaga gtgataagga ctttgttatt ggatttattg ctcaaaacga	840
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 <212> DNA
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<220>
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cgaggccctt tcgtc 3855

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<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer oGV394

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<210> 194
<211> 32
<212> DNA
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<223> Primer oGV395

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<210> 195
<211> 7273
<212> DNA
<213> Artificial Sequence

<220>
<223> linear fragment, KM_AFT, Ll_ilvD_coSc & G418

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<211> 1950

<212> DNA

<213> *Saccharomyces cerevisiae*

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 <213> *Saccharomyces cerevisiae*

<400> 203

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Leu	Pro	Arg	Ile	Pro	Ser	Leu	Glu	Leu	Pro	Leu	Asn	Val	Ser	Thr	Lys
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His	Ser	Ser	Ile	Gln	Lys	Ala	Ile	Lys	Met	Cys	Gly	Gly	Ile	Glu	Lys
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Val	Lys	Glu	Ala	Phe	Lys	Glu	His	Gly	Pro	Ile	Glu	Ser	Gln	His	Gly
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Leu	Gln	Leu	Tyr	Leu	Asn	Asp	Asp	Thr	Asp	Ser	Asp	Gly	Ser	Lys	Ser
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Tyr Phe Asn Glu His Pro Val Ile Gly Lys Arg Val Pro Phe Arg Asp
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Glu Ser Val Ile Leu Lys Val Thr Met Pro Lys Gly Thr Leu Ser Lys
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Asn Asn Asn Ser Val Lys Asp Ser Ile Lys Ser Leu Lys Asp Ser Asn
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Lys Leu Arg Val Thr Pro Val Ser Ile Val Asp Asn Thr Ile Lys Phe
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Arg Glu Met Ser Asp Phe Gln Ile Lys Leu Asp Asn Val Pro Ser Ala
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Arg Glu Phe Lys Ser Ser Phe Gly Ser Leu Glu Trp Asn Asn Phe Lys
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Ser Phe Val Asn Ser Val Pro Asp Asn Asp Ser Gln Pro Gln Glu Asn
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Ile Gly Asn Leu Ile Leu Asp Arg Ser Val Lys Ile Pro Ser Thr Asp
210 215 220

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

Leu Tyr Lys Tyr Lys Ala Asn Pro Phe Ala Lys Lys Lys Lys Asn Gly
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Val Thr Glu Val Lys Gly Thr Tyr Ile Lys Asn Tyr Gln Leu Phe Val
260 265 270

His Asp Leu Ser Asp Lys Thr Val Ile Pro Ser Gln Ala His Glu Gln
275 280 285

Val Leu Tyr Asp Phe Glu Val Ala Lys Lys Thr Lys Val Tyr Pro Gly
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Thr Lys Ser Asp Ser Lys Phe Tyr Glu Ser Leu Glu Glu Cys Leu Lys
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Ile Leu Arg Glu Leu Phe Ala Arg Arg Pro Ile Trp Val Lys Arg His

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Ser	Met	Val	Pro	Glu	Asn	Lys	Asn	Ser	Glu	Glu	Gly	Met	Gly	Val	Asn
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Thr	Asn	Lys	Asp	Ala	Asp	Gly	Asp	Ile	Asn	Met	Asp	Ala	Gly	Ser	Gln
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Asp Phe Asp Asp Asn Gly Ala Ile Thr Glu Glu Pro Asp Asp Ala Ala
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Leu Glu Asn Glu Glu Met Asp Thr Asp Gln Asn Leu Lys Val Pro Ala
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Ser Ile Asp Asp Asp Val Asp Asp Val Asp Ala Asp Glu Glu Glu Gln
595 600 605

Glu Ser Phe Asp Val Lys Thr Ala Ser Phe Gln Asp Ile Ile Asn Lys
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Ile Ala Lys Leu Asp Pro Lys Thr Ala Glu Thr Met Lys Ser Glu Leu
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Lys Gly Phe Val Asp Glu Val Asp Leu
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<211> 1713
<212> DNA
<213> Lactococcus lactis

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 <212> PRT
 <213> Lactococcus lactis

<400> 205

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Met Tyr Tyr Gly Ile Gly Phe Lys Asp Glu Asp Phe Lys Lys Ala Gln
 35 40 45

Val Gly Ile Val Ser Met Asp Trp Asp Gly Asn Pro Cys Asn Met His
 50 55 60

Leu Gly Thr Leu Gly Ser Lys Ile Lys Ser Ser Val Asn Gln Thr Asp
 65 70 75 80

Gly Leu Ile Gly Leu Gln Phe His Thr Ile Gly Val Ser Asp Gly Ile
 85 90 95

Ala Asn Gly Lys Leu Gly Met Arg Tyr Ser Leu Val Ser Arg Glu Val
100 105 110

Ile Ala Asp Ser Ile Glu Thr Asn Ala Gly Ala Glu Tyr Tyr Asp Ala
115 120 125

Ile Val Ala Ile Pro Gly Cys Asp Lys Asn Met Pro Gly Ser Ile Ile
130 135 140

Gly Met Ala Arg Leu Asn Arg Pro Ser Ile Met Val Tyr Gly Gly Thr
145 150 155 160

Ile Glu His Gly Glu Tyr Lys Gly Glu Lys Leu Asn Ile Val Ser Ala
165 170 175

Phe Glu Ser Leu Gly Gln Lys Ile Thr Gly Asn Ile Ser Asp Glu Asp
180 185 190

Tyr His Gly Val Ile Cys Asn Ala Ile Pro Gly Gln Gly Ala Cys Gly
195 200 205

Gly Met Tyr Thr Ala Asn Thr Leu Ala Ala Ala Ile Glu Thr Leu Gly
210 215 220

Met Ser Leu Pro Tyr Ser Ser Ser Asn Pro Ala Val Ser Gln Glu Lys
225 230 235 240

Gln Glu Glu Cys Asp Glu Ile Gly Leu Ala Ile Lys Asn Leu Leu Glu
245 250 255

Lys Asp Ile Lys Pro Ser Asp Ile Met Thr Lys Glu Ala Phe Glu Asn
260 265 270

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

His Ile Ile Ala Met Ala Asn Ala Ile Gly Val Glu Ile Thr Gln Asp
290 295 300

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

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

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Asp	Ile	Ile	Glu	Ile	Asp	Ala	Val	Asn	Asn	Ser	Ile	Ser	Leu	Lys	Val	
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Pro Ala Ser Glu Gly Cys Val Thr Asp Leu
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<211> 1713
<212> DNA
<213> *Lactococcus lactis*

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ccttccgaca taatgactaa ggaagctttt gaaaatgcta tcacaatagt gatggtcctt 840
ggtggctcta ccaacgcagt ttacacatc attgcaatgg caaatgcaat aggagttgaa 900
atcacacaag atgattttca acgtatctcc gatatcacac ctgtcctagg cgatttcaaa 960
ccatctggca agtatatgat ggaggatcta cacaagattg gaggacttcc tgcagtctta 1020
aagtatttgt tgaaagaggg taaattgcat ggtgattgtt taaccgtcac tggcaagacc 1080
ttggcagaaa atgtagaaac tgctttggat ttggatttcg atagtcaaga tatcatgagg 1140
ccattgaaaa accctatcaa ggctactggg cacttacaaa tcttatacgg caatctagca 1200
caaggtggtt ctgtcgctaa gattagtggg aaggaaggag agtttttcaa gggtagagca 1260
agagtttttg atggtgaaca acactttatc gatggcatag aaagtggtag attgcatgca 1320
ggcgatgtgg ctgtaattag aaacattgga ccagttggcg gacctggtat gcctgaaatg 1380
ctaaagccta ctccgcact aattggagct ggtcttggtg aatcatgtgc tttaatcacc 1440
gatggtagat tctccggtgg cacacatggt tttgtagttg gccatatcgt accagaagct 1500

gttgaaggag gtcttatagg cttagtagaa gatgatgaca taatcgaaat agacgcagtg 1560
aacaatagca tctcactaaa agtttctgat gaggaatatag caaagagaag ggctaattac 1620
cagaagccaa ctccaaaggc aaccagaggt gttctagcta agtttgctaa gttaactaga 1680
cctgctagcg aaggatgtgt tacagactta tga 1713

<210> 207
<211> 570
<212> PRT
<213> Lactococcus lactis

<400> 207

Met Glu Phe Lys Tyr Asn Gly Lys Val Glu Ser Val Glu Leu Asn Lys
1 5 10 15

Tyr Ser Lys Thr Leu Thr Gln Asp Pro Thr Gln Pro Ala Thr Gln Ala
20 25 30

Met Tyr Tyr Gly Ile Gly Phe Lys Asp Glu Asp Phe Lys Lys Ala Gln
35 40 45

Val Gly Ile Val Ser Met Asp Trp Asp Gly Asn Pro Cys Asn Met His
50 55 60

Leu Gly Thr Leu Gly Ser Lys Ile Lys Ser Ser Val Asn Gln Thr Asp
65 70 75 80

Gly Leu Ile Gly Leu Gln Phe His Thr Ile Gly Val Ser Asp Gly Ile
85 90 95

Ala Asn Gly Lys Leu Gly Met Arg Tyr Ser Leu Val Ser Arg Glu Val
100 105 110

Ile Ala Asp Ser Ile Glu Thr Asn Ala Gly Ala Glu Tyr Tyr Asp Ala
115 120 125

Ile Val Ala Ile Pro Gly Cys Asp Lys Asn Met Pro Gly Ser Ile Ile
130 135 140

Gly Met Ala Arg Leu Asn Arg Pro Ser Ile Met Val Tyr Gly Gly Thr
145 150 155 160

Ile Glu His Gly Glu Tyr Lys Gly Glu Lys Leu Asn Ile Val Ser Ala
165 170 175

Phe Glu Ser Leu Gly Gln Lys Ile Thr Gly Asn Ile Ser Asp Glu Asp
180 185 190

Tyr His Gly Val Ile Cys Asn Ala Ile Pro Gly Gln Gly Ala Cys Gly
195 200 205

Gly Met Tyr Thr Ala Asn Thr Leu Ala Ala Ala Ile Glu Thr Leu Gly
210 215 220

Met Ser Leu Pro Tyr Ser Ser Ser Asn Pro Ala Val Ser Gln Glu Lys
225 230 235 240

Gln Glu Glu Cys Asp Glu Ile Gly Leu Ala Ile Lys Asn Leu Leu Glu
245 250 255

Lys Asp Ile Lys Pro Ser Asp Ile Met Thr Lys Glu Ala Phe Glu Asn
260 265 270

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

His Ile Ile Ala Met Ala Asn Ala Ile Gly Val Glu Ile Thr Gln Asp
290 295 300

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

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

Pro Ala Val Leu Lys Tyr Leu Leu Lys Glu Gly Lys Leu His Gly Asp
340 345 350

Cys Leu Thr Val Thr Gly Lys Thr Leu Ala Glu Asn Val Glu Thr Ala
355 360 365

Leu Asp Leu Asp Phe Asp Ser Gln Asp Ile Met Arg Pro Leu Lys Asn
370 375 380

Pro Ile Lys Ala Thr Gly His Leu Gln Ile Leu Tyr Gly Asn Leu Ala
385 390 395 400

Gln Gly Gly Ser Val Ala Lys Ile Ser Gly Lys Glu Gly Glu Phe Phe

	405		410		415
Lys Gly Thr	Ala Arg Val Phe Asp Gly Glu Gln His Phe Ile Asp Gly				
	420		425		430
Ile Glu Ser Gly Arg Leu His Ala Gly Asp Val Ala Val Ile Arg Asn					
	435		440		445
Ile Gly Pro Val Gly Gly Pro Gly Met Pro Glu Met Leu Lys Pro Thr					
	450		455		460
Ser Ala Leu Ile Gly Ala Gly Leu Gly Lys Ser Cys Ala Leu Ile Thr					
	465		470		475
Asp Gly Arg Phe Ser Gly Gly Thr His Gly Phe Val Val Gly His Ile					
	485		490		495
Val Pro Glu Ala Val Glu Gly Gly Leu Ile Gly Leu Val Glu Asp Asp					
	500		505		510
Asp Ile Ile Glu Ile Asp Ala Val Asn Asn Ser Ile Ser Leu Lys Val					
	515		520		525
Ser Asp Glu Glu Ile Ala Lys Arg Arg Ala Asn Tyr Gln Lys Pro Thr					
	530		535		540
Pro Lys Ala Thr Arg Gly Val Leu Ala Lys Phe Ala Lys Leu Thr Arg					
	545		550		555
Pro Ala Ser Glu Gly Cys Val Thr Asp Leu					
	565		570		

<210> 208
 <211> 2073
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 208	
atggaaggct tcaatccggc tgacatagaa catgcgtcac cgattaattc atctgacagc	60
cattcatcct cctttgtata tgctctaccc aaaagtgcta gtgaatatgt agtcaaccat	120
aatgagggtc gtgcaagtgc aagtggaaat ccagccgcag tgccgtctcc cataatgaca	180
ctgaatctca aaagcacaca ttccctcaat attgatcagc atgttcatac ctcaacatcg	240
ccgacggaaa ctattgggca tattcatcat gtggaaaagc tgaatcaaaa caatttgatt	300

catctggatc cagtacccaa ctttgaagat aagtccgata ttaagccttg gttgcaaaaag	360
atTTTTtAtc ctcaaggaat agaacttgtg atagaaaggt cggacgcatt taaagttgtc	420
ttcaagtgtA aagctgctaa aaggggaagg aacgcgagaa ggaaaagaaa agataagccc	480
aaaggacagg accacgaaga cgagaaatcc aagatcaatg atgacgaatt agaatatgcg	540
agtccttcta atgccacagt aaccaatggg cctcaaacat cgcccgatca aacatcctcc	600
ataaagccaa agaaaaaaag atgtgtatcg aggtttaata actgtccgtt tagagtacga	660
gctacttatt cgtaaagag gaaaagatgg agcattgttg taatggacaa taaccattca	720
catcagctaa agtttaaccc tgattccgaa gagtacaaaa aattcaaaga aaaattaaga	780
aaggataatg acgtagatgc aatcaagaaa ttcgacgaat tggaatacag aactttggcc	840
aatttgccca ttccaacagc tacaatcccc tgtgattgtg gttaacaaa tgaaatacaa	900
agtttcaatg tcgtattgcc cactaacagt aatgttactt catcagcatc ctcttcaact	960
gtatcgtcca tatcccttga ttcatcgaat gcatctaaaa ggccatgctt accctctgta	1020
aataacaccg gtagtatcaa taccaataac gtaaggaaac cgaaaagcca gtgtaagaat	1080
aaagacacac tcttaaaaag aaccaccatg cagaactttc tcacaactaa atcaaggctg	1140
cgtaagaccg gtacgccaac atcttcgcaa cactcatcta cagcattttc aggatatatt	1200
gatgatcctt tcaatttgaa tgaaatcttg ccactgccgg catccgattt caagctaaac	1260
actgtaacaa atttgaacga aattgacttt acgaacattt ttaccaaate gccgcatcca	1320
catagcgggt ctacccatcc aagacaagtc ttcgaccaat tggacgattg ttcctctata	1380
ctcttctctc cattaactac aaacacgaat aatgaatttg aaggagagtc agatgatttt	1440
gttcattctc catatttgaa ctCagaggca gatttcagcc aaattcttag tagtgctccc	1500
ccagtccatc atgacccaaa tgaaacacat caggaaaacc aggatattat tgatagattt	1560
gctaatagtt cccaagaaca taatgagtat attctacaat atttgacgca ctccgatgct	1620
gctaaccaca ataacatcgg cgttccaaac aacaattcac attcgctaaa tactcagcat	1680
aacgtttctg atctgggcaa ctCactttta agacaagaag ctttagttgg cagctcttca	1740
acaaaaatct tcgacgaatt gaaatttgta caaatgggcc cacacgggtc tcaacatcct	1800
atagattttc aacatgttga ccatcgtcat ctCagctcta atgaacctca agtacgatca	1860
catcaatatg gtccgcaaca gcagccaccg cagcaattgc aatatacca aaatcagccc	1920
cacgacggcc ataaccacga acagcaccaa acagtacaaa aggatatgca aacgcatgaa	1980
tcgctagaaa taatgggaaa cacattattg gaagagttca aagacattaa aatgggtgaac	2040
ggcgagttga agtatgtgaa gccagaagat tag	2073

<210> 209
 <211> 690
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 209

Met Glu Gly Phe Asn Pro Ala Asp Ile Glu His Ala Ser Pro Ile Asn
 1 5 10 15

Ser Ser Asp Ser His Ser Ser Ser Phe Val Tyr Ala Leu Pro Lys Ser
 20 25 30

Ala Ser Glu Tyr Val Val Asn His Asn Glu Gly Arg Ala Ser Ala Ser
 35 40 45

Gly Asn Pro Ala Ala Val Pro Ser Pro Ile Met Thr Leu Asn Leu Lys
 50 55 60

Ser Thr His Ser Leu Asn Ile Asp Gln His Val His Thr Ser Thr Ser
 65 70 75 80

Pro Thr Glu Thr Ile Gly His Ile His His Val Glu Lys Leu Asn Gln
 85 90 95

Asn Asn Leu Ile His Leu Asp Pro Val Pro Asn Phe Glu Asp Lys Ser
 100 105 110

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

Leu Val Ile Glu Arg Ser Asp Ala Phe Lys Val Val Phe Lys Cys Lys
 130 135 140

Ala Ala Lys Arg Gly Arg Asn Ala Arg Arg Lys Arg Lys Asp Lys Pro
 145 150 155 160

Lys Gly Gln Asp His Glu Asp Glu Lys Ser Lys Ile Asn Asp Asp Glu
 165 170 175

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

Thr Ser Pro Asp Gln Thr Ser Ser Ile Lys Pro Lys Lys Lys Arg Cys
 195 200 205

Val Ser Arg Phe Asn Asn Cys Pro Phe Arg Val Arg Ala Thr Tyr Ser
210 215 220

Leu Lys Arg Lys Arg Trp Ser Ile Val Val Met Asp Asn Asn His Ser
225 230 235 240

His Gln Leu Lys Phe Asn Pro Asp Ser Glu Glu Tyr Lys Lys Phe Lys
245 250 255

Glu Lys Leu Arg Lys Asp Asn Asp Val Asp Ala Ile Lys Lys Phe Asp
260 265 270

Glu Leu Glu Tyr Arg Thr Leu Ala Asn Leu Pro Ile Pro Thr Ala Thr
275 280 285

Ile Pro Cys Asp Cys Gly Leu Thr Asn Glu Ile Gln Ser Phe Asn Val
290 295 300

Val Leu Pro Thr Asn Ser Asn Val Thr Ser Ser Ala Ser Ser Ser Thr
305 310 315 320

Val Ser Ser Ile Ser Leu Asp Ser Ser Asn Ala Ser Lys Arg Pro Cys
325 330 335

Leu Pro Ser Val Asn Asn Thr Gly Ser Ile Asn Thr Asn Asn Val Arg
340 345 350

Lys Pro Lys Ser Gln Cys Lys Asn Lys Asp Thr Leu Leu Lys Arg Thr
355 360 365

Thr Met Gln Asn Phe Leu Thr Thr Lys Ser Arg Leu Arg Lys Thr Gly
370 375 380

Thr Pro Thr Ser Ser Gln His Ser Ser Thr Ala Phe Ser Gly Tyr Ile
385 390 395 400

Asp Asp Pro Phe Asn Leu Asn Glu Ile Leu Pro Leu Pro Ala Ser Asp
405 410 415

Phe Lys Leu Asn Thr Val Thr Asn Leu Asn Glu Ile Asp Phe Thr Asn
420 425 430

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

307

Phe Lys Asp Ile Lys Met Val Asn Gly Glu Leu Lys Tyr Val Lys Pro
675 680 685

Glu Asp
690

<210> 210
<211> 2073
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 210
atggaaggct tcaatccggc tcacatagaa catgcgtcac cgattaattc atctgacagc 60
cattcatcct cttttgtata tgctctaccc aaaagtgtcta gtgaatatgt agtcaaccat 120
aatgaggggtc gtgcaagtgc aagtggaaat ccagccgcag tgccgtctcc cataatgaca 180
ctgaatctca aaagcacaca ttccctcaat agtgatcagc atgttcatac ctcaacatcg 240
ccgacggaaa ctattgggca tattcatcat gtggaaaagc tgaatcaaaa caatttgatt 300
catctggatc cagtacccaa ctttgaagat aagtccgata ttaagccttg gttgcaaaaag 360
atTTTTtata ctcaaggaat agaacttgtg atagaaaggt cggacacatt taaagttgtc 420
ttcaagtgtg aagctgctaa aaggggaagg aacgcgagaa ggaaaagaaa agataagccc 480
aaaggacagg accacgaaga cgagaaatcc aagatcaatg atgacgaatt agaatatgcg 540
agtccttcta atgccacagt aaccaatggg cctcaaacat cgcccgatca aacatcctcc 600
ataaagccaa agaaaaaag atgtgtatcg aggtttaata actgtccgtt tagagtacga 660
gctacttatt cgtaaagag gaaaagatgg agcattgttg taatgaacaa taaccattca 720
catcagctaa agtttaaccc tgattccgaa gagtacaaaa aattcaaaga aaaattaaga 780
aaggataatg acgtagatgc aatcaagaaa ttcgacgaat tggaatacag aactttggcc 840
aatttgccca ttccaacagc tacaatcccc tgtgattgtg gttaacaaa tgaaatacaa 900
agtttcaatg tcgtattgcc cactaacagt aatgttactt catcagcatc ctcttcaact 960
gtatcgtcca tatcccttga ttcacgaat gcatctaaaa ggccatgctt accctctgta 1020
aataacaccg gtagtatcaa taccaataac gtaaggaaac cgaaaagcca gtgtaagaat 1080
aaagacacac tcttaaaaag aaccaccatg cagaactttc tcacaactaa atcaaggctg 1140
cgtaagaccg gtacgccaac atcttcgcaa cactcatcta cagcattttc aggatatatt 1200
gatgatcctt tcaatttgaa tgaaatcttg ccactgccgg catccgattt caagctaaac 1260
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catagcgggt ctacccatcc aagacaagtc ttcgaccaat tggacgattg ttccctctata 1380

ctcttctctc cattaactac aaacacgaat aatgaatttg aaggagagtc agatgatttt 1440
 gttcattctc catatttgaa ctgagaggca gatttcagcc aaattcttag tagtgctccc 1500
 ccagtccatc atgacccaaa tgaacacat caggaaaacc aggatattat tgatagattt 1560
 gctaatagtt cccaagaaca taatgagtat attctacaat atttgacgca cttcgatgct 1620
 gctaaccaca ataacatcgg cgttccaaac aacaattcac attcgctaaa tactcagcat 1680
 aacgtttctg atctgggcaa cccactttta agacaagaag ctttagttgg cagctcttca 1740
 acaaaaatct tcgacgaatt gaaatttgta caaaatggcc cacacgggtc tcaacatcct 1800
 atagattttc aacatgttga ccatcgtcac ctgagctcta atgaacctca agtacgatca 1860
 catcaatatg gtccgcaaca gcagccaccg cagcaattgc aatatcacca aaatcagccc 1920
 cacgacggcc ataaccacga acagcaccaa acagtacaaa aggatatgca aacgcatgaa 1980
 tcgctagaaa taatgggaaa cacattattg gaagagttca aagacattaa aatggtgaac 2040
 ggcgagttga agtatgtgaa gccagaagat tag 2073

<210> 211
 <211> 690
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 211

Met Glu Gly Phe Asn Pro Ala His Ile Glu His Ala Ser Pro Ile Asn
1 5 10 15

Ser Ser Asp Ser His Ser Ser Ser Phe Val Tyr Ala Leu Pro Lys Ser
20 25 30

Ala Ser Glu Tyr Val Val Asn His Asn Glu Gly Arg Ala Ser Ala Ser
35 40 45

Gly Asn Pro Ala Ala Val Pro Ser Pro Ile Met Thr Leu Asn Leu Lys
50 55 60

Ser Thr His Ser Leu Asn Ser Asp Gln His Val His Thr Ser Thr Ser
65 70 75 80

Pro Thr Glu Thr Ile Gly His Ile His His Val Glu Lys Leu Asn Gln
85 90 95

Asn Asn Leu Ile His Leu Asp Pro Val Pro Asn Phe Glu Asp Lys Ser
100 105 110

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

Leu Val Ile Glu Arg Ser Asp Thr Phe Lys Val Val Phe Lys Cys Lys
130 135 140

Ala Ala Lys Arg Gly Arg Asn Ala Arg Arg Lys Arg Lys Asp Lys Pro
145 150 155 160

Lys Gly Gln Asp His Glu Asp Glu Lys Ser Lys Ile Asn Asp Asp Glu
165 170 175

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

Thr Ser Pro Asp Gln Thr Ser Ser Ile Lys Pro Lys Lys Lys Arg Cys
195 200 205

Val Ser Arg Phe Asn Asn Cys Pro Phe Arg Val Arg Ala Thr Tyr Ser
210 215 220

Leu Lys Arg Lys Arg Trp Ser Ile Val Val Met Asn Asn Asn His Ser
225 230 235 240

His Gln Leu Lys Phe Asn Pro Asp Ser Glu Glu Tyr Lys Lys Phe Lys
245 250 255

Glu Lys Leu Arg Lys Asp Asn Asp Val Asp Ala Ile Lys Lys Phe Asp
260 265 270

Glu Leu Glu Tyr Arg Thr Leu Ala Asn Leu Pro Ile Pro Thr Ala Thr
275 280 285

Ile Pro Cys Asp Cys Gly Leu Thr Asn Glu Ile Gln Ser Phe Asn Val
290 295 300

Val Leu Pro Thr Asn Ser Asn Val Thr Ser Ser Ala Ser Ser Ser Thr
305 310 315 320

Val Ser Ser Ile Ser Leu Asp Ser Ser Asn Ala Ser Lys Arg Pro Cys
325 330 335

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

Gly Ser Ser Ser Thr Lys Ile Phe Asp Glu Leu Lys Phe Val Gln Asn
580 585 590

Gly Pro His Gly Ser Gln His Pro Ile Asp Phe Gln His Val Asp His
595 600 605

Arg His Leu Ser Ser Asn Glu Pro Gln Val Arg Ser His Gln Tyr Gly
610 615 620

Pro Gln Gln Gln Pro Pro Gln Gln Leu Gln Tyr His Gln Asn Gln Pro
625 630 635 640

His Asp Gly His Asn His Glu Gln His Gln Thr Val Gln Lys Asp Met
645 650 655

Gln Thr His Glu Ser Leu Glu Ile Met Gly Asn Thr Leu Leu Glu Glu
660 665 670

Phe Lys Asp Ile Lys Met Val Asn Gly Glu Leu Lys Tyr Val Lys Pro
675 680 685

Glu Asp
690

<210> 212
<211> 2073
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 212
atggaaggct tcaatccggc tcacatagaa catgcgtcac cgattaattc atctgacagc 60
cattcatcct cctttgtata tgctctaccc aaaagtgcta gtgaatatgt agtcaaccat 120
aatgagggtc gtgcaagtgc aagtggaaat ccagccgcag tgccgtctcc cataatgaca 180
ctgaatctca aaagcacaca ttccctcaat agtgatcagc atgttcatac ctcaacatcg 240
ccgacggaaa ctattgggca tattcatcat gtggaaaagc tgaatcaaaa caatttgatt 300
catctggatc cagtacccaa ctttgaagat aagtccgata ttaagccttg gttgcaaaag 360
atTTTTtAtc ctcaaggaat agaacttgTg atagaaaggT cgGacacatt taaagttgtc 420
ttCaagtgtA aagctgctaa aaggggaagg aacgcgagaa ggaaaagaaa agataagccc 480
aaaggacagg accacgaaga cgagaaatcc aagatcaatg atgacgaatt agaatatgcg 540
agtccttcta atgccacagt aaccaatggg cctcaaacat cgcccgatca aacatcctcc 600
ataaagccaa agaaaaaag atgtgtatcg aggtttaata actgtccgtt tagagtacga 660

gctacttatt	cgttaaagag	gaaaagatgg	agcattgttg	taatgaacaa	taaccattca	720
catcagctaa	agtttaaccc	tgattccgaa	gagtacaaaa	aattcaaaga	aaaattaaga	780
aaggataatg	acgtagatgc	aatcaagaaa	ttcgacgaat	tggaatacag	aactttggcc	840
aatttgccca	ttccaacagc	tacaatcccc	tgtgattgtg	gtttaacaaa	tgaaatacaa	900
agtttcaatg	tcgtattgcc	cactaacagt	aatgttactt	catcagcatc	ctcttcaact	960
gtatcgtcca	tatcccttga	ttcatcgaat	gcatctaaaa	ggccatgctt	accctctgta	1020
aataacaccg	gtagtatcaa	taccaataac	gtaaggaaac	cgaaaagcca	gtgtaagaat	1080
aaagacacac	tcttaaaaag	aaccaccatg	cagaactttc	tcacaactaa	atcaaggctg	1140
cgtaagaccg	gtacgccaac	atcttcgcaa	cactcatcta	cagcattttc	aggatatatt	1200
gatgatcctt	tcaatttgaa	tgaaatcttg	ccactgccgg	catccgattt	caagctaaac	1260
actgtaacaa	atttgaacga	aattgacttt	acgaacattt	ttaccaaate	gccgcatcca	1320
catagcgggt	ctacccatcc	aagacaagtc	ttcgaccaat	tggaacgattg	ttcctctata	1380
ctctttctctc	cattaactac	aaacacgaat	aatgaatttg	aaggagagtc	agatgatttt	1440
gttcattctc	catatttgaa	ctcagaggca	gatttcagcc	aaattcttag	tagtgctccc	1500
ccagtccatc	atgacccaaa	tgaaacacat	caggaaaacc	aggatattat	tgatagattt	1560
gctaatagtt	cccaagaaca	taatgagtat	attctacaat	atttgacgca	cttcgatgct	1620
gctaaccaca	ataacatcgg	cgttccaaac	aacaattcac	attcgctaaa	tactcagcat	1680
aacgtttctg	atctgggcaa	cccactttta	agacaagaag	ctttagttgg	cagctcttca	1740
acaaaaatct	tcgacgaatt	gaaatttgta	caaaatggcc	cacacggttc	tcaacatcct	1800
atagattttc	aacatgttga	ccatcgtcac	ctcagctcta	atgaacctca	agtacgatca	1860
catcaatatg	gtccgcaaca	gcagccaccg	cagcaattgc	aatatcacca	aatcagccc	1920
cacgacggcc	ataaccacga	acagcaccaa	acagtacaaa	aggatatgca	aacgcatgaa	1980
tcgctagaaa	taatgggaaa	cacattattg	gaagagttca	aagacattaa	aatgggtgaac	2040
ggcgagttga	agtatgtgaa	gccagaagat	tag			2073

<210> 213
 <211> 690
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 213

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

Ala Ser Glu Tyr Val Val Asn His Asn Glu Gly Arg Ala Ser Ala Ser
35 40 45

Gly Asn Pro Ala Ala Val Pro Ser Pro Ile Met Thr Leu Asn Leu Lys
50 55 60

Ser Thr His Ser Leu Asn Ser Asp Gln His Val His Thr Ser Thr Ser
65 70 75 80

Pro Thr Glu Thr Ile Gly His Ile His His Val Glu Lys Leu Asn Gln
85 90 95

Asn Asn Leu Ile His Leu Asp Pro Val Pro Asn Phe Glu Asp Lys Ser
100 105 110

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

Leu Val Ile Glu Arg Ser Asp Thr Phe Lys Val Val Phe Lys Cys Lys
130 135 140

Ala Ala Lys Arg Gly Arg Asn Ala Arg Arg Lys Arg Lys Asp Lys Pro
145 150 155 160

Lys Gly Gln Asp His Glu Asp Glu Lys Ser Lys Ile Asn Asp Asp Glu
165 170 175

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

Thr Ser Pro Asp Gln Thr Ser Ser Ile Lys Pro Lys Lys Lys Arg Cys
195 200 205

Val Ser Arg Phe Asn Asn Cys Pro Phe Arg Val Arg Ala Thr Tyr Ser
210 215 220

Leu Lys Arg Lys Arg Trp Ser Ile Val Val Met Asn Asn Asn His Ser
225 230 235 240

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

				245						250						255
Glu	Lys	Leu	Arg	Lys	Asp	Asn	Asp	Val	Asp	Ala	Ile	Lys	Lys	Phe	Asp	
			260					265					270			
Glu	Leu	Glu	Tyr	Arg	Thr	Leu	Ala	Asn	Leu	Pro	Ile	Pro	Thr	Ala	Thr	
		275					280					285				
Ile	Pro	Cys	Asp	Cys	Gly	Leu	Thr	Asn	Glu	Ile	Gln	Ser	Phe	Asn	Val	
	290					295					300					
Val	Leu	Pro	Thr	Asn	Ser	Asn	Val	Thr	Ser	Ser	Ala	Ser	Ser	Ser	Thr	
305					310					315					320	
Val	Ser	Ser	Ile	Ser	Leu	Asp	Ser	Ser	Asn	Ala	Ser	Lys	Arg	Pro	Cys	
				325					330					335		
Leu	Pro	Ser	Val	Asn	Asn	Thr	Gly	Ser	Ile	Asn	Thr	Asn	Asn	Val	Arg	
			340					345					350			
Lys	Pro	Lys	Ser	Gln	Cys	Lys	Asn	Lys	Asp	Thr	Leu	Leu	Lys	Arg	Thr	
		355					360					365				
Thr	Met	Gln	Asn	Phe	Leu	Thr	Thr	Lys	Ser	Arg	Leu	Arg	Lys	Thr	Gly	
	370					375					380					
Thr	Pro	Thr	Ser	Ser	Gln	His	Ser	Ser	Thr	Ala	Phe	Ser	Gly	Tyr	Ile	
385					390					395					400	
Asp	Asp	Pro	Phe	Asn	Leu	Asn	Glu	Ile	Leu	Pro	Leu	Pro	Ala	Ser	Asp	
				405					410					415		
Phe	Lys	Leu	Asn	Thr	Val	Thr	Asn	Leu	Asn	Glu	Ile	Asp	Phe	Thr	Asn	
			420					425					430			
Ile	Phe	Thr	Lys	Ser	Pro	His	Pro	His	Ser	Gly	Ser	Thr	His	Pro	Arg	
		435					440					445				
Gln	Val	Phe	Asp	Gln	Leu	Asp	Asp	Cys	Ser	Ser	Ile	Leu	Phe	Ser	Pro	
	450					455					460					
Leu	Thr	Thr	Asn	Thr	Asn	Asn	Glu	Phe	Glu	Gly	Glu	Ser	Asp	Asp	Phe	
465					470					475					480	

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

Ser Ser Ala Pro Pro Val His His Asp Pro Asn Glu Thr His Gln Glu
500 505 510

Asn Gln Asp Ile Ile Asp Arg Phe Ala Asn Ser Ser Gln Glu His Asn
515 520 525

Glu Tyr Ile Leu Gln Tyr Leu Thr His Phe Asp Ala Ala Asn His Asn
530 535 540

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

Asn Val Ser Asp Leu Gly Asn Pro Leu Leu Arg Gln Glu Ala Leu Val
565 570 575

Gly Ser Ser Ser Thr Lys Ile Phe Asp Glu Leu Lys Phe Val Gln Asn
580 585 590

Gly Pro His Gly Ser Gln His Pro Ile Asp Phe Gln His Val Asp His
595 600 605

Arg His Leu Ser Ser Asn Glu Pro Gln Val Arg Ser His Gln Tyr Gly
610 615 620

Pro Gln Gln Gln Pro Pro Gln Gln Leu Gln Tyr His Gln Asn Gln Pro
625 630 635 640

His Asp Gly His Asn His Glu Gln His Gln Thr Val Gln Lys Asp Met
645 650 655

Gln Thr His Glu Ser Leu Glu Ile Met Gly Asn Thr Leu Leu Glu Glu
660 665 670

Phe Lys Asp Ile Lys Met Val Asn Gly Glu Leu Lys Tyr Val Lys Pro
675 680 685

Glu Asp
690

<210> 214
<211> 2073
<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 214

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cattcatcct cctttgtata tgctctaccc aaaagtgtga gtgaatatgt agtcaaccat	120
aatgaggggtc gtgcaagtgc aagtggaaat ccagccgcag tgccgtctcc cataatgaca	180
ctgaatctca aaagcacaca ttccctcaat agtgatcagc atgttcatac ctcaacatcg	240
ccgacggaaa ctattgggca tattcatcat gtggaaaagc tgaatcaaaa caatttgatt	300
catctggatc cagtacccaa ctttgaagat aagtccgata ttaagccttg gttgcaaaaag	360
atTTTTtata ctcaaggaat agaacttgtg atagaaagggt cggacacatt taaagttgtc	420
ttcaagtgtg aagctgctaa aaggggaagg aacgcgagaa ggaaaagaaa agataagccc	480
aaaggacagg accacgaaga cgagaaatcc aagatcaatg atgacgaatt agaatatgcg	540
agtccttcta atgccacagt aaccaatggg cctcaaacat cgcccgatca aacatcctcc	600
ataaagccaa agaaaaaag atgtgtatcg aggtttaata actgtccgtt tagagtacga	660
gctaacttatt cgtaaagag gaaaagatgg agcattgttg taatgaacaa taaccattca	720
catcagctaa agtttaaccc tgattccgaa gagtacaaaa aattcaaaga aaaattaaga	780
aaggataatg acgtagatgc aatcaagaaa ttcgacgaat tggaatacag aactttggcc	840
aatttgccca ttccaacagc tacaatcccc tgtgattgtg gttaacaaa tgaaatacaa	900
agtttcaatg tcgtattgcc cactaacagt aatgttactt catcagcatc ctcttcaact	960
gtatcgtcca tatcccttga ttcacgaaat gcattctaaa ggccatgctt accctctgta	1020
aataacaccg gtagtatcaa taccaataac gtaaggaaac cgaaaagcca gtgtaagaat	1080
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cgtaagaccg gtacgccaac atcttcgcaa cactcatcta cagcattttc aggatatatt	1200
gatgatcctt tcaatttgaa tgaaatcttg ccactgccgg catccgattt caagctaaac	1260
actgtaacaa atttgaacga aattgacttt acgaacattt ttaccaaata gccgcattca	1320
catagcgggt ctacccatcc aagacaagtc ttcgaccaat tggacgattg ttcctctata	1380
ctcttctctc cattaactac aaacacgaat aatgaatttg aaggagagtc agatgatttt	1440
gttcattctc catatttgaa ctgagaggca gatttcagcc aaattcttag tagtgctccc	1500
ccagtccatc atgacccaaa tgaaacacat caggaaaacc aggatattat tgatagattt	1560
gctaatagtt cccaagaaca taatgagtat attctacaat atttgacgca cttcgatgct	1620
gctaaccaca ataacatcgg cgttccaaac aacaattcac attcgctaaa tactcagcat	1680

aacgtttctg atctgggcaa cccactttta agacaagaag ctttagttgg cagctcttca 1740
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 atagattttc aacatgttga ccatcgtcat ctacagctcta atgaacctca agtacgatca 1860
 catcaatatg gtccgcaaca gcagccaccg cagcaattgc aatatcacca aaatcagccc 1920
 cagcagggcc ataaccacga acagcaccaa acagtacaaa aggatatgca aacgcatgaa 1980
 tcgctagaaa taatgggaaa cacattattg gaagagttca aagacattaa aatggtgaac 2040
 ggcgagttga agtatgtgaa gccagaagat tag 2073

<210> 215
 <211> 690
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 215

Met Glu Gly Phe Asn Pro Ala His Ile Glu His Ala Ser Pro Ile Asn
1 5 10 15

Ser Ser Asp Ser His Ser Ser Ser Phe Val Tyr Ala Leu Pro Lys Ser
20 25 30

Ala Ser Glu Tyr Val Val Asn His Asn Glu Gly Arg Ala Ser Ala Ser
35 40 45

Gly Asn Pro Ala Ala Val Pro Ser Pro Ile Met Thr Leu Asn Leu Lys
50 55 60

Ser Thr His Ser Leu Asn Ser Asp Gln His Val His Thr Ser Thr Ser
65 70 75 80

Pro Thr Glu Thr Ile Gly His Ile His His Val Glu Lys Leu Asn Gln
85 90 95

Asn Asn Leu Ile His Leu Asp Pro Val Pro Asn Phe Glu Asp Lys Ser
100 105 110

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

Leu Val Ile Glu Arg Ser Asp Thr Phe Lys Val Val Phe Lys Cys Lys
130 135 140

Ala Ala Lys Arg Gly Arg Asn Ala Arg Arg Lys Arg Lys Asp Lys Pro

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

Thr Pro Thr Ser Ser Gln His Ser Ser Thr Ala Phe Ser Gly Tyr Ile
 385 390 395 400

Asp Asp Pro Phe Asn Leu Asn Glu Ile Leu Pro Leu Pro Ala Ser Asp
 405 410 415

Phe Lys Leu Asn Thr Val Thr Asn Leu Asn Glu Ile Asp Phe Thr Asn
 420 425 430

Ile Phe Thr Lys Ser Pro His Pro His Ser Gly Ser Thr His Pro Arg
 435 440 445

Gln Val Phe Asp Gln Leu Asp Asp Cys Ser Ser Ile Leu Phe Ser Pro
 450 455 460

Leu Thr Thr Asn Thr Asn Asn Glu Phe Glu Gly Glu Ser Asp Asp Phe
 465 470 475 480

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

Ser Ser Ala Pro Pro Val His His Asp Pro Asn Glu Thr His Gln Glu
 500 505 510

Asn Gln Asp Ile Ile Asp Arg Phe Ala Asn Ser Ser Gln Glu His Asn
 515 520 525

Glu Tyr Ile Leu Gln Tyr Leu Thr His Phe Asp Ala Ala Asn His Asn
 530 535 540

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

Asn Val Ser Asp Leu Gly Asn Pro Leu Leu Arg Gln Glu Ala Leu Val
 565 570 575

Gly Ser Ser Ser Thr Lys Ile Phe Asp Glu Leu Lys Phe Val Gln Asn
 580 585 590

Gly Pro His Gly Ser Gln His Pro Ile Asp Phe Gln His Val Asp His
 595 600 605

Arg His Leu Ser Ser Asn Glu Pro Gln Val Arg Ser His Gln Tyr Gly
 610 615 620

Pro Gln Gln Gln Pro Pro Gln Gln Leu Gln Tyr His Gln Asn Gln Pro
625 630 635 640

His Asp Gly His Asn His Glu Gln His Gln Thr Val Gln Lys Asp Met
645 650 655

Gln Thr His Glu Ser Leu Glu Ile Met Gly Asn Thr Leu Leu Glu Glu
660 665 670

Phe Lys Asp Ile Lys Met Val Asn Gly Glu Leu Lys Tyr Val Lys Pro
675 680 685

Glu Asp
690

<210> 216
<211> 2073
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 216
atggaaggct tcaatccggc tcacatagaa catgcgtcac cgattaattc atctgacagc 60
cattcatcct cttttgtata tgctctaccc aaaagtgtga gtgaatatgt agtcaaccat 120
aatgaggggtc gtgcaagtgc aagtggaaat ccagccgcag tgccgtctcc cataatgaca 180
ctgaatctca aaagcacaca ttccctcaat agtgatcagc atgttcatac ctcaacatcg 240
ccgacggaaa ctattgggca tattcatcat gtggaaaagc tgaatcaaaa caatttgatt 300
catctggatc cagtacccaa ctttgaagat aagtccgata ttaagccttg gttgcaaaag 360
atTTTTtatt ctcaaggaat agaacttggt atagaaaggt cggacacatt taaagttgtc 420
ttcaagtgtg aagctgctaa aaggggaagg aacgcgagaa ggaaaagaaa agataagccc 480
aaaggacagg accacgaaga cgagaaatcc aagatcaatg atgacgaatt agaatatgcg 540
agtccttcta atgccacagt aaccaatggg cctcaaacad cgcccgatca aacatcctcc 600
ataaagccaa agaaaaaag atgtgtatcg aggtttaata actgtccgtt tagagtacga 660
gctacttatt cgtaaagag gaaaagatgg agcattgttg taatgaacaa taaccattca 720
catcagctaa agtttaaccc tgattccgaa gagtacaaaa aattcaaga aaaattaaga 780
aaggataatg acgtagatgc aatcaagaaa ttcgacgaat tggaatacag aactttggcc 840
aatttgccca ttccaacagc tacaatcccc tgtgattgtg gttaacaaa tgaaatacaa 900
agtttcaatg tcgtattgcc cactaacagt aatgttactt catcagcatc ctcttcaact 960

gtatcgtcca tatcccttga ttcacatgaat gcatctaaaa ggccatgctt accctctgta 1020
 aataacaccg gtagtatcaa taccaataac gtaaggaaac cgaaaagcca gtgtaagaat 1080
 aaagacacac tcttaaaaag aaccaccatg cagaactttc tcacaactaa atcaaggctg 1140
 cgtaagaccg gtacgccaac atcttcgcaa cactcatcta cagcattttc aggatatatt 1200
 gatgatcctt tcaatttgaa tgaaatcttg ccactgccgg catccgattt caagctaaac 1260
 actgtaacaa atttgaacga aattgacttt acgaacattt ttaccaaadc gccgcatcca 1320
 catagcgggt ctacccatcc aagacaagtc ttcgaccaat tggacgattg ttcctctata 1380
 ctcttctctc cattaactac aaacacgaat aatgaatttg aaggagagtc agatgatttt 1440
 gttcattctc catatttgaa ctacagaggca gatttcagcc aaattcttag tagtgctccc 1500
 ccagtccatc atgacccaaa tgaaacacat caggaaaacc aggatattat tgatagattt 1560
 gctaatagtt cccaagaaca taatgagtat attctacaat atttgacgca cttcgatgct 1620
 gctaaccaca ataacatcgg cgttccaaac aacaattcac attcgctaaa tactcagcat 1680
 aacgtttctg atctgggcaa cccactttta agacaagaag ctttagttgg cagctcttca 1740
 acaaaaatct tcgacgaatt gaaatttgta caaaatggcc cacacgggtc tcaacatcct 1800
 atagattttc aacatgttga ccatcgtcac ctacagctcta atgaacctca agtacgatca 1860
 catcaatatg gtccgcaaca gcagccaccg cagcaattgc aatatcacca aaatcagccc 1920
 cagcagggcc ataaccacga acagcaccaa acagtacaaa aggatatgca aacgcatgaa 1980
 tcgctagaaa taatgggaaa cacattattg gaagagttca aagacattaa aatgggtgaac 2040
 ggcgagttga agtatgtgaa gccagaagat tag 2073

<210> 217
 <211> 690
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 217

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

Ala Ser Glu Tyr Val Val Asn His Asn Glu Gly Arg Ala Ser Ala Ser
 35 40 45

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

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

Ile Pro Cys Asp Cys Gly Leu Thr Asn Glu Ile Gln Ser Phe Asn Val
 290 295 300

Val Leu Pro Thr Asn Ser Asn Val Thr Ser Ser Ala Ser Ser Ser Thr
 305 310 315 320

Val Ser Ser Ile Ser Leu Asp Ser Ser Asn Ala Ser Lys Arg Pro Cys
 325 330 335

Leu Pro Ser Val Asn Asn Thr Gly Ser Ile Asn Thr Asn Asn Val Arg
 340 345 350

Lys Pro Lys Ser Gln Cys Lys Asn Lys Asp Thr Leu Leu Lys Arg Thr
 355 360 365

Thr Met Gln Asn Phe Leu Thr Thr Lys Ser Arg Leu Arg Lys Thr Gly
 370 375 380

Thr Pro Thr Ser Ser Gln His Ser Ser Thr Ala Phe Ser Gly Tyr Ile
 385 390 395 400

Asp Asp Pro Phe Asn Leu Asn Glu Ile Leu Pro Leu Pro Ala Ser Asp
 405 410 415

Phe Lys Leu Asn Thr Val Thr Asn Leu Asn Glu Ile Asp Phe Thr Asn
 420 425 430

Ile Phe Thr Lys Ser Pro His Pro His Ser Gly Ser Thr His Pro Arg
 435 440 445

Gln Val Phe Asp Gln Leu Asp Asp Cys Ser Ser Ile Leu Phe Ser Pro
 450 455 460

Leu Thr Thr Asn Thr Asn Asn Glu Phe Glu Gly Glu Ser Asp Asp Phe
 465 470 475 480

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

Ser Ser Ala Pro Pro Val His His Asp Pro Asn Glu Thr His Gln Glu
 500 505 510

Asn Gln Asp Ile Ile Asp Arg Phe Ala Asn Ser Ser Gln Glu His Asn
 515 520 525

Glu Tyr Ile Leu Gln Tyr Leu Thr His Phe Asp Ala Ala Asn His Asn
 530 535 540

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

Asn Val Ser Asp Leu Gly Asn Pro Leu Leu Arg Gln Glu Ala Leu Val
 565 570 575

Gly Ser Ser Ser Thr Lys Ile Phe Asp Glu Leu Lys Phe Val Gln Asn
 580 585 590

Gly Pro His Gly Ser Gln His Pro Ile Asp Phe Gln His Val Asp His
 595 600 605

Arg His Leu Ser Ser Asn Glu Pro Gln Val Arg Ser His Gln Tyr Gly
 610 615 620

Pro Gln Gln Gln Pro Pro Gln Gln Leu Gln Tyr His Gln Asn Gln Pro
 625 630 635 640

His Asp Gly His Asn His Glu Gln His Gln Thr Val Gln Lys Asp Met
 645 650 655

Gln Thr His Glu Ser Leu Glu Ile Met Gly Asn Thr Leu Leu Glu Glu
 660 665 670

Phe Lys Asp Ile Lys Met Val Asn Gly Glu Leu Lys Tyr Val Lys Pro
 675 680 685

Glu Asp
 690

<210> 218
 <211> 2073
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 218
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 cattcatcct cctttgtata tgggtctaccc aaaagtgccta gtgaatatgt agtcaaccat 120
 aatgaggggtc gtgcaagtgc aagtggaaat ccagccgcag tgccgtctcc cataatgaca 180
 ctgaatctca aaagcacaca ttccctcaat agtgatcagc atgttcatac ctcaacatcg 240

ccgacggaaa ctattgggca tattcatcat gtggaaaagc tgaatcaaaa caatttgatt	300
catctggatc cagtacccaa ctttgaagat aagtccgata ttaagccttg gttgcaaaaag	360
atTTTTtatt ctcaaggaat agaacttggt atagaaaggt cggacacatt taaagttgtc	420
ttcaagtgtg aagctgctaa aaggggaagg aacgcgagaa ggaaaagaaa agataagccc	480
aaaggacagg accacgaaga cgagaaatcc aagatcaatg atgacgaatt agaatatgcy	540
agtccttcta atgccacagt aaccaatggg cctcaaacat cgcccgatca aacatcctcc	600
ataaagccaa agaaaaaaag atgtgtatcg aggtttaata actgtccgtt tagagtacga	660
gctacttatt cgtaaagag gaaaagatgg agcattgttg taatgaacaa taaccattca	720
catcagctaa agtttaaccc tgattccgaa gagtacaaaa aattcaaaga aaaattaaga	780
aaggataatg acgtagatgc aatcaagaaa ttcgacgaat tggaaatacag aactttggcc	840
aattttgcca ttccaacagc tacaatcccc tgtgattgtg gtttaacaaa tgaaatacaa	900
agtttcaatg tcgtattgcc cactaacagt aatgttactt catcagcatc ctcttcaact	960
gtatcgtcca tatcccttga ttcatcgaat gcatctaaaa ggccatgctt accctctgta	1020
aataacaccg gtagtatcaa taccaataac gtaaggaaac cgaaaagcca gtgtaagaat	1080
aaagacacac tcttaaaaag aaccaccatg cagaactttc tcacaactaa atcaaggctg	1140
cgtaagaccg gtacgccaac atcttcgcaa cactcatcta cagcattttc aggatatatt	1200
gatgatcctt tcaatttgaa tgaaatcttg ccactgccgg catccgattt caagctaaac	1260
actgtaacaa atttgaacga aattgacttt acgaacattt ttaccaaata gccgcatcca	1320
catagcgggt ctacccatcc aagacaagtc ttcgaccaat tggacgattg ttctctata	1380
ctcttctctc cattaactac aaacacgaat aatgaatttg aaggagagtc agatgatttt	1440
gttcattctc catatttgaa ctgagaggca gatttcagcc aaattcttag tagtgctccc	1500
ccagtccatc atgacccaaa tgaaacacat caggaaaacc tggatattat tgatagattt	1560
gctaatagtt cccaagaaca taatgagtat attctacaat atttgacgca cttcgatgct	1620
gctaaccaca ataacatcgg cgttccaaac aacaattcac attcgctaaa tactcagcat	1680
aacgtttctg atctgggcaa ccactttta agacaagaag ctttagttgg cagctcttca	1740
acaaaaatct tcgacgaatt gaaatttgta caaaatggcc cacacggttc tcaacatcct	1800
atagattttc aacatgttga ccatcgtcat ctgagctcta atgaacctca agtacgatca	1860
catcaatatg gtccgcaaca gcagccaccg cagcaattgc aatatcacca aaatcagccc	1920
cacgacggcc ataaccacga acagcaccaa acagtacaaa aggatatgca aacgcatgaa	1980
tcgctagaaa taatgggaaa cacattattg gaagagttca aagacattaa aatgggtgaac	2040

ggcgagttga agtatgtgaa gccagaagat tag

2073

<210> 219

<211> 690

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 219

Met Glu Gly Phe Asn Pro Ala His Ile Glu His Ala Ser Pro Ile Asn
1 5 10 15

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

Ala Ser Glu Tyr Val Val Asn His Asn Glu Gly Arg Ala Ser Ala Ser
35 40 45

Gly Asn Pro Ala Ala Val Pro Ser Pro Ile Met Thr Leu Asn Leu Lys
50 55 60

Ser Thr His Ser Leu Asn Ser Asp Gln His Val His Thr Ser Thr Ser
65 70 75 80

Pro Thr Glu Thr Ile Gly His Ile His His Val Glu Lys Leu Asn Gln
85 90 95

Asn Asn Leu Ile His Leu Asp Pro Val Pro Asn Phe Glu Asp Lys Ser
100 105 110

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

Leu Val Ile Glu Arg Ser Asp Thr Phe Lys Val Val Phe Lys Cys Lys
130 135 140

Ala Ala Lys Arg Gly Arg Asn Ala Arg Arg Lys Arg Lys Asp Lys Pro
145 150 155 160

Lys Gly Gln Asp His Glu Asp Glu Lys Ser Lys Ile Asn Asp Asp Glu
165 170 175

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

Thr Ser Pro Asp Gln Thr Ser Ser Ile Lys Pro Lys Lys Lys Arg Cys
195 200 205

Val Ser Arg Phe Asn Asn Cys Pro Phe Arg Val Arg Ala Thr Tyr Ser
210 215 220

Leu Lys Arg Lys Arg Trp Ser Ile Val Val Met Asn Asn Asn His Ser
225 230 235 240

His Gln Leu Lys Phe Asn Pro Asp Ser Glu Glu Tyr Lys Lys Phe Lys
245 250 255

Glu Lys Leu Arg Lys Asp Asn Asp Val Asp Ala Ile Lys Lys Phe Asp
260 265 270

Glu Leu Glu Tyr Arg Thr Leu Ala Asn Leu Pro Ile Pro Thr Ala Thr
275 280 285

Ile Pro Cys Asp Cys Gly Leu Thr Asn Glu Ile Gln Ser Phe Asn Val
290 295 300

Val Leu Pro Thr Asn Ser Asn Val Thr Ser Ser Ala Ser Ser Ser Thr
305 310 315 320

Val Ser Ser Ile Ser Leu Asp Ser Ser Asn Ala Ser Lys Arg Pro Cys
325 330 335

Leu Pro Ser Val Asn Asn Thr Gly Ser Ile Asn Thr Asn Asn Val Arg
340 345 350

Lys Pro Lys Ser Gln Cys Lys Asn Lys Asp Thr Leu Leu Lys Arg Thr
355 360 365

Thr Met Gln Asn Phe Leu Thr Thr Lys Ser Arg Leu Arg Lys Thr Gly
370 375 380

Thr Pro Thr Ser Ser Gln His Ser Ser Thr Ala Phe Ser Gly Tyr Ile
385 390 395 400

Asp Asp Pro Phe Asn Leu Asn Glu Ile Leu Pro Leu Pro Ala Ser Asp
405 410 415

Phe Lys Leu Asn Thr Val Thr Asn Leu Asn Glu Ile Asp Phe Thr Asn
420 425 430

Ile Phe Thr Lys Ser Pro His Pro His Ser Gly Ser Thr His Pro Arg
435 440 445

Gln Val Phe Asp Gln Leu Asp Asp Cys Ser Ser Ile Leu Phe Ser Pro
450 455 460

Leu Thr Thr Asn Thr Asn Asn Glu Phe Glu Gly Glu Ser Asp Asp Phe
465 470 475 480

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

Ser Ser Ala Pro Pro Val His His Asp Pro Asn Glu Thr His Gln Glu
500 505 510

Asn Leu Asp Ile Ile Asp Arg Phe Ala Asn Ser Ser Gln Glu His Asn
515 520 525

Glu Tyr Ile Leu Gln Tyr Leu Thr His Phe Asp Ala Ala Asn His Asn
530 535 540

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

Asn Val Ser Asp Leu Gly Asn Pro Leu Leu Arg Gln Glu Ala Leu Val
565 570 575

Gly Ser Ser Ser Thr Lys Ile Phe Asp Glu Leu Lys Phe Val Gln Asn
580 585 590

Gly Pro His Gly Ser Gln His Pro Ile Asp Phe Gln His Val Asp His
595 600 605

Arg His Leu Ser Ser Asn Glu Pro Gln Val Arg Ser His Gln Tyr Gly
610 615 620

Pro Gln Gln Gln Pro Pro Gln Gln Leu Gln Tyr His Gln Asn Gln Pro
625 630 635 640

His Asp Gly His Asn His Glu Gln His Gln Thr Val Gln Lys Asp Met
645 650 655

Gln Thr His Glu Ser Leu Glu Ile Met Gly Asn Thr Leu Leu Glu Glu
660 665 670

Phe Lys Asp Ile Lys Met Val Asn Gly Glu Leu Lys Tyr Val Lys Pro
675 680 685

Glu Asp
690

<210> 220
<211> 2073
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 220
atggaaggct tcaatccggc tcacatagaa catgcgtcac cgattaattc atctgacagc 60
cattcatcct cttttgtata tgctctaccc aaaagtgtga gtgaatatgt agtcaaccat 120
aatgaggggtc gtgcaagtgc aagtggaaat ccagccgcag tgccgtctcc cataatgaca 180
ctgaatctca aaagcacaca ttccctcaat agtgatcagc atgttcatac ctcaacatcg 240
ccgacggaaa ctattgggca tattcatcat gtggaaaagc tgaatcaaaa caatttgatt 300
catctggatc cagtacccaa ctttgaagat aagtccgata ttaagccttg gttgcaaaaag 360
atTTTTtAtc ctcaaggaat agaacttgtg atagaaaggt cggacacatt taaagttgtc 420
ttcaagtgtg aagctgctaa aaggggaagg aacgcgagaa ggaaaagaaa agataagccc 480
aaaggacagg aacacgaaga cgagaaatcc aagatcaatg atgacgaatt agaatatgcy 540
agtccttcta atgccacagt aaccaatggg cctcaaacat cgcctgatca aacatcctcc 600
ataaagccaa agaaaaaag atgtgtatcg aggtttaata actgtccgtt tagagtacga 660
gctacttatt cgttaaagag gaaaagatgg agcattgttg taatgaacaa taaccattca 720
catcagctaa agtttaaccc tgattccgaa gagtacaaaa aattcaaaga aaaattaaga 780
aaggataatg acgtagatgc aatcaagaaa ttcgacgaat tggaatacag aactttggcc 840
aatttgccca ttccaacagc tacaatccca tgtgattgtg gttaacaaa tgaaatacaa 900
agtttcaatg tcgtcttgcc cactaacagt aatgttactt catcagcatc ctcttcaact 960
gtatcgtcca tatcccttga ttcacgcaat gcatctaaaa ggccatgctt accctctgta 1020
aataacaccg gtagtatcaa taccaataac gtaaggaaac cgaaaagcca gtgtaagaat 1080
aaagacacac tcttaaaaag aaccaccatg cagaactttc tcacaactaa atcaaggctg 1140
cgtaagaccg gtacgccaac atcttcgcaa cactcatcta cagcattttc aggatatatt 1200
gatgatcctt tcaatttgaa tgaaatcttg ccactgccgg catccgattt caagctaaac 1260
actgtaacaa atttgaacga aattgacttt acgaacattt ttaccaaata gccgcatcca 1320

catagcgggt ctacccatcc aagacaagtc ttcgaccaat tggacgattg ttcctctata 1380
ctcttctctc cattaactac aaacacgaat aatgaatttg aaggagagtc agatgatttt 1440
gttcattctc catatttgaa ctgagaggca gatttcagcc aaattcttag tagtgctccc 1500
ccagtccatc atgacccaag tgaaacacat caggaaaacc aggatattat tgatagattt 1560
gctaatagct cccaagaaca taatgagtat attctacaat atttgacgca cttcgatgct 1620
gctaaccaca ataatatcgg cgttccaaac aacaattcac attcgctaaa tactcagcat 1680
aacgtttctg atctgggcaa cccactttta agacaagaag ctttagttgg cagctcttca 1740
acaaaaatct tcgatgaatt gaaatttgta caaaatggcc cacacgggtc tcaacatcct 1800
atagattttc aacatgttga ccatcgtcac ctgagctcta atgaacctca agtacgatca 1860
catcaatatg gtccgcaaca gcagccaccg cagcaattgc aatatcacca aaatcagccc 1920
cacgacgggc ataaccacga acagcttcaa acagtacaaa aggatatgca aacgcatgaa 1980
tcgctagaaa taatgggaaa cacattattg gaagagttca aagacattaa aatggtgaac 2040
ggcgagttga agtatgtgaa gccagaagat tag 2073

<210> 221
<211> 690
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 221

Met Glu Gly Phe Asn Pro Ala His Ile Glu His Ala Ser Pro Ile Asn
1 5 10 15

Ser Ser Asp Ser His Ser Ser Ser Phe Val Tyr Ala Leu Pro Lys Ser
20 25 30

Ala Ser Glu Tyr Val Val Asn His Asn Glu Gly Arg Ala Ser Ala Ser
35 40 45

Gly Asn Pro Ala Ala Val Pro Ser Pro Ile Met Thr Leu Asn Leu Lys
50 55 60

Ser Thr His Ser Leu Asn Ser Asp Gln His Val His Thr Ser Thr Ser
65 70 75 80

Pro Thr Glu Thr Ile Gly His Ile His His Val Glu Lys Leu Asn Gln
85 90 95

Asn Asn Leu Ile His Leu Asp Pro Val Pro Asn Phe Glu Asp Lys Ser
100 105 110

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

Leu Val Ile Glu Arg Ser Asp Thr Phe Lys Val Val Phe Lys Cys Lys
130 135 140

Ala Ala Lys Arg Gly Arg Asn Ala Arg Arg Lys Arg Lys Asp Lys Pro
145 150 155 160

Lys Gly Gln Glu His Glu Asp Glu Lys Ser Lys Ile Asn Asp Asp Glu
165 170 175

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

Thr Ser Pro Asp Gln Thr Ser Ser Ile Lys Pro Lys Lys Lys Arg Cys
195 200 205

Val Ser Arg Phe Asn Asn Cys Pro Phe Arg Val Arg Ala Thr Tyr Ser
210 215 220

Leu Lys Arg Lys Arg Trp Ser Ile Val Val Met Asn Asn Asn His Ser
225 230 235 240

His Gln Leu Lys Phe Asn Pro Asp Ser Glu Glu Tyr Lys Lys Phe Lys
245 250 255

Glu Lys Leu Arg Lys Asp Asn Asp Val Asp Ala Ile Lys Lys Phe Asp
260 265 270

Glu Leu Glu Tyr Arg Thr Leu Ala Asn Leu Pro Ile Pro Thr Ala Thr
275 280 285

Ile Pro Cys Asp Cys Gly Leu Thr Asn Glu Ile Gln Ser Phe Asn Val
290 295 300

Val Leu Pro Thr Asn Ser Asn Val Thr Ser Ser Ala Ser Ser Ser Thr
305 310 315 320

Val Ser Ser Ile Ser Leu Asp Ser Ser Asn Ala Ser Lys Arg Pro Cys
325 330 335

Leu Pro Ser Val Asn Asn Thr Gly Ser Ile Asn Thr Asn Asn Val Arg
340 345 350

Lys Pro Lys Ser Gln Cys Lys Asn Lys Asp Thr Leu Leu Lys Arg Thr
355 360 365

Thr Met Gln Asn Phe Leu Thr Thr Lys Ser Arg Leu Arg Lys Thr Gly
370 375 380

Thr Pro Thr Ser Ser Gln His Ser Ser Thr Ala Phe Ser Gly Tyr Ile
385 390 395 400

Asp Asp Pro Phe Asn Leu Asn Glu Ile Leu Pro Leu Pro Ala Ser Asp
405 410 415

Phe Lys Leu Asn Thr Val Thr Asn Leu Asn Glu Ile Asp Phe Thr Asn
420 425 430

Ile Phe Thr Lys Ser Pro His Pro His Ser Gly Ser Thr His Pro Arg
435 440 445

Gln Val Phe Asp Gln Leu Asp Asp Cys Ser Ser Ile Leu Phe Ser Pro
450 455 460

Leu Thr Thr Asn Thr Asn Asn Glu Phe Glu Gly Glu Ser Asp Asp Phe
465 470 475 480

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

Ser Ser Ala Pro Pro Val His His Asp Pro Ser Glu Thr His Gln Glu
500 505 510

Asn Gln Asp Ile Ile Asp Arg Phe Ala Asn Ser Ser Gln Glu His Asn
515 520 525

Glu Tyr Ile Leu Gln Tyr Leu Thr His Phe Asp Ala Ala Asn His Asn
530 535 540

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

Asn Val Ser Asp Leu Gly Asn Pro Leu Leu Arg Gln Glu Ala Leu Val
565 570 575

Gly Ser Ser Ser Thr Lys Ile Phe Asp Glu Leu Lys Phe Val Gln Asn
580 585 590

Gly Pro His Gly Ser Gln His Pro Ile Asp Phe Gln His Val Asp His
595 600 605

Arg His Leu Ser Ser Asn Glu Pro Gln Val Arg Ser His Gln Tyr Gly
610 615 620

Pro Gln Gln Gln Pro Pro Gln Gln Leu Gln Tyr His Gln Asn Gln Pro
625 630 635 640

His Asp Gly His Asn His Glu Gln Leu Gln Thr Val Gln Lys Asp Met
645 650 655

Gln Thr His Glu Ser Leu Glu Ile Met Gly Asn Thr Leu Leu Glu Glu
660 665 670

Phe Lys Asp Ile Lys Met Val Asn Gly Glu Leu Lys Tyr Val Lys Pro
675 680 685

Glu Asp
690

<210> 222
<211> 2073
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 222
atggaaggct tcaatccggc tcacatagaa catgcgtcac cgattaattc atctgacagc 60
cattcatcct cttttgtata tgctctaccc aaaagtgcta gtgaatatgt agtcaaccat 120
aatgaggatc gtgcaagtgc aagtggaaat ccagccgcag tgccgtctcc cataatgaca 180
ctgaatctca aaagcacaca ttccctcaat agtgatcagc atgttcatac ctcaacatcg 240
ccgacggaaa ctattgggca tattcatcat gtggaaaagc tgaatcaaaa caatttgatt 300
catctggatc cagtacccaa ctttgaagat aagtccgata ttaagccttg gttgcaaaag 360
atTTTTtata ctcaaggaat agaacttgtg atagaaaggt cggacacatt taaagttgtc 420
ttcaagtgta aagctgctaa aaggggaagg aacgcgagaa ggaaaagaaa agataagccc 480
aaaggacagg aacacgaaga cgagaaatcc aagatcaatg atgacgaatt agaatatgcg 540
agtccttcta atgccacagt aaccaatggg cctcaaacat cgcccgatca aacatcctcc 600

ataaagccaa agaaaaaaag atgtgtatcg aggtttaata actgtccggt tagagtacga	660
gctacttatt cgtaaagag gaaaagatgg agcattgttg taatgaacaa taaccattca	720
catcagctaa agtttaaccc tgattccgaa gagtacaaaa aattcaaaga aaaattaaga	780
aaggataatg acgtagatgc aatcaagaaa ttcgacgaat tggaatacag aactttggcc	840
aattttaccca ttccaacagc tacaatcccc tgtgattgtg gttaacaaa tgaaatacaa	900
agtttcaatg tcgtcttgcc cactaacagt aatgttactt catcagcatc ctcttcaact	960
gtatcgtcca tatcccttga ttcatcgaat gcatctaaaa ggccatgctt accctctgta	1020
aataacaccg gtagtatcaa taccaataac gtaaggaaac cgaaaagcca gtgtaagaat	1080
aaagacacac tcttaaaaag aaccaccatg cagaactttc tcacaactaa atcaaggctg	1140
cgtaagaccg gtacgccaac atcttcgcaa cactcatcta cagcattttc aggatatatt	1200
gatgatcctt tcaatttgaa tgaaatcttg ccactgccgg catccgattt caagctaaac	1260
actgtaacaa atttgaacga aattgacttt acgaacattt ttaccaaate gccgcatcca	1320
catagcgggt ctacccatcc aagacaagtc ttcgaccaat tggacgattg ttcctctata	1380
ctcttctctc cattaactac aaacacgaat aatgaatttg aaggagagtc agatgatttt	1440
gttcattctc catatttgaa ctgagaggca gatttcagcc aaattcttag tagtgctccc	1500
ccagtccatc atgacccaag tgaaacacat caggaaaacc aggatattat tgatagattt	1560
gctaatagct cccaagaaca taatgagtat attctacaat atttgacgca cttcgatgct	1620
gctaaccaca ataatatcgg cgttccaaac aacaattcac attcgctaaa tactcagcat	1680
aacgtttctg atctgggcaa cccactttta agacaagaag ctttagttgg cagctcttca	1740
acaaaaatct tcgatgaatt gaaatttgta caaatggcc cacacggttc tcaacatcct	1800
atagattttc aacatgttga ccatcgtcat ctgagctcta atgaacctca agtacgatca	1860
catcaatatg gtccgcaaca gcagccaccg cagcaattgc aatatcacca aaatcagccc	1920
cacgacgggc ataaccacga acagcttcaa acagtacaaa aggatatgca aacgcatgaa	1980
tcgctagaaa taatgggaaa cacattattg gaagagttca aagacattaa aatggtgaac	2040
ggcgagttga agtatgtgaa gccagaagat tag	2073

<210> 223
 <211> 690
 <212> PRT
 <213> *Saccharomyces cerevisiae*

 <400> 223

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

His Gln Leu Lys Phe Asn Pro Asp Ser Glu Glu Tyr Lys Lys Phe Lys
245 250 255

Glu Lys Leu Arg Lys Asp Asn Asp Val Asp Ala Ile Lys Lys Phe Asp
260 265 270

Glu Leu Glu Tyr Arg Thr Leu Ala Asn Leu Pro Ile Pro Thr Ala Thr
275 280 285

Ile Pro Cys Asp Cys Gly Leu Thr Asn Glu Ile Gln Ser Phe Asn Val
290 295 300

Val Leu Pro Thr Asn Ser Asn Val Thr Ser Ser Ala Ser Ser Ser Thr
305 310 315 320

Val Ser Ser Ile Ser Leu Asp Ser Ser Asn Ala Ser Lys Arg Pro Cys
325 330 335

Leu Pro Ser Val Asn Asn Thr Gly Ser Ile Asn Thr Asn Asn Val Arg
340 345 350

Lys Pro Lys Ser Gln Cys Lys Asn Lys Asp Thr Leu Leu Lys Arg Thr
355 360 365

Thr Met Gln Asn Phe Leu Thr Thr Lys Ser Arg Leu Arg Lys Thr Gly
370 375 380

Thr Pro Thr Ser Ser Gln His Ser Ser Thr Ala Phe Ser Gly Tyr Ile
385 390 395 400

Asp Asp Pro Phe Asn Leu Asn Glu Ile Leu Pro Leu Pro Ala Ser Asp
405 410 415

Phe Lys Leu Asn Thr Val Thr Asn Leu Asn Glu Ile Asp Phe Thr Asn
420 425 430

Ile Phe Thr Lys Ser Pro His Pro His Ser Gly Ser Thr His Pro Arg
435 440 445

Gln Val Phe Asp Gln Leu Asp Asp Cys Ser Ser Ile Leu Phe Ser Pro
450 455 460

Leu Thr Thr Asn Thr Asn Asn Glu Phe Glu Gly Glu Ser Asp Asp Phe
465 470 475 480

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

Ser Ser Ala Pro Pro Val His His Asp Pro Ser Glu Thr His Gln Glu
500 505 510

Asn Gln Asp Ile Ile Asp Arg Phe Ala Asn Ser Ser Gln Glu His Asn
515 520 525

Glu Tyr Ile Leu Gln Tyr Leu Thr His Phe Asp Ala Ala Asn His Asn
530 535 540

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

Asn Val Ser Asp Leu Gly Asn Pro Leu Leu Arg Gln Glu Ala Leu Val
565 570 575

Gly Ser Ser Ser Thr Lys Ile Phe Asp Glu Leu Lys Phe Val Gln Asn
580 585 590

Gly Pro His Gly Ser Gln His Pro Ile Asp Phe Gln His Val Asp His
595 600 605

Arg His Leu Ser Ser Asn Glu Pro Gln Val Arg Ser His Gln Tyr Gly
610 615 620

Pro Gln Gln Gln Pro Pro Gln Gln Leu Gln Tyr His Gln Asn Gln Pro
625 630 635 640

His Asp Gly His Asn His Glu Gln Leu Gln Thr Val Gln Lys Asp Met
645 650 655

Gln Thr His Glu Ser Leu Glu Ile Met Gly Asn Thr Leu Leu Glu Glu
660 665 670

Phe Lys Asp Ile Lys Met Val Asn Gly Glu Leu Lys Tyr Val Lys Pro
675 680 685

Glu Asp
690

<210> 224

<211> 2073
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 224
 atggaaggct tcaatccggc tcacatagaa catgcgtcac cgattaattc atctgacagc 60
 cattcatcct cctttgtata tgctctaccc aaaagtgtcta gtgaatatgt agtcaaccat 120
 aatgaggggtc gtgcaagtgc aagtggaaat ccagccgcag tgccgtctcc cataatgaca 180
 ctgaatctca aaagcacaca ttccctcaat agtgatcagc atgttcatac ctcaacatcg 240
 ccgacggaaa ctattgggca tattcatcat gtggaaaagc tgaatcaaaa caatttgatt 300
 catctggatc cagtacccaa ctttgaagat aagtccgata ttaagccttg gttgcaaaaag 360
 attttttatc ctcaaggaat agaacttgtg atagaaaggc cgacacatt taaagttgtc 420
 ttcaagtgtg aagctgctaa aaggggaagg aacgcgagaa ggaaaagaaa agataagccc 480
 aaaggacagg aacacgaaga cgagaaatcc aagatcaatg atgacgaatt agaatatgcg 540
 agtccttcta atgccacagt aaccaatggg cctcaaacat cgcccgatca aacatcctcc 600
 ataaagccaa agaaaaaag atgtgtatcg aggtttaata actgtccgtt tagagtacga 660
 gctacttatt cgttaaagag gaaaagatgg agcattgttg taatgaacaa taaccattca 720
 catcagctaa agtttaaccc tgattccgaa gagtacaaaa aattcaaaga aaaattaaga 780
 aaggataatg acgtagatgc aatcaagaaa ttcgacgaat tggaatacag aactttggcc 840
 aatttaccba ttccaacagc tacaatcccc tgtgattgtg gttaacaaa tgaaatacaa 900
 agtttcaatg tcgtcttgcc cactaacagt aatgttactt catcagcatc ctcttcaact 960
 gtatcgtcca tatcccttga ttcatcgaat gcatctaaaa ggccatgctt accctctgta 1020
 aataacaccg gtagtatcaa taccaataac gtaaggaaac cgaaaagcca gtgtaagaat 1080
 aaagacacac tcttaaaaag aaccaccatg cagaactttc tcacaactaa atcaaggctg 1140
 cgtaagaccg gtacgccaac atcttcgcaa cactcatcta cagcattttc aggatatatt 1200
 gatgatcctt tcaatttgaa tgaaatcttg ccactgccgg catccgattt caagctaaac 1260
 actgtaacaa atttgaacga aattgacttt acgaacattt ttaccaaata gccgcattca 1320
 catagcgggt ctacccatcc aagacaagtc ttcgaccaat tggacgattg ttcctctata 1380
 ctcttctctc cattaactac aaacacgaat aatgaatttg aaggagagtc agatgatttt 1440
 gttcattctc catatttgaa ctgagaggca gatttcagcc aaattcttag tagtgctccc 1500
 ccagtccatc atgacccaag tgaaacacat caggaaaacc aggatattat tgatagattt 1560
 gctaatagct cccaagaaca taatgagtat attctacaat atttgacgca cttcgatgct 1620

gctaaccaca ataatatcgg cgttccaaac aacaattcac attcgctaaa tactcagcat 1680
aacgtttctg atctgggcaa cccactttta agacaagaag ctttagttgg cagctcttca 1740
acaaaaatct tcgatgaatt gaaatttgta caaaatggcc cacacgggtc tcaacatcct 1800
atagattttc aacatgttga ccatcgtcat ctacagctcta atgaacctca agtacgatca 1860
catcaatatg gtccgcaaca gcagccaccg cagcaattgc aatatcacca aaatcagccc 1920
cacgacgggc ataaccacga acagcttcaa acagtacaaa aggatgtgca aacgcatgaa 1980
tcgctagaaa taatgggaaa cacattattg gaagagttca aagacattaa aatggtgaac 2040
ggcgagttga agtatgtgaa gccagaagat tag 2073

<210> 225
<211> 690
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 225

Met Glu Gly Phe Asn Pro Ala His Ile Glu His Ala Ser Pro Ile Asn
1 5 10 15

Ser Ser Asp Ser His Ser Ser Ser Phe Val Tyr Ala Leu Pro Lys Ser
20 25 30

Ala Ser Glu Tyr Val Val Asn His Asn Glu Gly Arg Ala Ser Ala Ser
35 40 45

Gly Asn Pro Ala Ala Val Pro Ser Pro Ile Met Thr Leu Asn Leu Lys
50 55 60

Ser Thr His Ser Leu Asn Ser Asp Gln His Val His Thr Ser Thr Ser
65 70 75 80

Pro Thr Glu Thr Ile Gly His Ile His His Val Glu Lys Leu Asn Gln
85 90 95

Asn Asn Leu Ile His Leu Asp Pro Val Pro Asn Phe Glu Asp Lys Ser
100 105 110

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

Leu Val Ile Glu Arg Ser Asp Thr Phe Lys Val Val Phe Lys Cys Lys
130 135 140

Ala Ala Lys Arg Gly Arg Asn Ala Arg Arg Lys Arg Lys Asp Lys Pro
 145 150 155 160

Lys Gly Gln Glu His Glu Asp Glu Lys Ser Lys Ile Asn Asp Asp Glu
 165 170 175

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

Thr Ser Pro Asp Gln Thr Ser Ser Ile Lys Pro Lys Lys Lys Arg Cys
 195 200 205

Val Ser Arg Phe Asn Asn Cys Pro Phe Arg Val Arg Ala Thr Tyr Ser
 210 215 220

Leu Lys Arg Lys Arg Trp Ser Ile Val Val Met Asn Asn Asn His Ser
 225 230 235 240

His Gln Leu Lys Phe Asn Pro Asp Ser Glu Glu Tyr Lys Lys Phe Lys
 245 250 255

Glu Lys Leu Arg Lys Asp Asn Asp Val Asp Ala Ile Lys Lys Phe Asp
 260 265 270

Glu Leu Glu Tyr Arg Thr Leu Ala Asn Leu Pro Ile Pro Thr Ala Thr
 275 280 285

Ile Pro Cys Asp Cys Gly Leu Thr Asn Glu Ile Gln Ser Phe Asn Val
 290 295 300

Val Leu Pro Thr Asn Ser Asn Val Thr Ser Ser Ala Ser Ser Ser Thr
 305 310 315 320

Val Ser Ser Ile Ser Leu Asp Ser Ser Asn Ala Ser Lys Arg Pro Cys
 325 330 335

Leu Pro Ser Val Asn Asn Thr Gly Ser Ile Asn Thr Asn Asn Val Arg
 340 345 350

Lys Pro Lys Ser Gln Cys Lys Asn Lys Asp Thr Leu Leu Lys Arg Thr
 355 360 365

Thr Met Gln Asn Phe Leu Thr Thr Lys Ser Arg Leu Arg Lys Thr Gly
 370 375 380

Thr Pro Thr Ser Ser Gln His Ser Ser Thr Ala Phe Ser Gly Tyr Ile
385 390 395 400

Asp Asp Pro Phe Asn Leu Asn Glu Ile Leu Pro Leu Pro Ala Ser Asp
405 410 415

Phe Lys Leu Asn Thr Val Thr Asn Leu Asn Glu Ile Asp Phe Thr Asn
420 425 430

Ile Phe Thr Lys Ser Pro His Pro His Ser Gly Ser Thr His Pro Arg
435 440 445

Gln Val Phe Asp Gln Leu Asp Asp Cys Ser Ser Ile Leu Phe Ser Pro
450 455 460

Leu Thr Thr Asn Thr Asn Asn Glu Phe Glu Gly Glu Ser Asp Asp Phe
465 470 475 480

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

Ser Ser Ala Pro Pro Val His His Asp Pro Ser Glu Thr His Gln Glu
500 505 510

Asn Gln Asp Ile Ile Asp Arg Phe Ala Asn Ser Ser Gln Glu His Asn
515 520 525

Glu Tyr Ile Leu Gln Tyr Leu Thr His Phe Asp Ala Ala Asn His Asn
530 535 540

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

Asn Val Ser Asp Leu Gly Asn Pro Leu Leu Arg Gln Glu Ala Leu Val
565 570 575

Gly Ser Ser Ser Thr Lys Ile Phe Asp Glu Leu Lys Phe Val Gln Asn
580 585 590

Gly Pro His Gly Ser Gln His Pro Ile Asp Phe Gln His Val Asp His
595 600 605

Arg His Leu Ser Ser Asn Glu Pro Gln Val Arg Ser His Gln Tyr Gly

610	615	620
Pro Gln Gln Gln Pro	Pro Gln Gln Leu Gln	Tyr His Gln Asn Gln Pro
625	630	635 640
His Asp Gly His Asn	His Glu Gln Leu Gln	Thr Val Gln Lys Asp Val
	645	650 655
Gln Thr His Glu Ser	Leu Glu Ile Met Gly	Asn Thr Leu Leu Glu Glu
	660	665 670
Phe Lys Asp Ile Lys	Met Val Asn Gly Glu	Leu Lys Tyr Val Lys Pro
	675	680 685
Glu Asp		
690		