

CL5510WOPCT_SeqListing_ST25.txt
SEQUENCE LISTING

<110> E.I. du Pont de Nemours and Co.
You, Zheng

<120> Recombinant Bacteria Having the Ability to Metabolize Sucrose

<130> CL5510 USNP

<160> 177

<170> PatentIn version 3.5

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<212> DNA

<213> *Saccharomyces cerevisiae*

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 Pro Gly Ile Thr Leu Pro Asp Asn Leu Val Ala Asn Pro Asp Leu Ile
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 Asp Ser Val Lys Asp Val Asp Ile Ile Val Phe Asn Ile Pro His Gln
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 Pro Tyr Phe His Val Ser Val Ile Glu Asp Val Ala Gly Ile Ser Ile
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285

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CL5510WOPCT_SeqListing_ST25.txt

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Ser Thr Phe Leu Arg Arg Ser Leu Leu Gln Thr Gln Leu His Ser Lys
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Met Thr Ala His Thr Asn Ile Lys Gln His Lys His Cys His Glu Asp
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Page 4

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180

185

190

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 195 200 205

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Cys Gly Ala Leu Ser Gly Ala Asn Leu Ala Pro Glu Val Ala Lys Glu
 225 230 235 240

His Trp Ser Glu Thr Thr Val Ala Tyr Gln Leu Pro Lys Asp Tyr Gln
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Gly Asp Gly Lys Asp Val Asp His Lys Ile Leu Lys Leu Leu Phe His
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Arg Pro Tyr Phe His Val Asn Val Ile Asp Asp Val Ala Gly Ile Ser
 275 280 285

Ile Ala Gly Ala Leu Lys Asn Val Val Ala Leu Ala Cys Gly Phe Val
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Glu Gly Met Gly Trp Gly Asn Asn Ala Ser Ala Ala Ile Gln Arg Leu
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Gly Leu Gly Glu Ile Ile Lys Phe Gly Arg Met Phe Phe Pro Glu Ser
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Gln Thr Cys Glu Leu Thr Gln Glu Phe Pro Leu Phe Glu Ala Val Tyr
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 Pro Ala Ile Ala Ala Phe Trp Arg Asp Phe Gly Lys Asp Lys Pro Tyr
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Gly Arg Asn Gly Leu Gly Phe Pro Ile Asn Glu Gln Asp Pro Ser Lys
180 185 190

Ser Lys Val Val Val Phe Glu Asp Ala Pro Ala Gly Ile Ala Ala Gly
195 200 205

Lys Ala Ala Gly Cys Lys Ile Val Gly Ile Ala Thr Thr Phe Asp Leu
210 215 220

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

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 130 135 140

Gln Gly Lys Pro His Pro Glu Pro Tyr Leu Lys Gly Arg Asn Gly Leu
 145 150 155 160

Gly Tyr Pro Ile Asn Glu Gln Asp Pro Ser Lys Ser Lys Val Val Val
 165 170 175

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 180 185 190

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

Lys Gly Cys Asp Ile Ile Val Lys Asn His Glu Ser Ile Arg Val Gly
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CL5510WOPCT_SeqListing_ST25.txt

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 Val Thr Asn Leu Lys Asp Asn Pro Val Gln Ile Ala Ala Asp Ala Ala
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 Glu Ala Gly Ile Arg Gly Phe Ser Glu Gln Glu Thr Thr Val Gly Ile
 165 170 175
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 485 490
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 85 90 95
 Val Ser Arg Glu Glu Ile Ile Ala Ile Thr Thr Ala Ile Thr Pro Ala
 100 105 110
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 115 120 125
 Ala Leu Gln Lys Met Arg Ala Arg Arg Thr Pro Ser Asn Gln Cys His
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210 215 220

Ser Val Tyr Gly Thr Glu Ala Val Phe Thr Asp Gly Asp Asp Thr Pro
225 230 235 240

Trp Ser Lys Ala Phe Leu Ala Ser Ala Tyr Ala Ser Arg Gly Leu Lys
245 250 255

Met Arg Tyr Thr Ser Gly Thr Gly Ser Glu Ala Leu Met Gly Tyr Ser
260 265 270

Glu Ser Lys Ser Met Leu Tyr Leu Glu Ser Arg Cys Ile Phe Ile Thr
275 280 285

Lys Gly Ala Gly Val Gln Gly Leu Gln Asn Gly Ala Val Ser Cys Ile
290 295 300

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

Asn Leu Ile Ala Ser Met Leu Asp Leu Glu Val Ala Ser Ala Asn Asp
325 330 335

Gln Thr Phe Ser His Ser Asp Ile Arg Arg Thr Ala Arg Thr Leu Met
340 345 350

Gln Met Leu Pro Gly Thr Asp Phe Ile Phe Ser Gly Tyr Ser Ala Val
355 360 365

Pro Asn Tyr Asp Asn Met Phe Ala Gly Ser Asn Phe Asp Ala Glu Asp
370 375 380

Phe Asp Asp Tyr Asn Ile Leu Gln Arg Asp Leu Met Val Asp Gly Gly
385 390 395 400

Leu Arg Pro Val Thr Glu Ala Glu Thr Ile Ala Ile Arg Gln Lys Ala
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Ala Arg Ala Ile Gln Ala Val Phe Arg Glu Leu Gly Leu Pro Pro Ile
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Ala Asp Glu Glu Val Glu Ala Ala Thr Tyr Ala His Gly Ser Asn Glu
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Met Lys Arg Asn Ile Thr Gly Leu Asp Ile Val Gly Ala Leu Ser Arg
465 470 475 480

Ser Gly Phe Glu Asp Ile Ala Ser Asn Ile Leu Asn Met Leu Arg Gln
485 490 495

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

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

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Met Pro His Gly Ala Ile Leu Lys Glu Leu Ile Ala Gly Val Glu Glu
50 55 60

gag ggg ctt cac gcc cgg gtg gtg cgc att ctg cgc acg tcc gac gtc 240
Glu Gly Leu His Ala Arg Val Val Arg Ile Leu Arg Thr Ser Asp Val
65 70 75 80

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Ile Gly Ile Gln Ser Lys Gly Thr Thr Val Ile His Gln Arg Asp Leu
100 105 110

ctg ccg ctc agc aac ctg gag ctg ttc tcc cag gcg ccg ctg ctg acg 384
Leu Pro Leu Ser Asn Leu Glu Leu Phe Ser Gln Ala Pro Leu Leu Thr
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ctg gag acc tac cgg cag att ggc aaa aac gct gcg cgc tat gcg cgc 432
Leu Glu Thr Tyr Arg Gln Ile Gly Lys Asn Ala Ala Arg Tyr Ala Arg
130 135 140

aaa gag tca cct tcg ccg gtg ccg gtg gtg aac gat cag atg gtg cgg 480
Lys Glu Ser Pro Ser Pro Val Pro Val Val Asn Asp Gln Met Val Arg
145 150 155 160

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Pro Lys Phe Met Ala Lys Ala Ala Leu Phe His Ile Lys Glu Thr Lys
165 170 175

cat gtg gtg cag gac gcc gag ccc gtc acc ctg cac atc gac tta gta 576
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50 55 60

Glu Gly Leu His Ala Arg Val Val Arg Ile Leu Arg Thr Ser Asp Val
65 70 75 80

Ser Phe Met Ala Trp Asp Ala Ala Asn Leu Ser Gly Ser Gly Ile Gly
85 90 95

Ile Gly Ile Gln Ser Lys Gly Thr Thr Val Ile His Gln Arg Asp Leu
100 105 110

Leu Pro Leu Ser Asn Leu Glu Leu Phe Ser Gln Ala Pro Leu Leu Thr
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115

120

125

Leu Glu Thr Tyr Arg Gln Ile Gly Lys Asn Ala Ala Arg Tyr Ala Arg
 130 135 140

Lys Glu Ser Pro Ser Pro Val Pro Val Val Asn Asp Gln Met Val Arg
 145 150 155 160

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 Thr Leu Glu Lys Val Leu Ser Gly Glu Val Gly Pro Gln Asp Val Arg
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 Gln Arg His Ala Val Ala Arg Asn Phe Arg Arg Ala Ala Glu Leu Ile
 65 70 75 80
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 Ala Ile Pro Asp Glu Arg Ile Leu Ala Ile Tyr Asn Ala Leu Arg Pro
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35 40 45

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50 55 60

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

Phe Arg Ser Ser Gln Ala Glu Leu Leu Ala Ile Ala Asp Glu Leu Glu
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Phe Pro Leu Lys Leu Lys Ala Arg Tyr Asp Asn Phe Ile Gly Gly Glu
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ggg caa ctg gaa acc atc ctc aac tac att gat atc ggt aaa aaa gag Gly Gln Leu Glu Thr Ile Leu Asn Tyr Ile Asp Ile Gly Lys Lys Glu 355 360 365	1104
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35

40

45

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305 310 315 320

Glu Arg Phe Met Glu Arg Ala Ile Arg Arg Val Glu Ser Ile Arg Ser
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405 410 415

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48

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96

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Glu	Arg	Val	Tyr	Val	Gln	Lys	Gly	Ile	Tyr	Asp	Gln	Phe	Val	Asn	Arg										

CL5510WOPCT_SeqListing_ST25.txt

290

295

300

ctg Leu 305	ggt Gly	gaa Glu	gcg Ala	atg Met	cag Gln 310	gcg Ala	ggt Val	caa Gln	ttt Phe	ggt Gly 315	aac Asn	ccc Pro	gct Ala	gaa Glu	cg Arg 320	960
aac Asn	gac Asp	att Ile	gcg Ala	atg Met 325	ggg Gly	ccg Pro	ttg Leu	att Ile	aac Asn 330	gcc Ala	gcg Ala	gcg Ala	ctg Leu	gaa Glu 335	agg Arg	1008
gtc Val	gag Glu	caa Gln	aaa Lys 340	gtg Val	gcg Ala	cg Arg	gca Ala	gta Val 345	gaa Glu	gaa Glu	ggg Gly	gcg Ala	aga Arg 350	gtg Val	gcg Ala	1056
ttc Phe	ggt Gly	ggc Gly 355	aaa Lys	gcg Ala	gta Val	gag Glu	ggg Gly 360	aaa Lys	gga Gly	tat Tyr	tat Tyr	tat Tyr 365	ccg Pro	ccg Pro	aca Thr	1104
ttg Leu	ctg Leu 370	ctg Leu	gat Asp	gtt Val	cg Arg	cag Gln 375	gaa Glu	atg Met	tcg Ser	att Ile	atg Met 380	cat His	gag Glu	gaa Glu	acc Thr	1152
ttt Phe 385	ggc Gly	ccg Pro	gtg Val	ctg Leu	cca Pro 390	gtt Val	gtc Val	gca Ala	ttt Phe	gac Asp 395	acg Thr	ctg Leu	gaa Glu	gat Asp	gct Ala 400	1200
atc Ile	tca Ser	atg Met	gct Ala	aat Asn 405	gac Asp	agt Ser	gat Asp	tac Tyr	ggc Gly 410	ctg Leu	acc Thr	tca Ser	tca Ser	atc Ile 415	tat Tyr	1248
acc Thr	caa Gln	aat Asn	ctg Leu 420	aac Asn	gtc Val	gcg Ala	atg Met	aaa Lys 425	gcc Ala	att Ile	aaa Lys	ggg Gly 430	ctg Leu	aag Lys	ttt Phe	1296
ggt Gly	gaa Glu	act Thr 435	tac Tyr	atc Ile	aac Asn	cgt Arg	gaa Glu 440	aac Asn	ttc Phe	gaa Glu	gct Ala	atg Met 445	caa Gln	ggc Gly	ttc Phe	1344
cac His 450	gcc Ala	gga Gly	tgg Trp	cgt Arg	aaa Lys	tcc Ser 455	ggt Gly	att Ile	ggc Gly	ggc Gly	gca Ala 460	gat Asp	ggt Gly	aaa Lys	cat His	1392
ggc Gly 465	ttg Leu	cat His	gaa Glu	tat Tyr	ctg Leu 470	cag Gln	acc Thr	cag Gln	gtg Val	gtt Val 475	tat Tyr	tta Leu	cag Gln	tct Ser	taa	1440

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 <211> 479
 <212> PRT
 <213> Escherichia coli

<400> 18

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Thr Trp Arg Gly Asp Ala Trp Ile Asp Val Val Asn Pro Ala Thr Glu
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Ala Val Ile Ser Arg Ile Pro Asp Gly Gln Ala Glu Asp Ala Arg Lys
 35 40 45

Ala Ile Asp Ala Ala Glu Arg Ala Gln Pro Glu Trp Glu Ala Leu Pro
 50 55 60

CL5510WOPCT_SeqListing_ST25.txt

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

Glu Arg Ala Ser Glu Ile Ser Ala Leu Ile Val Glu Glu Gly Gly Lys
85 90 95

Ile Gln Gln Leu Ala Glu Val Glu Val Ala Phe Thr Ala Asp Tyr Ile
100 105 110

Asp Tyr Met Ala Glu Trp Ala Arg Arg Tyr Glu Gly Glu Ile Ile Gln
115 120 125

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

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

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

Pro Ser Glu Phe Thr Pro Asn Asn Ala Ile Ala Phe Ala Lys Ile Val
180 185 190

Asp Glu Ile Gly Leu Pro Arg Gly Val Phe Asn Leu Val Leu Gly Arg
195 200 205

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

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

Ala Ala Lys Asn Ile Thr Lys Val Cys Leu Glu Leu Gly Gly Lys Ala
245 250 255

Pro Ala Ile Val Met Asp Asp Ala Asp Leu Glu Leu Ala Val Lys Ala
260 265 270

Ile Val Asp Ser Arg Val Ile Asn Ser Gly Gln Val Cys Asn Cys Ala
275 280 285

Glu Arg Val Tyr Val Gln Lys Gly Ile Tyr Asp Gln Phe Val Asn Arg
290 295 300

Leu Gly Glu Ala Met Gln Ala Val Gln Phe Gly Asn Pro Ala Glu Arg
305 310 315 320

Asn Asp Ile Ala Met Gly Pro Leu Ile Asn Ala Ala Ala Leu Glu Arg
325 330 335

CL5510WOPCT_SeqListing_ST25.txt

Val Glu Gln Lys Val Ala Arg Ala Val Glu Glu Gly Ala Arg Val Ala
340 345 350

Phe Gly Gly Lys Ala Val Glu Gly Lys Gly Tyr Tyr Tyr Pro Pro Thr
355 360 365

Leu Leu Leu Asp Val Arg Gln Glu Met Ser Ile Met His Glu Glu Thr
370 375 380

Phe Gly Pro Val Leu Pro Val Val Ala Phe Asp Thr Leu Glu Asp Ala
385 390 395 400

Ile Ser Met Ala Asn Asp Ser Asp Tyr Gly Leu Thr Ser Ser Ile Tyr
405 410 415

Thr Gln Asn Leu Asn Val Ala Met Lys Ala Ile Lys Gly Leu Lys Phe
420 425 430

Gly Glu Thr Tyr Ile Asn Arg Glu Asn Phe Glu Ala Met Gln Gly Phe
435 440 445

His Ala Gly Trp Arg Lys Ser Gly Ile Gly Gly Ala Asp Gly Lys His
450 455 460

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465 470 475

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<212> DNA
<213> Escherichia coli

<220>
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gcc att gaa aac cgc tta ttt att aac ggt gaa tat act gct gcg gcg 96
Ala Ile Glu Asn Arg Leu Phe Ile Asn Gly Glu Tyr Thr Ala Ala Ala
20 25 30

gaa aat gaa acc ttt gaa acc gtt gat ccg gtc acc cag gca ccg ctg 144
Glu Asn Glu Thr Phe Glu Thr Val Asp Pro Val Thr Gln Ala Pro Leu
35 40 45

gcg aaa att gcc cgc gcc aag agc gtc gat atc gac cgt gcg atg agc 192
Ala Lys Ile Ala Arg Gly Lys Ser Val Asp Ile Asp Arg Ala Met Ser
50 55 60

gca gca cgc gcc gta ttt gaa cgc gcc gac tgg tca ctc tct tct ccg 240
Ala Ala Arg Gly Val Phe Glu Arg Gly Asp Trp Ser Leu Ser Ser Pro
65 70 75 80

CL5510WOPCT_SeqListing_ST25.txt

gct Ala	aaa Lys	cgt Arg	aaa Lys	gcg Ala 85	gta Val	ctg Leu	aat Asn	aaa Lys	ctc Leu 90	gcc Ala	gat Asp	tta Leu	atg Met	gaa Glu 95	gcc Ala	288
cac His	gcc Ala	gaa Glu	gag Glu 100	ctg Leu	gca Ala	ctg Leu	ctg Leu	gaa Glu 105	act Thr	ctc Leu	gac Asp	acc Thr	ggc Gly 110	aaa Lys	ccg Pro	336
att Ile	cgt Arg	cac His 115	agt Ser	ctg Leu	cgt Arg	gat Asp	gat Asp 120	att Ile	ccc Pro	ggc Gly	gcg Ala	gcg Ala	cgc Arg	gcc Ala	att Ile	384
cgc Arg	tgg Trp 130	tac Tyr	gcc Ala	gaa Glu	gcg Ala	atc Ile 135	gac Asp	aaa Lys	gtg Val	tat Tyr	ggc Gly 140	gaa Glu	gtg Val	gcg Ala	acc Thr	432
acc Thr 145	agt Ser	agc Ser	cat His	gag Glu	ctg Leu 150	gcg Ala	atg Met	atc Ile	gtg Val	cgt Arg 155	gaa Glu	ccg Pro	gtc Val	ggc Gly	gtg Val 160	480
att Ile	gcc Ala	gcc Ala	atc Ile	gtg Val 165	ccg Pro	tgg Trp	aac Asn	ttc Phe	ccg Pro 170	ctg Leu	ttg Leu	ctg Leu	act Thr	tgc Cys 175	tgg Trp	528
aaa Lys	ctc Leu	ggc Gly	ccg Pro 180	gcg Ala	ctg Leu	gcg Ala	gcg Ala	gga Gly 185	aac Asn	agc Ser	gtg Val	att Ile	cta Leu 190	aaa Lys	ccg Pro	576
tct Ser	gaa Glu	aaa Lys 195	tca Ser	ccg Pro	ctc Leu	agt Ser	gcg Ala 200	att Ile	cgt Arg	ctc Leu	gcg Ala	ggg Gly 205	ctg Leu	gcg Ala	aaa Lys	624
gaa Glu	gca Ala 210	ggc Gly	ttg Leu	ccg Pro	gat Asp	ggt Gly 215	gtg Val	ttg Leu	aac Asn	gtg Val	gtg Val 220	acg Thr	ggt Gly	ttt Phe	ggt Gly	672
cat His 225	gaa Glu	gcc Ala	ggg Gly	cag Gln 230	gcg Ala	ctg Leu	tcg Ser	cgt Arg	cat His	aac Asn 235	gat Asp	atc Ile	gac Asp	gcc Ala	att Ile 240	720
gcc Ala	ttt Phe	acc Thr	ggt Gly	tca Ser 245	acc Thr	cgt Arg	acc Thr	ggg Gly	aaa Lys 250	cag Gln	ctg Leu	ctg Leu	aaa Lys	gat Asp 255	gcg Ala	768
ggc Gly	gac Asp	agc Ser	aac Asn 260	atg Met	aaa Lys	cgc Arg	gtc Val	tgg Trp 265	ctg Leu	gaa Glu	gcg Ala	ggc Gly	ggc Gly 270	aaa Lys	agc Ser	816
gcc Ala	aac Asn	atc Ile 275	gtt Val	ttc Phe	gct Ala	gac Asp	tgc Cys 280	ccg Pro	gat Asp	ttg Leu	caa Gln	cag Gln 285	gcg Ala	gca Ala	agc Ser	864
gcc Ala	acc Thr 290	gca Ala	gca Ala	ggc Gly	att Ile	ttc Phe 295	tac Tyr	aac Asn	cag Gln	gga Gly	cag Gln 300	gtg Val	tgc Cys	atc Ile	gcc Ala	912
gga Gly 305	acg Thr	cgc Arg	ctg Leu	ttg Leu	ctg Leu 310	gaa Glu	gag Glu	agc Ser	atc Ile	gcc Ala 315	gat Asp	gaa Glu	ttc Phe	tta Leu	gcc Ala 320	960
ctg Leu	tta Leu	aaa Lys	cag Gln 325	cag Gln	gcg Ala	caa Gln	aac Asn	tgg Trp	cag Gln 330	ccg Pro	ggc Gly	cat His	cca Pro	ctt Leu 335	gat Asp	1008
ccc Pro	gca Ala	acc Thr	acc Thr 340	atg Met	ggc Gly	acc Thr	tta Leu	atc Ile 345	gac Asp	tgc Cys	gcc Ala	cac His	gcc Ala 350	gac Asp	tcg Ser	1056

CL5510WOPCT_SeqListing_ST25.txt

gtc	cat	agc	ttt	att	cgg	gaa	ggc	gaa	agc	aaa	ggg	caa	ctg	ttg	ttg	1104
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		355					360					365				
gat	ggc	cgt	aac	gcc	ggg	ctg	gct	gcc	gcc	atc	ggc	ccg	acc	atc	ttt	1152
Asp	Gly	Arg	Asn	Ala	Gly	Leu	Ala	Ala	Ala	Ile	Gly	Pro	Thr	Ile	Phe	
	370					375					380					
gtg	gat	gtg	gac	ccg	aat	gcg	tcc	tta	agt	cgc	gaa	gag	att	ttc	ggg	1200
Val	Asp	Val	Asp	Pro	Asn	Ala	Ser	Leu	Ser	Arg	Glu	Glu	Ile	Phe	Gly	
385					390					395					400	
ccg	gtg	ctg	gtg	gtc	acg	cgt	ttc	aca	tca	gaa	gaa	cag	gcg	cta	cag	1248
Pro	Val	Leu	Val	Val	Thr	Arg	Phe	Thr	Ser	Glu	Glu	Gln	Ala	Leu	Gln	
				405					410					415		
ctt	gcc	aac	gac	agc	cag	tac	ggc	ctt	ggc	gcg	gcg	gta	tgg	acg	cgc	1296
Leu	Ala	Asn	Asp	Ser	Gln	Tyr	Gly	Leu	Gly	Ala	Ala	Val	Trp	Thr	Arg	
			420				425						430			
gac	ctc	tcc	cgc	gcg	cac	cgc	atg	agc	cga	cgc	ctg	aaa	gcc	ggg	tcc	1344
Asp	Leu	Ser	Arg	Ala	His	Arg	Met	Ser	Arg	Arg	Leu	Lys	Ala	Gly	Ser	
		435					440					445				
gtc	ttc	gtc	aat	aac	tac	aac	gac	ggc	gat	atg	acc	gtg	ccg	ttt	ggc	1392
Val	Phe	Val	Asn	Asn	Tyr	Asn	Asp	Gly	Asp	Met	Thr	Val	Pro	Phe	Gly	
	450					455					460					
ggc	tat	aag	cag	agc	ggc	aac	ggg	cgc	gac	aaa	tcc	ctg	cat	gcc	ctt	1440
Gly	Tyr	Lys	Gln	Ser	Gly	Asn	Gly	Arg	Asp	Lys	Ser	Leu	His	Ala	Leu	
465					470				475						480	
gaa	aaa	ttc	act	gaa	ctg	aaa	acc	atc	tgg	ata	agc	ctg	gag	gcc	tga	1488
Glu	Lys	Phe	Thr	Glu	Leu	Lys	Thr	Ile	Trp	Ile	Ser	Leu	Glu	Ala		
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<210> 20
 <211> 495
 <212> PRT
 <213> Escherichia coli

<400> 20

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 20 25 30

Glu Asn Glu Thr Phe Glu Thr Val Asp Pro Val Thr Gln Ala Pro Leu
 35 40 45

Ala Lys Ile Ala Arg Gly Lys Ser Val Asp Ile Asp Arg Ala Met Ser
 50 55 60

Ala Ala Arg Gly Val Phe Glu Arg Gly Asp Trp Ser Leu Ser Ser Pro
 65 70 75 80

Ala Lys Arg Lys Ala Val Leu Asn Lys Leu Ala Asp Leu Met Glu Ala
 85 90 95

CL5510WOPCT_SeqListing_ST25.txt

His Ala Glu Glu Leu Ala Leu Leu Glu Thr Leu Asp Thr Gly Lys Pro
 100 105 110
 Ile Arg His Ser Leu Arg Asp Asp Ile Pro Gly Ala Ala Arg Ala Ile
 115 120 125
 Arg Trp Tyr Ala Glu Ala Ile Asp Lys Val Tyr Gly Glu Val Ala Thr
 130 135 140
 Thr Ser Ser His Glu Leu Ala Met Ile Val Arg Glu Pro Val Gly Val
 145 150 155 160
 Ile Ala Ala Ile Val Pro Trp Asn Phe Pro Leu Leu Leu Thr Cys Trp
 165 170 175
 Lys Leu Gly Pro Ala Leu Ala Ala Gly Asn Ser Val Ile Leu Lys Pro
 180 185 190
 Ser Glu Lys Ser Pro Leu Ser Ala Ile Arg Leu Ala Gly Leu Ala Lys
 195 200 205
 Glu Ala Gly Leu Pro Asp Gly Val Leu Asn Val Val Thr Gly Phe Gly
 210 215 220
 His Glu Ala Gly Gln Ala Leu Ser Arg His Asn Asp Ile Asp Ala Ile
 225 230 235 240
 Ala Phe Thr Gly Ser Thr Arg Thr Gly Lys Gln Leu Leu Lys Asp Ala
 245 250 255
 Gly Asp Ser Asn Met Lys Arg Val Trp Leu Glu Ala Gly Gly Lys Ser
 260 265 270
 Ala Asn Ile Val Phe Ala Asp Cys Pro Asp Leu Gln Gln Ala Ala Ser
 275 280 285
 Ala Thr Ala Ala Gly Ile Phe Tyr Asn Gln Gly Gln Val Cys Ile Ala
 290 295 300
 Gly Thr Arg Leu Leu Leu Glu Glu Ser Ile Ala Asp Glu Phe Leu Ala
 305 310 315 320
 Leu Leu Lys Gln Gln Ala Gln Asn Trp Gln Pro Gly His Pro Leu Asp
 325 330 335
 Pro Ala Thr Thr Met Gly Thr Leu Ile Asp Cys Ala His Ala Asp Ser
 340 345 350
 Val His Ser Phe Ile Arg Glu Gly Glu Ser Lys Gly Gln Leu Leu Leu
 355 360 365

CL5510WOPCT_SeqListing_ST25.txt

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

Val Asp Val Asp Pro Asn Ala Ser Leu Ser Arg Glu Glu Ile Phe Gly
385 390 395 400

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

Leu Ala Asn Asp Ser Gln Tyr Gly Leu Gly Ala Ala Val Trp Thr Arg
420 425 430

Asp Leu Ser Arg Ala His Arg Met Ser Arg Arg Leu Lys Ala Gly Ser
435 440 445

Val Phe Val Asn Asn Tyr Asn Asp Gly Asp Met Thr Val Pro Phe Gly
450 455 460

Gly Tyr Lys Gln Ser Gly Asn Gly Arg Asp Lys Ser Leu His Ala Leu
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Glu Lys Phe Thr Glu Leu Lys Thr Ile Trp Ile Ser Leu Glu Ala
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<210> 21
<211> 1395
<212> DNA
<213> Escherichia coli

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ccgtttattg cagatgaatt ccagattact tcgcacacgc aagaatgggt cgtaagctcc 180
atgatgttcg gtgcggcagt cgggtgcggtg ggcagcggct ggctctcctt taaactcggg 240
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gataccgcct tcagctacac cgggtgcatg cgctggatgc tgggtgtgat tatcatcccg 540
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ctgtttaaag agaacagcaa cttccgccgc gcggtgttcc ttggcgact gttgcaggta 780
atgcagcaat tcaccgggat gaacgtcatc atgtattacg cgccgaaaat cttcgaactg 840
gcgggttata ccaacactac cgagcaaattg tgggggaccg tgattgtcgg cctgaccaac 900

CL5510WOPCT_SeqListing_ST25.txt

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ggtattcact ctccgtcggc gcagtatttc gccatcgcca tgctgctgat gtttattgtc      1080
ggttttgcca tgagtgccgg tccgctgatt tgggtactgt gtcctgaaat tcagccgctg      1140
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gttggcgcaa cgttcctgac catgctcaac acgctgggta acgccaacac cttctgggtg      1260
tatgcggctc tgaacgtact gtttatcctg ctgacattgt ggctgggtacc ggaaacaaaa      1320
cacgtttcgc tggaacatat tgaacgtaat ctgatgaaag gtcgtaaact gcgcgaaata      1380
ggcgctcacg attaa                                          1395

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<210> 22
<211> 464
<212> PRT
<213> Escherichia coli

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<400> 22
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          20          25          30

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Ile Gly Val Ile Ala Gly Ala Leu Pro Phe Ile Ala Asp Glu Phe Gln
          35          40          45

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```
Ile Thr Ser His Thr Gln Glu Trp Val Val Ser Ser Met Met Phe Gly
50          55          60

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Ala Ala Val Gly Ala Val Gly Ser Gly Trp Leu Ser Phe Lys Leu Gly
65          70          75          80

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Arg Lys Lys Ser Leu Met Ile Gly Ala Ile Leu Phe Val Ala Gly Ser
          85          90          95

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Leu Phe Ser Ala Ala Ala Pro Asn Val Glu Val Leu Ile Leu Ser Arg
100          105          110

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Val Leu Leu Gly Leu Ala Val Gly Val Ala Ser Tyr Thr Ala Pro Leu
115          120          125

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Tyr Leu Ser Glu Ile Ala Pro Glu Lys Ile Arg Gly Ser Met Ile Ser
130          135          140

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Met Tyr Gln Leu Met Ile Thr Ile Gly Ile Leu Gly Ala Tyr Leu Ser
145          150          155          160

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Asp Thr Ala Phe Ser Tyr Thr Gly Ala Trp Arg Trp Met Leu Gly Val

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165

170

175

Ile Ile Ile Pro Ala Ile Leu Leu Leu Ile Gly Val Phe Phe Leu Pro
 180 185 190

Asp Ser Pro Arg Trp Phe Ala Ala Lys Arg Arg Phe Val Asp Ala Glu
 195 200 205

Arg Val Leu Leu Arg Leu Arg Asp Thr Ser Ala Glu Ala Lys Arg Glu
 210 215 220

Leu Asp Glu Ile Arg Glu Ser Leu Gln Val Lys Gln Ser Gly Trp Ala
 225 230 235 240

Leu Phe Lys Glu Asn Ser Asn Phe Arg Arg Ala Val Phe Leu Gly Val
 245 250 255

Leu Leu Gln Val Met Gln Gln Phe Thr Gly Met Asn Val Ile Met Tyr
 260 265 270

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

Gln Met Trp Gly Thr Val Ile Val Gly Leu Thr Asn Val Leu Ala Thr
 290 295 300

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

Thr Leu Gly Phe Leu Val Met Ala Ala Gly Met Gly Val Leu Gly Thr
 325 330 335

Met Met His Ile Gly Ile His Ser Pro Ser Ala Gln Tyr Phe Ala Ile
 340 345 350

Ala Met Leu Leu Met Phe Ile Val Gly Phe Ala Met Ser Ala Gly Pro
 355 360 365

Leu Ile Trp Val Leu Cys Ser Glu Ile Gln Pro Leu Lys Gly Arg Asp
 370 375 380

Phe Gly Ile Thr Cys Ser Thr Ala Thr Asn Trp Ile Ala Asn Met Ile
 385 390 395 400

Val Gly Ala Thr Phe Leu Thr Met Leu Asn Thr Leu Gly Asn Ala Asn
 405 410 415

Thr Phe Trp Val Tyr Ala Ala Leu Asn Val Leu Phe Ile Leu Leu Thr
 420 425 430

Leu Trp Leu Val Pro Glu Thr Lys His Val Ser Leu Glu His Ile Glu

435

440

445

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 450 455 460

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 <211> 1248
 <212> DNA
 <213> Escherichia coli

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 ctaggattaa cagggacgga attaggtaca ctttattcgg tcaaccagtt taccagcatt 180
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 ttactgcaaa gcaatttttc tgtaggtcta attctggggg cgctcttttt tggcctgggg 360
 tatctggcgg gatgcggttt gcttgacagc ttcaccgaaa aaatggcgcg aaattttcat 420
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 gccggtatat tttttagtat cagtcccat atcaacttct ggttgggtctc gctatttggc 540
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<210> 24
 <211> 415
 <212> PRT
 <213> Escherichia coli

<400> 24

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

290

Ala Leu Phe Val Asn Pro Trp Ile Ile Ser Leu Val Lys Leu Leu His
305 310 315 320

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

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

Gln Ile Ala Ser Ser Leu Gly Ile Val Leu Leu Ser Thr Pro Thr Gly
355 360 365

Ile Leu Phe Asp His Ala Gly Tyr Gln Thr Val Phe Phe Ala Ile Ser
370 375 380

Gly Ile Val Cys Leu Met Leu Leu Phe Gly Ile Phe Phe Leu Ser Lys
385 390 395 400

Lys Arg Glu Gln Ile Val Met Glu Thr Pro Val Pro Ser Ala Ile
405 410 415

<210> 25
<211> 1248
<212> DNA
<213> Escherichia coli

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ctatttatga tgttctacgg catcgttcag gataaactcg gtctgaagaa accgctcatc 240
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CL5510WOPCT_SeqListing_ST25.txt

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gtgctgcttt caacgccgac tgggatactc tttgaccacg caggctacca gacagttttc      1140
ttcgcaattt cgggtattgt ctgcctgatg ttgctatttg gcattttctt cttgagtaaa      1200
aaacgcgagc aaatagttat ggaaacgcct gtaccttcag caatatag                      1248

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<210> 26
<211> 415
<212> PRT
<213> Escherichia coli

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<400> 26
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1           5           10           15

```

```
Ser Tyr Ser Phe Leu Phe Phe Ile Ser Trp Ser Leu Trp Trp Ser Leu
           20           25           30

```

```
Tyr Ala Ile Trp Leu Lys Gly His Leu Gly Leu Thr Gly Thr Glu Leu
           35           40           45

```

```
Gly Thr Leu Tyr Ser Val Asn Gln Phe Thr Ser Ile Leu Phe Met Met
           50           55           60

```

```
Phe Tyr Gly Ile Val Gln Asp Lys Leu Gly Leu Lys Lys Pro Leu Ile
65           70           75           80

```

```
Trp Cys Met Ser Phe Ile Leu Val Leu Thr Gly Pro Phe Met Ile Tyr
           85           90           95

```

```
Val Tyr Glu Pro Leu Leu Gln Ser Asn Phe Ser Val Gly Leu Ile Leu
           100          105          110

```

```
Gly Ala Leu Phe Phe Gly Leu Gly Tyr Leu Ala Gly Cys Gly Leu Leu
           115          120          125

```

```
Asp Ser Phe Thr Glu Lys Met Ala Arg Asn Phe His Phe Glu Tyr Gly
           130          135          140

```

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Thr Ala Arg Ala Trp Gly Ser Phe Gly Tyr Ala Ile Gly Ala Phe Phe
145          150          155          160

```

```
Ala Gly Ile Phe Phe Ser Ile Ser Pro His Ile Asn Phe Trp Leu Val
           165          170          175

```

```
Ser Leu Phe Gly Ala Val Phe Met Met Ile Asn Met Arg Phe Lys Asp
           180          185          190

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```
Lys Asp His Gln Cys Val Ala Ala Asp Ala Gly Gly Val Lys Lys Glu

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195

200

205

Asp Phe Ile Ala Val Phe Lys Asp Arg Asn Phe Trp Val Phe Val Ile
 210 215 220

Phe Ile Val Gly Thr Trp Ser Phe Tyr Asn Ile Phe Asp Gln Gln Leu
 225 230 235 240

Phe Pro Val Phe Tyr Ser Gly Leu Phe Glu Ser His Asp Val Gly Thr
 245 250 255

Arg Leu Tyr Gly Tyr Leu Asn Ser Phe Gln Val Val Leu Glu Ala Leu
 260 265 270

Cys Met Ala Ile Ile Pro Phe Phe Val Asn Arg Val Gly Pro Lys Asn
 275 280 285

Ala Leu Leu Ile Gly Val Val Ile Met Ala Leu Arg Ile Leu Ser Cys
 290 295 300

Ala Leu Phe Val Asn Pro Trp Ile Ile Ser Leu Val Lys Leu Leu His
 305 310 315 320

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

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

Gln Ile Ala Ser Ser Leu Gly Ile Val Leu Leu Ser Thr Pro Thr Gly
 355 360 365

Ile Leu Phe Asp His Ala Gly Tyr Gln Thr Val Phe Phe Ala Ile Ser
 370 375 380

Gly Ile Val Cys Leu Met Leu Leu Phe Gly Ile Phe Phe Leu Ser Lys
 385 390 395 400

Lys Arg Glu Gln Ile Val Met Glu Thr Pro Val Pro Ser Ala Ile
 405 410 415

<210> 27

<211> 1434

<212> DNA

<213> Escherichia coli

<400> 27

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aacggcctga tctggtttta cgatcgttat cacgcgtttt atcaacatca cccgatgagc 180

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CL5510WOPCT_SeqListing_ST25.txt

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 attcatttcg agaaacaggg tgtgatcctc actccaccag aaggcatcat gcacttccgc 480
 gatcctaaag tgtggcgtga agccgacaca tgggtggatgg tagtcggggc gaaagaccca 540
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 gaggcggtga tgagtagccg aatatatccg cagccagaag aacgggaact gtcgctctat 1380
 gcctcccacg gagtggctgt gctgcaacat ggagcactct ggcaactggg ttaa 1434

<210> 28
 <211> 477
 <212> PRT
 <213> Escherichia coli

<400> 28

Met Thr Gln Ser Arg Leu His Ala Ala Gln Asn Ala Leu Ala Lys Leu
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His Glu Arg Arg Gly Asn Thr Phe Tyr Pro His Phe His Leu Ala Pro
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Pro Ala Gly Trp Met Asn Asp Pro Asn Gly Leu Ile Trp Phe Asn Asp
 35 40 45

Arg Tyr His Ala Phe Tyr Gln His His Pro Met Ser Glu His Trp Gly
 50 55 60

Pro Met His Trp Gly His Ala Thr Ser Asp Asp Met Ile His Trp Gln
 65 70 75 80

CL5510WOPCT_SeqListing_ST25.txt

His Glu Pro Ile Ala Leu Ala Pro Gly Asp Glu Asn Asp Lys Asp Gly
 85 90 95
 Cys Phe Ser Gly Ser Ala Val Asp Asp Asn Gly Val Leu Ser Leu Ile
 100 105 110
 Tyr Thr Gly His Val Trp Leu Asp Gly Ala Gly Asn Asp Asp Ala Ile
 115 120 125
 Arg Glu Val Gln Cys Leu Ala Thr Ser Arg Asp Gly Ile His Phe Glu
 130 135 140
 Lys Gln Gly Val Ile Leu Thr Pro Pro Glu Gly Ile Met His Phe Arg
 145 150 155 160
 Asp Pro Lys Val Trp Arg Glu Ala Asp Thr Trp Trp Met Val Val Gly
 165 170 175
 Ala Lys Asp Pro Gly Asn Thr Gly Gln Ile Leu Leu Tyr Arg Gly Ser
 180 185 190
 Ser Leu Arg Glu Trp Thr Phe Asp Arg Val Leu Ala His Ala Asp Ala
 195 200 205
 Gly Glu Ser Tyr Met Trp Glu Cys Pro Asp Phe Phe Ser Leu Gly Asp
 210 215 220
 Gln His Tyr Leu Met Phe Ser Pro Gln Gly Met Asn Ala Glu Gly Tyr
 225 230 235 240
 Ser Tyr Arg Asn Arg Phe Gln Ser Gly Val Ile Pro Gly Met Trp Ser
 245 250 255
 Pro Gly Arg Leu Phe Ala Gln Ser Gly His Phe Thr Glu Leu Asp Asn
 260 265 270
 Gly His Asp Phe Tyr Ala Pro Gln Ser Phe Val Ala Lys Asp Gly Arg
 275 280 285
 Arg Ile Val Ile Gly Trp Met Asp Met Trp Glu Ser Pro Met Pro Ser
 290 295 300
 Lys Arg Glu Gly Trp Ala Gly Cys Met Thr Leu Ala Arg Glu Leu Ser
 305 310 315 320
 Glu Ser Asn Gly Lys Leu Leu Gln Arg Pro Val His Glu Ala Glu Ser
 325 330 335
 Leu Arg Gln Gln His Gln Ser Ile Ser Pro Arg Thr Ile Ser Asn Lys
 340 345 350

CL5510WOPCT_SeqListing_ST25.txt

Tyr Val Leu Gln Glu Asn Ala Gln Ala Val Glu Ile Gln Leu Gln Trp
355 360 365

Ala Leu Lys Asn Ser Asp Ala Glu His Tyr Gly Leu Gln Leu Gly Ala
370 375 380

Gly Met Arg Leu Tyr Ile Asp Asn Gln Ser Glu Arg Leu Val Leu Trp
385 390 395 400

Arg Tyr Tyr Pro His Glu Asn Leu Asp Gly Tyr Arg Ser Ile Pro Leu
405 410 415

Pro Gln Gly Asp Met Leu Ala Leu Arg Ile Phe Ile Asp Thr Ser Ser
420 425 430

Val Glu Val Phe Ile Asn Asp Gly Glu Ala Val Met Ser Ser Arg Ile
435 440 445

Tyr Pro Gln Pro Glu Glu Arg Glu Leu Ser Leu Tyr Ala Ser His Gly
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Val Ala Val Leu Gln His Gly Ala Leu Trp Gln Leu Gly
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<210> 29
<211> 1434
<212> DNA
<213> Escherichia coli

<400> 29
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aacggcctga tctggtttta cgatcggttat cacgcgtttt atcaacatca tccgatgagc 180
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catgagccta ttgcgctagc gccaggagac gataatgaca aagacgggtg tttttcaggt 300
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attcatttcg agaaacaggg tgtgatcctc actccaccag aaggaatcat gcacttcgcg 480
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ggcaacacgg ggcagatcct gctttatcgc ggcagttcgt tgcgtgaatg gaccttcgat 600
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agttaccgaa atcgctttca aagtggcgta atacccggaa tgtggtcgcc aggacgactt 780
tttgcaaat ccgggcattt tactgaactt gataacgggc atgactttta tgcaccacaa 840
agcttttttag cgaaggatgg tcggcggtatt gttatcggct ggatggatat gtgggaatcg 900

CL5510WOPCT_SeqListing_ST25.txt

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catcaatctg tctctccccg cacaatcagc aataaatatg ttttgcagga aaacgcgcaa      1080
gcagttgaga ttcagttgca gtgggcgctg aagaacagtg atgccgaaca ttacggatta      1140
cagctcggca ctggaatgcg gctgtatatt gataaccaat ctgagcgact tgttttgtgg      1200
cggattacc cacacgagaa tttagacggc taccgtagta ttcccctccc gcagcgtgac      1260
acgctcgccc taaggatatt tatcgataca tcatccgtgg aagtatttat taacgacggg      1320
gaagcgggtga tgagtagtcg aatctatccg cagccagaag aacgggaact gtcgctttat      1380
gcctcccacg gagtggctgt gctgcaacat ggagcactct ggctactggg ttaa          1434

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<210> 30
<211> 477
<212> PRT
<213> Escherichia coli

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```
<400> 30
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Met Thr Gln Ser Arg Leu His Ala Ala Gln Asn Ala Leu Ala Lys Leu
1          5          10          15
```

```
His Glu His Arg Gly Asn Thr Phe Tyr Pro His Phe His Leu Ala Pro
          20          25          30
```

```
Pro Ala Gly Trp Met Asn Asp Pro Asn Gly Leu Ile Trp Phe Asn Asp
          35          40          45
```

```
Arg Tyr His Ala Phe Tyr Gln His His Pro Met Ser Glu His Trp Gly
50          55          60
```

```
Pro Met His Trp Gly His Ala Thr Ser Asp Asp Met Ile His Trp Gln
65          70          75          80
```

```
His Glu Pro Ile Ala Leu Ala Pro Gly Asp Asp Asn Asp Lys Asp Gly
          85          90          95
```

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

```
Tyr Thr Gly His Val Trp Leu Asp Gly Ala Gly Asn Asp Asp Ala Ile
115          120          125
```

```
Arg Glu Val Gln Cys Leu Ala Thr Ser Arg Asp Gly Ile His Phe Glu
130          135          140
```

```
Lys Gln Gly Val Ile Leu Thr Pro Pro Glu Gly Ile Met His Phe Arg
145          150          155          160
```

```
Asp Pro Lys Val Trp Arg Glu Ala Asp Thr Trp Trp Met Val Val Gly
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165

170

175

Ala Lys Asp Pro Gly Asn Thr Gly Gln Ile Leu Leu Tyr Arg Gly Ser
 180 185 190

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

Gly Glu Ser Tyr Met Trp Glu Cys Pro Asp Phe Phe Ser Leu Gly Asp
 210 215 220

Gln His Tyr Leu Met Phe Ser Pro Gln Gly Met Asn Ala Glu Gly Tyr
 225 230 235 240

Ser Tyr Arg Asn Arg Phe Gln Ser Gly Val Ile Pro Gly Met Trp Ser
 245 250 255

Pro Gly Arg Leu Phe Ala Gln Ser Gly His Phe Thr Glu Leu Asp Asn
 260 265 270

Gly His Asp Phe Tyr Ala Pro Gln Ser Phe Leu Ala Lys Asp Gly Arg
 275 280 285

Arg Ile Val Ile Gly Trp Met Asp Met Trp Glu Ser Pro Met Pro Ser
 290 295 300

Lys Arg Glu Gly Trp Ala Gly Cys Met Thr Leu Ala Arg Glu Leu Ser
 305 310 315 320

Glu Ser Asn Gly Lys Leu Leu Gln Arg Pro Val His Glu Ala Glu Ser
 325 330 335

Leu Arg Gln Gln His Gln Ser Val Ser Pro Arg Thr Ile Ser Asn Lys
 340 345 350

Tyr Val Leu Gln Glu Asn Ala Gln Ala Val Glu Ile Gln Leu Gln Trp
 355 360 365

Ala Leu Lys Asn Ser Asp Ala Glu His Tyr Gly Leu Gln Leu Gly Thr
 370 375 380

Gly Met Arg Leu Tyr Ile Asp Asn Gln Ser Glu Arg Leu Val Leu Trp
 385 390 395 400

Arg Tyr Tyr Pro His Glu Asn Leu Asp Gly Tyr Arg Ser Ile Pro Leu
 405 410 415

Pro Gln Arg Asp Thr Leu Ala Leu Arg Ile Phe Ile Asp Thr Ser Ser
 420 425 430

Val Glu Val Phe Ile Asn Asp Gly Glu Ala Val Met Ser Ser Arg Ile

435

440

445

Tyr Pro Gln Pro Glu Glu Arg Glu Leu Ser Leu Tyr Ala Ser His Gly
 450 455 460

Val Ala Val Leu Gln His Gly Ala Leu Trp Leu Leu Gly
 465 470 475

<210> 31
 <211> 1599
 <212> DNA
 <213> Bifidobacterium lactis

<400> 31
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 aatggcgggt ggatcaacga cccgaacggc ctgtgccgct acaacggacg ctggcacgtg 240
 ttctaccagc tgcattccca cggcacacag tggggcccga tgcattgggg ccacgtctcc 300
 tccgacaaca tggctgactg gcaccgcgaa cccatcgctt tcgcgccaag cctcgaacag 360
 gaacgccacg gtgtgtttctc cggttccgcc gtgattggcg acgacggcaa gccgtggatt 420
 ttctacaccg gccaccgctg ggccaacggc aaggacaaca ccggaggcga ctggcaggtg 480
 cagatgctcg ccaagccgaa cgacgacgaa ctgaagacct tcacgaagga gggcatgata 540
 atcgactgcc ccaccgacga ggtggaccac cacttccgcg acccgaaggt gtggaagacc 600
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ctcaccatgc actcgctcaa gtccatcgga ctcgagtga

1599

<210> 32
 <211> 532
 <212> PRT
 <213> Bifidobacterium lactis

<400> 32

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 20 25 30

Gln Leu Ser Leu Ala Glu Ala Gly Val Ser Ala Leu Glu Thr Thr Arg
 35 40 45

Asn Asp Arg Trp Tyr Pro Lys Phe His Ile Ala Ser Asn Gly Gly Trp
 50 55 60

Ile Asn Asp Pro Asn Gly Leu Cys Arg Tyr Asn Gly Arg Trp His Val
 65 70 75 80

Phe Tyr Gln Leu His Pro His Gly Thr Gln Trp Gly Pro Met His Trp
 85 90 95

Gly His Val Ser Ser Asp Asn Met Val Asp Trp His Arg Glu Pro Ile
 100 105 110

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

Ser Ala Val Ile Gly Asp Asp Gly Lys Pro Trp Ile Phe Tyr Thr Gly
 130 135 140

His Arg Trp Ala Asn Gly Lys Asp Asn Thr Gly Gly Asp Trp Gln Val
 145 150 155 160

Gln Met Leu Ala Lys Pro Asn Asp Asp Glu Leu Lys Thr Phe Thr Lys
 165 170 175

Glu Gly Met Ile Ile Asp Cys Pro Thr Asp Glu Val Asp His His Phe
 180 185 190

Arg Asp Pro Lys Val Trp Lys Thr Gly Asp Thr Trp Tyr Met Thr Phe
 195 200 205

Gly Val Ser Ser Lys Glu His Arg Gly Gln Met Trp Leu Tyr Thr Ser
 210 215 220

Ser Asp Met Val His Trp Ser Phe Asp Arg Val Leu Phe Glu His Pro
 Page 42

225 230 235 240
 Asp Pro Asn Val Phe Met Leu Glu Cys Pro Asp Phe Phe Pro Ile Arg
 245 250 255
 Asp Ala Arg Gly Asn Glu Lys Trp Val Ile Gly Phe Ser Ala Met Gly
 260 265 270
 Ala Lys Pro Asn Gly Phe Met Asn Arg Asn Val Asn Asn Ala Gly Tyr
 275 280 285
 Met Val Gly Thr Trp Lys Pro Gly Glu Ser Phe Lys Pro Glu Thr Glu
 290 295 300
 Phe Arg Leu Trp Asp Glu Gly His Asn Phe Tyr Ala Pro Gln Ser Phe
 305 310 315 320
 Asn Thr Glu Gly Arg Gln Ile Met Tyr Gly Trp Met Ser Pro Phe Val
 325 330 335
 Ala Pro Ile Pro Met Glu Glu Asp Gly Trp Cys Gly Asn Leu Thr Leu
 340 345 350
 Pro Arg Glu Ile Thr Leu Gly Asp Asp Gly Asp Leu Val Thr Ala Pro
 355 360 365
 Thr Ile Glu Met Glu Gly Leu Arg Glu Asn Thr Ile Gly Phe Asp Ser
 370 375 380
 Leu Asp Leu Gly Thr Asn Gln Thr Ser Thr Ile Leu Asp Asp Asp Gly
 385 390 395 400
 Gly Ala Leu Glu Ile Glu Met Arg Leu Asp Leu Asn Lys Thr Thr Ala
 405 410 415
 Glu Arg Ala Gly Leu His Val His Ala Thr Ser Asp Gly His Tyr Thr
 420 425 430
 Ala Ile Val Phe Asp Ala Gln Ile Gly Gly Val Val Ile Asp Arg Gln
 435 440 445
 Asn Val Ala Asn Gly Asp Lys Gly Tyr Arg Val Ala Lys Leu Ser Asp
 450 455 460
 Thr Glu Leu Ala Ala Asp Thr Leu Asp Leu Arg Val Phe Ile Asp Arg
 465 470 475 480
 Gly Cys Val Glu Val Tyr Val Asp Gly Gly Lys His Ala Met Ser Ser
 485 490 495
 Tyr Ser Phe Pro Gly Asp Gly Ala Arg Ala Val Glu Leu Val Ser Glu
 Page 43

500

505

510

Ser Gly Thr Thr His Ile Asp Thr Leu Thr Met His Ser Leu Lys Ser
 515 520 525

Ile Gly Leu Glu
 530

<210> 33
 <211> 1599
 <212> DNA
 <213> *Saccharomyces cerevisiae*

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1599

<210> 34
 <211> 532
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 34

Met Leu Leu Gln Ala Phe Leu Phe Leu Leu Ala Gly Phe Ala Ala Lys
 1 5 10 15

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

Phe Thr Pro Asn Lys Gly Trp Met Asn Asp Pro Asn Gly Leu Trp Tyr
 35 40 45

Asp Glu Lys Asp Ala Lys Trp His Leu Tyr Phe Gln Tyr Asn Pro Asn
 50 55 60

Asp Thr Val Trp Gly Thr Pro Leu Phe Trp Gly His Ala Thr Ser Asp
 65 70 75 80

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

Asn Asp Ser Gly Ala Phe Ser Gly Ser Met Val Val Asp Tyr Asn Asn
 100 105 110

Thr Ser Gly Phe Phe Asn Asp Thr Ile Asp Pro Arg Gln Arg Cys Val
 115 120 125

Ala Ile Trp Thr Tyr Asn Thr Pro Glu Ser Glu Glu Gln Tyr Ile Ser
 130 135 140

Tyr Ser Leu Asp Gly Gly Tyr Thr Phe Thr Glu Tyr Gln Lys Asn Pro
 145 150 155 160

Val Leu Ala Ala Asn Ser Thr Gln Phe Arg Asp Pro Lys Val Phe Trp
 165 170 175

Tyr Glu Pro Ser Gln Lys Trp Ile Met Thr Ala Ala Lys Ser Gln Asp
 180 185 190

Tyr Lys Ile Glu Ile Tyr Ser Ser Asp Asp Leu Lys Ser Trp Lys Leu
 195 200 205

Glu Ser Ala Phe Ala Asn Glu Gly Phe Leu Gly Tyr Gln Tyr Glu Cys
 210 215 220

Pro Gly Leu Ile Glu Val Pro Thr Glu Gln Asp Pro Ser Lys Ser Tyr
 Page 45

225 230 235 240
 Trp Val Met Phe Ile Ser Ile Asn Pro Gly Ala Pro Ala Gly Gly Ser
 245 250 255
 Phe Asn Gln Tyr Phe Val Gly Ser Phe Asn Gly Thr His Phe Glu Ala
 260 265 270
 Phe Asp Asn Gln Ser Arg Val Val Asp Phe Gly Lys Asp Tyr Tyr Ala
 275 280 285
 Leu Gln Thr Phe Phe Asn Thr Asp Pro Thr Tyr Gly Ser Ala Leu Gly
 290 295 300
 Ile Ala Trp Ala Ser Asn Trp Glu Tyr Ser Ala Phe Val Pro Thr Asn
 305 310 315 320
 Pro Trp Arg Ser Ser Met Ser Leu Val Arg Lys Phe Ser Leu Asn Thr
 325 330 335
 Glu Tyr Gln Ala Asn Pro Glu Thr Glu Leu Ile Asn Leu Lys Ala Glu
 340 345 350
 Pro Ile Leu Asn Ile Ser Asn Ala Gly Pro Trp Ser Arg Phe Ala Thr
 355 360 365
 Asn Thr Thr Leu Thr Lys Ala Asn Ser Tyr Asn Val Asp Leu Ser Asn
 370 375 380
 Ser Thr Gly Thr Leu Glu Phe Glu Leu Val Tyr Ala Val Asn Thr Thr
 385 390 395 400
 Gln Thr Ile Ser Lys Ser Val Phe Ala Asp Leu Ser Leu Trp Phe Lys
 405 410 415
 Gly Leu Glu Asp Pro Glu Glu Tyr Leu Arg Met Gly Phe Glu Val Ser
 420 425 430
 Ala Ser Ser Phe Phe Leu Asp Arg Gly Asn Ser Lys Val Lys Phe Val
 435 440 445
 Lys Glu Asn Pro Tyr Phe Thr Asn Arg Met Ser Val Asn Asn Gln Pro
 450 455 460
 Phe Lys Ser Glu Asn Asp Leu Ser Tyr Tyr Lys Val Tyr Gly Leu Leu
 465 470 475 480
 Asp Gln Asn Ile Leu Glu Leu Tyr Phe Asn Asp Gly Asp Val Val Ser
 485 490 495
 Thr Asn Thr Tyr Phe Met Thr Thr Gly Asn Ala Leu Gly Ser Val Asn
 Page 46

500

505

510

Met Thr Thr Gly Val Asp Asn Leu Phe Tyr Ile Asp Lys Phe Gln Val
 515 520 525

Arg Glu Val Lys
 530

<210> 35
 <211> 1302
 <212> DNA
 <213> Corynebacterium glutamicum

<400> 35
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 accacgccgt tgaccggacc gcagcgattg cagtggacgc acctgcccga cgctctttac 240
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 agctctgacc agtgcggata tgtcgtcggc aagcttgaag gaacgacctt ccgcgtcttg 840
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<210> 36
 <211> 433
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 36

CL5510WOPCT_SeqListing_ST25.txt

Met Cys Gly Ala Met His Thr Glu Leu Ser Ser Leu Arg Pro Ala Tyr
1 5 10 15

His Val Thr Pro Pro Gln Gly Arg Leu Asn Asp Pro Asn Gly Met Tyr
20 25 30

Val Asp Gly Asp Thr Leu His Val Tyr Tyr Gln His Asp Pro Gly Phe
35 40 45

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

Thr Gly Pro Gln Arg Leu Gln Trp Thr His Leu Pro Asp Ala Leu Tyr
65 70 75 80

Pro Asp Ala Ser Tyr Asp Leu Asp Gly Cys Tyr Ser Gly Gly Ala Val
85 90 95

Phe Thr Asp Gly Thr Leu Lys Leu Phe Tyr Thr Gly Asn Leu Lys Ile
100 105 110

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

Thr Gly Leu Met Gly Gly Ile His Arg Arg Ser Pro Lys Asn Pro Leu
130 135 140

Ile Asp Gly Pro Ala Ser Gly Phe Thr Pro His Tyr Arg Asp Pro Met
145 150 155 160

Ile Ser Pro Asp Gly Asp Gly Trp Lys Met Val Leu Gly Ala Gln Arg
165 170 175

Glu Asn Leu Thr Gly Ala Ala Val Leu Tyr Arg Ser Thr Asp Leu Glu
180 185 190

Asn Trp Glu Phe Ser Gly Glu Ile Thr Phe Asp Leu Ser Asp Ala Gln
195 200 205

Pro Gly Ser Ala Pro Asp Leu Val Pro Gly Gly Tyr Met Trp Glu Cys
210 215 220

Pro Asn Leu Phe Thr Leu Arg Asp Glu Glu Thr Gly Glu Asp Leu Asp
225 230 235 240

Val Leu Ile Phe Cys Pro Gln Gly Leu Asp Arg Ile His Asp Glu Val
245 250 255

Thr His Tyr Ala Ser Ser Asp Gln Cys Gly Tyr Val Val Gly Lys Leu
260 265 270

CL5510WOPCT_SeqListing_ST25.txt

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

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

Trp Leu Val Gly Trp Met Gly Leu Pro Ala Gln Asp Asp His Pro Thr
305 310 315 320

Val Ala Arg Glu Gly Trp Val His Cys Leu Thr Val Pro Arg Lys Leu
325 330 335

His Leu Arg Asn His Ala Ile Tyr Gln Glu Leu Leu Leu Pro Glu Gly
340 345 350

Glu Ser Gly Val Ile Arg Ser Val Leu Gly Ser Glu Pro Val Arg Val
355 360 365

Asp Ile Arg Gly Asn Ile Ser Leu Glu Trp Asp Gly Val Arg Leu Ser
370 375 380

Val Asp Arg Gly Gly Asp Arg Arg Val Ala Glu Val Lys Pro Gly Glu
385 390 395 400

Leu Val Ile Ala Asp Asp Asn Thr Ala Ile Glu Ile Thr Ala Gly Asp
405 410 415

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

Arg

<210> 37
<211> 1473
<212> DNA
<213> Leuconostoc mesenteroides

<400> 37
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gccggcgaaa accgtccaac acaagccgat gttgacttaa tttacaagcg taaagataag 420
gcaccaacgc aagaaatcac ttttgatgat ggcacaacag aaaacttgtg gaatactttt 480
ggtgaagaac aaattgacat tgatgttaat tcagccattg ccaaggaatt tattaagaca 540

CL5510WOPCT_SeqListing_ST25.txt

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gcagttaaaa aagttgacac aaatgacttc ttcgttgagc cagaaatctg ggacactttg      660
aatgaagtac gtgaaatfff gacaccatta aaggctgaaa ttttaccaga aattcatgaa      720
cattactcaa tccctaaaaa gatcaatgat catggttact tcacctatga ctttgcatta      780
ccaatgacaa cgctttacac attgtattca ggtaagacaa atcaattggc aaagtgggtg      840
aagatgtcac caatgaagca attcacaaca ttggacacgc atgatgggat tggtgtcgtt      900
gatgcccgtg atattctaac tgatgatgaa attgactacg cttctgaaca actttacaag      960
gttggcgcgga atgtcaaaaa gacatattca tctgcttcac acaacaacct tgatattttac    1020
caaattaact caacttatta ttcagcattg ggaaatgatg atgcagcata cttgttgagt    1080
cgtgtcttcc aagtctttgc gcctggaatt ccacaaatff attacgttgg tttgttgga    1140
ggtgaaaacg atatcgcgct tttggagtca actaaagaag gtcgtaatat taaccgtcat    1200
tactatacgc gtgaagaagt taagtcagaa gttaagcgac cagttgttgc taacttattg    1260
aagctattgt catggcgtaa tgaaagccct gcatttgatt tggctggctc aatcacagtt    1320
gacacgcaa ctgatacaac aattgtggtg acacgtcaag atgaaaatgg tcaaaacaaa    1380
gctgtattaa cagccgatgc ggccaacaaa acttttgaaa tcgttgagaa tgggtcaaact    1440
gttatgagca gtgataatff gactcagaac taa                                  1473

```

```

<210> 38
<211> 490
<212> PRT
<213> Leuconostoc mesenteroides

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<400> 38
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Met Glu Ile Gln Asn Lys Ala Met Leu Ile Thr Tyr Ala Asp Ser Leu
1           5           10          15
```

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

```
Asp Ala Ile Gly Gly Val His Leu Leu Pro Phe Phe Pro Ser Thr Gly
35           40          45
```

```
Asp Arg Gly Phe Ala Pro Ala Asp Tyr Thr Arg Val Asp Ala Ala Phe
50           55          60
```

```
Gly Asp Trp Ala Asp Val Glu Ala Leu Gly Glu Glu Tyr Tyr Leu Met
65           70          75          80
```

```
Phe Asp Phe Met Ile Asn His Ile Ser Arg Glu Ser Val Met Tyr Gln
85           90          95
```

```
Asp Phe Lys Lys Asn His Asp Asp Ser Lys Tyr Lys Asp Phe Phe Ile
100          105         110
```

CL5510WOPCT_SeqListing_ST25.txt

Arg Trp Glu Lys Phe Trp Ala Lys Ala Gly Glu Asn Arg Pro Thr Gln
 115 120 125
 Ala Asp Val Asp Leu Ile Tyr Lys Arg Lys Asp Lys Ala Pro Thr Gln
 130 135 140
 Glu Ile Thr Phe Asp Asp Gly Thr Thr Glu Asn Leu Trp Asn Thr Phe
 145 150 155 160
 Gly Glu Glu Gln Ile Asp Ile Asp Val Asn Ser Ala Ile Ala Lys Glu
 165 170 175
 Phe Ile Lys Thr Thr Leu Glu Asp Met Val Lys His Gly Ala Asn Leu
 180 185 190
 Ile Arg Leu Asp Ala Phe Ala Tyr Ala Val Lys Lys Val Asp Thr Asn
 195 200 205
 Asp Phe Phe Val Glu Pro Glu Ile Trp Asp Thr Leu Asn Glu Val Arg
 210 215 220
 Glu Ile Leu Thr Pro Leu Lys Ala Glu Ile Leu Pro Glu Ile His Glu
 225 230 235 240
 His Tyr Ser Ile Pro Lys Lys Ile Asn Asp His Gly Tyr Phe Thr Tyr
 245 250 255
 Asp Phe Ala Leu Pro Met Thr Thr Leu Tyr Thr Leu Tyr Ser Gly Lys
 260 265 270
 Thr Asn Gln Leu Ala Lys Trp Leu Lys Met Ser Pro Met Lys Gln Phe
 275 280 285
 Thr Thr Leu Asp Thr His Asp Gly Ile Gly Val Val Asp Ala Arg Asp
 290 295 300
 Ile Leu Thr Asp Asp Glu Ile Asp Tyr Ala Ser Glu Gln Leu Tyr Lys
 305 310 315 320
 Val Gly Ala Asn Val Lys Lys Thr Tyr Ser Ser Ala Ser Tyr Asn Asn
 325 330 335
 Leu Asp Ile Tyr Gln Ile Asn Ser Thr Tyr Tyr Ser Ala Leu Gly Asn
 340 345 350
 Asp Asp Ala Ala Tyr Leu Leu Ser Arg Val Phe Gln Val Phe Ala Pro
 355 360 365
 Gly Ile Pro Gln Ile Tyr Tyr Val Gly Leu Leu Ala Gly Glu Asn Asp
 370 375 380

CL5510WOPCT_SeqListing_ST25.txt

Ile Ala Leu Leu Glu Ser Thr Lys Glu Gly Arg Asn Ile Asn Arg His
385 390 395 400

Tyr Tyr Thr Arg Glu Glu Val Lys Ser Glu Val Lys Arg Pro Val Val
405 410 415

Ala Asn Leu Leu Lys Leu Leu Ser Trp Arg Asn Glu Ser Pro Ala Phe
420 425 430

Asp Leu Ala Gly Ser Ile Thr Val Asp Thr Pro Thr Asp Thr Thr Ile
435 440 445

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

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

Val Met Ser Ser Asp Asn Leu Thr Gln Asn
485 490

<210> 39
<211> 1515
<212> DNA
<213> Bifidobacterium adolescentis

<400> 39
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tcgatgaccg acattctgcg caccgccttc gacggcgtgt acgacggcgt tcacatcctg 120
ccgttcttca ccccgcttca cggcgccgac gcaggcttcg acccgatcga ccacaccaag 180
gtcgacgaac gtctcggcag ctgggacgac gtcgccgaac tctccaagac ccacaacatc 240
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gccaagggcg aggagtccga atactatccg atgttcctca ccatgagctc cgtgttcccg 360
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gccggcacca gctgcttcac gaccccgaag acctcaagc tgatctcccg tctgcgtgag 660
gaaggcgtca agcgcggtct ggaaatcctc atcgaagtgc actcctacta caagaagcag 720
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cagctcgacc gctcgctcaa gggctctctg ccggatgagg acgtggacaa cctcgtcaac 960
accatccacg ccaacacca cggcgaatcc caggcagcca ctggcgccgc cgcacccaat 1020

CL5510WOPCT_SeqListing_ST25.txt

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ggcgcgctcg ccggcaagaa cgacatggag ctgctgcgta agacgaataa cggccgcgac      1200
atcaatcgcc attactactc caccgcggaa atcgacgaga acctcaagcg tccggtcgtc      1260
aaggccctga acgcgctcgc caagttccgc aacgagctcg acgcgttcga cggcacgttc      1320
tcgtacacca ccgatgacga cacgtccatc agcttcacct ggcgcggcga aaccagccag      1380
gccacgctga cgttcgagcc gaagcgcggt ctcggtgtgg acaacactac gccggtcgcc      1440
atgttggaat gggaggattc cgcgggagac caccgttcgg atgatctgat cgccaatccg      1500
cctgtcgtcg cctga                                                         1515

```

```

<210> 40
<211> 504
<212> PRT
<213> Bifidobacterium adolescentis

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<400> 40
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Met Lys Asn Lys Val Gln Leu Ile Thr Tyr Ala Asp Arg Leu Gly Asp
 1          5          10          15

```

```
Gly Thr Ile Lys Ser Met Thr Asp Ile Leu Arg Thr Arg Phe Asp Gly
          20          25          30

```

```
Val Tyr Asp Gly Val His Ile Leu Pro Phe Phe Thr Pro Phe Asp Gly
          35          40          45

```

```
Ala Asp Ala Gly Phe Asp Pro Ile Asp His Thr Lys Val Asp Glu Arg
 50          55          60

```

```
Leu Gly Ser Trp Asp Asp Val Ala Glu Leu Ser Lys Thr His Asn Ile
65          70          75          80

```

```
Met Val Asp Ala Ile Val Asn His Met Ser Trp Glu Ser Lys Gln Phe
          85          90          95

```

```
Gln Asp Val Leu Ala Lys Gly Glu Glu Ser Glu Tyr Tyr Pro Met Phe
100          105          110

```

```
Leu Thr Met Ser Ser Val Phe Pro Asn Gly Ala Thr Glu Glu Asp Leu
115          120          125

```

```
Ala Gly Ile Tyr Arg Pro Arg Pro Gly Leu Pro Phe Thr His Tyr Lys
130          135          140

```

```
Phe Ala Gly Lys Thr Arg Leu Val Trp Val Ser Phe Thr Pro Gln Gln
145          150          155          160

```

```
Val Asp Ile Asp Thr Asp Ser Asp Lys Gly Trp Glu Tyr Leu Met Ser
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```

165

170

175

Ile Phe Asp Gln Met Ala Ala Ser His Val Ser Tyr Ile Arg Leu Asp
 180 185 190

Ala Val Gly Tyr Gly Ala Lys Glu Ala Gly Thr Ser Cys Phe Met Thr
 195 200 205

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

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

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

Pro Leu Leu Leu His Ala Leu Ser Thr Gly His Val Glu Pro Val Ala
 260 265 270

His Trp Thr Asp Ile Arg Pro Asn Asn Ala Val Thr Val Leu Asp Thr
 275 280 285

His Asp Gly Ile Gly Val Ile Asp Ile Gly Ser Asp Gln Leu Asp Arg
 290 295 300

Ser Leu Lys Gly Leu Val Pro Asp Glu Asp Val Asp Asn Leu Val Asn
 305 310 315 320

Thr Ile His Ala Asn Thr His Gly Glu Ser Gln Ala Ala Thr Gly Ala
 325 330 335

Ala Ala Ser Asn Leu Asp Leu Tyr Gln Val Asn Ser Thr Tyr Tyr Ser
 340 345 350

Ala Leu Gly Cys Asn Asp Gln His Tyr Ile Ala Ala Arg Ala Val Gln
 355 360 365

Phe Phe Leu Pro Gly Val Pro Gln Val Tyr Tyr Val Gly Ala Leu Ala
 370 375 380

Gly Lys Asn Asp Met Glu Leu Leu Arg Lys Thr Asn Asn Gly Arg Asp
 385 390 395 400

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

Arg Pro Val Val Lys Ala Leu Asn Ala Leu Ala Lys Phe Arg Asn Glu
 420 425 430

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

435

440

445

Ser Ile Ser Phe Thr Trp Arg Gly Glu Thr Ser Gln Ala Thr Leu Thr
 450 455 460

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

Met Leu Glu Trp Glu Asp Ser Ala Gly Asp His Arg Ser Asp Asp Leu
 485 490 495

Ile Ala Asn Pro Pro Val Val Ala
 500

<210> 41
 <211> 927
 <212> DNA
 <213> Agrobacterium tumefaciens

<400> 41
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 gacatcgtca agttctcgga tgaggacctg gcgtgggttcg gtctggaagg cgacgaggac 600
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<210> 42
 <211> 308
 <212> PRT
 <213> Agrobacterium tumefaciens

<400> 42

Met Ile Leu Cys Cys Gly Glu Ala Leu Ile Asp Met Leu Pro Arg Gln
 1 5 10 15

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Thr Thr Leu Gly Glu Ala Gly Phe Ala Pro Tyr Ala Gly Gly Ala Val
20 25 30

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

Phe Thr Gly Leu Ser Asp Asp Met Met Gly Asp Ile Leu Arg Glu Thr
50 55 60

Leu Arg Ala Ser Lys Val Asp Phe Ser Tyr Cys Ala Thr Leu Ser Arg
65 70 75 80

Pro Thr Thr Ile Ala Phe Val Lys Leu Val Asp Gly His Ala Thr Tyr
85 90 95

Ala Phe Tyr Asp Glu Asn Thr Ala Gly Arg Met Ile Thr Glu Ala Glu
100 105 110

Leu Pro Ala Leu Gly Ala Asp Cys Glu Ala Leu His Phe Gly Ala Ile
115 120 125

Ser Leu Ile Pro Glu Pro Cys Gly Ser Thr Tyr Glu Ala Leu Met Thr
130 135 140

Arg Glu His Glu Thr Arg Val Ile Ser Leu Asp Pro Asn Ile Arg Pro
145 150 155 160

Gly Phe Ile Gln Asn Lys Gln Ser His Met Ala Arg Ile Arg Arg Met
165 170 175

Ala Ala Met Ser Asp Ile Val Lys Phe Ser Asp Glu Asp Leu Ala Trp
180 185 190

Phe Gly Leu Glu Gly Asp Glu Asp Thr Leu Ala Arg His Trp Leu His
195 200 205

His Gly Ala Lys Leu Val Val Val Thr Arg Gly Ala Lys Gly Ala Val
210 215 220

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

Val Val Asp Thr Val Gly Ala Gly Asp Thr Phe Asp Ala Gly Ile Leu
245 250 255

Ala Ser Leu Lys Met Gln Gly Leu Leu Thr Lys Ala Gln Val Ala Ser
260 265 270

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

CL5510WOPCT_SeqListing_ST25.txt

Ala Ala Val Thr Val Ser Arg Ala Gly Ala Asn Pro Pro Phe Ala His
 290 295 300

Glu Ile Gly Leu
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<210> 43
 <211> 1404
 <212> DNA
 <213> Streptococcus mutans

<400> 43
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 gcttaaaaga ttcagtaaca atagtattaa agccttttgg ctaactaata cttgaaattt 180
 agcaaattat gatataatgt taagtagtcc ttaagggtag attaagggta ttcaaattcc 240
 aaaattgatt tggtaagtta agtaaaatat aagaggttta ttatgtctaa attatatggc 300
 agcatcgaag ctggcggaac aaaatttgct tgtgctgtag gtgatgaaaa ttttcaaatt 360
 ttagaaaaag ttcagttccc aacaacaaca ctttatgaaa caatagaaaa aacagttgct 420
 ttctttaaaa aatttgaagc tgatttagcc agtgttgcca ttggttcttt tggccctatt 480
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 agtgaatata attactcttg atttcctctg aaactagata gtggtatatt gaaaaacaga 1320
 aaggagaaca ctatggaagg acctttgttt ttacaatcac aaatgcataa aaaaatctgg 1380
 ggcggcaatc ggctcagaaa agaa 1404

<210> 44
 <211> 293
 <212> PRT
 <213> Streptococcus mutans

<400> 44

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 1 5 10 15

Cys Ala Val Gly Asp Glu Asn Phe Gln Ile Leu Glu Lys Val Gln Phe
 20 25 30

Pro Thr Thr Thr Pro Tyr Glu Thr Ile Glu Lys Thr Val Ala Phe Phe
 35 40 45

Lys Lys Phe Glu Ala Asp Leu Ala Ser Val Ala Ile Gly Ser Phe Gly
 50 55 60

Pro Ile Asp Ile Asp Gln Asn Ser Asp Thr Tyr Gly Tyr Ile Thr Ser
 65 70 75 80

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

Lys Asp Phe Lys Ile Pro Phe Tyr Phe Thr Thr Asp Val Asn Ser Ser
 100 105 110

Ala Tyr Gly Glu Thr Ile Ala Arg Ser Asn Val Lys Ser Leu Val Tyr
 115 120 125

Tyr Thr Ile Gly Thr Gly Ile Gly Ala Gly Ala Ile Gln Asn Gly Glu
 130 135 140

Phe Ile Gly Gly Met Gly His Thr Glu Ala Gly His Val Tyr Met Ala
 145 150 155 160

Pro His Pro Asn Asp Val His His Gly Phe Val Gly Thr Cys Pro Phe
 165 170 175

His Lys Gly Cys Leu Glu Gly Leu Ala Ala Gly Pro Ser Leu Glu Ala
 180 185 190

Arg Thr Gly Ile Arg Gly Glu Leu Ile Glu Gln Asn Ser Glu Val Trp
 195 200 205

Asp Ile Gln Ala Tyr Tyr Ile Ala Gln Ala Ala Ile Gln Ala Thr Val
 210 215 220

Leu Tyr Arg Pro Gln Val Ile Val Phe Gly Gly Gly Val Met Ala Gln
 225 230 235 240

Glu His Met Leu Asn Arg Val Arg Glu Lys Phe Thr Ser Leu Leu Asn
 245 250 255

Asp Tyr Leu Pro Val Pro Asp Val Lys Asp Tyr Ile Val Thr Pro Ala
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260

265

270

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

Lys Ile Ala Ala Arg
 290

<210> 45
 <211> 915
 <212> DNA
 <213> Escherichia coli

<400> 45
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 ttaggcggaa caagtgggtt tataggtcgg gtgggggatg atccttttg tgcgttaatg 180
 caaagaacgc tgctaactga gggagtcgat atcacgtatc tgaagcaaga tgaatggcac 240
 cggacatcca cggtgcttgt cgatctgaac gatcaagggg aacgttcatt tacgtttatg 300
 gtccgccccg gtgccgatct ttttttagag acgacagact tgccctgctg gcgacatggc 360
 gaatggttac atctctgttc aattgcgttg tctgccgagc cttcgcgtac cagcgcattt 420
 actgcgatga cggcgatccg gcatgccgga ggttttgtca gcttcgatcc taatattcgt 480
 gaagatctat ggcaagacga gcatttgctc cgcttggtgt tgccggcaggc gctacaactg 540
 gcggatgtcg tcaagctctc ggaagaagaa tggcgactta tcagtggaaa aacacagaac 600
 gatcaggata tatgcgccct ggcaaaagag tatgagatcg ccatgctgtt ggtgactaaa 660
 ggtgcagaag ggggtgggtgt ctgttatcga ggacaagttc accattttgc tggaatgtct 720
 gtgaattgtg tcgatagcac gggggcgagg gatgcgttcg ttgccgggtt actcacaggt 780
 ctgtcctcta cgggattatc tacagatgag agagaaatgc gacgaattat cgatctcgct 840
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 caagaactgg aatag 915

<210> 46
 <211> 304
 <212> PRT
 <213> Escherichia coli

<400> 46

Met Ser Ala Lys Val Trp Val Leu Gly Asp Ala Val Val Asp Leu Leu
 1 5 10 15

Pro Glu Ser Asp Gly Arg Leu Leu Pro Cys Pro Gly Gly Ala Pro Ala
 20 25 30

Asn Val Ala Val Gly Ile Ala Arg Leu Gly Gly Thr Ser Gly Phe Ile
 35 40 45

CL5510WOPCT_SeqListing_ST25.txt

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

Leu Thr Glu Gly Val Asp Ile Thr Tyr Leu Lys Gln Asp Glu Trp His
65 70 75 80

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

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

Asp Leu Pro Cys Trp Arg His Gly Glu Trp Leu His Leu Cys Ser Ile
115 120 125

Ala Leu Ser Ala Glu Pro Ser Arg Thr Ser Ala Phe Thr Ala Met Thr
130 135 140

Ala Ile Arg His Ala Gly Gly Phe Val Ser Phe Asp Pro Asn Ile Arg
145 150 155 160

Glu Asp Leu Trp Gln Asp Glu His Leu Leu Arg Leu Cys Leu Arg Gln
165 170 175

Ala Leu Gln Leu Ala Asp Val Val Lys Leu Ser Glu Glu Glu Trp Arg
180 185 190

Leu Ile Ser Gly Lys Thr Gln Asn Asp Gln Asp Ile Cys Ala Leu Ala
195 200 205

Lys Glu Tyr Glu Ile Ala Met Leu Leu Val Thr Lys Gly Ala Glu Gly
210 215 220

Val Val Val Cys Tyr Arg Gly Gln Val His His Phe Ala Gly Met Ser
225 230 235 240

Val Asn Cys Val Asp Ser Thr Gly Ala Gly Asp Ala Phe Val Ala Gly
245 250 255

Leu Leu Thr Gly Leu Ser Ser Thr Gly Leu Ser Thr Asp Glu Arg Glu
260 265 270

Met Arg Arg Ile Ile Asp Leu Ala Gln Arg Cys Gly Ala Leu Ala Val
275 280 285

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

<210> 47
<211> 924
<212> DNA

<213> *Klebsiella pneumoniae*

<400> 47

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ctcggcggtg acagcggggt tatcggccgc gtcggcgacg atcccttcgg ccgttttatg      180
cgtcacaccc tggcgcagga gcaagtggat gtgaactata tgcgcctcga tgcggcgag      240
cgcacctcca cggtggtggt cgatctcgat agccacgggg agcgcacctt tacctttatg      300
gtccgtccga gcgccgacct gttccttcag cccgaggatc tcccgccgtt tgccgccggt      360
cagtggctgc acgtctgctc catcgctctc agcgcggagc cgagccgcag cagcacattc      420
gcggcgatgg aggcgataaa gcgcgccggg ggctatgtca gtttcgacct caatatccgc      480
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gccgacgcca taaaactttc ggaagaggag ctggcgttta tcagcggcag cgacgacatc      600
gtcagcggca ccgcccggt gaacgccgcg ttccagccga cgctactgct ggtgacctag      660
ggtaaagcgg ggggtccaggc cgccctgcgc gggcaggtta gccacttccc tgcccgcccg      720
gtggtggccg tcgataccac cggcgccggc gatgcctttg tcgccgggct actcgccggc      780
ctcgccgccc acggtatccc ggacaacctc gcagccctgg ctcccgacct cgcgctggcg      840
caaacctgcg gcgcctggc caccaccgcc aaaggcgcca tgaccgccct gccctacagg      900
gacgatcttc agcgctcgct gtga                                           924

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<210> 48

<211> 307

<212> PRT

<213> *Klebsiella pneumoniae*

<400> 48

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Met Asn Gly Lys Ile Trp Val Leu Gly Asp Ala Val Val Asp Leu Leu
1           5           10          15

Pro Asp Gly Glu Gly Arg Leu Leu Gln Cys Pro Gly Gly Ala Pro Ala
           20           25           30

Asn Val Ala Val Gly Val Ala Arg Leu Gly Gly Asp Ser Gly Phe Ile
           35           40           45

Gly Arg Val Gly Asp Asp Pro Phe Gly Arg Phe Met Arg His Thr Leu
           50           55           60

Ala Gln Glu Gln Val Asp Val Asn Tyr Met Arg Leu Asp Ala Ala Gln
65           70           75           80

Arg Thr Ser Thr Val Val Val Asp Leu Asp Ser His Gly Glu Arg Thr
           85           90           95

Phe Thr Phe Met Val Arg Pro Ser Ala Asp Leu Phe Leu Gln Pro Glu

```

100

105

110

Asp Leu Pro Pro Phe Ala Ala Gly Gln Trp Leu His Val Cys Ser Ile
 115 120 125

Ala Leu Ser Ala Glu Pro Ser Arg Ser Thr Thr Phe Ala Ala Met Glu
 130 135 140

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

Ser Asp Leu Trp Gln Asp Pro Gln Asp Leu Arg Asp Cys Leu Asp Arg
 165 170 175

Ala Leu Ala Leu Ala Asp Ala Ile Lys Leu Ser Glu Glu Glu Leu Ala
 180 185 190

Phe Ile Ser Gly Ser Asp Asp Ile Val Ser Gly Thr Ala Arg Leu Asn
 195 200 205

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

Val Gln Ala Ala Leu Arg Gly Gln Val Ser His Phe Pro Ala Arg Pro
 225 230 235 240

Val Val Ala Val Asp Thr Thr Gly Ala Gly Asp Ala Phe Val Ala Gly
 245 250 255

Leu Leu Ala Gly Leu Ala Ala His Gly Ile Pro Asp Asn Leu Ala Ala
 260 265 270

Leu Ala Pro Asp Leu Ala Leu Ala Gln Thr Cys Gly Ala Leu Ala Thr
 275 280 285

Thr Ala Lys Gly Ala Met Thr Ala Leu Pro Tyr Arg Asp Asp Leu Gln
 290 295 300

Arg Ser Leu
 305

<210> 49
 <211> 915
 <212> DNA
 <213> Escherichia coli

<400> 49
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 ttaggcggaa caagtgggtt tataggtcgg gtgggggatg atccttttg tgcgttaatg 180
 caaagaacgc tgctaactga gggagtcgat atcacgtatc tgaagcaaga tgaatggcac 240

CL5510WOPCT_SeqListing_ST25.txt

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cggacatcca cggtgcttgt cgatctgaac gatcaagggg aacgttcatt tacgtttatg      300
gtccgccccca gtgccgatct ttttttagag acgacagact tgccctgctg gcgacatggc      360
gaatgggttac atctctgttc aattgcgttg tctgccgagc cttcgcgtac cagcgcattt      420
actgcgatga cggcgatccg gcatgccgga ggttttgtca gcttcgatcc taatattcgt      480
gaagatctat ggcaagacga gcatttgctc cgcttggtgtt tgcggcaggc gctacaactg      540
gcggatgtcg tcaagctctc ggaagaagaa tggcgactta tcagtggaaa aacacagaac      600
gatcaggata tatgcgccct ggcaaaagag tatgagatcg ccatgctgtt ggtgactaaa      660
ggtgcagaag ggggtgggtgt ctgttatcga ggacaagttc accattttgc tggaatgtct      720
gtgaattgtg tcgatagcac gggggcgggg gatgcgttcg ttgccggggtt actcacaggt      780
ctgtcctcta cgggattatc tacagatgag agagaaatgc gacgaattat cgatctcgct      840
caacgttgcg gagcgcttgc agtaacggcg aaagggggcaa tgacagcgct gccatgtcga      900
caagaactgg aatag                                                                915

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<210> 50
<211> 304
<212> PRT
<213> Escherichia coli

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<400> 50

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Met Ser Ala Lys Val Trp Val Leu Gly Asp Ala Val Val Asp Leu Leu
1          5          10          15

```

```

Pro Glu Ser Asp Gly Arg Leu Leu Pro Cys Pro Gly Gly Ala Pro Ala
          20          25          30

```

```

Asn Val Ala Val Gly Ile Ala Arg Leu Gly Gly Thr Ser Gly Phe Ile
          35          40          45

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```

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

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Leu Thr Glu Gly Val Asp Ile Thr Tyr Leu Lys Gln Asp Glu Trp His
65          70          75          80

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```

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

```

```

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

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Asp Leu Pro Cys Trp Arg His Gly Glu Trp Leu His Leu Cys Ser Ile
115          120          125

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Ala Leu Ser Ala Glu Pro Ser Arg Thr Ser Ala Phe Thr Ala Met Thr
130          135          140

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CL5510WOPCT_SeqListing_ST25.txt

Ala Ile Arg His Ala Gly Gly Phe Val Ser Phe Asp Pro Asn Ile Arg
145 150 155 160

Glu Asp Leu Trp Gln Asp Glu His Leu Leu Arg Leu Cys Leu Arg Gln
165 170 175

Ala Leu Gln Leu Ala Asp Val Val Lys Leu Ser Glu Glu Glu Trp Arg
180 185 190

Leu Ile Ser Gly Lys Thr Gln Asn Asp Gln Asp Ile Cys Ala Leu Ala
195 200 205

Lys Glu Tyr Glu Ile Ala Met Leu Leu Val Thr Lys Gly Ala Glu Gly
210 215 220

Val Val Val Cys Tyr Arg Gly Gln Val His His Phe Ala Gly Met Ser
225 230 235 240

Val Asn Cys Val Asp Ser Thr Gly Ala Gly Asp Ala Phe Val Ala Gly
245 250 255

Leu Leu Thr Gly Leu Ser Ser Thr Gly Leu Ser Thr Asp Glu Arg Glu
260 265 270

Met Arg Arg Ile Ile Asp Leu Ala Gln Arg Cys Gly Ala Leu Ala Val
275 280 285

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

<210> 51
<211> 879
<212> DNA
<213> Enterococcus faecalis

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acaatgaaaa aagtaataga atttttccaa caatatcctt taaaagcgat tgggattggt 180
tcatttggtc cgattgatat tcacgttgat tctcctacgt atggttatat cacttctaca 240
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cgtcgtcatc ctgaagatac gtatgcagga aattgtcctt atcatggaga ttgtttagaa 540
gggattgcag caggaccagc agttgaaggt cgttctggta aaaaaggaca tttattggaa 600
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 tttgccttgg caaaaaaagc tttaatggct caaaaataa 879

<210> 52
 <211> 292
 <212> PRT
 <213> Enterococcus faecalis

<400> 52

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

Phe Pro Thr Thr Thr Pro Glu Glu Thr Met Lys Lys Val Ile Glu Phe
 35 40 45

Phe Gln Gln Tyr Pro Leu Lys Ala Ile Gly Ile Gly Ser Phe Gly Pro
 50 55 60

Ile Asp Ile His Val Asp Ser Pro Thr Tyr Gly Tyr Ile Thr Ser Thr
 65 70 75 80

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

His Phe Asp Val Pro Met Ala Trp Thr Thr Asp Val Asn Ala Ala Ala
 100 105 110

Tyr Gly Glu Tyr Val Ala Gly Asn Gly Gln His Thr Ser Ser Cys Val
 115 120 125

Tyr Tyr Thr Ile Gly Thr Gly Val Gly Ala Gly Ala Ile Gln Asn Gly
 130 135 140

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

Arg Arg His Pro Glu Asp Thr Tyr Ala Gly Asn Cys Pro Tyr His Gly
 165 170 175

Asp Cys Leu Glu Gly Ile Ala Ala Gly Pro Ala Val Glu Gly Arg Ser
 180 185 190

Gly Lys Lys Gly His Leu Leu Glu Glu Asp His Lys Thr Trp Glu Leu
 195 200 205

CL5510WOPCT_SeqListing_ST25.txt

Glu Ala Tyr Tyr Leu Ala Gln Ala Ala Tyr Asn Thr Thr Leu Leu Leu
210 215 220

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

Leu Met Pro Lys Val Arg Glu Lys Phe Ala Glu Leu Val Asn Gly Tyr
245 250 255

Val Glu Thr Pro Pro Leu Glu Lys Tyr Leu Val Thr Pro Leu Leu Glu
260 265 270

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

Met Ala Gln Lys
290

<210> 53
<211> 1458
<212> DNA
<213> Saccharomyces cerevisiae

<400> 53
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ttgagaaagg ttgttaagca ctttatcgac gaattgaata aaggtttgac aaagaagggg 180
ggtaacattc caatgattcc cggttggttc atggaattcc caacaggtaa agaactctggt 240
aactatttgg ccattgattt gggtggtact aacttaagag tcgtgttggt caagttgagc 300
ggtaaccata ctttgacac cactcaatcc aagtataaac taccacatga catgagaacc 360
actaagcacc aagaggagtt atggtccttt attgccgact ctttgaagga ctttatggtc 420
gagcaagaat tgctaaacac caaggacacc ttaccattag gtttcacctt ctctgaccca 480
gcttcccaaa acaagattaa cgaaggtatt ttgcaaagat ggaccaaggg tttcgatatt 540
ccaaatgtcg aaggccacga tgtcgtccca ttgctacaaa acgaaatttc caagagagag 600
ttgcctattg aaattgtagc attgattaat gatactgttg gtactttaat tgcctcatatc 660
tacactgacc cagagactaa gatgggtgtg attttcggta ctggtgtcaa cggtgctttc 720
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aactctcaa tggctatcaa ttgtgaatat ggttccttcg ataataaaca tttggtcttg 840
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tttgaaaaga tgacctcgg ttactacttg ggtgaattgt tgcgtctagt gttacttgaa 960
ttaaacgaga agggcttgat gttgaaggat caagatctaa gcaagttgaa acaaccatac 1020
atcatggata cctcctaccc agcaagaatc gaggatgatc catttgaaaa cttggaagat 1080
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CL5510WOPCT_SeqListing_ST25.txt

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tataacaaat acccaggttt caaggaagcc gccgctaagg gtttgagaga tatctatgga 1320
tggtactggtg acgcaagcaa agatccaatt acgattgttc cagctgagga tggttcaggt 1380
gcaggtgctg ctgttattgc tgcattgtcc gaaaaaagaa ttgccgaagg taagtctctt 1440
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<210> 54
<211> 485
<212> PRT
<213> *Saccharomyces cerevisiae*
<400> 54

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20 25 30

Met Phe Thr Val Asp Ser Glu Thr Leu Arg Lys Val Val Lys His Phe
35 40 45

Ile Asp Glu Leu Asn Lys Gly Leu Thr Lys Lys Gly Gly Asn Ile Pro
50 55 60

Met Ile Pro Gly Trp Val Met Glu Phe Pro Thr Gly Lys Glu Ser Gly
65 70 75 80

Asn Tyr Leu Ala Ile Asp Leu Gly Gly Thr Asn Leu Arg Val Val Leu
85 90 95

Val Lys Leu Ser Gly Asn His Thr Phe Asp Thr Thr Gln Ser Lys Tyr
100 105 110

Lys Leu Pro His Asp Met Arg Thr Thr Lys His Gln Glu Glu Leu Trp
115 120 125

Ser Phe Ile Ala Asp Ser Leu Lys Asp Phe Met Val Glu Gln Glu Leu
130 135 140

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

Ala Ser Gln Asn Lys Ile Asn Glu Gly Ile Leu Gln Arg Trp Thr Lys
165 170 175

Gly Phe Asp Ile Pro Asn Val Glu Gly His Asp Val Val Pro Leu Leu
180 185 190

CL5510WOPCT_SeqListing_ST25.txt

Gln Asn Glu Ile Ser Lys Arg Glu Leu Pro Ile Glu Ile Val Ala Leu
 195 200 205
 Ile Asn Asp Thr Val Gly Thr Leu Ile Ala Ser Tyr Tyr Thr Asp Pro
 210 215 220
 Glu Thr Lys Met Gly Val Ile Phe Gly Thr Gly Val Asn Gly Ala Phe
 225 230 235 240
 Tyr Asp Val Val Ser Asp Ile Glu Lys Leu Glu Gly Lys Leu Ala Asp
 245 250 255
 Asp Ile Pro Ser Asn Ser Pro Met Ala Ile Asn Cys Glu Tyr Gly Ser
 260 265 270
 Phe Asp Asn Glu His Leu Val Leu Pro Arg Thr Lys Tyr Asp Val Ala
 275 280 285
 Val Asp Glu Gln Ser Pro Arg Pro Gly Gln Gln Ala Phe Glu Lys Met
 290 295 300
 Thr Ser Gly Tyr Tyr Leu Gly Glu Leu Leu Arg Leu Val Leu Leu Glu
 305 310 315 320
 Leu Asn Glu Lys Gly Leu Met Leu Lys Asp Gln Asp Leu Ser Lys Leu
 325 330 335
 Lys Gln Pro Tyr Ile Met Asp Thr Ser Tyr Pro Ala Arg Ile Glu Asp
 340 345 350
 Asp Pro Phe Glu Asn Leu Glu Asp Thr Asp Asp Ile Phe Gln Lys Asp
 355 360 365
 Phe Gly Val Lys Thr Thr Leu Pro Glu Arg Lys Leu Ile Arg Arg Leu
 370 375 380
 Cys Glu Leu Ile Gly Thr Arg Ala Ala Arg Leu Ala Val Cys Gly Ile
 385 390 395 400
 Ala Ala Ile Cys Gln Lys Arg Gly Tyr Lys Thr Gly His Ile Ala Ala
 405 410 415
 Asp Gly Ser Val Tyr Asn Lys Tyr Pro Gly Phe Lys Glu Ala Ala Ala
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 Lys Gly Leu Arg Asp Ile Tyr Gly Trp Thr Gly Asp Ala Ser Lys Asp
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 Pro Ile Thr Ile Val Pro Ala Glu Asp Gly Ser Gly Ala Gly Ala Ala
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CL5510WOPCT_SeqListing_ST25.txt

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 ttacaagccg ttaccaagca cttcatttcc gaattggaaa agggtttgtc caagaagggt 180
 ggtaacattc caatgattcc aggttgggtt atggatttcc caactggtaa ggaatccggt 240
 gatttcttgg ccattgattt ggggtgtacc aacttgagag ttgtcttagt caagttgggc 300
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 gagcaattcc cacaaggtat ctctgagcca attccattgg gtttcacctt ttctttccca 480
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CL5510WOPCT_SeqListing_ST25.txt

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<213> *Saccharomyces cerevisiae*

<400> 56

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 35 40 45

Ile Ser Glu Leu Glu Lys Gly Leu Ser Lys Lys Gly Gly Asn Ile Pro
 50 55 60

Met Ile Pro Gly Trp Val Met Asp Phe Pro Thr Gly Lys Glu Ser Gly
 65 70 75 80

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

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

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

Gln Gly Ile Ser Glu Pro Ile Pro Leu Gly Phe Thr Phe Ser Phe Pro
 145 150 155 160

Ala Ser Gln Asn Lys Ile Asn Glu Gly Ile Leu Gln Arg Trp Thr Lys
 165 170 175

Gly Phe Asp Ile Pro Asn Ile Glu Asn His Asp Val Val Pro Met Leu
 180 185 190

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

Ile Asn Asp Thr Thr Gly Thr Leu Val Ala Ser Tyr Tyr Thr Asp Pro
 210 215 220

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

Tyr Asp Val Cys Ser Asp Ile Glu Lys Leu Gln Gly Lys Leu Ser Asp
 245 250 255

CL5510WOPCT_SeqListing_ST25.txt

Asp Ile Pro Pro Ser Ala Pro Met Ala Ile Asn Cys Glu Tyr Gly Ser
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Phe Asp Asn Glu His Val Val Leu Pro Arg Thr Lys Tyr Asp Ile Thr
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Ile Asp Glu Glu Ser Pro Arg Pro Gly Gln Gln Thr Phe Glu Lys Met
290 295 300

Ser Ser Gly Tyr Tyr Leu Gly Glu Ile Leu Arg Leu Ala Leu Met Asp
305 310 315 320

Met Tyr Lys Gln Gly Phe Ile Phe Lys Asn Gln Asp Leu Ser Lys Phe
325 330 335

Asp Lys Pro Phe Val Met Asp Thr Ser Tyr Pro Ala Arg Ile Glu Glu
340 345 350

Asp Pro Phe Glu Asn Leu Glu Asp Thr Asp Asp Leu Phe Gln Asn Glu
355 360 365

Phe Gly Ile Asn Thr Thr Val Gln Glu Arg Lys Leu Ile Arg Arg Leu
370 375 380

Ser Glu Leu Ile Gly Ala Arg Ala Ala Arg Leu Ser Val Cys Gly Ile
385 390 395 400

Ala Ala Ile Cys Gln Lys Arg Gly Tyr Lys Thr Gly His Ile Ala Ala
405 410 415

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

Asn Ala Leu Lys Asp Ile Tyr Gly Trp Thr Gln Thr Ser Leu Asp Asp
435 440 445

Tyr Pro Ile Lys Ile Val Pro Ala Glu Asp Gly Ser Gly Ala Gly Ala
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Val Gly Ile Ile Gly Ala
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<211> 1164

<212> DNA

<213> Klebsiella pneumoniae

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 35 40 45

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

Glu Val Ala Ile Phe Asp Gly Val Glu Pro Asn Pro Lys Asp Thr Asn
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Val Thr Val Gly Gly Gly Ser Pro His Asp Cys Gly Lys Gly Ile Gly
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 Ile Ala Ala Thr His Glu Gly Asp Leu Tyr Gln Tyr Ala Gly Ile Glu
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 130 135 140
 Gly Thr Ala Ser Glu Val Thr Arg His Cys Val Leu Thr Asn Thr Glu
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 Thr Lys Val Lys Phe Val Ile Val Ser Trp Arg Asn Leu Pro Ser Val
 165 170 175
 Ser Ile Asn Asp Pro Leu Leu Met Ile Gly Lys Pro Ala Ala Leu Thr
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 Ala Ala Thr Gly Met Asp Ala Leu Thr His Ala Val Glu Ala Tyr Ile
 195 200 205
 Ser Lys Asp Ala Asn Pro Val Thr Asp Ala Ala Ala Met Gln Ala Ile
 210 215 220
 Arg Leu Ile Ala Arg Asn Leu Arg Gln Ala Val Ala Leu Gly Ser Asn
 225 230 235 240
 Leu Gln Ala Arg Glu Asn Met Ala Tyr Ala Ser Leu Leu Ala Gly Met
 245 250 255
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 260 265 270
 Leu Gly Gly Leu Tyr Asp Met Pro His Gly Val Ala Asn Ala Val Leu
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 Leu Pro His Val Ala Arg Tyr Asn Leu Ile Ala Asn Pro Glu Lys Phe
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 Ala Asp Ile Ala Glu Leu Met Gly Glu Asn Ile Thr Gly Leu Ser Thr
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 Leu Asp Ala Ala Glu Lys Ala Ile Ala Ala Ile Thr Arg Leu Ser Met
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 Asp Ile Gly Ile Pro Gln His Leu Arg Asp Leu Gly Val Lys Glu Ala
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 Asp Phe Pro Tyr Met Ala Glu Met Ala Leu Lys Asp Gly Asn Ala Phe

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360

365

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 Ala Leu Ala Ser Asp Tyr Pro Gln Ala Arg Ala Phe Val Ala Ser Gly
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 Ile Val Ala Thr Thr Gly Met Lys Gly Thr Arg Asp Asn Ile Ala Gly
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 Thr Leu Ala Ala Leu Glu Gln Ala Leu Ala Lys Thr Pro Trp Ser Met
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 65 70 75 80
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 Asp Val Ala Met Glu Thr Ile Thr Glu Thr Ile Ile Thr Glu Ser Thr
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 Met Ile Gly His Asn Pro Gln Thr Pro Gly Gly Val Gly Val Val
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 Gly Thr Thr Ile Ala Leu Gly Arg Leu Ala Thr Leu Pro Ala Ala Gln
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 Tyr Ala Glu Gly Trp Ile Val Leu Ile Asp Asp Ala Val Asp Phe Leu
 130 135 140
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 Asp Ala Val Trp Trp Leu Asn Glu Ala Leu Asp Arg Gly Ile Asn Val
 145 150 155 160
 gtg gcg gcg atc ctc aaa aag gac gac ggc gtg ctg gtg aac aac cgc 528
 Val Ala Ala Ile Leu Lys Lys Asp Asp Gly Val Leu Val Asn Asn Arg
 165 170 175
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CL5510WOPCT_SeqListing_ST25.txt

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acg	gcg	gtc	cat	ctc	gcc	ggg	gcg	ggg	aat	atg	gtc	agc	ctg	ttg	att	1344									
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CL5510WOPCT_SeqListing_ST25.txt

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 <213> Klebsiella pneumoniae

<400> 60

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CL5510WOPCT_SeqListing_ST25.txt

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195 200 205

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Gln Ser Arg Val Ile Pro Ala Gly Asn Leu Tyr Ile Ser Gly Glu Lys
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Ala Met Ser Ala Cys Ala Pro Val Arg Asp Ile Arg Gly Glu Pro Gly
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Thr His Ala Gly Gly Met Leu Glu Arg Val Arg Lys Val Met Ala Ser
305 310 315 320

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325 330 335

Val Asp Thr Phe Ile Pro Arg Lys Val Gln Gly Gly Met Ala Gly Glu
340 345 350

Cys Ala Met Glu Asn Ala Val Gly Met Ala Ala Met Val Lys Ala Asp
355 360 365

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405 410 415

Gly Ala Gly Ser Thr Asp Ala Ala Ile Val Asn Ala Glu Gly Gln Ile
420 425 430

Thr Ala Val His Leu Ala Gly Ala Gly Asn Met Val Ser Leu Leu Ile
435 440 445

Lys Thr Glu Leu Gly Leu Glu Asp Leu Ser Leu Ala Glu Ala Ile Lys
450 455 460

Lys Tyr Pro Leu Ala Lys Val Glu Ser Leu Phe Ser Ile Arg His Glu
465 470 475 480

Asn Gly Ala Val Glu Phe Phe Arg Glu Ala Leu Ser Pro Ala Val Phe
485 490 495

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

Ala Ser Pro Leu Glu Lys Ile Arg Leu Val Arg Arg Gln Ala Lys Glu
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Lys Val Phe Val Thr Asn Cys Leu Arg Ala Leu Arg Gln Val Ser Pro
530 535 540

Gly Gly Ser Ile Arg Asp Ile Ala Phe Val Val Leu Val Gly Gly Ser
545 550 555 560

Ser Leu Asp Phe Glu Ile Pro Gln Leu Ile Thr Glu Ala Leu Ser His
565 570 575

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<400> 61

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CL5510WOPCT_SeqListing_ST25.txt

aaaactcaca	aggcaaatat	agagattagc	cttgatgaat	ttaagttcat	gttaatgctt	13560
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gatttaaaca	cttacagcaa	tatgaaattg	gtggttgata	agcgaggccg	cccgactgat	13680
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aaccagataa	aaatgaatgg	tgacaaaata	ccaacaacca	ttacatcaga	ttcctaccta	13800
cataacggac	taagaaaaac	actacacgat	gctttaactg	caaaaattca	gctcaccagt	13860
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aacaactgtt	caccgttaca	tatcaaagg	aaaactgtcc	atatgcacag	atgaaaacgg	14100
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<210> 67
 <211> 1260
 <212> DNA
 <213> Citrobacter sp

<400> 67	
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tggctgatgg	ggatagtcac cacgctcagc ggcccgttcc tgatttatgt ttacgaaccg 300
ctgctgacct	ccaacttcaa acttggtatg gcgctgggag ccattttctt tggccttggc 360
tacctcgcg	gttgtggtct ggtagaaagc ttcgtcgaaa aagttagccg caaattcaac 420
tttgaattcg	gcaccgccc cttgtgggga tcgcttggct acgccgcagg gacatttggt 480
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gtgttattcc	tgttgattaa cgtgttggtt aaaaccaact caccgcccc atcttctgta 600
aaaacgcgtt	ctcctgaacc tgacgcgctg acccgaaagg attttctcac tatctttaaa 660
gatacgcagt	tctgggtttt cgttatcttt gtcgtcggta cctggctcgt ctatagcatc 720
tacgatcagc	agatgttccc ggtgttttac gccagcttat ttgacgatcc cgaactggca 780
ccacgcgtat	acggctacct caactcggt caggtcttta tggaagccgt cggatggcg 840
ctggttccat	tcctgattaa ccgcatcggg cctaaatccg cattgctgct ggggtggcaca 900

CL5510WOPCT_SeqListing_ST25.txt

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gtagcgaatt ttgataaacg cctgtcatca acgatatatc tcattggcctt caatatcgcc      1080
agttccattg gcattatcgt gctgtcactg cctgtcggta agttgtttga taaagtgggc      1140
tatcaggaaa tcttcctgat tatggccagc attgtgataa taacactaat atttggctat      1200
ttctcgttga gcaaaaagca tcatcagcag aagatgggaa atgaactggt gacagagtag      1260

```

```

<210> 68
<211> 419
<212> PRT
<213> Citrobacter sp
<400> 68

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```

Met Lys Ile Asn Met Pro Phe Ser Asn Asp Lys Tyr Arg Tyr Ser Ser
1      5      10      15

```

```

Gly Tyr Leu Leu Phe Phe Phe Ala Ala Trp Ser Leu Trp Trp Ser Phe
      20      25      30

```

```

Tyr Ala Ile Trp Leu Lys Asn Lys Leu Gly Leu Ser Gly Thr Glu Leu
      35      40      45

```

```

Gly Met Leu Tyr Ala Val Asn Gln Phe Phe Ser Met Leu Phe Met Leu
      50      55      60

```

```

Val Tyr Gly Phe Leu Gln Asp Lys Leu Gly Thr Arg Lys His Leu Ile
      65      70      75      80

```

```

Trp Leu Met Gly Ile Val Ile Thr Leu Ser Gly Pro Phe Leu Ile Tyr
      85      90      95

```

```

Val Tyr Glu Pro Leu Leu Thr Ser Asn Phe Lys Leu Gly Met Ala Leu
      100      105      110

```

```

Gly Ala Ile Phe Phe Gly Leu Gly Tyr Leu Ala Gly Cys Gly Leu Val
      115      120      125

```

```

Glu Ser Phe Val Glu Lys Val Ser Arg Lys Phe Asn Phe Glu Phe Gly
      130      135      140

```

```

Thr Ala Arg Leu Trp Gly Ser Leu Gly Tyr Ala Ala Gly Thr Phe Val
      145      150      155      160

```

```

Gly Gly Ile Phe Phe Ser Ile Asn Pro His Ile Asn Phe Trp Cys Val
      165      170      175

```

```

Ser Val Met Gly Val Leu Phe Leu Leu Ile Asn Val Leu Phe Lys Thr
      180      185      190

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CL5510WOPCT_SeqListing_ST25.txt

Asn Ser Pro Ala Pro Ser Ser Val Lys Thr Arg Ser Pro Glu Pro Asp
195 200 205

Ala Leu Thr Arg Lys Asp Phe Leu Thr Ile Phe Lys Asp Thr Gln Phe
210 215 220

Trp Phe Phe Val Ile Phe Val Val Gly Thr Trp Ser Phe Tyr Ser Ile
225 230 235 240

Tyr Asp Gln Gln Met Phe Pro Val Phe Tyr Ala Ser Leu Phe Asp Asp
245 250 255

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

Phe Met Glu Ala Val Gly Met Ala Leu Val Pro Phe Leu Ile Asn Arg
275 280 285

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

Arg Ile Leu Gly Ser Ala Leu Phe Thr Asp Ile Tyr Ile Ile Ser Leu
305 310 315 320

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

Phe Lys Phe Ser Val Ala Asn Phe Asp Lys Arg Leu Ser Ser Thr Ile
340 345 350

Tyr Leu Ile Gly Phe Asn Ile Ala Ser Ser Ile Gly Ile Ile Val Leu
355 360 365

Ser Leu Pro Val Gly Lys Leu Phe Asp Lys Val Gly Tyr Gln Glu Ile
370 375 380

Phe Leu Ile Met Ala Ser Ile Val Ile Ile Thr Leu Ile Phe Gly Tyr
385 390 395 400

Phe Ser Leu Ser Lys Lys His His Gln Gln Lys Met Gly Asn Glu Leu
405 410 415

Val Thr Glu

<210> 69
<211> 1314
<212> DNA
<213> Enterococcus faecium

<400> 69
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Page 117

CL5510WOPCT_SeqListing_ST25.txt

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ggcagtgctg taggaacagt attctcggca aattcgtagg ttaccttaat tttgatgttt 240
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gtattagcga cacttgttgg accatttttt atatggatat atgggccatt gctagataac 360
aattttaatt taggcattat tatgggagcg ctatttttgt cagctggata tttagcttct 420
gtaggagttt ttgaagctgt gtcagaaagg tttagtcgtt ttttggctt tgaatatgga 480
caagcaaggg cgtggggatc atttggttat gccttggtag cgcttttggc aggattttta 540
tttgtaaaaa atcctcattt aaacttttgg gcgggatcctt tctttggttc tttactattg 600
ttaaatatat tatttttgaa ccctaaagt gaacgggaag caaatcaaaa ttttaatcaa 660
gaacaagctg aatcaaatag ttttccttct ttaaaagaaa tgtttgatct aatgaaactg 720
cctcaattat ggacgataat catctttatt gtttttacat ggacatttta tacggtatct 780
gatcaacaaa tgtttccggg attttatact ggtttgtttt caacatcagc taatggtgaa 840
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gttccaatca ttatgagaaa attaggggtt cgaaatactt tgttattagg tgtaaccatt 960
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caaattgggc aagtgatttt atcaacacca ttgggaatat taagagacaa cgttggctat 1200
caaccaacat ttaaaattat ttctcttatt gtattactag caggcatata tgcattcttt 1260
attcttaaac aagatgatag agatgttcaa ggggatccat ttattcgagg ataa 1314

```

<210> 70
 <211> 437
 <212> PRT
 <213> Enterococcus faecium

<400> 70

Met Lys Gly Asp Thr Asn Ile Ser Leu Glu Asp Lys Asn Met Ser Lys
 1 5 10 15

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

Leu Leu Phe Phe Ala Ser Trp Gly Val Trp Trp Ser Phe Phe Gln Leu
 35 40 45

Trp Leu Thr Ser Glu Ser Asn Gly Leu Gly Leu Ser Gly Ser Ala Val
 50 55 60

Gly Thr Val Phe Ser Ala Asn Ser Leu Val Thr Leu Ile Leu Met Phe
 Page 118

65 70 75 80
 Ile Tyr Gly Thr Leu₈₅ Gln Asp Lys Leu Tyr₉₀ Ile Lys Arg Asn Leu₉₅ Leu
 Ile Phe Ala Ser₁₀₀ Val Leu Ala Thr Leu₁₀₅ Val Gly Pro Phe Phe₁₁₀ Ile Trp
 Ile Tyr Gly₁₁₅ Pro Leu Leu Asp Asn₁₂₀ Asn Phe Asn Leu Gly₁₂₅ Ile Ile Met
 Gly Ala₁₃₀ Leu Phe Leu Ser Ala₁₃₅ Gly Tyr Leu Ala Ser₁₄₀ Val Gly Val Phe
 Glu Ala Val Ser Glu Arg₁₅₀ Phe Ser Arg Leu Phe₁₅₅ Gly Phe Glu Tyr Gly₁₆₀
 Gln Ala Arg Ala Trp₁₆₅ Gly Ser Phe Gly Tyr₁₇₀ Ala Leu Val Ala Leu₁₇₅ Leu
 Ala Gly Phe Leu₁₈₀ Phe Val Lys Asn Pro₁₈₅ His Leu Asn Phe Trp₁₉₀ Ala Gly
 Ser Phe Phe₁₉₅ Gly Ser Leu Leu Leu₂₀₀ Asn Leu Leu Phe₂₀₅ Trp Asn Pro
 Lys Val₂₁₀ Glu Arg Glu Ala Asn₂₁₅ Gln Asn Phe Asn Gln Glu Gln Ala Glu
 Ser Asn Ser Ile Pro Ser₂₃₀ Leu Lys Glu Met Phe₂₃₅ Asp Leu Met Lys Leu₂₄₀
 Pro Gln Leu Trp Thr₂₄₅ Ile Ile Ile Phe Ile₂₅₀ Val Phe Thr Trp Thr₂₅₅ Phe
 Tyr Thr Val Phe₂₆₀ Asp Gln Gln Met Phe₂₆₅ Pro Gly Phe Tyr Thr₂₇₀ Gly Leu
 Phe Ser Thr₂₇₅ Ser Ala Asn Gly Glu₂₈₀ Lys Ile Tyr Gly Thr₂₈₅ Leu Asn Ala
 Ile Gln Val Phe Cys Glu Ala₂₉₅ Leu Met Met Gly Ile₃₀₀ Val Pro Ile Ile
 Met Arg Lys Leu Gly Val₃₁₀ Arg Asn Thr Leu Leu₃₁₅ Leu Gly Val Thr Ile₃₂₀
 Met Cys Val Arg Ile₃₂₅ Gly Leu Cys Gly Phe₃₃₀ Ala Ser Thr Pro Leu₃₃₅ Ser
 Val Ser Cys Ile Lys Met Leu His Ala Leu Glu Val Pro Leu Phe Thr
 Page 119

340

345

350

Leu Pro Met Phe Arg Tyr Phe Thr Leu His Phe Asp Thr Lys Leu Ser
 355 360 365

Ala Thr Leu Tyr Met Ile Gly Phe Gln Ile Ala Ala Gln Ile Gly Gln
 370 375 380

Val Ile Leu Ser Thr Pro Leu Gly Ile Leu Arg Asp Asn Val Gly Tyr
 385 390 395 400

Gln Pro Thr Phe Lys Ile Ile Ser Leu Ile Val Leu Leu Ala Gly Ile
 405 410 415

Tyr Ala Phe Phe Ile Leu Lys Gln Asp Asp Arg Asp Val Gln Gly Asp
 420 425 430

Pro Phe Ile Arg Gly
 435

<210> 71
 <211> 1299
 <212> DNA
 <213> Corynebacterium glucuronolyticum

<400> 71
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 ctgctcttct tcatgtcctg gggcatcttg tggctcttct tccagctttg gctctccagc 120
 gaaacccgcg gtctcggctt caacggcagt gagatcggca ccatctactc ggtgaactcc 180
 gccgtcacgc tcgtcctcat gctcgtctac ggaactgccc aagataagct tcgtactcgc 240
 cgtaatttgg tgatcgggat tgcagttcta atgagcttga ccggcccggt cttcatgtgg 300
 gtctactggc cactgctgca gagcgagtcg ctctatgtcc tcggtggttg acttggcgca 360
 atcttcatcg gtacggcttt tgtgggggtca tgcccgtgt tcgaggcgct tgccgagcgc 420
 atgtcccgaa aacacaactt cgaatatggc caggcccgcg cgtgggggtt ctttggttac 480
 gccatcgtcg cactcctcgc cggcttcaac ttcacatca accggcgat taacttctgg 540
 atggcctcgg ccttcggcgt tctgttgctt ctatcctcg ttttctggaa ggaaccggta 600
 ggcctcgtg acgaaattgc agaggaggaa gtggaaaaca ccacacctag cgtcaaggaa 660
 atggtgtctg ttctcaaagt gcccgcctc tgggtcgtca ttgtcctcgt gttcttcacg 720
 tggacgttct acacgggtct cgaccagcag atgttcccg agttctacac ctacttttt 780
 agtgactccg ccaccggcga gcgaacctat ggcgtgctca actccgtcca agtggtcgtc 840
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 ctcatgacgg gcttcgccgt catggcactg cgcacctag gttgcgcggt cttcgcggac 960
 ccagtcacca tctcctttgt caagatgttc cagctctcg aggtaccact gtgcatcctc 1020
 cccatcttcc gctacttcac cctgcacttc cccacgaaga tctcgccac cttgtacatg 1080

CL5510WOPCT_SeqListing_ST25.txt

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tccgctatct tcgcctgggt ggctctcaag ggcgataagg aacaagtgga gggcgatccc      1260
ttctaccgcg attcggaact taaggagata caccaatga                               1299

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<210> 72
<211> 432
<212> PRT
<213> Corynebacterium glucuronolyticum

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<400> 72
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Met Ser Lys Phe Met Gln Gln Leu Lys Asn Thr Ala Tyr Gln Gln Ser
1          5          10          15
```

```
Ser Ala Gln Leu Leu Leu Phe Phe Met Ser Trp Gly Ile Trp Trp Ser
          20          25          30
```

```
Phe Phe Gln Leu Trp Leu Ser Ser Glu Thr Arg Gly Leu Gly Phe Asn
          35          40          45
```

```
Gly Ser Glu Ile Gly Thr Ile Tyr Ser Val Asn Ser Ala Val Thr Leu
          50          55          60
```

```
Val Leu Met Leu Val Tyr Gly Thr Ala Gln Asp Lys Leu Arg Thr Arg
65          70          75          80
```

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

```
Phe Phe Met Trp Val Tyr Trp Pro Leu Leu Gln Ser Glu Ser Leu Tyr
          100          105          110
```

```
Val Leu Gly Val Gly Leu Gly Ala Ile Phe Ile Gly Thr Ala Phe Val
          115          120          125
```

```
Gly Ser Cys Pro Leu Phe Glu Ala Leu Ala Glu Arg Met Ser Arg Lys
          130          135          140
```

```
His Asn Phe Glu Tyr Gly Gln Ala Arg Ala Trp Gly Ser Phe Gly Tyr
145          150          155          160
```

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

```
Ile Asn Phe Trp Met Ala Ser Ala Phe Gly Val Leu Leu Leu Leu Ile
          180          185          190
```

```
Leu Val Phe Trp Lys Glu Pro Val Ala Pro Arg Asn Glu Ile Ala Glu
          195          200          205
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CL5510WOPCT_SeqListing_ST25.txt

Glu Glu Val Glu Asn Thr Thr Pro Ser Val Lys Glu Met Val Ser Val
210 215 220

Leu Lys Val Pro Ala Leu Trp Val Val Ile Val Leu Val Phe Phe Thr
225 230 235 240

Trp Thr Phe Tyr Thr Val Phe Asp Gln Gln Met Phe Pro Gln Phe Tyr
245 250 255

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

Leu Asn Ser Val Gln Val Phe Val Glu Ala Leu Met Met Gly Ile Val
275 280 285

Pro Ile Tyr Met Arg Lys Val Gly Val Lys Asn Thr Leu Met Thr Gly
290 295 300

Phe Ala Val Met Ala Leu Arg Ile Leu Gly Cys Ala Val Phe Ala Asp
305 310 315 320

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

Leu Cys Ile Leu Pro Ile Phe Arg Tyr Phe Thr Leu His Phe Pro Thr
340 345 350

Lys Ile Ser Ala Thr Leu Tyr Met Val Gly Phe Gln Ile Ala Ser Gln
355 360 365

Val Gly Asn Val Val Met Ser Pro Ile Leu Gly Ser Leu Arg Asp Arg
370 375 380

Leu Gly Phe Gln Pro Thr Phe Tyr Val Ile Ser Gly Ile Val Leu Val
385 390 395 400

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

Glu Gly Asp Pro Phe Tyr Arg Asp Ser Glu Leu Lys Glu Ile His Gln
420 425 430

<210> 73
<211> 1326
<212> DNA
<213> Bifidobacterium animalis

<400> 73
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ttcctgttct tctgctcctg gggcatctgg tggtcgttct tccagcgctg gctcaactcg 120

atgggactca acggcgcgga agtgggcacg atctattcga tcaactcgct ggccacgctc 180

CL5510WOPCT_SeqListing_ST25.txt

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ctgatgagga cgaacatgat ggccgccgca ctcgtgggct ccgtcgttct ctccgcgggc      360
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gccggcttcg tgttcaacat caacccgatg atcaacttct ggctcggctc cgcattcggc      540
gtgggcatgc tcatcgtgta cctcacctgg tatccggccg agcagcgcgga agcgctcaag      600
gaagccgccg atccgaatgc cgcgccaaact aaccggacca tcaaagacat gctcggcggtg      660
ctcaagatgc ccacgctgtg ggtgctcatc gtgttcatgc tgctcaccaa cacgttctac      720
accgtattcg accagcagat gttccccacc tactacgcct cgctcttccc gaatgaggcc      780
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atgtaa                                                                    1326

```

```

<210> 74
<211> 441
<212> PRT
<213> Bifidobacterium animalis
<400> 74

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```

Met Ala Thr Thr Thr Lys Val Trp Arg Asn Pro Ser Tyr Leu Gln Ser
1           5           10          15

```

```

Ser Thr Gly Ile Phe Leu Phe Phe Cys Ser Trp Gly Ile Trp Trp Ser
          20          25          30

```

```

Phe Phe Gln Arg Trp Leu Asn Ser Met Gly Leu Asn Gly Ala Glu Val
          35          40          45

```

```

Gly Thr Ile Tyr Ser Ile Asn Ser Leu Ala Thr Leu Ile Leu Met Phe
          50          55          60

```

```

Gly Tyr Gly Leu Ile Gln Asp Asn Leu Gly Leu Lys Arg Arg Leu Val
65          70          75          80

```

CL5510WOPCT_SeqListing_ST25.txt

Leu Val Ile Ser Ala Ile Ala Ala Leu Val Gly Pro Phe Val Gln Phe
 85 90 95
 Val Tyr Ala Pro Leu Met Arg Thr Asn Met Met Ala Ala Ala Leu Val
 100 105 110
 Gly Ser Val Val Leu Ser Ala Gly Phe Met Ala Gly Cys Ser Leu Ile
 115 120 125
 Glu Ala Val Thr Glu Arg Tyr Ser Arg Arg Phe Asn Phe Glu Tyr Gly
 130 135 140
 Gln Ser Arg Ala Trp Gly Ser Phe Gly Tyr Ala Ile Val Ala Leu Val
 145 150 155 160
 Ala Gly Phe Val Phe Asn Ile Asn Pro Met Ile Asn Phe Trp Leu Gly
 165 170 175
 Ser Ala Phe Gly Val Gly Met Leu Ile Val Tyr Leu Thr Trp Tyr Pro
 180 185 190
 Ala Glu Gln Arg Glu Ala Leu Lys Glu Ala Ala Asp Pro Asn Ala Ala
 195 200 205
 Pro Thr Asn Pro Thr Ile Lys Asp Met Leu Gly Val Leu Lys Met Pro
 210 215 220
 Thr Leu Trp Val Leu Ile Val Phe Met Leu Leu Thr Asn Thr Phe Tyr
 225 230 235 240
 Thr Val Phe Asp Gln Gln Met Phe Pro Thr Tyr Tyr Ala Ser Leu Phe
 245 250 255
 Pro Asn Glu Ala Thr Gly Asn Ala Val Tyr Gly Thr Leu Asn Ser Val
 260 265 270
 Gln Val Phe Cys Glu Ser Ala Met Met Gly Val Val Pro Ile Ile Met
 275 280 285
 Arg Lys Val Gly Val Arg Asn Ala Leu Leu Leu Gly Ser Thr Val Met
 290 295 300
 Phe Leu Arg Ile Gly Leu Cys Gly Ile Phe His Asp Pro Val Ser Ile
 305 310 315 320
 Ser Ile Val Lys Met Phe His Ala Ile Glu Val Pro Leu Phe Cys Leu
 325 330 335
 Pro Ala Phe Arg Tyr Phe Thr Leu His Phe Asn Pro Lys Leu Ser Ala
 340 345 350

CL5510WOPCT_SeqListing_ST25.txt

Thr Leu Tyr Met Val Gly Phe Gln Ile Ala Ser Gln Ile Gly Gln Val
355 360 365

Val Phe Ser Thr Pro Leu Gly Met Leu His Asp Arg Met Gly Asp Arg
370 375 380

Thr Thr Phe Leu Thr Ile Ser Ala Ile Val Leu Ala Ala Thr Val Tyr
385 390 395 400

Gly Phe Phe Val Ile Lys Arg Asp Asp Glu Gln Val Asp Gly Asp Pro
405 410 415

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

Ile Leu Ser Ala Asp Ser Glu Asp Met
435 440

<210> 75
<211> 1398
<212> DNA
<213> Bifidobacterium gallicum

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<400> 76

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

Arg Leu Val Val Val Ile Ala Thr Ile Ala Ala Leu Ile Gly Pro Phe
 85 90 95

Val Gln Phe Val Tyr Ala Pro Leu Met Gln Thr Asn Ile Met Ala Ala
 100 105 110

Ala Leu Ile Gly Ser Val Val Leu Ser Ala Gly Phe Met Ser Gly Cys
 115 120 125

Ser Leu Ile Glu Ala Leu Thr Glu Arg Tyr Ser Arg Lys Phe Gly Phe
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Glu Tyr Gly Gln Ser Arg Ala Trp Gly Ser Phe Gly Tyr Ala Ile Val
 145 150 155 160

Ala Leu Ile Ala Gly Ile Val Phe Asn Ile Asn Pro Met Ile Asn Phe
 165 170 175

Trp Leu Gly Ser Ala Phe Gly Val Gly Met Leu Ile Val Tyr Leu Thr
 180 185 190

Trp Tyr Pro Ala Glu Gln Arg Gln Ala Leu Lys Glu Ala Ala Asp Pro
 Page 126

195

200

205

Asn Ala Glu Lys Ser Asn Pro Ser Phe Lys Asp Met Val Asn Val Leu
 210 215 220

Lys Met Pro Thr Leu Trp Val Leu Ile Ile Phe Met Leu Leu Thr Asn
 225 230 235 240

Thr Phe Tyr Thr Val Phe Asp Gln Gln Met Phe Pro Thr Tyr Tyr Ala
 245 250 255

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

Asn Ser Ile Gln Val Phe Cys Glu Ser Ala Met Met Gly Val Val Pro
 275 280 285

Ile Ile Met Arg Lys Ile Gly Val Arg Asn Ala Leu Leu Leu Gly Ala
 290 295 300

Thr Val Met Phe Leu Arg Ile Gly Leu Cys Gly Ile Phe His Asp Pro
 305 310 315 320

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

Phe Cys Leu Pro Ala Phe Arg Tyr Phe Thr Leu His Phe Asn Pro Lys
 340 345 350

Leu Ser Ala Thr Leu Tyr Met Val Gly Phe Gln Ile Ala Ser Gln Ile
 355 360 365

Gly Gln Val Ile Phe Ser Thr Pro Leu Gly Met Leu His Asp Arg Phe
 370 375 380

Gly Asp Arg Thr Thr Phe Leu Ser Ile Ser Gly Ile Val Leu Leu Ala
 385 390 395 400

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

Gly Asp Pro Phe Leu Arg Asp Arg Asp Arg Lys Glu Met Glu Leu Ile
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 <213> Bifidobacterium longum

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Ser Ser Phe Gly Ile Phe Met Phe Phe Cys Ser Trp Gly Ile Trp Trp
 Page 128

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 Glu Val Gly Thr Ile Tyr Ser Ile Asn Ser Leu Ala Thr Leu Val Ile
 50 55 60
 Met Phe Val Tyr Gly Val Ile Gln Asp Gln Leu Gly Ile Lys Arg Lys
 65 70 75 80
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 Gln Phe Val Tyr Ala Pro Met Ile Leu Ala Gly Gly Thr Thr Arg Trp
 100 105 110
 Ile Gly Ala Leu Ile Gly Ser Ile Val Leu Ser Ala Gly Phe Met Ser
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 Gly Cys Ser Leu Phe Glu Ala Val Thr Glu Arg Tyr Ser Arg Lys Phe
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 Gly Phe Glu Tyr Gly Gln Ser Arg Ala Trp Gly Ser Phe Gly Tyr Ala
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 195 200 205
 Asp Pro Asn Ala Ala Pro Thr Asn Pro Ser Leu Lys Glu Met Val Ala
 210 215 220
 Val Leu Lys Met Pro Thr Leu Trp Val Leu Ile Val Phe Met Leu Leu
 225 230 235 240
 Thr Asn Thr Phe Tyr Thr Val Phe Asp Gln Gln Met Phe Pro Thr Tyr
 245 250 255
 Tyr Ala Asn Leu Phe Pro Thr Glu Glu Ile Gly Asn Ala Thr Tyr Gly
 260 265 270
 Thr Leu Asn Gly Phe Gln Val Phe Leu Glu Ser Ala Met Met Gly Val
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 Val Pro Ile Ile Met Lys Lys Ile Gly Val Arg Asn Ala Leu Leu Leu

290

295

300

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

Pro Leu Phe Cys Leu Pro Ala Phe Arg Tyr Phe Thr Leu His Phe Asp
 340 345 350

Thr Lys Leu Ser Ala Thr Leu Tyr Met Val Gly Phe Gln Ile Ala Ser
 355 360 365

Gln Val Gly Gln Val Ile Phe Ser Thr Pro Leu Gly Ala Phe His Asp
 370 375 380

Lys Met Ala Gln Ile Leu Pro Asn Asn Asp Met Gly Ser Arg Val Thr
 385 390 395 400

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

Phe Val Ile Lys His Asp Asp Gln Glu Val Gly Gly Asp Pro Phe Tyr
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<210> 79

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<213> Bifidobacterium adolescentis

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ttcctgttca acatcaaccc gctgctgaac ttctgggttg gttccatctg cggcctcagc 660

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<212> PRT
<213> Bifidobacterium adolescentis

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

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100          105          110

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Lys Leu Val Ile Phe Ile Ser Ala Val Ala Ala Cys Val Gly Pro Phe
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Val Gln Phe Val Tyr Gln Pro Met Leu Thr Ala Gly Gly Thr Thr Arg
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 165 170 175
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 180 185 190
 Ala Val Val Ala Leu Cys Ala Gly Phe Leu Phe Asn Ile Asn Pro Leu
 195 200 205
 Leu Asn Phe Trp Val Gly Ser Ile Cys Gly Leu Ser Met Leu Cys Val
 210 215 220
 Tyr Ala Phe Trp Val Pro Ala Glu Gln Lys Glu Glu Leu Lys Lys Glu
 225 230 235 240
 Ala Asp Pro Asn Ala Thr Pro Thr Asn Pro Ser Phe Lys Glu Met Val
 245 250 255
 Ser Val Leu Lys Met Pro Thr Leu Trp Val Leu Ile Val Phe Met Leu
 260 265 270
 Phe Thr Asn Thr Phe Tyr Thr Val Phe Asp Gln Gln Met Phe Pro Asn
 275 280 285
 Tyr Tyr Ala Ser Leu Phe Pro Thr Thr Glu Ile Gly Asn Ala Thr Tyr
 290 295 300
 Gly Thr Leu Asn Ser Phe Gln Val Phe Leu Glu Ser Ala Met Met Gly
 305 310 315 320
 Val Val Pro Ile Ile Met Lys Lys Ile Gly Val Arg Asn Ser Leu Leu
 325 330 335
 Leu Gly Ala Thr Val Met Phe Ala Arg Ile Gly Leu Cys Gly Val Phe
 340 345 350
 His Asp Pro Val Ser Val Ser Ile Val Lys Leu Phe His Ser Ile Glu
 355 360 365
 Val Pro Leu Phe Cys Leu Pro Ala Phe Arg Tyr Phe Thr Leu His Phe
 370 375 380
 Asp Thr Lys Leu Ser Ala Thr Leu Tyr Met Val Gly Phe Gln Ile Ala
 385 390 395 400
 Ser Gln Val Gly Gln Val Ile Phe Ser Thr Pro Met Gly Ala Leu His
 405 410 415

CL5510WOPCT_SeqListing_ST25.txt

Asp Ala Met Gly Asp Arg Pro Thr Phe Phe Thr Ile Ser Ala Ile Val
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Phe Ala Ala Leu Val Tyr Gly Phe Phe Val Ile Lys Lys Asp Asp Gln
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Glu Val Gly Gly Asp Pro Phe Tyr Thr Asp Lys Gln Leu Lys Ala Met
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Lys Ala Ala Asp Ala Glu Val Lys Ala
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 <211> 1503
 <212> DNA
 <213> Bifidobacterium longum

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<210> 82
 <211> 500
 <212> PRT
 <213> Bifidobacterium longum
 <400> 82

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 35 40 45

Ser Ser Asn Gln Arg Met Ile Met Ala Ser Ala Thr Lys Ser Ala Trp
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Cys Ser Trp Gly Ile Trp Trp Ser Phe Phe Gln Arg Trp Leu Ile Ser
 85 90 95

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

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Trp Gly Ser Phe Gly Tyr Ala Ile Val Ala Leu Cys Ala Gly Phe Leu
 Page 134

210

215

220

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Glu Glu Leu Lys Lys Glu Thr Asp Pro Asn Ala Ala Pro Thr Asn Pro
 260 265 270

Ser Leu Lys Glu Met Val Ala Val Leu Lys Met Pro Thr Leu Trp Val
 275 280 285

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

Leu Phe His Ser Ile Glu Val Pro Leu Phe Cys Leu Pro Ala Phe Arg
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Tyr Phe Thr Leu His Phe Asp Thr Lys Leu Ser Ala Thr Leu Tyr Met
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Val Gly Phe Gln Ile Ala Ser Gln Val Gly Gln Val Ile Phe Ser Thr
 420 425 430

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

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<212> DNA
<213> Mitsuokella multacida

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<213> Mitsuokella multacida

<400> 84

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CL5510WOPCT_SeqListing_ST25.txt

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

CL5510WOPCT_SeqListing_ST25.txt

Pro Ile Leu Met Arg Arg Ile Gly Val Arg Lys Ala Ile Leu Leu Gly
290 295 300

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

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

Leu Phe Ile Leu Ala Val Phe Arg Tyr Phe Thr Leu His Phe Asp Thr
340 345 350

Arg Ile Ser Ala Thr Leu Tyr Met Val Gly Phe Gln Ile Ala Ala Gln
355 360 365

Val Gly Gln Ile Ile Phe Ser Thr Pro Leu Gly Ala Leu His Asp Ser
370 375 380

Ile Gly Tyr Gln Ser Thr Phe Leu Val Ile Ser Gly Ile Val Cys Val
385 390 395 400

Ala Ser Leu Tyr Ala Phe Val Ile Leu Lys Lys Asp Asp Gln Gln Val
405 410 415

Asp Gly Gln Pro Leu
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<210> 85
<211> 1275
<212> DNA
<213> Lactobacillus antri

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acgctggtct taatgttcat ctacgggtca gtgcaagaca agctcggcat taaacgccgg 240
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gcccgttacg agaataaggc cgaggaagaa cacgacgcgg ataagccgag tttcaaagag 660
atcatcagtg ttttcaagct caagcagttg tgggaattgg ttttcttcat tattttcagc 720
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CL5510WOPCT_SeqListing_ST25.txt

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 ctcttgattg gggtcaccat tatgttcttg cggatcggcc tctgcggcct ggtcgtcagc 960
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<210> 86
 <211> 424
 <212> PRT
 <213> Lactobacillus antri

<400> 86

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 20 25 30

Ser Phe Phe Gln Ile Trp Leu Thr Asn Asp Leu Gly Phe Ser Gly Ala
 35 40 45

Lys Val Gly Met Ile Tyr Thr Phe Asp Ser Ala Ile Thr Leu Val Leu
 50 55 60

Met Phe Ile Tyr Gly Ser Val Gln Asp Lys Leu Gly Ile Lys Arg Arg
 65 70 75 80

Leu Leu Ile Gly Val Thr Ile Leu Glu Met Leu Leu Gly Pro Phe Phe
 85 90 95

Thr Trp Ile Tyr Ala Pro Leu Leu His Ser Asn Phe Ile Leu Gly Ala
 100 105 110

Phe Leu Gly Ser Leu Tyr Leu Ser Phe Ala Phe Leu Ala Ala Ser Pro
 115 120 125

Thr Phe Glu Ala Leu Ala Glu Arg Met Ser Arg Arg Tyr Ser Phe Glu
 130 135 140

Tyr Gly Arg Ala Arg Ala Trp Gly Ser Phe Gly Tyr Ala Val Ser Ala
 145 150 155 160

Leu Cys Ala Gly Tyr Leu Phe Thr Ile Ser Pro Tyr Ile Val Phe Trp

165

170

175

Leu Ser Ser Gly Ile Ser Leu Leu Thr Phe Leu Leu Leu Cys Phe Gly
 180 185 190
 Arg Thr Lys Ser Pro Thr Gln Val Ala Arg Tyr Glu Asn Lys Ala Glu
 195 200 205
 Glu Glu His Asp Ala Asp Lys Pro Ser Phe Lys Glu Ile Ile Ser Val
 210 215 220
 Phe Lys Leu Lys Gln Leu Trp Glu Leu Val Phe Phe Ile Ile Phe Ser
 225 230 235 240
 Gly Ser Phe Tyr Thr Val Phe Asp Gln Gln Met Phe Pro Gln Phe Phe
 245 250 255
 Thr Gln Phe Phe Lys Thr Ala Ala Gln Gly Asn Thr Ala Tyr Gly Ile
 260 265 270
 Leu Asn Ser Ile Glu Val Phe Leu Glu Ala Ile Met Met Ala Ile Val
 275 280 285
 Pro Trp Ile Met Lys Lys Ile Gly Val Arg Lys Thr Leu Leu Ile Gly
 290 295 300
 Val Thr Ile Met Phe Leu Arg Ile Gly Leu Cys Gly Leu Val Val Ser
 305 310 315 320
 Pro Val Gly Ile Ser Ile Val Lys Leu Phe His Ala Pro Glu Thr Ala
 325 330 335
 Ile Phe Ala Leu Ala Met Phe Arg Tyr Leu Thr Leu His Phe Asp Thr
 340 345 350
 Arg Leu Ser Ala Thr Met Tyr Met Val Val Gly Gln Ile Ala Gly Gln
 355 360 365
 Ile Gly Gln Ile Ile Leu Ser Thr Pro Leu Gly Met Leu His Asp Arg
 370 375 380
 Ile Gly Tyr Arg Ala Thr Phe Leu Val Ile Ser Leu Ile Val Ile Cys
 385 390 395 400
 Ala Ala Val Tyr Ala Phe Val Ile Leu Arg Lys Asp Asn Gln Glu Val
 405 410 415
 Asp Gly Gln Pro Leu Glu Asn Asn
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<210> 87

CL5510WOPCT_SeqListing_ST25.txt

<211> 1323

<212> DNA

<213> Lactobacillus ruminis

<400> 87

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ttctttgctg gctggggcat ctggttgtca ttcttcaga tctggctgac aaccaagcag      180
gggttcaccg gagcccaggt tggcgagata tactccttca actcggcggt ctcactgatt      240
gccaaccttg tttacagcaa cattcaggac aggctcggcc tcaaacgcaa ccttttgatc      300
ttctgcgctt gcctgcaggt gttcctcggg cccttcttca cgttcctctt cgtgccgatg      360
cttcatgcca accttgaact cggcgctctg atcggttcat gctacctgac gcttgccat      420
ctttccgcat ccccgatgtt cgaggcactg acggaacgtg caagccgccg cttcaactat      480
cagtatgggt cagcgcgtgc ctggggctcg ttcggatatg ccgtatccgc cttgcttgca      540
ggattcgtct tcacaatcaa tccgtcgtcg ctgttctgga tcggctctgc catcgctgtt      600
gtccttcttc tcctgctttt gttctggaac cctgtccgca acaaggagac ggttgccaga      660
tttgaaaatg aaatggctag ggaacgtgag aactccaagc ctgggtcaag ggacttcctc      720
aatgtcttca aggttcgcag cctttgggaa atcgccattt tccttgtctt cagcgggtaca      780
ttctacacga ttttcgatca gcagatgttt cctcagttct tcactcagtt cttcaagacc      840
caggcaatgg gcgatcacat gtatgggatc ctgaactcgg ttgaggtgtt cctcgaagca      900
ctcatgatgg gcctggttcc gcttctcatg aagaagatcg gcgtccgccg cacgattctt      960
gtcggcgtga cgttcatgtt catcagaatc ggtggctgcg gtctgattac gaaccctctt     1020
ggcgtttcaa tgatcaagct tctccatgcg cctgaaacgg ccattttctg cgtcgtaatg     1080
ttccgttact acactctgca ctacgatccg cgagtatcag ccacgatcaa tatcgtaacg     1140
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cacatcgggt atcagccgac cttcctggta atcgccggca tcgtattctg cgccggcatc     1260
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taa                                                                    1323

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<210> 88

<211> 440

<212> PRT

<213> Lactobacillus ruminis

<400> 88

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Met Met Pro Ile Ser Asp Asn Trp Lys Gly Ile Leu Phe Met Asn Asp
1           5           10          15

```

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Met Asn Lys Ser Gly Arg Met Ser Gln Leu Lys Asn Pro Phe Phe Thr
20          25          30

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Ser Asn Ala Thr Asn Ile Leu Met Phe Phe Ala Gly Trp Gly Ile Trp

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

305 310 315 320

Val Gly Val Thr Phe Met Phe Ile Arg Ile Gly Gly Cys Gly Leu Ile
325 330 335

Thr Asn Pro Leu Gly Val Ser Met Ile Lys Leu Leu His Ala Pro Glu
340 345 350

Thr Ala Ile Phe Cys Val Val Met Phe Arg Tyr Tyr Thr Leu His Tyr
355 360 365

Asp Pro Arg Val Ser Ala Thr Ile Asn Ile Val Thr Gly Ile Ala Gly
370 375 380

Ser Phe Gly Gln Ile Leu Leu Ser Thr Pro Leu Gly Leu Leu Arg Asp
385 390 395 400

His Ile Gly Tyr Gln Pro Thr Phe Leu Val Ile Ala Gly Ile Val Phe
405 410 415

Cys Ala Gly Ile Tyr Gly Leu Phe Ile Ile Arg Arg Asp Asp Gln Glu
420 425 430

Val Asn Gly Glu Arg Leu Ser Glu
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<210> 89

<211> 1242

<212> DNA

<213> Yersinia frederiksenii

<400> 89

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aaaggtaccg aaacaggggc gactttttcc gccattgcct taacggcact ttgcgctcaa 180

ccgctttatg gcgtgataca agataagttg gggctaaaaa aacatctttt atggggcatt 240

ggtattttgc tgctgatcag tggccctttt tttatttatg tttatgcccc tttattgcgt 300

gtcaacatgc tggttggtgc cgttaccggt ggcttatata tggggatgac gttctttgcc 360

ggtattggtg cgcttgagtc ttataccgaa cgagtgaagg gtattagtgg gtttgagttt 420

ggtaaagccc gtatgtgggg atcgctgggg tgggcgggtg caaccttttt tgctggcatg 480

ttgtttaata ttaatccaa cattaatttc tggatggcat cggcatcggc cgcatatatt 540

ttactgttgt tgtggcactt acatgaagtt aaaacagcgg ctatggggca gttggaatac 600

ggtaagaata gtgccctgac actgagtgat acattgtcac tgtttcgtat gccgcgtttc 660

tgggcgctgg tggatattgt caccggtgtg agcgtttata acgtctatga ccagcaattt 720

ccggtctatt tctcctctct atttactgac cgacgccacg gcaatgaaat gtacggcttt 780

cttaattcac tacaggtatt cctagaggct ggtggtatgt tcctcgcgcc ttttctggtt 840

CL5510WOPCT_SeqListing_ST25.txt

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gtggagttgc ctattttgct cattgcatg ttttaagtata tcgccgcaa tttcgacccg     1020
cgtttgtcag ccacgcttta tctggtggga tttcagttta ttaccaagt ctatgccagc     1080
gtattttcgc cgttggcagg taaaggctat gacctgatcg ggttcgctga tacctatctg     1140
atcatgggag gcattgtcct cggattaaca gcaatttctt gttttatgct gcgcggcgag     1200
tcgcgtacgg atgatccttc cctacaatta accactaagt ga                          1242

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<210> 90
<211> 413
<212> PRT
<213> Yersinia frederiksenii
<400> 90

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Met Lys His Ser Val Arg Asn Gln Tyr Leu Ile Leu Ser Gly Leu Leu
1          5          10          15

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Phe Thr Phe Phe Phe Thr Trp Ser Ser Ala Phe Ser Leu Phe Ser Ile
          20          25          30

```

```

Trp Leu Asn Gln Tyr Val Gly Leu Lys Gly Thr Glu Thr Gly Ala Thr
          35          40          45

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```

Phe Ser Ala Ile Ala Leu Thr Ala Leu Cys Ala Gln Pro Leu Tyr Gly
          50          55          60

```

```

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

```

```

Gly Ile Leu Leu Leu Ile Ser Gly Pro Phe Phe Ile Tyr Val Tyr Ala
          85          90          95

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```

Pro Leu Leu Arg Val Asn Met Leu Val Gly Ala Val Thr Gly Gly Leu
          100          105          110

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```

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

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```

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

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Met Trp Gly Ser Leu Gly Trp Ala Gly Ala Thr Phe Phe Ala Gly Met
          145          150          155          160

```

```

Leu Phe Asn Ile Asn Pro Asn Ile Asn Phe Trp Met Ala Ser Ala Ser
          165          170          175

```

```

Ala Ala Ile Phe Leu Leu Leu Leu Trp His Leu His Glu Val Lys Thr
Page 144

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180

185

190

Ala Ala Met Gly Gln Leu Glu Tyr Gly Lys Asn Ser Ala Leu Thr Leu
 195 200 205

Ser Asp Thr Leu Ser Leu Phe Arg Met Pro Arg Phe Trp Ala Leu Val
 210 215 220

Val Phe Val Thr Gly Val Ser Val Tyr Asn Val Tyr Asp Gln Gln Phe
 225 230 235 240

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

Met Tyr Gly Phe Leu Asn Ser Leu Gln Val Phe Leu Glu Ala Gly Gly
 260 265 270

Met Phe Leu Ala Pro Phe Leu Val Asn Arg Ile Gly Ala Lys Lys Gly
 275 280 285

Leu Leu Leu Ser Gly Leu Ile Met Ala Met Arg Ile Leu Gly Ser Gly
 290 295 300

Leu Ala Gln Asp Ala Val Thr Ile Ser Leu Met Lys Leu Leu His Ala
 305 310 315 320

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

Asn Phe Asp Pro Arg Leu Ser Ala Thr Leu Tyr Leu Val Gly Phe Gln
 340 345 350

Phe Ile Thr Gln Val Tyr Ala Ser Val Phe Ser Pro Leu Ala Gly Lys
 355 360 365

Gly Tyr Asp Leu Ile Gly Phe Ala Asp Thr Tyr Leu Ile Met Gly Gly
 370 375 380

Ile Val Leu Gly Leu Thr Ala Ile Ser Cys Phe Met Leu Arg Gly Glu
 385 390 395 400

Ser Arg Thr Asp Asp Pro Ser Leu Gln Leu Thr Thr Lys
 405 410

<210> 91

<211> 1260

<212> DNA

<213> Serratia proteamaculans

<400> 91

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tttacctggt catccagctt ttcactgatc tccatctggc tgaaccagaa aatcggcctg 120

CL5510WOPCT_SeqListing_ST25.txt

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ggatttggcg cgctggaatc ctataccgaa cgagtcagcc gcatcgtcgg tttcgaattc      420
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aactacaata tcgaccccaa tatcaacttc tggatcgctt cggcctcggc ggcagtgttt      540
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tgggcgctgg tgggtgtttg gctgggcacc agcatctacg gcggtgttga ccagcagttc      720
ccggtgtatt tcgcctcgca gttccccacc cacgaagaag gcaaccgat gtacggtttc      780
cttaattcgc tgcaggtgtt tctggaggcc ggtggcatgt tcctggcccc gctgctgggt      840
aaccgcattg gcataaagca aagcctgttg ctggccagca gcgtgatggc gctgcgcatg      900
gtcggttccg gctttgccag cggcgccctg atgatttccg ccatgaaact gctgcacgcc      960
gtagaattgc caatcctgct ggtggcgatg ttcaagtaca tcaccaccg tttcgacagc     1020
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<210> 92
 <211> 419
 <212> PRT
 <213> *Serratia proteamaculans*

<400> 92

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 20 25 30

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

Phe Ala Ala Met Ser Ile Met Ala Leu Cys Ala Gln Pro Leu Tyr Gly
 50 55 60

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

Gly Val Leu Leu Leu Leu Thr Gly Pro Phe Phe Ile Tyr Val Tyr Ala
 Page 146

Pro Leu Leu Gln Ser Asn Leu Val Val Gly Ala Leu Val Gly Gly Val
100 105 110

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

Thr Glu Arg Val Ser Arg Ile Val Gly Phe Glu Phe Gly Arg Ala Arg
130 135 140

Met Trp Gly Ser Leu Gly Trp Ala Ser Ala Thr Phe Phe Ala Gly Phe
145 150 155 160

Asn Tyr Asn Ile Asp Pro Asn Ile Asn Phe Trp Ile Ala Ser Ala Ser
165 170 175

Ala Ala Val Phe Leu Leu Leu Leu Trp Gln Val Arg Glu Leu Lys Pro
180 185 190

Asn Ala Met Ala Gly Leu Glu Tyr Gly Lys Pro Glu Asn Leu Lys Leu
195 200 205

Gln Asp Ala Leu Ala Leu Leu Arg Leu Pro Gly Phe Trp Ala Leu Val
210 215 220

Val Phe Val Leu Gly Thr Ser Ile Tyr Gly Val Phe Asp Gln Gln Phe
225 230 235 240

Pro Val Tyr Phe Ala Ser Gln Phe Pro Thr His Glu Glu Gly Asn Arg
245 250 255

Met Tyr Gly Phe Leu Asn Ser Leu Gln Val Phe Leu Glu Ala Gly Gly
260 265 270

Met Phe Leu Ala Pro Leu Leu Val Asn Arg Ile Gly Ile Lys Gln Ser
275 280 285

Leu Leu Leu Ala Ser Ser Val Met Ala Leu Arg Met Val Gly Ser Gly
290 295 300

Phe Ala Ser Gly Ala Leu Met Ile Ser Ala Met Lys Leu Leu His Ala
305 310 315 320

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

Arg Phe Asp Ser Arg Leu Ser Ser Thr Leu Tyr Leu Val Gly Phe Gln
340 345 350

Phe Ile Ser Gln Ile Val Ala Gly Phe Leu Ala Pro Leu Ala Gly Tyr
Page 147

355

360

365

Gly Tyr Asp Arg Ile Gly Phe Ala Asp Thr Tyr Leu Leu Met Gly Cys
 370 375 380

Ala Val Ala Gly Thr Thr Leu Ile Ser Cys Phe Leu Leu Arg Gly Glu
 385 390 395 400

Thr Val Ala Ser Ala Pro Gln Phe Gln Ser Thr Leu Lys Ser Ser Glu
 405 410 415

Pro Thr Gln

<210> 93
 <211> 1239
 <212> DNA
 <213> Escherichia coli

<400> 93
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 aaagcatcgg aaaccggcat ttttttttca gtattatccg tctccgcgct cttcgcgcag 180
 gtctgttatg gctttattca ggaccgactt ggtctgcgca aacatttggt atggtttatc 240
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 aatattctgc tgggcagcgt attcgggggc ttatttatcg ggctgacgtt taatgggggt 360
 atcggcggtt tggagtccta taccgagcgc gtcgcgcgct aaagtacctt tgagtttggg 420
 cgggcacgca tgtgggggtc tctgggctgg gcagttgccg cgttttttgc cgggttactg 480
 tttaatatca accctgacct taacttctcg gtggcttcat gctcaggggt aatcttcttc 540
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 gctaaaaaag tttctctgga agacgccctg cgtctgctta ctctgccgcg cttctgggca 660
 ctgatattct tcgtggtcgg aacctgcatt tacggcgtat acgatcagca attcccggtc 720
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CL5510WOPCT_SeqListing_ST25.txt

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 <213> Escherichia coli

<400> 94

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 35 40 45

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Phe Ile Gln Asp Arg Leu Gly Leu Arg Lys His Leu Leu Trp Phe Ile
 65 70 75 80

Thr Ala Leu Leu Ile Leu Ser Gly Pro Ala Tyr Leu Leu Phe Ser Tyr
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Ile Gly Leu Thr Phe Asn Gly Gly Ile Gly Val Leu Glu Ser Tyr Thr
 115 120 125

Glu Arg Val Ala Arg Gln Ser Thr Phe Glu Phe Gly Arg Ala Arg Met
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Trp Gly Ser Leu Gly Trp Ala Val Ala Thr Phe Phe Ala Gly Leu Leu
 145 150 155 160

Phe Asn Ile Asn Pro Asp Leu Asn Phe Leu Val Ala Ser Cys Ser Gly
 165 170 175

Leu Ile Phe Phe Cys Leu Leu Ala Arg Leu Lys Val Ala Ala Pro Ala
 180 185 190

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

Ala Leu Arg Leu Leu Thr Leu Pro Arg Phe Trp Ala Leu Ile Phe Phe
 210 215 220

Val Val Gly Thr Cys Ile Tyr Gly Val Tyr Asp Gln Gln Phe Pro Val
 225 230 235 240

Tyr Phe Ser Ser Gln Phe Pro Thr Leu Arg Glu Gly Asn Glu Met Phe
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245

250

255

Gly Tyr Leu Asn Ser Phe Gln Val Phe Leu Glu Ala Ala Gly Met Phe
 260 265 270

Cys Ala Pro Trp Leu Val Asn Arg Ile Gly Ala Lys Asn Gly Leu Ile
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 290 295 300

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

Asp Lys Arg Leu Ser Ser Thr Ile Tyr Leu Val Gly Phe Ala Cys Thr
 340 345 350

Ser Ser Val Ile Gly Thr Val Leu Ser Pro Leu Ala Gly Phe Ser Tyr
 355 360 365

Glu Arg Phe Gly Phe Ala Gln Ser Tyr Leu Ile Met Gly Ile Met Val
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<212> DNA

<213> Weissella paramesenteroides

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ttatgggttaa ctgcaaaaag cggtttgaat ttggatggta gtgccgttgg aacaatttat 180

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CL5510WOPCT_SeqListing_ST25.txt

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<213> Weissella paramesenteroides

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CL5510WOPCT_SeqListing_ST25.txt

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 260 265 270
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 275 280 285
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 325 330 335
 Glu Thr Pro Leu Phe Ile Leu Ser Ile Phe Arg Tyr Phe Thr Leu His
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 355 360 365
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 Arg Asp Asn Ser Gly Tyr Ala Val Thr Phe His Ile Ile Thr Ile Ile
 385 390 395 400
 Val Ile Ala Ala Gly Ile Tyr Ala Phe Phe Val Ile Lys Lys Asp Asn
 405 410 415

CL5510WOPCT_SeqListing_ST25.txt

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 <212> DNA
 <213> Bifidobacterium pseudocatenuatum

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 225 230 235 240
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 260 265 270
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305 310 315 320

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340 345 350

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gcataa 1086

CL5510WOPCT_SeqListing_ST25.txt

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 <213> Bifidobacterium catenulatum
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 35 40 45
 Phe Phe Ser Arg Trp Leu Thr Asp Pro Thr His Gly Leu Gly Met Thr
 50 55 60
 Ser Ala Glu Gln Gly Gln Ile Tyr Ser Ile Asn Ser Leu Ala Thr Leu
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 Val Ile Met Phe Ala Tyr Gly Ala Ile Gln Asp Gln Leu Gly Ile Lys
 85 90 95
 Arg Lys Leu Val Ile Phe Val Ser Ala Ile Ala Ala Leu Val Gly Pro
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 115 120 125
 Arg Phe Ile Gly Val Leu Ile Gly Ser Ile Val Leu Ser Ser Gly Phe
 130 135 140
 Met Ala Gly Cys Ser Leu Phe Glu Ala Leu Thr Glu Arg Tyr Ser Arg
 145 150 155 160
 Lys Phe Gly Phe Glu Tyr Gly Gln Ser Arg Ala Trp Gly Ser Phe Gly
 165 170 175
 Tyr Ala Ile Val Ala Leu Cys Ala Gly Phe Leu Phe Asn Ile Asn Pro
 180 185 190
 Leu Leu Asn Phe Trp Val Gly Ser Ile Cys Gly Leu Gly Met Leu Cys
 195 200 205
 Val Tyr Ala Phe Trp Val Pro Ala Lys Gln Lys Glu Glu Leu Lys Lys
 210 215 220
 Glu Ala Asp Pro Asn Ala Ala Pro Thr Asn Pro Ser Phe Lys Glu Met
 225 230 235 240
 Ile Ser Val Leu Lys Met Pro Thr Leu Trp Val Leu Ile Val Phe Met
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250

255

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 260 265 270

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

Gly Val Val Pro Ile Ile Met Lys Lys Ile Gly Val Arg Asn Ser Leu
 305 310 315 320

Leu Leu Gly Ala Thr Val Met Phe Leu Arg Ile Gly Leu Cys Gly Val
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Glu Val Pro Leu Phe Cys Leu Pro Ala
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 <211> 1176
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 <213> Clostridium thermocellum

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<210> 102
 <211> 391
 <212> PRT
 <213> Clostridium thermocellum

<400> 102

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Phe Met Pro Val Tyr Leu Glu Gly Leu Gly Tyr Asp Asn Thr Asp Ile
 35 40 45

Gly Thr Phe Leu Ser Ile Ser Ser Phe Val Gly Leu Phe Ala Gln Pro
 50 55 60

Ile Trp Gly Val Ile Ser Asp Arg Ala Lys Ser Lys Asn Asn Val Leu
 65 70 75 80

Lys Met Leu Val Leu Phe Ser Ser Ile Ala Ile Phe Met Phe Arg Leu
 85 90 95

Ser Gly Asn Tyr Tyr Tyr Ile Phe Ala Val Met Val Val Tyr Ala Phe
 100 105 110

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

Ile Thr Asp Thr Lys Trp Lys Tyr Gly Pro Ile Arg Leu Ala Gly Ala
 130 135 140

Leu Gly Tyr Ala Val Met Ala Phe Ile Gly Gly Ala Leu Thr Arg Lys
 145 150 155 160

Asn Ile Asn Ala Ile Phe Phe Ile Cys Phe Val Ile Gly Ile Met Ser
 165 170 175

Leu Ile Thr Val Phe Arg Met Pro Thr Val Lys Gly His Gln Ser Asp
 180 185 190

Gly Asn Lys Leu Ser Ile Leu Glu Val Phe Lys Asn Ser Glu Leu Val
 195 200 205

CL5510WOPCT_SeqListing_ST25.txt

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

Leu Val Phe Gly Asp Arg Ile Ile Lys Arg Leu Gly Ile Lys Phe Thr
260 265 270

Leu Phe Gly Ala Ala Val Val Ala Val Val Arg Trp Ala Ser Leu Gly
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Leu Ile Asn Asn Ile Phe Ala Val Leu Ala Leu Gln Ile Leu His Gly
290 295 300

Phe Ile Phe Ile Val Leu Ala Tyr Ser Met Ala Thr Tyr Ile Asn Asn
305 310 315 320

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

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<212> DNA
<213> Granulibacter bethesdensis

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CL5510WOPCT_SeqListing_ST25.txt

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<210> 104
 <211> 436
 <212> PRT
 <213> Granulibacter bethesdensis

<400> 104

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

Val Leu Ser Asp Gly Gln Pro Pro Ser Asp Ser Arg Gln Lys Gln Gly
20 25 30

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

Asp Gly Leu Gly Pro Tyr Leu Ala Val Tyr Leu Leu Ser Ala Ser Gly
50 55 60

Arg Asp Gly Arg Trp Asp Glu Ser Ser Val Gly Leu Val Leu Thr Ile
65 70 75 80

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

Asp Arg Ser Arg Asn Lys Pro Arg Leu Leu Ala Val Ala Ile Leu Leu
100 105 110

Val Thr Leu Ser Thr Leu Leu Leu Pro Phe Met Ser Gly Leu Pro Leu

115

120

125

Val Thr Leu Thr Gln Ser Met Ala Ala Val Ala Gly Ala Ile Phe Ala
 130 135 140
 Pro Val Ile Ala Ala Met Thr Leu Gly Leu Val Gly Thr Asp Gly Phe
 145 150 155 160
 Ala Arg Arg Ile Gly Arg Asn Glu Ser Phe Asn His Leu Gly Asn Ala
 165 170 175
 Val Ser Ala Ala Ile Ala Gly Leu Leu Ala Trp His Tyr Gly Pro Val
 180 185 190
 Val Val Phe Trp Leu Met Gly Leu Leu Ala Ile Ala Gly Leu Val Thr
 195 200 205
 Val Leu Arg Ile Asp Asn Arg His Ile Asp Asn Asp Leu Ala Asn Gly
 210 215 220
 Gly Glu Ala Asn Gly Met Asp Gly Ala Ala Leu Lys Asp Gln Ala Ser
 225 230 235 240
 Pro Gly Leu Trp Arg Ile Leu Ala Asp His Pro Gly Leu Met Thr Phe
 245 250 255
 Ala Val Leu Val Phe Leu Phe His Leu Ala Asn Ala Ala Met Leu Thr
 260 265 270
 Ser Val Ser Gln Leu Leu Met Arg Glu Val Gly Lys Asp Met Ala Thr
 275 280 285
 Ser Leu Ala Ala Ala Cys Ile Val Ala Ala Gln Met Val Met Val Pro
 290 295 300
 Val Ala Met Leu Val Gly Arg Phe Val Asp Arg Ile Gly Thr Arg Pro
 305 310 315 320
 Ile Phe Leu Leu Ala Phe Gly Ile Leu Ala Leu Arg Gly Met Leu Tyr
 325 330 335
 Pro Leu Ser Gly Asn Pro Trp Trp Leu Leu Gly Val Gln Leu Leu Asp
 340 345 350
 Gly Val Gly Ala Gly Ile Phe Gly Ala Leu Phe Pro Val Val Val Ala
 355 360 365
 Asp Leu Thr Lys Gly Thr Gly Arg Phe Asn Ile Ser Gln Gly Ala Val
 370 375 380
 Ala Thr Ala Gln Gly Ile Gly Ala Ala Leu Ser Ala Gly Val Ala Gly
 Page 161

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

<210> 105
 <211> 1263
 <212> DNA
 <213> Cronobacter turicensis

<400> 105
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 gcgggactga gtgcaattga tatcgggtacg gtttttgccg tcaacgggtgt gtttgccgtc 180
 ctgggttaaac ctgtatatgg ctttatcatg gacaaaaccg gcatgaaaaa gcatttgctc 240
 tatttcgtct gccttatttc cgcactgatg gccccttttt atctgtggtg ctacttgccc 300
 ttactacaaa gtcactttct ggcaggcatg atcattggcg cgttattttt cagcttcggc 360
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 atggagttcg gtcgtatcag aatgtgggcc gactgggat gggcggttgc tgcacgtttt 480
 tctggctacg tttataacat ttccccaata attaaacttta ccatcggcag cgtatctgca 540
 gtgtgtatgt tgctgggtgt aatttcactt aaagttgatc atttcgggca ggaagaaaat 600
 agcgttctgt ctaaagataa aattgttatc gcggatgtgt ttcattctgtt cagaaatcca 660
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 ttcgacaaaa ggattaacgc gaccatgtat ctgcttggct atcaggccat ggtttatgtg 1080
 ggctccatcg tggttgcccc tcccgtggc tacgcctatg acaccatagg ttttgaacat 1140
 acgtatctga ttatgggcac catttcacta ctgtttacga ttgtgtcggc tttcacactt 1200
 tctgattgtc aaaagcataa aaaagtcacc tccgcctccc atacagatca agcattaaat 1260
 taa 1263

<210> 106
 <211> 420

CL5510WOPCT_SeqListing_ST25.txt

<212> PRT

<213> Cronobacter turicensis

<400> 106

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

Tyr Ala Ile Trp Leu Gly Asp Lys Ala Gly Leu Ser Ala Ile Asp Ile
 35 40 45

Gly Thr Val Phe Ala Val Asn Gly Val Phe Ala Val Leu Val Lys Pro
 50 55 60

Val Tyr Gly Phe Ile Met Asp Lys Thr Gly Met Lys Lys His Leu Leu
 65 70 75 80

Tyr Phe Val Cys Leu Ile Ser Ala Leu Met Ala Pro Phe Tyr Leu Trp
 85 90 95

Cys Tyr Leu Pro Leu Leu Gln Ser His Phe Leu Ala Gly Met Ile Ile
 100 105 110

Gly Ala Leu Phe Phe Ser Phe Gly Trp Tyr Ala Gly Val Ala Ala Glu
 115 120 125

Glu Ser Tyr Val Asp Arg Phe Ser Arg Leu Tyr Asn Met Glu Phe Gly
 130 135 140

Arg Ile Arg Met Trp Ala Ala Leu Gly Trp Ala Val Ala Ala Ser Phe
 145 150 155 160

Ser Gly Tyr Val Tyr Asn Ile Ser Pro Ile Ile Asn Phe Thr Ile Gly
 165 170 175

Ser Val Ser Ala Val Cys Met Leu Leu Val Leu Ile Ser Leu Lys Val
 180 185 190

Asp His Phe Gly Gln Glu Glu Asn Ser Val Leu Ser Lys Asp Lys Ile
 195 200 205

Val Ile Ala Asp Val Phe His Leu Phe Arg Asn Pro Lys Phe Trp Met
 210 215 220

Phe Ala Leu Tyr Ile Ala Gly Val Ala Trp Met Met Phe Ile Ala Glu
 225 230 235 240

Gln Gln Phe Ser Arg Tyr Phe Val Thr Phe Phe Asn Thr Lys Glu Gln
 245 250 255

CL5510WOPCT_SeqListing_ST25.txt

Gly Asn Ala Met Phe Gly Tyr Met Ser Thr Thr Gln Ser Cys Thr Glu
260 265 270

Phe Phe Gly Met Met Leu Val Pro Ala Leu Val Asn Arg Ile Gly Ala
275 280 285

Lys Gln Gly Met Leu Leu Thr Gly Leu Ile Val Ser Leu Arg Leu Ile
290 295 300

Ile Ser Gly Leu Thr Thr Asp Pro Leu Ile Ile Cys Leu Val Lys Pro
305 310 315 320

Leu Tyr Gly Ile Glu Ile Ala Leu Ile Leu Val Ser Val Phe Lys Tyr
325 330 335

Ile Ala Glu His Phe Asp Lys Arg Ile Asn Ala Thr Met Tyr Leu Leu
340 345 350

Gly Tyr Gln Ala Met Val Tyr Val Gly Ser Ile Val Val Ala Pro Pro
355 360 365

Ala Gly Tyr Ala Tyr Asp Thr Ile Gly Phe Glu His Thr Tyr Leu Ile
370 375 380

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

Ser Asp Cys Gln Lys His Lys Lys Val Thr Ser Ala Ser His Thr Asp
405 410 415

Gln Ala Leu Asn
420

<210> 107
<211> 1269
<212> DNA
<213> Enterobacter sp

<400> 107
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gccaatctca gcgggtcggg tatcgggacg gtatttgctgg ttaacgggtat tttctccgtg 180
attttaaaac cgatctacgg ctatattctc gataagatcg ggatgagcaa atacctgctc 240
tattttgtgg tggcgtatgc ggccctgatg gcaccgttct ttatttatgt ctatcagccg 300
ctgttaatgt ccaacacgat gctgggtatt attatcggcg cgctctatct aagctttgccc 360
tggtatgcgg gcgtggcagc gtgtgaatcc tattccgatc gtttcagtcg tctaaacggc 420
atggagtttg gtcagattcg catgtggggg tcacttggct gggcgggtggc gtcgtcgttc 480
tcgggcctgc tgtttaacct ctgcctgcg tataatttta ttctgggtag cgtggcgtca 540

CL5510WOPCT_SeqListing_ST25.txt

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gtcatcatgc tcattgttct gctgaacctg aaagtgaaca ctaactccgt tcatgccagt      600
gacgtactga ccaaagagaa aatcgcccct tcggatgttt acgcgctgct gcgcagccgc      660
aagttttggg ctttctgcct gtatgtcgcg ggcgtggcgt ggatgatgtt tatcgccgag      720
cagcagttct cgcgctactt cgtcaccttc tttgacgata tccatcaggg caacgcggta      780
ttcggctacc tcggcacggt tcagtcgggt atggaatttg tcatgtatat ggtgattccg      840
ctgttcgtga actttatcgg tgccaagcgc ggattactca tcgtcggggt gttcgtcggg      900
gcgcgtctga ttatttccgg cctgtgcgat tcccacttat taatttccgt tctcaagcct      960
ttatacggtc tggaaatctg tttgctgctg gtgtcggtat ttaaataatat cgccgagcat     1020
ttcgataaac gtgtaaatgc caccatgtat ttattgggct atcaggcgat gctgtatgtc     1080
ggaaatgtgg ttatctcgtc accggcggga tatatgtatg accgcatcgg atttgaacag     1140
acctatatca ttatgggcgc aacggcgctg acctttacgc tgctctctgc ctttacgtta     1200
tccgcctgcc aaagcaaatg gcgtggcaca tctgcaatct ctgtagcaga acagaatcca     1260
tctcgataa                                     1269

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<210> 108
<211> 422
<212> PRT
<213> Enterobacter sp

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<400> 108
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Met Glu Asn Thr Ser Thr Asn Asn Arg Thr Glu Tyr Tyr Lys Ile Ser
1           5           10           15
```

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Ile Phe Ile Phe Leu Tyr Phe Phe Thr Trp Ser Ala Ser Ile Gly Leu
                20                25                30
```

```
Leu Ala Ile Trp Leu Gly Gln Lys Ala Asn Leu Ser Gly Ser Val Ile
          35          40          45
```

```
Gly Thr Val Phe Ala Val Asn Gly Ile Phe Ser Val Ile Leu Lys Pro
          50          55          60
```

```
Ile Tyr Gly Tyr Ile Leu Asp Lys Ile Gly Met Ser Lys Tyr Leu Leu
65          70          75          80
```

```
Tyr Phe Val Val Ala Met Ser Ala Leu Met Ala Pro Phe Phe Ile Tyr
          85          90          95
```

```
Val Tyr Gln Pro Leu Leu Met Ser Asn Thr Met Leu Gly Ile Ile Ile
          100          105          110
```

```
Gly Ala Leu Tyr Leu Ser Phe Ala Trp Tyr Ala Gly Val Ala Ala Cys
          115          120          125
```

```
Glu Ser Tyr Ser Asp Arg Phe Ser Arg Leu Asn Gly Met Glu Phe Gly
                                     Page 165

```

130

135

140

Gln Ile Arg Met Trp Gly Ser Leu Gly Trp Ala Val Ala Ser Ser Phe
 145 150 155 160

Ser Gly Leu Leu Phe Asn Leu Ser Pro Ala Tyr Asn Phe Ile Leu Gly
 165 170 175

Ser Val Ala Ser Val Ile Met Leu Ile Val Leu Leu Asn Leu Lys Val
 180 185 190

Asn Thr Asn Ser Val His Ala Ser Asp Val Leu Thr Lys Glu Lys Ile
 195 200 205

Ala Pro Ser Asp Val Tyr Ala Leu Leu Arg Ser Arg Lys Phe Trp Ala
 210 215 220

Phe Cys Leu Tyr Val Ala Gly Val Ala Trp Met Met Phe Ile Ala Glu
 225 230 235 240

Gln Gln Phe Ser Arg Tyr Phe Val Thr Phe Phe Asp Asp Ile His Gln
 245 250 255

Gly Asn Ala Val Phe Gly Tyr Leu Gly Thr Val Gln Ser Gly Met Glu
 260 265 270

Phe Val Met Tyr Met Val Ile Pro Leu Phe Val Asn Phe Ile Gly Ala
 275 280 285

Lys Arg Gly Leu Leu Ile Val Gly Leu Phe Val Gly Ala Arg Leu Ile
 290 295 300

Ile Ser Gly Leu Cys Asp Ser His Leu Leu Ile Ser Val Leu Lys Pro
 305 310 315 320

Leu Tyr Gly Leu Glu Ile Cys Leu Leu Leu Val Ser Val Phe Lys Tyr
 325 330 335

Ile Ala Glu His Phe Asp Lys Arg Val Asn Ala Thr Met Tyr Leu Leu
 340 345 350

Gly Tyr Gln Ala Met Leu Tyr Val Gly Asn Val Val Ile Ser Ser Pro
 355 360 365

Ala Gly Tyr Met Tyr Asp Arg Ile Gly Phe Glu Gln Thr Tyr Ile Ile
 370 375 380

Met Gly Ala Thr Ala Leu Thr Phe Thr Leu Leu Ser Ala Phe Thr Leu
 385 390 395 400

Ser Ala Cys Gln Ser Lys Trp Arg Gly Thr Ser Ala Ile Ser Val Ala
 Page 166

Glu Gln Asn Pro Ser Arg
420

<210> 109
<211> 1260
<212> DNA
<213> Citrobacter koseri

<400> 109
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tcagaaaaga taggccttga tgggtgttgcg attggtattg tttttgccgc aaacggcttt 180
tgtgcggtac taatcaaacc tgtatatggg tttcttatcg atcggctagg gttaaggaaa 240
gatctgttat tctttatctc gcttatctcg ataaccgttt tccccctttt cttttatata 300
tacaaaccac tattgcagtc tgcgttgtat gctgggtattg cgttggggcg tatattttta 360
agtatgggat actacgcagg gtgtgcagcc gcagaatcat accttgatcg ctttgccgt 420
ttgtttgatc ttgagtttgg tcaaaccgc atgtggggcg cgattggttc tgtattctct 480
gctgcaagta caggctatat ttttaatat aaccaatga tcaatttcgg gttaagttcc 540
gcagggtgcg tgataattct tattattgtt ttacgatga agatcgaagt caatgaagag 600
gtaaaaaatc gcatcattgc taaagataaa gcgacaatat acgatattat agcattatct 660
agcacacgca atttctggac gtttgtttta tatgtttgtg gtgttgtgtg gattatcttt 720
gtcgcagaac aacaatatcc acgtttcttt atcacatttt atgccagtaa agaaatcggg 780
catcaaatgt ttggttatct tgggtctgcc agtctgggag tagagtttct gttcatgatg 840
attgcacctg gcattgtcaa ccgtctgggg ccaaaaaccg gcttgctgat tacaggcttt 900
gttggtggccg ctagatttat tggttctggt ttggttacia gtgcaataac aattggaatt 960
atcaaattgt cgtgggggat agaaatgtca ttcctgttgg tttcaatttt caaatatctg 1020
gaaattaact ttgataaaaa agtaaatggt tcaatgtatt tattaggcta tcaaagcgtt 1080
aactatatcg gaacagttat cttgtcgccg ttgagtgggt acttgatga gcgattaggt 1140
ttttcacata catatcttat gatgggatgt acagtattgt ttttcactat tatatccgca 1200
tttcttcttc aaaataacaa acgaacagaa ccagtcattg cggagaatgc gcatgcttga 1260

<210> 110
<211> 577
<212> PRT
<213> Citrobacter koseri

<400> 110

Met Arg Met Leu Glu Arg Asn Met Leu Arg Glu Asn Ile Ile Asp Lys
1 5 10 15

Leu Tyr Asp Val Leu Asp Ser Val Val Asn Arg Thr Ile Asn Lys Glu
Page 167

20

25

30

Gln Ser Phe Gly Val Val Leu Thr Leu Asp Asp Asp Pro Tyr Ala Ser
 35 40 45

Gly Lys Phe Ala Leu Ala Leu Ser Phe Leu Ile Glu Arg Phe Pro Ala
 50 55 60

Arg Ala Asp Gln Trp Ser Gly Val Trp His Glu Leu Val Lys Ala Pro
 65 70 75 80

Ser Glu Asn Trp Gly Lys Tyr Tyr Phe Leu Gln Ala Leu Trp Lys Leu
 85 90 95

His Cys Leu Gly Leu Leu Asn Thr Ile Phe Ser Asp Gln Gln Leu Gln
 100 105 110

Arg Leu Thr Glu Lys Leu Arg Trp Gln Glu Leu Val Asp Glu Glu Ser
 115 120 125

Trp Lys Leu Asn Pro Pro Phe Pro Thr Asn Tyr Tyr Gly Val Ala Phe
 130 135 140

Ser Ile Ala Arg Leu Arg Phe Leu Leu Gly Trp Glu Thr Gln Phe Ala
 145 150 155 160

Ser Gln Lys Ile Leu Gln Gln Leu Val Glu His Tyr Arg Thr Tyr Ser
 165 170 175

Gln His Gly Cys Val Asp Glu Thr Glu Gly Lys Gly Arg Phe Asp Arg
 180 185 190

Tyr Ser Ile Leu Leu Ile Ala Glu Ile Cys Gln Arg His Ile Asp Thr
 195 200 205

Gly Leu Glu Ile Cys Asp Trp Leu Lys Asp Ala Leu Arg Gln Val Ser
 210 215 220

Thr Leu Ile Leu Ala Met Leu Asn Asp Glu Gly Val Gly Phe Leu Trp
 225 230 235 240

Gly Arg Ser Ile Gly Ala Tyr Gly Asp Ser Ala Phe Asn Glu Ile Leu
 245 250 255

Thr Ile Ser Met Arg Leu Gly Leu Leu Asp Arg Gln Glu Cys Ala Ala
 260 265 270

Ala Ser Arg Phe Thr Leu Ala Cys Ser Glu Arg Phe Leu Asn Phe Trp
 275 280 285

Tyr Asp Ser Asn Glu Gln Ser Val Asn Leu Trp Phe Tyr Gly Arg Gln
 Page 168

290

295

300

Thr Asp Ala Tyr Arg Ala Glu His Arg Leu Val Gly Glu Asn Ile Ser
305 310 315 320

Leu Ser Cys Gln His Leu Cys Val Gln Arg Ala Trp Ala Asp Val Ser
325 330 335

Phe Asp Ala Thr Pro Phe Val Leu Pro Glu Gln Thr Leu Lys Phe Thr
340 345 350

Pro Phe Cys Asn Asp Lys Tyr Thr Arg Gly Leu Phe His Trp Tyr Asp
355 360 365

Gly Lys Arg Leu Phe Val Leu Pro Leu Ile Asn Gly Asp Lys His Tyr
370 375 380

Phe Ala Thr Ser Pro Tyr Phe Pro Val Pro Phe Ser Ala Gly Leu Ile
385 390 395 400

Thr Gly Val Ala Gln Gly His Ala Pro Leu Trp Val Pro Gly Leu Val
405 410 415

Asp Ser Arg Gly Cys Ile Leu Arg Pro Leu Val Trp Phe Gly Asp Cys
420 425 430

Gly Tyr Gln Lys Thr Lys Asn Gly Trp Glu Ile Glu Ile Asn Tyr Ser
435 440 445

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

Lys Asp Tyr Ser Cys Gln Cys Arg Thr Arg Tyr Phe Ile Glu Pro Ser
465 470 475 480

Thr Leu Thr Arg Val Asp Thr Phe Ser Phe Leu Lys His Ser Glu Met
485 490 495

Tyr Leu Glu Leu Gln Cys Ala Val Phe Pro Glu Lys Met Arg Met Ile
500 505 510

His Ser Ala Asp Ser Leu His Ile Asp Tyr Glu Ser Asn Gly Ile Gln
515 520 525

Ser Leu Glu Leu Asn Gly Phe Glu Asp Tyr Cys Val Glu Arg Thr Ala
530 535 540

Leu Cys Ser Pro Tyr Gly Ala Leu Gly Gln Gln Ile Thr Gly Arg Arg
545 550 555 560

Asp Val Ser Gly Ala Lys Asp Val Thr Val Ser Trp Gln Ile Cys Tyr
Page 169

Cys

<210> 111
<211> 1242
<212> DNA
<213> Bacillus megaterium

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<400> 111
atgaaaagtt caaaaagttt atattggaag ctgagtgcac attttttctt cttctttttt      60
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ggatcagcaa caggcttaat cttttctgtg aacgctatct ttgctttgtg tatgcagcct      180
ttgtacggat atatatctga caggataggt ttaaagaaac acgttttatt ttttattagc      240
tgtcttttag tgttttagg accattttat atttttgttt atggaccttt gcttcaatac      300
aatgtggtga taggggctat tattggaggc ttatatattag gagtagcggt tttggcgggc      360
atcggagcga ttgaaacata catagagaaa gtcagccgaa aatataaatt tgagtatgga      420
aaatctagaa tgtgggggtc attaggctgg gctgcagcta cgttttttgc aggacaatta      480
tttaatatta atcctcacat taatttttgg gtggcatctg tttcagcggg tatcctagtc      540
gctattattt tttctgtaaa agtagaaatg agcagttatg aaatggaaaa agctgaatcc      600
gtcacgctaa gagatgtagg tagttttattt ttattgaagg aattttgggt ttttatgatt      660
tatgtttgtt gtgttacatg cgtatatggg gtatacgatc agcaatttcc tatctattat      720
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caagtatttt tagaagctgg aatgatgttc gcagcaccgt ttattgtaaa taagatcggt      840
gcaaaaaata gtttaatttt agcaggattt ctaatgggat ttcgtattat tggggtcaggg      900
cttggtgttg gtccaatcgg aatatcttca atgaaactca ttcattgcatt agaacttcct      960
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atcctttatt tggttggatt ccaatttgct tcgcaaatag gtgcttcagt tctttcacc     1080
atagtgggag gattatatga tagcgtaggt ttttcccgtc cctatttaat tatgggaggt     1140
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tttataagaa aagatgtaca agaaaacacg cagattatat ag                        1242
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<210> 112
<211> 413
<212> PRT
<213> Bacillus megaterium

<400> 112

Met Lys Ser Ser Lys Ser Leu Tyr Trp Lys Leu Ser Ala Tyr Phe Phe
1 5 10 15

Phe Phe Phe Phe Thr Trp Ser Ser Ser Tyr Ser Leu Phe Ser Ile Trp
Page 170

Leu Gly Gln Glu Ile Lys Leu Asn Gly Ser Ala Thr Gly Leu Ile Phe
 35 40 45
 Ser Val Asn Ala Ile Phe Ala Leu Cys Met Gln Pro Leu Tyr Gly Tyr
 50 55 60
 Ile Ser Asp Arg Ile Gly Leu Lys Lys His Val Leu Phe Phe Ile Ser
 65 70 75 80
 Cys Leu Leu Val Phe Val Gly Pro Phe Tyr Ile Phe Val Tyr Gly Pro
 85 90 95
 Leu Leu Gln Tyr Asn Val Val Ile Gly Ala Ile Ile Gly Gly Leu Tyr
 100 105 110
 Leu Gly Val Ala Phe Leu Ala Gly Ile Gly Ala Ile Glu Thr Tyr Ile
 115 120 125
 Glu Lys Val Ser Arg Lys Tyr Lys Phe Glu Tyr Gly Lys Ser Arg Met
 130 135 140
 Trp Gly Ser Leu Gly Trp Ala Ala Ala Thr Phe Phe Ala Gly Gln Leu
 145 150 155 160
 Phe Asn Ile Asn Pro His Ile Asn Phe Trp Val Ala Ser Val Ser Ala
 165 170 175
 Val Ile Leu Val Ala Ile Ile Phe Ser Val Lys Val Glu Met Ser Ser
 180 185 190
 Tyr Glu Met Glu Lys Ala Glu Ser Val Thr Leu Arg Asp Val Gly Ser
 195 200 205
 Leu Phe Leu Leu Lys Glu Phe Trp Phe Phe Met Ile Tyr Val Val Gly
 210 215 220
 Val Thr Cys Val Tyr Gly Val Tyr Asp Gln Gln Phe Pro Ile Tyr Tyr
 225 230 235 240
 Ala Ser Leu Phe Pro Thr Glu Ser Ile Gly Asn Gln Val Phe Gly Tyr
 245 250 255
 Leu Asn Ser Phe Gln Val Phe Leu Glu Ala Gly Met Met Phe Ala Ala
 260 265 270
 Pro Phe Ile Val Asn Lys Ile Gly Ala Lys Asn Ser Leu Ile Leu Ala
 275 280 285
 Gly Phe Leu Met Gly Phe Arg Ile Ile Gly Ser Gly Leu Val Val Gly
 Page 171

290

Pro Ile Gly Ile Ser Ser Met Lys Leu Ile His Ala Leu Glu Leu Pro
305 310 315 320

Ile Met Leu Ile Ala Ile Phe Lys Tyr Leu Ala Ala Asn Phe Asp Thr
325 330 335

Arg Leu Ser Ser Ile Leu Tyr Leu Val Gly Phe Gln Phe Ala Ser Gln
340 345 350

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

Val Gly Phe Ser Arg Thr Tyr Leu Ile Met Gly Gly Met Val Leu Val
370 375 380

Phe Asn Val Ile Ser Met Phe Thr Leu Leu Asn Ser Lys Lys His Arg
385 390 395 400

Phe Ile Arg Lys Asp Val Gln Glu Asn Thr Gln Ile Ile
405 410

<210> 113
<211> 1263
<212> DNA
<213> Providencia rustigianii

<400> 113
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gtgggcttaa aggggacgga tacgggaatt atcttctcgg tgatcagttt aaccgcattc 180
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tggtacattg gtgtgatgct ggtgatcagt ggtccatggt ttatttttgt ttgtactcca 300
ttgttacgtt ggaatatttt cctcggatca atcagtttag gcgtgtatgt cggggcaacg 360
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gccggtatct tattcaatat taatccaaat tataatttcg cgatgggatc ggtatccgca 540
ttaattttca tcattttatt atggagatta agtgatgttc gtcctcaagc gatgaatgag 600
ctggaatttg gtaaaagtaa tgcactaaaa ctgtcagatg ccttgggggt actcaaaatg 660
cgttcatttt ggtctctggt cgtttttgtg tgtggcgta gcgtttataa cgtatatgac 720
caacaattcc caatctattt tgcctcacta tttagtgaac aaagtcatgg taatgaaatg 780
tttggttacc tgaattcact gcaagttttt ctagaagcag gcggcatggt tttagcccca 840
ttcttagtca accgaattgg cgccaagaat ggattactcc tcagtggatt tgtaatggcg 900
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CL5510WOPCT_SeqListing_ST25.txt

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cttcatgccg ttgaacttcc taccctactg atatctttat ttaaataatat cactacagtt 1020
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acctatatga ttttggcggg tattgtcttt acgttaacca ttatttcttg tgtgctgctg 1200
aaatctgaaa acagctcaaa agttcacaat gtcagtattc agaaaaaac ggtagaacta 1260
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```

<210> 114
<211> 420
<212> PRT
<213> Providencia rustigianii
<400> 114

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

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CL5510WOPCT_SeqListing_ST25.txt

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

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

Ser Leu Val Val Phe Val Cys Gly Val Ser Val Tyr Asn Val Tyr Asp
225 230 235 240

Gln Gln Phe Pro Ile Tyr Phe Ala Ser Leu Phe Ser Glu Gln Ser His
245 250 255

Gly Asn Glu Met Phe Gly Tyr Leu Asn Ser Leu Gln Val Phe Leu Glu
260 265 270

Ala Gly Gly Met Phe Leu Ala Pro Phe Leu Val Asn Arg Ile Gly Ala
275 280 285

Lys Asn Gly Leu Leu Leu Ser Gly Phe Val Met Ala Leu Arg Ile Leu
290 295 300

Gly Ser Gly Leu Ala Asp Asp Thr Ile Thr Ile Ser Phe Met Lys Leu
305 310 315 320

Leu His Ala Val Glu Leu Pro Ile Leu Leu Ile Ser Leu Phe Lys Tyr
325 330 335

Ile Thr Thr Val Phe Asp Lys Arg Leu Ser Ala Thr Ile Tyr Leu Val
340 345 350

Gly Phe Gln Phe Ile Ala Ser Leu Cys Ala Thr Val Leu Ser Pro Leu
355 360 365

Ala Gly Ile Ser Tyr Asp Arg Ile Gly Phe Ala Asp Thr Tyr Met Ile
370 375 380

Leu Ala Gly Ile Val Phe Thr Leu Thr Ile Ile Ser Cys Val Leu Leu
385 390 395 400

Lys Ser Glu Asn Ser Ser Lys Val His Asn Val Ser Ile Gln Lys Lys
405 410 415

Thr Val Glu Leu
420

<210> 115
<211> 1266
<212> DNA
<213> Providencia alcalifaciens

<400> 115
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Page 174

CL5510WOPCT_SeqListing_ST25.txt

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tgtgcacagc ctctgtatgg atttattcag gacagactcg gtttacgcaa aaatttatta 240
tggtttctgg gtgggttggt attaatcagt ggaccttggg ttatttttgt ctgtactccg 300
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```

<210> 116
<211> 421
<212> PRT
<213> Providencia alcalifaciens

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<400> 116
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Met Gly Lys Lys Thr Arg Ala Asn Ile His Ala Tyr Leu Thr Leu Ser
1 5 10 15
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Gly Leu Leu Phe Thr Phe Phe Trp Thr Trp Ser Ser Val Phe Ser Leu
20 25 30
```

```
Val Ser Leu Trp Leu Ser Gln Lys Ile Gly Leu Lys Gly Thr Asp Thr
35 40 45
```

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Gly Ile Ile Phe Ser Val Ile Ser Leu Thr Ala Phe Cys Ala Gln Pro
50 55 60
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```
Leu Tyr Gly Phe Ile Gln Asp Arg Leu Gly Leu Arg Lys Asn Leu Leu
Page 175
```

65 70 75 80
 Trp Phe Leu Gly Gly Leu Leu Leu Ile Ser Gly Pro Trp Phe Ile Phe
 85 90 95
 Val Cys Thr Pro Leu Leu Lys Trp Asn Ile Phe Ala Gly Ala Ala Ala
 100 105 110
 Leu Gly Ile Tyr Val Gly Ala Thr Phe Phe Ala Gly Ile Gly Ala Leu
 115 120 125
 Glu Ser Tyr Thr Glu Arg Val Ser Arg Ile Ala Ser Phe Glu Tyr Gly
 130 135 140
 Arg Ala Arg Met Trp Gly Ser Leu Gly Trp Ala Gly Ala Thr Phe Phe
 145 150 155 160
 Ala Gly Leu Leu Phe Asn Ile Asp Pro Asn Leu Asn Phe Ala Met Gly
 165 170 175
 Ser Val Ser Ala Leu Leu Phe Ile Ile Leu Leu Trp Arg Leu Arg Asn
 180 185 190
 Val Arg Pro His Thr Met Asn Glu Leu Glu Phe Gly Lys Thr Gln Ser
 195 200 205
 Leu Thr Val Ser Asp Ala Leu Gly Leu Leu Arg Met Arg Ser Phe Trp
 210 215 220
 Ser Leu Val Ile Phe Val Cys Gly Val Ser Val Tyr Asn Val Tyr Asp
 225 230 235 240
 Gln Gln Phe Pro Val Tyr Phe Ala Ser Leu Phe Ala Asn Gln Asn Glu
 245 250 255
 Gly Asn Glu Met Phe Gly Tyr Leu Asn Ser Leu Gln Val Phe Leu Glu
 260 265 270
 Ala Gly Gly Met Phe Leu Ala Pro Phe Leu Val Asn Arg Ile Gly Ala
 275 280 285
 Lys Arg Gly Leu Leu Leu Ser Gly Leu Ile Met Ala Leu Arg Ile Leu
 290 295 300
 Gly Ser Gly Leu Ala Asp Asp Ala Ile Thr Ile Ser Phe Met Lys Leu
 305 310 315 320
 Leu His Ala Val Glu Leu Pro Ile Leu Leu Ile Ser Leu Phe Lys Tyr
 325 330 335
 Ile Thr Ser Val Phe Asp Lys Arg Leu Ser Ala Thr Ile Tyr Leu Val
 Page 176

340

345

350

Gly Phe Gln Phe Thr Ala Ser Leu Cys Ala Ser Phe Leu Ser Pro Leu
 355 360 365

Ala Gly Tyr Gly Tyr Asp Thr Leu Gly Phe Ala Asp Thr Tyr Met Ile
 370 375 380

Leu Ala Ala Ile Val Ile Ser Met Thr Ile Ile Ser Ser Val Leu Leu
 385 390 395 400

Gln Ser Glu Asn Thr Ser Thr Val Ser Asn Pro Met Thr Thr Ser Lys
 405 410 415

Lys Thr Val Glu Leu
 420

<210> 117
 <211> 1371
 <212> DNA
 <213> Serratia odorifera

<400> 117
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 ctgtggcagg tgcgagagct gaaacccaac gccatggccg gggttgaata cggcaaaccg 720
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 ccgattctgc tggtagccat gttcaaatac atcaccaccc gcttcgacag ccgcctgtcc 1140
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CL5510WOPCT_SeqListing_ST25.txt

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 cgcgcacctc aatttcaatc cacgataaaa tcaagtgagc caatccaatg a 1371

<210> 118
 <211> 456
 <212> PRT
 <213> Serratia odorifera

<400> 118

Met Leu Thr Leu Thr Phe Val Ile Asn Ile Ala Ile Pro Asp Val Gly
 1 5 10 15

Gly Phe Ile Trp Pro Lys Val Asn Val Asn Asn Lys Ala Asp Ile Ile
 20 25 30

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

Leu Ser Gly Leu Leu Phe Phe Phe Phe Thr Trp Ser Ala Ser Phe
 50 55 60

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

Glu Thr Gly Leu Ile Phe Ser Ala Met Ser Ile Met Ala Leu Cys Val
 85 90 95

Gln Pro Leu Tyr Gly Phe Val Gln Asp Lys Leu Gly Leu Arg Lys His
 100 105 110

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

Ile Tyr Val Tyr Ala Pro Leu Leu Gln Thr Asn Leu Val Ala Gly Ala
 130 135 140

Leu Val Gly Gly Leu Phe Val Ser Leu Ala Phe Asn Ala Gly Ile Gly
 145 150 155 160

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

Phe Gly Arg Ala Arg Met Trp Gly Ser Leu Gly Trp Ala Ser Ala Thr
 180 185 190

Phe Phe Ala Gly Phe Ile Tyr Asn Ile Asn Pro Asn Ile Asn Phe Trp
 195 200 205

Ile Ala Ser Ala Ser Ala Ala Val Phe Leu Leu Leu Leu Trp Gln Val
 Page 178

210

215

220

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

Glu Asn Leu Lys Leu Gln Asp Ala Leu Ala Leu Leu Arg Leu Pro Gly
 245 250 255

Phe Trp Ala Leu Val Val Phe Val Leu Gly Thr Ser Ile Tyr Gly Val
 260 265 270

Phe Asp Gln Gln Phe Pro Val Tyr Phe Ala Ser Gln Phe Ala Thr His
 275 280 285

Glu Glu Gly Asn Arg Met Tyr Gly Phe Leu Asn Ser Leu Gln Val Phe
 290 300

Leu Glu Ala Gly Gly Met Phe Leu Ala Pro Leu Leu Val Asn Arg Ile
 305 310 315 320

Gly Ile Lys Gln Ser Leu Leu Leu Ala Ser Ser Val Met Ala Phe Arg
 325 330 335

Met Phe Gly Ser Gly Phe Ala Asn Gly Ala Leu Met Ile Ser Ala Met
 340 345 350

Lys Leu Leu His Ala Val Glu Leu Pro Ile Leu Leu Val Ala Met Phe
 355 360 365

Lys Tyr Ile Thr Thr Arg Phe Asp Ser Arg Leu Ser Ser Thr Leu Tyr
 370 375 380

Leu Val Gly Phe Gln Phe Ile Ser Gln Ile Val Ala Gly Ile Leu Ala
 385 390 395 400

Pro Leu Ala Gly Leu Gly Tyr Asp Arg Ile Gly Phe Ala Asp Thr Tyr
 405 410 415

Leu Leu Met Gly Cys Ala Val Ala Gly Thr Thr Leu Val Ser Cys Phe
 420 425 430

Leu Leu Arg Gly Glu Thr Pro Ala Arg Ala Pro Gln Phe Gln Ser Thr
 435 440 445

Ile Lys Ser Ser Glu Pro Ile Gln
 450 455

<210> 119
 <211> 1314
 <212> DNA
 <213> Streptomyces albus

CL5510WOPCT_SeqListing_ST25.txt

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<400> 119
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ctctcctggg cactcttctc catctggctg acccaggaca tcggcctgag cccggggccgc      180
agttcgctgg tgatcggcgc caactcgctc ggctgcctgg tcacgatgcc ggtctacggc      240
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ccgaagaagt ccctgctggg ctccggctgc gtcattggcg cccggatctt cctctccggc      960
atcgtcacgg acccggtcgc gatctcggcg gtgaagctcc tgcacgccgt cgaactgccc     1020
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ctggtggcca cttcacctt ggtctcggtc ttcacctgc gcgccgacgc caagggcacg     1260
cacgggctgc ccgcgggtgg agccgccgag ggccgctccc cggcagcggg ctga           1314

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<210> 120
<211> 437
<212> PRT
<213> Streptomyces albus

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<400> 120
Met Thr Val Gln Ser Pro Ala Ala Pro Ser Pro Ala Ala Ala Val Pro
1          5          10         15

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

Phe Met Phe Phe Val Thr Trp Ser Leu Ser Trp Ser Leu Phe Ser Ile
35         40         45

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

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CL5510WOPCT_SeqListing_ST25.txt

Ile Gly Ala Asn Ser Leu Gly Cys Leu Val Thr Met Pro Val Tyr Gly
65 70 75 80

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

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

Pro Leu Leu Lys Ser His Phe Ala Leu Gly Leu Val Val Gly Ser Ala
115 120 125

Tyr Leu Ala Met Ala Phe Ala Val Ala Val Ala Thr Leu Glu Ser Tyr
130 135 140

Ala Glu Arg Leu Ser Arg Phe His Gly Phe Glu Phe Gly Arg Ala Arg
145 150 155 160

Met Phe Gly Ser Leu Gly Trp Ala Ala Ala Thr Phe Leu Ala Gly Arg
165 170 175

Leu Phe Asn Ile Asp Pro Asp Leu Thr Phe Trp Ala Ala Ser Gly Thr
180 185 190

Ala Val Val Phe Val Gly Leu Leu Val Ala Ile Arg Val Thr Asp Gly
195 200 205

Arg Arg Ala Ala Ala Val Asp His Ala Ala Ala Ser Val Ser Leu Ala
210 215 220

Asp Val Ala Ala Leu Leu Arg Tyr Pro Ala Phe Trp Gly Leu Leu Leu
225 230 235 240

Phe Val Val Ala Val Thr Ala Thr Tyr Asn Thr Tyr Asp Ala Met Phe
245 250 255

Pro Ser Tyr Phe Ser Ser Leu Phe Ala Thr Asp Ala Asp Gly Asn Arg
260 265 270

Met Tyr Ser Asp Leu Asn Ser Val Gln Val Phe Leu Glu Ala Gly Gly
275 280 285

Met Ala Leu Ala Pro Phe Leu Val Asn Arg Leu Gly Pro Lys Lys Ser
290 295 300

Leu Leu Val Ser Gly Cys Val Met Ala Thr Arg Ile Phe Leu Ser Gly
305 310 315 320

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

CL5510WOPCT_SeqListing_ST25.txt

Val Glu Leu Pro Ile Met Leu Ile Ala Ile Phe Lys Tyr Val Asn Arg
340 345 350

His Phe Glu Pro Arg Leu Ser Ser Thr Ile Tyr Leu Ile Gly Phe Gln
355 360 365

Met Ala Thr Gln Val Gly Ala Ala Val Ile Ser Pro Leu Ala Gly Leu
370 375 380

Gly Tyr Asp Arg Leu Gly Tyr Ala Pro Thr Tyr Leu Val Met Ser Ala
385 390 395 400

Leu Val Ala Thr Phe Thr Leu Val Ser Val Phe Thr Leu Arg Ala Asp
405 410 415

Ala Lys Gly Thr His Gly Leu Pro Ala Val Gly Ala Ala Glu Gly Arg
420 425 430

Ser Pro Ala Ala Gly
435

<210> 121
<211> 1284
<212> DNA
<213> Azobactervinelandii

<400> 121
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atcgagggtg cgatcctggt ggtcgcgggt ttcaagtaca tctgcgtcaa cttcgatcgc 1020

CL5510WOPCT_SeqListing_ST25.txt

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 ctgctggcca gtctggtcgg cgcctgcctg ctgctgtcct ggctcgtgct gcgcgccgac 1200
 ccgtccagca agaccacccg ggcggcggac ggcgccccgg aactgccggc catcgcccag 1260
 gcggccaacc attacgaacc ctga 1284

<210> 122
 <211> 427
 <212> PRT
 <213> *Azobacter vinelandii*

<400> 122

Met His Leu Pro Leu Lys Arg Glu Tyr Trp Leu Ile Ser Gly Leu Leu
1 5 10 15

Phe Phe Phe Phe Phe Ala Trp Ser Ser Tyr Ser Leu Phe Ser Ile
20 25 30

Trp Leu His Arg Val Ile Gly Leu Ser Gly Thr Glu Thr Gly Phe Ile
35 40 45

Phe Ala Ala Asn Ala Ile Ala Ala Leu Phe Ile Gln Pro Phe Tyr Gly
50 55 60

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

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

Gly Leu Leu Ala His Asp Val Val Leu Gly Ala Leu Val Gly Ala Ala
100 105 110

Phe Leu Ala Phe Ala Met Leu Ala Gly Val Gly Val Ile Glu Ser Tyr
115 120 125

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

Met Trp Gly Ser Leu Gly Trp Ala Ala Ala Thr Gly Val Ala Gly Val
145 150 155 160

Val Phe Asp Ile Asp Pro Asp Ile Ala Phe Tyr Met Ser Ser Ala Ala
165 170 175

Gly Leu Ala Phe Leu Leu Ile Leu Ser Arg Leu Asp Met Asp Ala Phe
180 185 190

Arg Asn His Glu Thr Arg Ala Gly Glu Ser Ala Pro Val Arg Thr Ala
Page 183

195

200

205

Asp Ile Leu Gln Leu Leu Arg Leu Pro Arg Phe Trp Ala Phe Ser Leu
 210 215 220

Phe Leu Thr Gly Val Ala Gly Val Tyr Met Ile Tyr Glu Gln Gln Phe
 225 230 235 240

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

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

Met Leu Val Ala Pro Trp Val Val Ala Arg Thr Gly Ala Lys Tyr Gly
 275 280 285

Leu Leu Leu Ala Gly Thr Ile Met Phe Val Arg Ile Leu Gly Ser Gly
 290 295 300

Leu Ala Ser Asp Ala Trp Thr Ile Ala Ala Cys Lys Met Leu His Ala
 305 310 315 320

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

Asn Phe Asp Ala Arg Leu Ser Ala Thr Leu Tyr Leu Val Ser Phe Gln
 340 345 350

Phe Ala Gln Gln Leu Thr Ala Met Leu Leu Ser Pro Ala Val Gly Tyr
 355 360 365

Gly Tyr Asp Arg Leu Gly Phe Ala Ser Val Tyr Leu Leu Leu Ala Ser
 370 375 380

Leu Val Gly Ala Cys Leu Leu Leu Ser Trp Ser Leu Leu Arg Ala Asp
 385 390 395 400

Pro Ser Ser Lys Thr Thr Arg Ala Ala Asp Gly Ala Pro Glu Leu Pro
 405 410 415

Ala Ile Ala Gln Ala Ala Asn His Tyr Glu Pro
 420 425

<210> 123
 <211> 1278
 <212> DNA
 <213> Oenococcus oeni

<400> 123
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tttcattct ctactttac ctatTTTTTT atttggcaaa tcattaacgg ttattttaact 120
 Page 184

CL5510WOPCT_SeqListing_ST25.txt

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ctatggatgg aacagatagg acacctaaat ggtgcagaag ctggagttgt attttctatg      180
atggctggat tttctctcat ttttcaacca tcatttggaa ttatttccga taaattaatt      240
tttaagaaaa atttgattct gacaatttca atcgctggaa tcttgattgg accatatttt      300
cagtggcttt tcctaccgtt aatgaaaata aactcaacat tcgttgctat tattactggt      360
atttttttta gtttcatttt gaatggtggc gttagcgtaa tagaacaata tgttcaaaga      420
gcaagtctcg ctaaccattt tgaatacggg cattcaagaa tgggtggatc tttggcagga      480
atgtgtgcct cttttcttgg tgggcaacta tttttgtgga gtcctaattc tatttttttg      540
gcctgcacta tttcagcaat gatccttaca ggcttgttat tatttaatga caagatccat      600
atggaaaatg caaatcttgc cggtggaact tccagtcgtt taaacctaaa acagatctct      660
tcaatattta aaataaagaa tttttggttc ctctcactat tttatattgg cacggcctct      720
atttacgata tctttgatca gcaatttatt atatttttta aatctttttt tgataccgca      780
tcacaaggaa cagctgccta tagttatatg acaactgcgc agattggtat cgaatttata      840
cttatgtttc caatgccttg gataattaat cgaattggag cgcgtaatgg cctaatagca      900
tatggaacaa ttttagctat tagaattatt ggtagtgcac tatctccaaa tcttttttgg      960
gttattttgc tacgcttgct ggctggatta gaaatgcctc ttatcctagt ttcaatcatg     1020
aaatatatat cgggtgcctt tgaccttcgc ctttatgcca ctatatatgc gctgtcatca     1080
aactttgcaa aacaaataac tgaattcttt ttagcaactg ctgcaggaaa aatgtatgat     1140
tcaatcggct ttcaccatac ttatttaatt cttggagtca tcgtcgcaat ctttacgatt     1200
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ggaaacccca aagcttaa                                     1278

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<210> 124
<211> 425
<212> PRT
<213> Oenococcus oeni
<400> 124

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

Gln Ile Ile Asn Gly Tyr Leu Thr Leu Trp Met Glu Gln Ile Gly His
          35          40          45

Leu Asn Gly Ala Glu Ala Gly Val Val Phe Ser Met Met Ala Gly Phe
          50          55          60

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

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CL5510WOPCT_SeqListing_ST25.txt

Phe Lys Lys Asn Leu Ile Leu Thr Ile Ser Ile Ala Gly Ile Leu Ile
 85 90 95
 Gly Pro Tyr Phe Gln Trp Leu Phe Leu Pro Leu Met Lys Ile Asn Ser
 100 105 110
 Thr Phe Val Ala Ile Ile Thr Gly Ile Phe Leu Ser Phe Ile Leu Asn
 115 120 125
 Gly Gly Val Ser Val Ile Glu Gln Tyr Val Gln Arg Ala Ser Leu Ala
 130 135 140
 Asn His Phe Glu Tyr Gly His Ser Arg Met Gly Gly Ser Leu Ala Gly
 145 150 155 160
 Met Cys Ala Ser Phe Leu Gly Gly Gln Leu Phe Leu Trp Ser Pro Asn
 165 170 175
 Ser Ile Phe Trp Ala Cys Thr Ile Ser Ala Met Ile Leu Thr Gly Leu
 180 185 190
 Leu Leu Phe Asn Asp Lys Ile His Met Glu Asn Ala Asn Leu Ala Gly
 195 200 205
 Gly Thr Ser Ser Arg Leu Asn Leu Lys Gln Ile Ser Ser Ile Phe Lys
 210 215 220
 Ile Lys Asn Phe Trp Phe Leu Ser Leu Phe Tyr Ile Gly Thr Ala Ser
 225 230 235 240
 Ile Tyr Asp Ile Phe Asp Gln Gln Phe Ile Ile Phe Phe Lys Ser Phe
 245 250 255
 Phe Asp Thr Ala Ser Gln Gly Thr Ala Ala Tyr Ser Tyr Met Thr Thr
 260 265 270
 Ala Gln Ile Gly Ile Glu Phe Ile Leu Met Phe Pro Met Pro Trp Ile
 275 280 285
 Ile Asn Arg Ile Gly Ala Arg Asn Gly Leu Ile Ala Tyr Gly Thr Ile
 290 295 300
 Leu Ala Ile Arg Ile Ile Gly Ser Ala Leu Ser Pro Asn Leu Phe Trp
 305 310 315 320
 Val Ile Leu Leu Arg Leu Leu Ala Gly Leu Glu Met Pro Leu Ile Leu
 325 330 335
 Val Ser Ile Met Lys Tyr Ile Ser Gly Ala Phe Asp Leu Arg Leu Tyr
 340 345 350

CL5510WOPCT_SeqListing_ST25.txt

Ala Thr Ile Tyr Ala Leu Ser Ser Asn Phe Ala Lys Gln Ile Thr Glu
 355 360 365

Phe Phe Leu Ala Thr Ala Ala Gly Lys Met Tyr Asp Ser Ile Gly Phe
 370 375 380

His His Thr Tyr Leu Ile Leu Gly Val Ile Val Ala Ile Phe Thr Ile
 385 390 395 400

Phe Thr Ala Leu Phe Leu Lys Lys Glu Asn Pro Val Gln Ala Gly Glu
 405 410 415

Arg Asp Arg Ala Gly Asn Pro Lys Ala
 420 425

<210> 125
 <211> 1290
 <212> DNA
 <213> Lactobacillus brevis

<400> 125
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 cacttaaacg ggaccgaatc tgggtgccgtc ttctcaatga tggcgggtat ttccttgatc 180
 ttccaaccta tctttggggg tgtttctgat aaattactct tcaagaaaaa cttaatctta 240
 acgattgcga tcgtcgggat cttcatcggg cttacttcc aatgggtctt catgcccac 300
 ttacacatta gcgccttctt agtagccatc gttactggga cttttctgag tttcatccta 360
 aacgggtgggg tgtccgcatc tgaacaatac gtacagcggg ctagtttggc taacggcttc 420
 gaatatgccc actcccgggt cgggtggttcc gtcgccgggtg tcgttgcttc attagttgcc 480
 gggcgaatct tcctctggaa gcctaactcc atcttctggg catgtaccat tgccgctatt 540
 atcttaactt tcttattact cttctctgac aagggttaact tagataacgc tgccgctgct 600
 ggtgacacgt ccgattcact tgatatgaag acggttctgt ctgtcttcaa acttaagaac 660
 ctctggggtt tagctatctt ctacatgggc gcttctgcct tattcgatgt atttgatcaa 720
 cagtttatca tcttctttaa gactttcttt gataccgctg ctacaggggac cctgggtttac 780
 tcttacatga gttctgctca aacagctatc gaattttggt taatgttccc aatgccatgg 840
 attatcaaca aaattgggtc tcgtaatggg ttgttaattt acggtttcat tacctgcatc 900
 cggatcttag gttctgcttt atctcctaac tggatctggg ttgttggttt ccgtttggtta 960
 gctgggtttg aaatgccatt gctattaact tccatcatga aatacattgc tgggtgccttt 1020
 gatattcggg tatacggcac gggttacgca ttggcgtcaa actttgctaa acaggtatcc 1080
 gtcttcatct tctccacagt tgctgggtcgg atgtatgacg ttatcgggta tcaacacacg 1140
 tacatcatca tggggatcgt ggtcttcttc attaccttgt ttgccgtctt cttcctgaag 1200
 aaagaagatc cgattcaagc cgggtgaagtc gaggatccta atgttaaagc taaagtggaa 1260

gcggcttctt caactgatag tcgtgaatga

1290

<210> 126
 <211> 429
 <212> PRT
 <213> Lactobacillus brevis

<400> 126

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

Thr Leu Trp Met Glu Gln Val Ala His Leu Asn Gly Thr Glu Ser Gly
 35 40 45

Ala Val Phe Ser Met Met Ala Gly Ile Ser Leu Ile Phe Gln Pro Ile
 50 55 60

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

Thr Ile Ala Ile Val Gly Ile Phe Ile Gly Pro Tyr Phe Gln Trp Val
 85 90 95

Phe Met Pro Ile Leu His Ile Ser Ala Phe Leu Val Ala Ile Val Thr
 100 105 110

Gly Thr Phe Leu Ser Phe Ile Leu Asn Gly Gly Val Ser Val Ile Glu
 115 120 125

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

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

Gly Arg Ile Phe Leu Trp Lys Pro Asn Ser Ile Phe Trp Ala Cys Thr
 165 170 175

Ile Ala Ala Ile Ile Leu Thr Phe Leu Leu Leu Phe Ser Asp Lys Val
 180 185 190

Asn Leu Asp Asn Ala Ala Ala Ala Gly Asp Thr Ser Asp Ser Leu Asp
 195 200 205

Met Lys Thr Val Leu Ser Val Phe Lys Leu Lys Asn Leu Trp Val Leu
 210 215 220

Ala Ile Phe Tyr Met Gly Ala Ser Ala Leu Phe Asp Val Phe Asp Gln
 Page 188

225 230 235 240

Gln Phe Ile Ile Phe Phe Lys Thr Phe Phe Asp Thr Ala Ala Gln Gly
245 250 255

Thr Leu Val Tyr Ser Tyr Met Ser Ser Ala Gln Thr Ala Ile Glu Phe
260 265 270

Cys Leu Met Phe Pro Met Pro Trp Ile Ile Asn Lys Ile Gly Ser Arg
275 280 285

Asn Gly Leu Leu Ile Tyr Gly Phe Ile Thr Cys Ile Arg Ile Leu Gly
290 295 300

Ser Ala Leu Ser Pro Asn Trp Ile Trp Val Val Gly Phe Arg Leu Leu
305 310 315 320

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

Ala Gly Ala Phe Asp Ile Arg Leu Tyr Ala Thr Val Tyr Ala Leu Ala
340 345 350

Ser Asn Phe Ala Lys Gln Val Ser Val Phe Ile Phe Ser Thr Val Ala
355 360 365

Gly Arg Met Tyr Asp Val Ile Gly Tyr Gln His Thr Tyr Ile Ile Met
370 375 380

Gly Ile Val Val Phe Phe Ile Thr Leu Phe Ala Val Phe Phe Leu Lys
385 390 395 400

Lys Glu Asp Pro Ile Gln Ala Gly Glu Val Glu Asp Pro Asn Val Lys
405 410 415

Ala Lys Val Glu Ala Ala Ser Ser Thr Asp Ser Arg Glu
420 425

<210> 127
<211> 1245
<212> DNA
<213> Weissella paramesenteroides

<400> 127
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agttatttct ttatttggca aattgtacaa ggtttcttgg tactttgggtt aaaacaagaa 120
gccgatttga gtggtggcca agccggattt gttttttcat ttttggcatt tgcctcatta 180
tttatcaac cagtatttgg tataatttcg gataaattgg tctttaaaaa gacgttgcta 240
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CL5510WOPCT_SeqListing_ST25.txt

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gcaggattgg tgtttgtaa aaatccattt ttggttttct ggatttgctc acttgctggt      540
attattttga cttgcttggg aatctttggg gatcggatta attttgctaa tgcagatgcg      600
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gatcaacagt tcccgggtatt ttatcaaaca ttcttcacga gtgctgcagc tgggtaccgta      780
gcctacagcc gcctactaac gacacaaatt gcgttagaag ccctattaat gattccaatg      840
ccttggataa ttaataaaat tgggtgctaag aatggattga ttgcttatgg tgtgcttact      900
tttctacgta ttacgttaag cgcaattgct cctaatttct ggttcttaac atttgttcgt      960
ctacttgcat catttgaaat gccactcttc ttagtctcaa caatgaagta tattgccgga     1020
gcatttgatt taagattata cgcaaccatt tatgctttgg cgttcaattt tgctaaacag     1080
atatcgttat ttattttctc tacagttgcc ggtgatcttt atgatagcgt gggattccat     1140
acgacatatt tcatcttagc tgcattagtc gctttggtaa caatcgttgc tgtatttatg     1200
ttgaagaaag aaaatccagc tcaggcgggt gaagtcgcgg agtga                       1245

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<210> 128
<211> 414
<212> PRT
<213> Weissella paramesenteroides

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<400> 128
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1           5           10           15
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Gly Thr Asp Val Ser Tyr Phe Phe Ile Trp Gln Ile Val Gln Gly Phe
20           25           30
```

```
Leu Val Leu Trp Leu Lys Gln Glu Ala Asp Leu Ser Gly Gly Gln Ala
35           40           45
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Gly Phe Val Phe Ser Phe Leu Ala Phe Ala Ser Leu Phe Tyr Gln Pro
50           55           60
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Val Phe Gly Ile Ile Ser Asp Lys Leu Val Phe Lys Lys Thr Leu Leu
65           70           75           80
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Leu Ser Ile Thr Ile Ala Ala Ile Leu Ile Gly Pro Phe Phe Gln Trp
85           90           95
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Leu Phe Ile Pro Leu Leu His Phe Ser Ser Leu Leu Gly Ala Ile Ile
100          105          110
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Gly Gly Phe Ala Leu Ala Tyr Val Leu Asn Gly Gly Val Ala Val Ile
Page 190

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115

120

125

Glu Ser Tyr Val Glu Arg Ala Ser Leu Ala Asn Gly Phe Glu Tyr Gly
 130 135 140

His Ala Arg Met Gly Gly Ser Ile Gly Gly Ala Leu Ala Ser Phe Val
 145 150 155 160

Ala Gly Leu Val Phe Val Lys Asn Pro Phe Leu Val Phe Trp Ile Cys
 165 170 175

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

Ile Asn Phe Ala Asn Ala Asp Ala Ala Glu Gly Ala Ser Ser Ala Pro
 195 200 205

Leu Asn Ala Lys Thr Ile Leu Ser Ile Phe Lys Ile Lys Asn Phe Trp
 210 215 220

Ile Leu Ser Ile Phe Phe Met Gly Thr Ser Ala Ile Tyr Asp Val Phe
 225 230 235 240

Asp Gln Gln Phe Pro Val Phe Tyr Gln Thr Phe Phe Thr Ser Ala Ala
 245 250 255

Ala Gly Thr Val Ala Tyr Ser Arg Leu Leu Thr Thr Gln Ile Ala Leu
 260 265 270

Glu Ala Leu Leu Met Ile Pro Met Pro Trp Ile Ile Asn Lys Ile Gly
 275 280 285

Ala Lys Asn Gly Leu Ile Ala Tyr Gly Val Leu Thr Phe Leu Arg Ile
 290 295 300

Thr Leu Ser Ala Ile Ala Pro Asn Phe Trp Phe Leu Thr Phe Val Arg
 305 310 315 320

Leu Leu Ala Ser Phe Glu Met Pro Leu Phe Leu Val Ser Thr Met Lys
 325 330 335

Tyr Ile Ala Gly Ala Phe Asp Leu Arg Leu Tyr Ala Thr Ile Tyr Ala
 340 345 350

Leu Ala Phe Asn Phe Ala Lys Gln Ile Ser Leu Phe Ile Phe Ser Thr
 355 360 365

Val Ala Gly Asp Leu Tyr Asp Ser Val Gly Phe His Thr Thr Tyr Phe
 370 375 380

Ile Leu Ala Ala Leu Val Ala Leu Val Thr Ile Val Ala Val Phe Met

385

390

395

400

Leu Lys Lys Glu Asn Pro Ala Gln Ala Gly Glu Val Ala Glu
 405 410

<210> 129

<211> 1278

<212> DNA

<213> Mannheimia succinicproduces

<400> 129

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acatgttatc ctttcttagg catttggttg ggagatatta acggtctgtc gggagaagat      180
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aatcctaata tggctttttg gcttggttct atagcctctc taatcctttt acttttgata      600
gccctagcta agccggaaca aaccagcact gtgcaaatcg cggagaaatt aggggctaata      660
aaaaatccgg ttaacctcag acaggcattc gctctcctca aactaccgaa attctgggcg      720
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gaagtccctt tttacctagt aggactatth aaatacattg ctaatgtggt tgaagtacat     1080
ttttctgcga ccatttatct ggtagcctgc cactttgcc aacagatcgg caatatgctg     1140
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ctaggctgca ttgccgccgg attcaccctg ctttcggttt ttacacttac cggcaaatcc     1260
ttatcgtctc aatcataa                                     1278

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<210> 130

<211> 425

<212> PRT

<213> Mannheimia succiniciproduces

<400> 130

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 1 5 10 15

CL5510WOPCT_SeqListing_ST25.txt

Asn Phe Tyr Leu Asn Asn Arg Asn Tyr Trp Ile Phe Ser Gly Tyr Phe
 20 25 30
 Phe Val Tyr Phe Phe Ile Met Ala Thr Cys Tyr Pro Phe Leu Gly Ile
 35 40 45
 Trp Leu Gly Asp Ile Asn Gly Leu Ser Gly Glu Asp Arg Gly Thr Val
 50 55 60
 Phe Ala Met Met Ser Phe Phe Ala Leu Cys Phe Gln Pro Val Phe Gly
 65 70 75 80
 Tyr Val Ser Asp Lys Leu Gly Leu Lys Lys His Leu Leu Trp Val Leu
 85 90 95
 Gly Ile Ser Leu Leu Ile Tyr Ala Pro Phe Phe Ile Tyr Ile Phe Ala
 100 105 110
 Pro Leu Leu Lys Val Asn Val Trp Leu Gly Ser Leu Val Gly Gly Ala
 115 120 125
 Tyr Ile Gly Phe Val Phe Gln Ala Gly Ala Pro Ala Ser Glu Ala Tyr
 130 135 140
 Ile Glu Arg Val Ser Arg Arg Ser Lys Phe Glu Tyr Gly Arg Val Arg
 145 150 155 160
 Met Phe Gly Met Phe Gly Trp Ala Ile Cys Ala Ser Ile Ala Gly Val
 165 170 175
 Leu Tyr Ala Thr Asn Pro Asn Leu Val Phe Trp Leu Gly Ser Ile Ala
 180 185 190
 Ser Leu Ile Leu Leu Leu Leu Ile Ala Leu Ala Lys Pro Glu Gln Thr
 195 200 205
 Ser Thr Val Gln Ile Ala Glu Lys Leu Gly Ala Asn Lys Asn Pro Val
 210 215 220
 Asn Leu Arg Gln Ala Phe Ala Leu Leu Lys Leu Pro Lys Phe Trp Ala
 225 230 235 240
 Leu Leu Ala Tyr Val Met Gly Ile Ala Cys Val Tyr Asp Ile Phe Asp
 245 250 255
 Gln Gln Phe Gly Asn Phe Phe Asn Thr Phe Phe Glu Ser His Glu Gln
 260 265 270
 Gly Ile Lys Met Phe Gly Tyr Val Thr Thr Ala Gly Glu Leu Leu Asn
 275 280 285

CL5510WOPCT_SeqListing_ST25.txt

Ala Leu Ile Met Phe Phe Val Pro Leu Ile Ile Asn Arg Ile Gly Ala
290 295 300

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

Gly Ser Ser Tyr Ala Ile Glu Ala Trp His Val Val Val Leu Lys Thr
325 330 335

Leu His Met Phe Glu Val Pro Phe Tyr Leu Val Gly Leu Phe Lys Tyr
340 345 350

Ile Ala Asn Val Phe Glu Val His Phe Ser Ala Thr Ile Tyr Leu Val
355 360 365

Ala Cys His Phe Ala Lys Gln Ile Gly Asn Met Leu Val Ser Pro Leu
370 375 380

Val Gly Ala Trp Tyr Asp Thr Tyr Gly Phe Gln Asp Thr Tyr Leu Ile
385 390 395 400

Leu Gly Cys Ile Ala Ala Gly Phe Thr Leu Leu Ser Val Phe Thr Leu
405 410 415

Thr Gly Lys Ser Leu Ser Ser Gln Ser
420 425

<210> 131
<211> 1257
<212> DNA
<213> Aggregatibacter aphrophilus

<400> 131
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tggctcgggtg atattcacgg attaaaagg gagaaaattg gctacgtctt ttcgttcatt 180
tctctttttg ctttactctt tcagcctatt ttaggatttt tatctgataa attaggtatt 240
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ggctccgcca ccgccgttgt gttattgggt ctgattttcc ttgcgaaaac agatagcagt 600
aatacggctc aagtcgtgga taaattaggt gtaaataaaa gtccaattac actaaaacaa 660
gccttaaagc tcttttctct acctcgtttc tgggcactat taacctatgt tgttggagtg 720
gcttgtgttt atgacatttt tgaccagcaa ttcggtaatt tcttcaatac gttttttgaa 780

CL5510WOPCT_SeqListing_ST25.txt

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gcaacaatta tgttttttcgt gccttttattg attaatcgta ttggggcgaa gaatgcgtta 900
ttgattgcag gatcaattat gagtattcgc attatgggct catcttttgc aacagaagca 960
tggcacgtga ttgtattaaa aacattacat atgtttgaag tgccattcta tttggttgga 1020
gtatttaagt atattgctga tgttttttgaa gtccgttttt ctgcaaccat ttacttagtc 1080
tcttgccact tttcaaagca gattggtaat atgattttat cgcctgccgt agggacttta 1140
tatgacatgt atggttttca atctacctat tttatcttag gttgtattgc tcttacattt 1200
acatcagttt ctgtattttac tttagtaaata accaagaaat tagtgaacaa cgcttaa 1257

<210> 132
<211> 417
<212> PRT
<213> Aggregatibacter aphrophilus

<400> 132

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Tyr Trp Ile Phe Ser Ala Tyr Phe Phe Ala Phe Phe Phe Ile Met Ala
20 25 30

Thr Cys His Pro Phe Leu Gly Ile Trp Leu Gly Asp Ile His Gly Leu
35 40 45

Lys Gly Glu Lys Ile Gly Tyr Val Phe Ser Phe Ile Ser Leu Phe Ala
50 55 60

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

Arg Lys His Leu Leu Trp Leu Leu Ala Ile Leu Leu Leu Phe Tyr Ala
85 90 95

Pro Phe Phe Ile Tyr Val Phe Ala Pro Leu Leu Lys Thr Asn Leu Trp
100 105 110

Leu Gly Val Ile Ala Gly Gly Ala Tyr Met Gly Phe Val Phe Gln Ala
115 120 125

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

Gly Phe Glu Tyr Gly Arg Thr Arg Leu Phe Gly Met Leu Gly Trp Ala
145 150 155 160

Ile Cys Ala Ser Ile Ala Gly Asn Leu Tyr Ser Ser Gln Pro Asn Ala
165 170 175

CL5510WOPCT_SeqListing_ST25.txt

Val Phe Trp Leu Gly Ser Ala Thr Ala Val Val Leu Leu Val Leu Ile
180 185 190

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

Leu Gly Val Asn Lys Ser Pro Ile Thr Leu Lys Gln Ala Leu Lys Leu
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tcatcgattg gtattatcgt gctgagtctg ccggttggca aactgttcga taaagttggt	1140
tatcaggaaa tttttctgat catggccagc atcgtcatta tcaccctgat tttcggctac	1200
tttagcctgt ctaaaaaaca tcaccagcaa aaaatgggta acgaactggg gacggaataa	1260

<210> 142
 <211> 1314
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon optimized CDS from *Enterococcus faecium*

CL5510WOPCT_SeqListing_ST25.txt

```

<400> 142
atgaaagggtg ataccaacat tagcctggaa gacaaaaata tgagcaaagt caacgtgttc      60
aaaaaccaat cctatctgca atcgtccgcc accctgctgc tgtttttcgc atcatggggc      120
gtttggtggt cgtttttcca actgtggctg accagcgaat ctaatggcct gggctctgagt      180
ggctccgctg tcggtacggt gttttcagcg aactcgctgg tcaccctgat cctgatgttc      240
atztatggta cgctgcagga taaactgtac atcaaacgta atctgctgat ttttgcttct      300
gttctggcga ccctggtcgg cccgtttttc atctggattt atgggtccgct gctggacaac      360
aattttaacc tgggcattat catgggtgct ctgttcctga gcgccggcta cctggcatct      420
gtgggtgttt ttgaagcggg tagcgaacgt ttctctcgcc tgtttggctt cgaatatggt      480
caggcacgtg cttggggcag ctttggttac gcgctggttg ccctgctggc aggctttctg      540
ttcgtcaaaa atccgcatct gaacttctgg gccggcagct ttttcggttc cctgctgctg      600
ctgaatctgc tgttttggaa cccgaaagtg gaacgcgaag ctaaccagaa tttcaaccag      660
gaacaagcgg aatcaaattc gatcccagac ctgaaagaaa tgtttgatct gatgaaactg      720
ccgcaactgt ggaccattat cttttttatt gtcttcacct ggacgtttta tacggtgttc      780
gaccagcaaa tgtttccggg cttctacacc ggtctgttta gcacgtctgc aaatggcgaa      840
aaaatctatg gcaccctgaa cgccattcag gttttctgcg aagcactgat gatgggcatc      900
gtgccgatca ttatgcgtaa actgggcggt cgcaatacgc tgctgctggg tgtgaccatc      960
atgtgctgtc gtattggcct gtgtgggttt gccagcacc cgtgagtggt ctctgtatt      1020
aaaatgctgc atgactgga agtgccgctg ttacgctgc cgatgtttcg ctatttcacc      1080
ctgcacttcg atacgaaact gagtgccacc ctgtacatga tcggccttca gattgcggcc      1140
cagatcggtc aagttattct gtccaccccg ctgggcatcc tgcgcgataa cgtcggttat      1200
caaccgacgt ttaaaatcat tagtctgatt gtgctgctgg ctggtatcta cgcgtttttc      1260
attctgaaac aggatgaccg tgatgtgcaa ggcgaccgtt ttattcgcgg ttaa          1314

```

```

<210> 143
<211> 1299
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> codon optimized CDS from Corynebacterium glucuronolyticum

```

```

<400> 143
atgtcaaaat tcatgcaaca actgaaaaat acggcttacc aacaatcatc ggcacaactg      60
ctgctgttct ttatgtcgtg gggcatttgg tggagctttt tccaactgtg gctgagctct      120
gaaacccgtg gcctgggttt taatggttcc gaaattggca cgatctatag cgtgaactct      180
gcagtgacct tggttctgat gctggtttac ggcacggctc aggataaact gcgcaccgt      240
cgcaatctgg ttattggtat cgcggctctg atgagcctga cgggcccgtt tttcatgtgg      300
gtgtattggc cgctgctgca aagtgaatcc ctgtacgtcc tgggtgtggg tctgggtgcg      360

```

CL5510WOPCT_SeqListing_ST25.txt

atttttatcg gcaccgcatt cgtgggcagt tgcccgcgtg ttgaagcgct ggccgaacgt	420
atgtcccgca aacataactt tgaatatggt caggcacgtg cttggggtag tttcggctac	480
gcaattgtgg ctctgctggc gggctttaac ttcaccatta atccggcaat caacttttgg	540
atggcgagcg ctttcggtgt tctgctgctg ctgattctgg tgttttgga agaaccgggt	600
gcaccgcgca atgaaatcgc tgaagaagaa gtggaaaaca ccacgccgtc agtgaaagaa	660
atggtttcgg tcctgaaagt gccggccctg tgggtgggta tcgtgctggg gtttttcacc	720
tggacgtttt atacggtttt cgatcagcaa atgtttccgc agttctacac cagcctgttt	780
tcagactcgg cgaccggtga acgtacgtat ggcgtcctga acagcgcca agtgtttgtt	840
gaagccctga tgatgggcat tgttccgac tacatgcgta aagtcggtgt gaaaaacacc	900
ctgatgacgg gctttgccgt gatggcactg cgcattctgg gttgcgctgt gttcgcggat	960
ccggttacca tcagctttgt caaaatgttc catgcgctgg aagtgccgct gtgtattctg	1020
ccgatctttc gctatttcac cctgcacttt ccgacgaaaa tttcagcgac cctgtacatg	1080
gttggtttcc agatcgctc gcaagtcggc aatgtcgtga tgagtccgat tctgggttcc	1140
ctgctgcatc gcctgggctt tcagccgacc ttctatgtga ttagcgggtat cgttctggtc	1200
tctgccatct ttgcatggct ggctctgaaa ggtgacaaag aacagggtga aggcgatccg	1260
ttctatcgtg actctgaact gaaagaaatt caccaataa	1299

<210> 144
 <211> 1326
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon optimized CDS from Bifidobacterium animalis

<400> 144	
atggcgacca cgaccaaagt ctggcgtaat ccgagttatc tgcaatcctc cacgggcatt	60
tttctgttct tctgttcctg gggcatctgg tggagctttt tccagcgttg gctgaactcc	120
atgggcctga atgggtgctga agttggcacc atttatagta tcaactccct ggcgacgctg	180
attctgatgt ttggctacgg tctgatccag gataatctgg gcctgaaacg tcgcctgggtg	240
ctgggttatta gcgcaatcgc agccctgggtg ggtccgtttg tgcaattcgt ttatgcaccg	300
ctgatgcgca ccaacatgat ggcggcggcg ctggttggca gcgtgggttct gtctgcaggc	360
tttatggctg gttgcagcct gattgaagcc gtcacggaac gttattctcg tcgctttaac	420
ttcgaatacg gtcagagtcg cgcgtggggc tccttcgggtt acgctatcgt cgcgctgggt	480
gcgggctttg ttttcaacat caaccgatg atcaacttct ggctggggtt tgccttcggc	540
gtgggtatgc tgattgttta tctgacctgg tatccggcgg aacaacgtga agcactgaaa	600
gaagccgcag atccgaacgc tgcgccgacc aatccgacga ttaaagacat gctgggcgtg	660
ctgaaaatgc cgaccctgtg ggttctgac gtctttatgc tgctgaccaa cacgttttat	720
accgttttcg atcagcaaat gtttccgacg tattacgcga gtctgttccc gaacgaagcg	780

CL5510WOPCT_SeqListing_ST25.txt

```

accggcaatg ccgtttacgg tacgctgaac agcgtccagg tgttttgtga atctgctatg      840
atgggtgtcg tgccgattat catgcgtaaa gttggcgctcc gcaatgcact gctgctgggt      900
agcaccgtga tgtttctgcg tattggcctg tgcggtatct tccatgatcc ggtcagcatt      960
tctatcgtga aaatgtttca cgctattgaa gtcccgtgtg tctgtctgcc ggcgtttcgc     1020
tatttcaccc tgcattttaa tccgaaactg agtgccacgc tgtacatggg gggctttcag     1080
attgcatcac agatcgggtca agttgtcttc tcgaccccg c tgggcatgct gcacgatcgt     1140
atgggtgacc gcaccacgtt tctgaccatt tccgcgatcg ttctggccgc aacgggtctat     1200
ggctttttcg tgattaaacg tgatgacgaa caagtggatg gtgaccggtt catccgcgat     1260
agcaaaaaac tgccgtcgct ggcaaccgac gaagctattc tgtcagcgga ttcggaagac     1320
atgtaa                                           1326

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```

<210> 145
<211> 1398
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> codon optimized CDS from Bifidobacterium gallicum

```

```

<400> 145
atggtcaata aaccgaaaac cgctaaaatc tggagcaatc cgtcatacct gcaatcttcc      60
tttggcatct tcctgttctt ctgttcctgg ggcattctgg ggagcttttt ccagcgctgg     120
ctgaacacca ttggcctgaa tgggtgcgaa gtcggcaccg tgtatagtat caactccctg     180
gccacgctga ttctgatgtt tggctacggg attatccaag ataatctggg catcaaacgt     240
cgcctgggtg ttgtcattgc aaccatcgcg gccctgattg gtccgtttgt tcagttcgtc     300
tatgtccgcg tgatgcaaac gaacatcatg gcggcggcac tgattggcag tgtggttctg     360
tccgcaggct ttatgtcagg ttgctcgctg atcgaagctc tgaccgaacg ctatagccgt     420
aaatttggct tcgaatacgg tcagagccgc gcgtggggct cttttggtta cgccattgtc     480
gactgattg ctggcatcgt gttcaacatc aaccgatga tcaacttctg gctgggttcc     540
gcgttcggcg tcggtatgct gattgtgtat ctgacctggg atccggcgga acagcgtcaa     600
gccctgaaag aagccgcaga tccgaacgcc gaaaaaagca atccgtcttt taaagacatg     660
gttaacgtcc tgaaaatgcc gacgctgtgg gttctgatta tcttcatgct gctgaccaat     720
acgttttata ccgtgttcga tcagcaaagt tttccgacgt attacgcctc actgttcccg     780
tcgatcgaac ccggcaacac ggtgtacggg gttctgaata gtattcagggt gttttgcgaa     840
tccgcaatga tgggtgtcgt gccgattatc atgcgcaaaa tcggcgttcg taacgcactg     900
ctgctgggtg ctaccgtgat gtttctgctg atcggcctgt gcggtatttt ccatgatccg     960
gttgcaatta gtatcgtcaa aatgtttcac gctattgaag tgccgctgtt ctgtctgccg     1020
gcgtttcgtt atttcaccct gcattttaat ccgaaactgt ctgcgacgct gtacatgggt     1080
ggctttcaga ttgcctcaca gatcgggtcaa gtgattttct cgaccccgct gggcatgctg     1140

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CL5510WOPCT_SeqListing_ST25.txt

cacgatcgct ttggtgaccg taccacgttc ctgagcattt ctggcatcgt gctgctggca	1200
acgatctatg gctttttcgt tattaaacgt gatgacgaac atgtcgatgg cgacccgttt	1260
ctgcgtgatc gcgaccgtaa agaaatggaa ctgattgaag aaaacctgca gccggatgcc	1320
gaactggaaa ccagcccggg ggggtgttgct gcacaagtgc gtgacaatcg tgcggttcaa	1380
ccggaatatg cctcttaa	1398

<210> 146
 <211> 1338
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon optimized CDS from Bifidobacterium longum

<400> 146	
atggcgtcag cgaccaaadc ggcgtggaaa aacccgtcct atctgcaatc ctcattcggc	60
atcttcatgt tcttctgttc gtggggcatt tgggtggtcat ttttccagcg ttggctgatc	120
tcgggcgtgg gtctgacgaa cgccgaagtt ggcaccattt atagcatcaa ttctctggca	180
accctgggtga ttatgtttgt gtacggcggtt attcaggatc aactgggtat caaacgtaaa	240
ctggttattg tggtagcgt catcgcgggc tgcgtgggtc cgtttgtcca gtctgtgtat	300
gcaccgatga ttctggcggg cggcaccacg cgttggatcg gtgctctgat tggttcaatc	360
gtgctgtcgg cgggctttat gagtgggttc tccctgttcg aagctgttac cgaacgttat	420
tctcgcaaat ttggcttcga atacggtcag agccgcgcct ggggctcttt tggttatgca	480
attgtggctc tgtgtgcggg ctttctgttc aacattaatc cgctgatcaa cttttgggtt	540
ggttcagcat tcgggtccgg catgctgctg gtttacgctt tttgggtccc ggcggaacaa	600
aaagaagaac tgaaaaaaga aacggatccg aacgcagctc cgaccaatcc gtcgctgaaa	660
gaaatggttg cggctctgaa aatgccgacg ctgtgggttc tgattgtctt tatgctgctg	720
accaacacgt tttataccgt gttcgaccag caaatgtttc cgacgtatta cgctaacctg	780
tttccgaccg aagaaatcgg caacgcgacc tacggcacgc tgaatggttt tcaggttttc	840
ctggaaagcg ccatgatggg tgtcgtgccg attatcatga agaaaattgg cgttcgtaat	900
gccctgctgc tgggtgcaac ggtcatgttt ctgcgcacgc gcctgtgcgg tgtgttccat	960
gatccgggta ccattagtat cgtcaaactg tttcactcca ttgaagtgcc gctgttctgt	1020
ctgccggcgt ttcgttattt caccctgcat tttgacacga aactgagcgc caccctgtac	1080
atggttggct tccagattgc aagccaagtg ggtcaagtta tcttttctac gccgctgggc	1140
gccttccacg ataaaatggc acaaactctg ccgaacaatg acatgggtag tcgtgtcacc	1200
ttttgggtga tttccgctat cgtgctgtgt gcgctgattt atggcttttt cgtcatcaaa	1260
catgatgacc aggaagtggg cggatgatccg ttctacaccg acaacaact gcgccaaatg	1320
gaagcggcca aagcgtaa	1338

<210> 147

CL5510WOPCT_SeqListing_ST25.txt

<211> 1422

<212> DNA

<213> Artificial Sequence

<220>

<223> codon optimized CDS from Bifidobacterium adolescentis

<400> 147

```

atgaaatcgg aacagggtca ggctaaaacg acctcagaag caatcgcggc tgcccgtcaa      60
cgccaacgtg aagaaaaaaa acgcatcaaa atggcggtcaa aaacccgttc ggtgtggaaa      120
aacccgagtt atctgcagag ctcttttggc attttcatgt ttttctgctc ctgggggtatc      180
tggtggagct ttttctctcg ctggctgacc gatccgacgc atggcctggg tatgagttcc      240
gccgaacagg gccaaattta tagtatcaat tccctggcaa cgctgggtcat tatgtttgtg      300
tacggcacca ttcaggacca actgggtatc aaacgtaaac tggttatttt catcagcgca      360
gttgccgcct gtgtcgggtc gtttgtccag ttcgtgtatc aaccgatgct gaccgcgggc      420
ggcaccacgc gttttatttg tgtcctgctg ggtagcatcg tgctgtctgc cggctttatg      480
gcaggttgca gcctgttcga agctattacc gaacgttatt ctgcaaatt tggcttcgaa      540
tacggtcaga gtcgtgcctg gggctccttt ggttatgcag tggttgctct gtgtgcgggc      600
tttctgttca acattaatcc gctgctgaac ttttgggtgg gctcaatctg cggctctgtc      660
atgctgtgtg tgtacgcctt ctgggttccg gcagaacaga aagaagaact gaaaaaagaa      720
gctgatccga acgcgacccc gacgaatccg agctttaaag aaatggtttc tgtcctgaaa      780
atgccgacgc tgtgggttct gattgtcttt atgctgttca ccaacacggt ttataccgtg      840
ttcgatcagc aaatgtttcc gaattattac gctagtctgt tcccgaccac ggaaatcggc      900
aacgcgacct acggtacgct gaatagtttt caggttttcc tggaatccgc catgatgggc      960
gtcgtgccga ttatcatgaa gaaaattggc gtgcgtaatt ctctgctgct gggtgctacc     1020
gttatgtttg cgcgcatcgg cctgtgcggg gtcttccatg atccggtgtc agtttcgatt     1080
gttaaactgt ttcacagcat cgaagtcccg ctgttctgtc tgccggcggt tcgttatttc     1140
accctgcatt ttgacacgaa actgtcagcc accctgtaca tgggtgggctt tcagattgca     1200
tcacaagtgg gtcaagttat cttctcgacc ccgatgggtg cactgcacga tgcaatgggt     1260
gaccgcccga cttttttcac gattagcgcc atcgtctttg cagctctggg gtatggcttt     1320
ttcgttatca aaaaagatga ccaggaagtg ggcggtgatc cgtttttacac cgacaaacaa     1380
ctgaaagcaa tgaaagcggc cgatgctgaa gttaaagcgt aa                        1422

```

<210> 148

<211> 1503

<212> DNA

<213> Artificial Sequence

<220>

<223> codon optimized CDS from Bifidobacterium longum

<400> 148

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atgctgtgtc aacaagtccg ccatgctgat ctgcgccagt ccattgacgt gaaccgcctg      60

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CL5510WOPCT_SeqListing_ST25.txt

acctcacata	acaactacta	cattaccacc	agcacgaaag	ctcgtccgcc	ggaacagaaa	120
cgctatatta	cgaacaatca	gccgagctct	aaccaacgta	tgatcatggc	aagtgtctacc	180
aaatccgcat	ggaaaaatcc	gtcatacctg	cagagttcct	ttggcatttt	catgtttttc	240
tgcatgtggg	gtatctggtg	gtcctttttc	caacgctggc	tgatttcggg	cgtgggtctg	300
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ttcgaatacg	gtcagagccg	tgcatggggc	tcttttggtt	atgcgattgt	ggccctgtgt	660
gcaggctttc	tgttcaacat	taatccgctg	atcaactttt	gggttggttag	cgctttcggt	720
ccgggcatgc	tgctggttta	tgccttttgg	gtcccggcag	aacagaaaga	agaactgaaa	780
aaagaaacgg	atccgaacgc	agctccgacc	aatccgtctc	tgaaagaaat	ggttgcggtc	840
ctgaaaatgc	cgacgctgtg	ggttctgatt	gtctttatgc	tgctgaccaa	cacgttttat	900
accgtgttcg	accagcaaat	gtttccgacg	tattacgcca	acctgtttcc	gaccgaagaa	960
atcggcaacg	caacctacgg	cacgctgaat	ggttttcagg	ttttcctgga	atccgccatg	1020
atgggtgtcg	tgccgattat	catgaagaaa	attggcgttc	gtaatgctct	gctgctgggt	1080
gcgacggtca	tgtttctgcg	catcggcctg	tgcggtgtgt	tccatgatcc	ggttaccatt	1140
tcaatcgta	aactgtttca	ctcgattgaa	gtgccgctgt	tctgtctgcc	ggcgtttcgc	1200
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attgcgagcc	aagtgggtca	agttatcttt	tctaccccg	tgggcgcttt	ccacgataaa	1320
atggcgcaaa	ttctgccgaa	caatgacatg	ggtagtcgtg	tcaccttttg	ggtgatttcc	1380
gccatcgtgc	tgtgcgact	gatttatggc	tttttcgtca	tcaaacaatga	tgaccaggaa	1440
gtgggcggtg	atccgtttta	caccgacaaa	caactgcgcc	aaatggaagc	ggccaaagcg	1500
taa						1503

<210> 149
 <211> 1266
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon optimized CDS from Mitsuokella multacida

<400> 149	
atgggtaatc	tgctgaaagc gttctcgaat ccgttttatc gcacctctc cctggaaatc 60
ctgctgttct	ttgctggttg gggatatttg tggagctttt tccagatttg gctgaccacg 120
aaacagggct	ttacgggtgc acaagtgggc accatctaca gctttggttc tgcagtcgct 180
ctggtgctga	tgttcgttta tggcagcctg caggataaac tgggtatgaa gaaaaccatg 240

CL5510WOPCT_SeqListing_ST25.txt

ctgaaat	ttt	tcg	cgg	ttt	g	ccaa	att	ctg	g	tcg	g	ccc	g	t	ttt	cac	ctg	g	g	ttt	at	g	t	g
300																								
ccgat	g	ctg	t	g	g	c	ca	a	act	t	ttac	g	t	g	g	g	g	c	g	g	t	g	t	g
360																								
gcctt	t	ctg	t	g	g	c	ag	ctt	g	ccc	ggt	ctt	c	gaa	gcc	g	t	g	acc	c	aac	g	t	g
420																								
tcctt	t	ga	at	ac	g	gt	c	ag	g	c	ac	g	c	t	t	g	g	g	c	t	t	g	t	g
480																								
tgt	g	c	g	g	g	g	c	t	tt	c	t	g	t	t	c	a	c	g	a	t	a	a	c	c
540																								
g	c	g	g	c	g	g	t	g	c	a	a	c	t	g	a	t	c	g	t	c	t	g	a	t
600																								
g	c	t	c	a	a	t	a	t	a	g	t	g	a	a	a	g	c	a	a	a	a	c	c	c
660																								
a	t	t	g	t	g	g	t	g	t	t	t	c	a	a	a	c	t	g	a	a	a	a	t	a
720																								
t	g	g	a	c	t	t	t	t	t	t	c	g	a	a	a	a	a	a	a	a	a	a	a	a
780																								
g	c	g	a	c	g	c	c	g	a	a	g	c	c	g	c	c	a	a	a	a	a	a	a	a
840																								
g	a	a	t	t	t	c	t	g	a	t	g	g	c	c	t	g	g	c	c	a	a	a	a	a
900																								
a	t	t	c	t	g	c	t	g	g	a	a	t	a	a	t	a	a	a	a	a	a	a	a	a
960																								
c	c	g	c	t	g	g	g	t	g	t	c	a	t	a	a	a	a	a	a	a	a	a	a	a
1020																								
g	c	t	g	t	g	t	t	t	c	g	a	a	c	c	g	c	g	c	t	g	t	a	t	a
1080																								
g	t	t	g	g	c	t	t	t	c	a	a	g	a	t	a	t	a	t	a	t	a	t	a	a
1140																								
c	t	g	c	a	t	g	a	c	t	a	c	c	t	a	a	a	a	a	a	a	a	a	a	a
1200																								
g	c	c	t	c	a	c	t	g	t	a	a	a	a	a	a	a	a	a	a	a	a	a	a	a
1260																								
c	t	g	t	a	a																			
1266																								

<210> 150
 <211> 1275
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon optimized CDS from Lactobacillus antri

<400> 150																				
atg	aaaaa	act	ctaa	act	gag	cgc	att	caaa	aact	cgt	tct	atct	gg	aaa	ag	tag	cct	gtcc		60
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aac	gat	ctgg	gct	tt	agt	gg	tg	caaa	agtc	gg	cat	gatt	at	ac	gtt	cga	ctcc	gc	gac	180
acc	ctg	gttc	tgat	gt	ttat	ttac	gg	ctca	gtcc	agg	ata	aact	gg	gtat	ttaa	ac	gtc	gc	240	
ctg	ctg	attg	gc	gt	tac	gat	cct	gg	aaat	g	ctg	ctg	gtc	cg	tttt	tt	cac	ctg	gat	300
gcg	ccg	ctgc	tg	cat	ag	taa	ttt	catt	ctg	gg	c	catt	ttc	tg	gg	tt	cact	gt	acct	360
ttt	g	cttt	cc	tg	gc	gg	ccag	ccc	gac	ctt	ga	ag	cact	g	ctga	ac	gtat	gag	ccg	420
tatt	cttt	cg	aata	c	ggt	cg	tg	cg	ctg	cg	tg	gg	g	ct	cat	tt	gg	ttat	gc	480
ctg	tg	cg	cag	g	tac	ct	gtt	tac	gatt	tcg	ccg	tac	at	cg	tg	ttt	tg	gct	gag	540
att	ag	cct	gc	tg	ac	tt	cct	g	ctg	ct	gt	gt	gt	ttt	gg	tc	gta	ccaa	ag	600
g	ct	cg	tat	g	aaa	caa	agc	gga	aga	gaa	cac	gat	g	ccg	acaa	acc	gag	ctt	caa	660

CL5510WOPCT_SeqListing_ST25.txt

```

atcatctctg tcttcaaact gaaacaactg tgggaactgg tgtttttcat tatcttttagt 720
ggctccttct atacggtttt tgatcagcaa atgtttccgc agtttttcac ccaatttttc 780
aaaacggcag ctcagggcaa caccgcctac ggcattctga acagcatcga agtttttctg 840
gaagctatta tgatggcgat cgtcccgtgg attatgaaga aaattggcgt gcgtaaaacg 900
ctgctgattg gtgttaccat catgtttctg cgcacgcggc tgtgcggtct ggtgggttagc 960
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gtcgtgggtc agattgccgg ccagatcggg caaattatcc tgagtacgcc gctgggcatg 1140
ctgcatgacc gtatcgggta tcgcgccacc ttcctgggtca tttccctgat tgtgatctgt 1200
gcggccgttt acgcatttgt cattctgcgc aaagataatc aggaagtgga cgggtcaaccg 1260
ctggaaaaca attaa 1275

```

```

<210> 151
<211> 1323
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> codon optimized CDS from Lactobacillus ruminis

```

```

<400> 151
atgatgccga ttagcgacaa ctggaaaggt atcctgttta tgaatgacat gaacaaaagc 60
ggctcgtatga gccaaactgaa aaacccgttt ttcacctcaa acgctacgaa tattctgatg 120
tttttcgcgg gctgggggtat ttggtgggtc tttttccaga tctggctgac cacgaaacag 180
ggctttaccg gtgcccaagt ggggtgaaatt tatagtttta actccgcttt ctactgatt 240
gcgaacctgg ttacagcaa tatccaggat cgtctgggtc tgaaacgcaa tctgctgata 300
ttttgcgcgt gtctgcaagt cttcctgggc ccgtttttca cttttctggt cgttccgatg 360
ctgcatgcta acctggaact ggggtgcgtg attggtagct gctatctgac cctggcttac 420
ctgagcgcgt ctccgatgtt cgaagccctg acggaacgtg catctcgtcg ctttaactat 480
cagtacgggt ctgcgcgtgc gtggggcagt ttcggttatg cggtttccgc cctgctggca 540
ggttttgtct tcaccatcaa tccgtcactg ctgttttgga ttggctcggc aatcgctgtg 600
gttctgctgc tgctgctgct gttctggaac ccggtgcgta ataaagaaac cgttgcccgc 660
tttgaacacg aaatgggtgcg tgaacgcgaa aattcgaaac cgggtagccg tgattttctg 720
aatgtcttca aagtgcgcag tctgtgggaa attgcaatct ttctggtttt ctccggcacc 780
ttctacacga tcttcgatca gcaaattgtt ccgcagtttt tcacccaatt tttcaaacg 840
caggctatgg gtgaccatat gtacggcatc ctgaatagcg ttgaagtctt tctggaagcg 900
ctgatgatgg gtctgggtgc gctgctgatg aagaaaattg gtgttcgtcg caccatcctg 960
gtgggcgtta cgtttatgtt cattcgtatc ggcggttgcg gtctgattac caaccgctg 1020
ggcgtgagta tgatcaaact gctgcatgcc ccggaaaccg caatcttttg cgctcgtgatg 1080

```

CL5510WOPCT_SeqListing_ST25.txt

ttccgttatt acacgctgca ctatgatccg cgcgtctctg ccaccattaa tatcgtgacg	1140
ggcattgcag gtagctttgg ccagatcctg ctgtctaccc cgctgggtct gctgcgtgac	1200
cacattgggt atcaaccgac gtttctgggt attgccggta tcgtcttctg tgcaggatct	1260
tacggcctgt ttattatccg tcgcatgac caggaagtga atggcgaacg cctgtccgaa	1320
taa	1323

<210> 152
 <211> 1248
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon optimized CDS from Yersinia frederiksenii

<400> 152	
aagcttatga aacatagcgt ccgtaaccaa tacctgattc tgagcgggtct gctgttcacc	60
ttcttcttta cctggctgct ggcatttagc ctgttcagta tttggctgaa ccagtatggt	120
ggcctgaaag gcaccgaaac ggggtgcgacc ttttccgcaa ttgctctgac ggcactgtgc	180
gcacagccgc tgtacggtgt catccaagat aaactgggccc tgaaaaaaca tctgctgtgg	240
gcgattggta tcctgctgct gattagcggc ccgtttttca tctatgtcta cgcgccgctg	300
ctgctgtgta atatgctggt tgggtgccgtc accggcgggtc tgtatatggg catgacgttt	360
ttcgcgggca ttgggtgccct ggaatcatac accgaacgtg tgtcacgcat ctcgggtttt	420
gaatttggca aagcccgcat gtggggctcg ctgggttggg caggtgcaac gtttttcgca	480
ggcatgctgt tcaacatcaa cccgaacatc aacttctgga tggcaagtgc ttccgcggcc	540
atctttctgc tgctgctgtg gcatctgcac gaagtgaana cgcagctat gggtaactg	600
gaatatggca aaaacagcgc actgaccctg agtgatacgc tgtccctgtt ccgtatgccg	660
cgtttttggg ccctgggtgt ttttgttacc ggtgtctctg tgtataatgt ttacgatcag	720
caatttccgg tctatttcag ctctctgttt acggaccgtc gccatggtaa cgaaatgtac	780
ggcttcctga atagtctgca ggtctttctg gaagcaggcg gtatgttcct ggctccgttt	840
ctggtgaacc gtattggtgc gaaaaaaggc ctgctgctgt ctggcctgat tatggctatg	900
cgcacccctg gcagcgggtc ggcacaagat gctgtgacca tctctctgat gaaactgctg	960
cacgcagttg aactgccgat tctgctgac gctatgttca aatatattgc ggccaatttt	1020
gacccgcgtc tgagcgcgac cctgtatctg gtgggttttc agttcattac gcaagtgtac	1080
gcgagcgttt tctctccgct ggccggcaaa ggttatgac tgatcggctt tgcggacacc	1140
tacctgatta tgggcgggtat cgttctgggt ctgacggcca tttcctgttt tatgctgcgt	1200
ggcgaatcac gcaccgatga cccgtcgtg caactgacca cgaaataa	1248

<210> 153
 <211> 1260
 <212> DNA
 <213> Artificial Sequence

CL5510WOPCT_SeqListing_ST25.txt

<220>

<223> codon optimized CDS from *Serratia proteamaculans*

<400> 153

```

atgaatcgtg aaaccaaaaa atactatgtc ctgctgtcgg gtctgctggt cttcttcttc      60
tttacctggg cttcgtcgtt ctcgctgatt tcaatctggc tgaaccagaa aattggcctg      120
aaaggcaccg aaacgggcct gatctttgcg gccatgtcga ttatggcgct gtgcgcccag      180
ccgctgtatg gctttatcca agataaactg ggtctgcgta aacatctgct gctgttcgtt      240
ggcgtcctgc tgctgctgac cgggtccgtt ttcatctatg tgtacgcacc gctgctgcag      300
tcaaacctgg tggttggcgc tctggttggc ggtgtgtttg tttcgtggc attcaatgct      360
ggcatcgggt cgctggaaag ctataccgaa cgtgtctctc gcattgtggg ctttgaattt      420
ggtcgtgcac gcatgtgggg ctactgggt tgggcatcgg caacgttttt cgcggttttc      480
aactacaata ttgacccgaa catcaatttt tggattgcaa gcgctagcgc ggcggtgttt      540
ctgctgctgc tgtggcaggt ccgtgaactg aaaccgaacg cgatggccgg cctggaatat      600
ggtaaaccgg aaaatctgaa actgcaagat gactggctc tgctgctcct gccgggtttt      660
tgggcgctgg tcgtgttcgt gctgggcacc agcatctatg gtgtgtttga ccagcaattc      720
ccggtttact ttgcctctca gttcccgcac catgaagaag gcaaccgcat gtacggcttt      780
ctgaacagcc tgcaagtctt cctggaagca ggcggtatgt ttctggctcc gctgctgggt      840
aatcgtattg gcatcaaaca gtctctgctg ctggcgagct ctgttatggc cctgcgcatg      900
gtcggcagtg gttttgcgtc cgggtgccctg atgattagtg cgatgaaact gctgcacgcc      960
gtcgaaactg cgatcctgct ggttgcgatg ttcaaataa ttaccacgcg ttttgatagt     1020
cgcctgagtt ccaccctgta cctgggtggc tttcagttca tttcccaaat cgttgccggt     1080
tttctggcac cgctggctgg ctatgggttac gatcgtatcg gctttgcaga cacctatctg     1140
ctgatgggtt gcgcagtggc aggcaccacg ctgattagct gttttctgct gcgcggtgaa     1200
acggttgcaa gtgctccgca gttccaatcc accctgaaat catcggaacc gacgcagtaa     1260

```

<210> 154

<211> 1239

<212> DNA

<213> Artificial Sequence

<220>

<223> codon optimized CDS from *Escherichia coli*

<400> 154

```

atgaaaaaac gcccgaccg ctcatcatg ctgctgtccg cactgctggt cttcttcttc      60
gtgacctgga gttcgtcctc ttctctgctg agcatttggc tgcatacagga agtgggcctg      120
aaagcgtctg aaaccggtat tatctttagt gtcctgtccg tgtcagcact gtttgctcag      180
gtttgctatg gcttcatcca agatcgtctg ggtctgcgca aacacctgct gtggtttatt      240
accgcactgc tgatcctgtc gggcccggct tatctgctgt tctcttacct gctgagtgtg      300
aacattctgc tgggtagcgt ttttggcggc ctgttcattg gcctgacgtt taatggcggc      360

```

CL5510WOPCT_SeqListing_ST25.txt

```

atcgggtgtgc ttggaatcgta taccgaacgt gttgcgcgcc agagcacgtt tgaatttggt 420
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tttaacatta atccggacct gaacttcctg gttgcctcgt gcagcggcct gatctttttc 540
tgtctgctgg cacgtctgaa agtggcagca ccggcctcca tggaaaaact ggaaattggt 600
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ctgattttct ttgtgggttg cacgtgcatc tatggtgtct acgaccagca atttccgggtg 720
tatttcagct ctcagtttcc gaccctgcgc gaaggcaacg aaatgtttgg ttacctgaat 780
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agttccacca ttacctgggt gggctttgca tgtacctcat cggttatcgg tacggtcctg 1080
tcgccgctgg caggcttcag ctatgaacgt tttggtttcg ctcagagtta cctgattatg 1140
ggcatcatgg tgttctccac cacgtttatt tcaatcttcc tgctgcgctc cacgaaaagc 1200
tctagtgaac cgtcatttct gcagcaaaaa gccgtttaa 1239

```

```

<210> 155
<211> 1263
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> codon optimized CDS from Cronobacter turicensis

```

```

<400> 155
atgagcgaag tcctgcaatc aaccggttcc gcctacatca aactgagcct gttcgtcttt 60
ctgttcacct ttacctggag tgctggcttt ggcattgatg cgatttggct gggcgataaa 120
gccggtctga gtgcaattga catcggcacg gtctttgctg tgaacggtgt tttcgcggctc 180
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tctggctatg ttacaacat tagccccgatt atcaatttca ccacggttag tgtctccgca 540
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agcgtgctgt ctaaagataa aattgttatc gcggacgtct ttacctgtt ccgtaatccg 660
aaattttgga tgttcgcact gtatatcgcg ggtgttgctt ggatgatgtt tattgctgaa 720
cagcaattta gccgctatct cgtgaccttt ttcaacacga aagaacaggg caatgccatg 780
ttcggttaca tgagtaccac gcaatcctgc acggaatttt tcggcatgat gctggtgccg 840

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CL5510WOPCT_SeqListing_ST25.txt

gccctggtta accgtatcgg cgcaaaacag ggtatgctgc tgaccgggtct gattgttagt	900
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ctgtatggta ttgaaatcgc actgattctg gtttctgtct ttaaatacat cgctgaacat	1020
ttcgacaaac gtattaatgc gaccatgtat ctgctgggct accaagccat ggtgtatgtt	1080
ggtagtatcg tggttgcacc gccggctggc tatgcgtagc ataccattgg ttttgaacac	1140
acgtacctga ttatgggcac catctccctg ctgtttacga ttgtctcagc cttcacccctg	1200
tcggattgtc agaaacataa aaaagtgacc tcagcttcgc acacggacca agcgctgaac	1260
taa	1263

<210> 156
 <211> 1269
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon optimized CDS from Enterobacter sp

<400> 156	
atggaaaata cctcaacgaa caatcgcacc gaatactata aaatcagcat cttcatcttc	60
ctgtacttct tcacctgggtc agcgtcaatt ggcctgctgg ctatctggct gggtcagaaa	120
gcgaacctgt caggctcggg gatcggcacc gtgtttgcag ttaatggcat cttcagcgtt	180
attctgaaac cgatctatgg ctacattctg gacaaaatcg gcatgtcgaa atatctgctg	240
tactttgtgg ttgcaatgag cgctctgatg gcgccgtttt tcattttatgt ttaccagccg	300
ctgctgatgt ctaacaccat gctgggcatt atcattgggt ccctgtatct gagtttcgca	360
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tctggcctgc tgttcaacct gagtccggcc tataatttta ttctgggtag tgtcgcattc	540
gtgatcatgc tgattgttct gctgaacctg aaagttaaca ccaatagcgt ccatgcgtct	600
gatgtgctga cgaaagaaaa aatcgccccg tccgacgtct atgcactgct gcgttcacgc	660
aaattttggg ctttctgtct gtacgttgct ggcgtcgcgt ggatgatgtt tatcgcagaa	720
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gctcgctga tcatttcagg cctgtgcgat tcgcatctgc tgattagcgt gctgaaaccg	960
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ggtaatgtcg tgatcagttc cccggcgggt tatatgtacg atcgattgg ttttgaacaa	1140
acctacatca ttatgggcgc gacggccctg acctttacgc tgctgtctgc tttcacccctg	1200
agtgcgtgcc agtccaaatg gcgtggtacg agcgccattt cgggtggcaga acaaaatccg	1260

agccgctaa

1269

<210> 157
 <211> 1260
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon optimized CDS from *Citrobacter koseri*

<400> 157
 atgaacaaaa atgactcggc ggaaaaaaat cgtcgcaaaa tctacatcac gctgtcgcctg 60
 tttattcttg tttacttctt ctcctggaaa gcgaccctgg atacgtactc cttttggctg 120
 tcagaaaaaa ttggcctgga cgggtgtcgcg attggcatcg tgtttgcggc caacggtttc 180
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 gccgcaagca ccggttacat cttcaacatc aaccgatga tcaacttcgg cctgagctct 540
 gctggtgcgc tgatcatcct gatcatcgtt ttcacatga aaatcgaagt gaacgaagaa 600
 gttaaaaacc gtatcatcgc aaaagataaa gctacgatct acgacatcat cgccctgttt 660
 agcacccgca atttctggac gtttgttctg tacgtctgcg gcgtgggttg gattatcttc 720
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 gtcgtggccg cacgcttcat cggtcgggt ctggttacca gcgcaattac gatcggcatt 960
 atcaaaactga gctggggtat tgaaatgtct tttctgctgg ttagcatctt caaatacctg 1020
 gaaatcaact tcgataaaaa agtcaacggc tccatgtatc tgctgggtta ccagtcagtg 1080
 aactacattg gcaccgttat cctgtctccg ctgagtggct atctgtacga acgtctgggt 1140
 ttttcccata cgtatttcat gatgggttgt accgtgctgt tctttacgat tatcagtgcg 1200
 tttctgctgc aaaacaataa acgcaccgaa ccggttattg ccgaaaatgc ccacgcataa 1260

<210> 158
 <211> 1242
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon optimized CDS from *Bacillus megaterium*

<400> 158
 atgaaatcct caaaatcgct gtattggaaa ctgtcggctt acttcttctt cttcttcttt 60
 acctggtcat cctcttattc gctgttcagc atttggtcgg gccaggaaat caaactgaac 120

CL5510WOPCT_SeqListing_ST25.txt

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ggctcagcca ccggtctgat ttttagcgtg aatgctatct tcgcgctgtg catgcaaccg      180
ctgtatggct acatttcaga tcgtatcggg ctgaaaaaac atgttctgtt tttcatttcg      240
tgtctgctgg tgtttggtgg cccgttttat atcttcgtgt acgggtccgct gctgcagtat      300
aacgtgggta ttggcgctat tatcggcggg ctgtacctgg gtgttgccct tctggcaggc      360
attggtgcaa tcgaaacgta catcgaaaaa gtcagtcgta aatacaaatt cgaatacggc      420
aaaagccgta tgtgggggctc tctggggttg gcggccgcaa cctttttcgc ggggtcaactg      480
tttaacatta atccgcacat caatttctgg gtggctagcg tttctgcggg cattctgggtg      540
gcgattatct ttagcgtcaa agtggaatg agctcttatg aaatggaaaa agccgaaagt      600
gttacgctgc gtgatgtcgg ctccctgttt ctgctgaaag aattttgggt tttcatgata      660
tacgtcgtgg gcgttacgtg cgtctatggg gtgtacgacc agcaatttcc gatttattac      720
gcaagtctgt tcccgaccga atccatcggc aaccagggtct ttggctatct gaacagcttt      780
caagtgttcc tggaagcggg catgatgttt gctgcgccgt tcattgtgaa caaaatcggg      840
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ctggttgctg gcccgattgg tatcagttcc atgaaactga ttcatgccct ggaactgccg      960
atcatgctga ttgcaatctt taaatatctg gccgcaaact tcgatacccg tctgtcatcg     1020
attctgtacc tggttggctt tcagttcgcc tctcaaattg gtgcaagtgt gctgtccccg     1080
atcgttggcg gtctgtatga ctcagttggg ttttcgcgca cctacctgat tatgggcggg     1140
atggttctgg tctttaacgt gatcagcatg ttcacgctgc tgaacagcaa aaaacaccgt     1200
tttattcgca aagacgtgca ggaaaatacc caaattatct aa                          1242

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```

<210> 159
<211> 1263
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> codon optimized CDS from Providencia rustigianii

```

```

<400> 159
atgggcaaaa tcattggtgc gacccgtcac gcctacttta tcctgagcgg cctgctgttt      60
accttcttct ggacctggag ttcggcattt agcctggttt ctctgtggct gtctcagaaa     120
gtcggcctga aaggcaccga tacgggtatt atcttcagtg ttatctccct gaccgcattt     180
tgcgctcagc cgctgtatgg tttcattcaa gacaaactgg gcctgcgtaa aaacctgctg     240
tggtacattg gtgtgatgct gggttatcagt ggcccgtggg ttattttcgt ttgtaccccg     300
ctgctgcgct ggaatatttt tctgggcagt atctccctgg gtgtctatgt gggcgcgacc     360
tttttcgccg gcatcgggtg actggaatcc tatacggaac gtgtgtcacg cattgctggg     420
tttgaatacg gtcgtgcacg tatgtggggc tcgctggggt gggcagggtg aacctttttc     480
gcaggatttc tgttcaacat caaccgaac tacaatttcg ccatgggctc agtgtcggca     540
ctgatcttta ttatcctgct gtggcgtctg agcgatgttc gccgcaggc aatgaacgaa     600

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CL5510WOPCT_SeqListing_ST25.txt

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cagcaatttc cgatttattt	cgccagcctg ttttctgaac	agagtcattg taacgaaatg	780	
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tgcgcaacgg tgctgtctcc	gctggcaggt attagttatg	atcgcatcgg ctttgccgac	1140	
acctacatga ttctggcagg	catcgtcttc accctgacga	ttatctcctg tgtgctgctg	1200	
aaatcagaaa acagctctaa	agtccataat gtgagcattc	agaagaaaac cgtggaactg	1260	
taa			1263	

<210> 160
 <211> 1266
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon optimized CDS from Providencia alcalifaciens

<400> 160	
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ccctgagcgg cctgctgttc	60
accttcttct ggacgtggtc	gagcgtgttt tctactggtgt
cgctgtggct gtctcagaaa	120
attggcctga aaggcaccga	tacgggtatt atcttcagcg
ttatctctct gaccgctttt	180
tgcgcgagc cgctgtatgg	tttcattcaa gaccgtctgg
gcctgcgcaa aaacctgctg	240
tggtttctgg gcggtctgct	gctgattagc ggtccgtgggt
ttatcttcgt gtgtaccccg	300
ctgctgaaat ggaatatttt	tgcgggcgcg gccgcactgg
gtatctacgt tggcgctacc	360
tttttcgcyg gcattgggtgc	cctggaatcc tatacggaac
gtgtcagtcg catcgcatcc	420
tttgaatacg gtcgtgctcg	tatgtggggc tctactgggtt
gggcaggtgc aacctttttc	480
gccggtctgc tgtttaacat	tgatccgaac ctgaatttcg
caatgggcag tgtctccgct	540
ctgctgttta ttatcctgct	gtggcgtctg cgcaacgtgc
gtccgcatac catgaatgaa	600
ctggaatttg gtaaaaccca	gtcactgacg gtgtcggatg
cactgggtct gctgcgtatg	660
cgagtttct ggtccctggt	catctttgtg tgcggtgtgt
ctgtttataa cgtttacgac	720
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gcggtatggt cctggccccg	840
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tcaaatacat cacgtctggt	1020

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ttcgataaac gcctgagtgc aaccatctac ctggtcgggtt ttcagttcac ggcgagcctg	1080
tgtgcctcat ttctgtcgcc gctggcgggc tatggttacg ataccctggg cttcgccgac	1140
acgtatatga ttctggctgc gattgtgatc tcgatgacca ttatcagctc tgttctgctg	1200
caaagcgaag acaccagcac ggtctctaata ccgatgacca cgagcaagaa aaccgtggaa	1260
ctgtaa	1266

<210> 161
 <211> 1290
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon optimized CDS from weissella paramesenteroides

<400> 161	
atgggtgggc gccgtatgtc aaaatatatg aaagccttca aaaacgaaag ctacctgcaa	60
tcctcgggtca cgatgctgct gtacttcgct agctggggca tttgggtggag ctttttccaa	120
ctgtggctga ccgcgaaatc aggtctgaac ctggatggct cggccgtggg tacgatctat	180
agtgcgaatt ccctgggttac cctgggtcctg atgttttttct acggcacgct gcaagacaaa	240
ctgggtatta aacgtcatct gctgatcttt agcgggtgttt gcgcagccct ggtcgggtccg	300
tttttcattt atgcgtacga accgatgctg cacaccaact ttacgatggg cctgggtggtt	360
ggttcaattt ttctgtcggc tggcttcctg gcgaccacgg gtatctatga agccctgggtc	420
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gttcgtgaaa tgctgtccct gctgaaaatg cgcgatctgt gggttgtcat tgtgtgatc	720
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ggcctgttta gctctgtggc gcagggccag caaatgtatg gtaacctgaa cagcattcaa	840
gtgttcgttg aagccattat gatgggtatc gtcccgggtga ttatgaacaa aatcggcggtt	900
cgtaataccc tgctgctggg tattgccatc atggcaattc gcacggcct gtgcgggtttt	960
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ctgggcatgc tgcgcgataa ttccgggttat gccgttacgt ttcacattat caccattatc	1200
gtcattgcgg cgggtatcta cgcatttttc gtgatcaaaa aagataacca ggacgtgaat	1260
ggtgaaccgc tggtttctaa agcagcttaa	1290

<210> 162
 <211> 1185
 <212> DNA

<213> Artificial Sequence

<220>

<223> codon optimized CDS from Bifidobacterium pseudocatenuatum

<400> 162

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atgacctcgg cggaacaagg ccaaattctac tcaatcaact cgctggctac cctgggttatt      60
atgttcgctt atgggtgctat ccaagaccaa ctgggcatca aacgtaaact ggttatcttt      120
gtcagcgcgga ttgcggccct gggttggtccg tttgtgcaat tcgtttatgc accgatgctg      180
accgcgggcg gcaccacgcg tttcattggt gttctgattg gttcaatcgt cctgtcggca      240
ggctttatgg ctggttgtag tctgttcgaa gactgaccg aacgttattc ccgcaaattt      300
ggcttcgaat acggtcagag ccgtgcttg ggctcttttg gttatgctat cgtggcgctg      360
tgtgccggct ttctgttcaa cattaatccg ctgctgaact tttgggtggg tagcatctgc      420
ggcctgggta tgctgtgtat ttacgcgttc tgggttcgg ccgaacaaaa agaagaactg      480
aaaaaagaag cggatccgaa cgcagctccg acgaatccga gttttaaaga aatgatctcc      540
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tataccgtgt tcgatcagca aatgtttccg aattattacg cgagtctgtt ctccaccacg      660
gaaattggca acgccaccta cggtagctg aacagctttc aggttttcct ggaatcggcc      720
atgatgggcg tggttccgat tatcatgaag aaaattggcg ttcgtaatag cctgctgctg      780
ggtgcaaccg tcatgtttct gcgcattggc ctgtgcggtg tgttccatga tccggtcagc      840
gtgtctatcg tgaaactggt tcaactcaatt gaagttccgc tgttctgtct gccggcgttt      900
cgttatttca ccctgcattt tgacacgaaa ctgtcggcaa ccctgtacat ggttggcttt      960
cagattgcta gccagatcgg tcaagtcatt ttctctacgc cgatgggtgc actgcacgat      1020
gcaatgggtg accgcccagc ctttttcacg atttctggca tcgtgctggc ggccctgata      1080
tatggctttt tcgtcatcaa aaaagatgac caggaagtgg gcggtgatcc gttttacacc      1140
gacaaacaac tgaaagccca agcggcgggc gaagccaacg cataa      1185

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<210> 163

<211> 1086

<212> DNA

<213> Artificial Sequence

<220>

<223> codon oprimized CDS from Bifidobacterium catenuatum

<400> 163

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atgctgcgtg gctctggcac caataaaaaa aaacaacgta ataacatgac ctcaaacacc      60
cgctccgcct ggaaaaatcc gtcctacctg cagagctctt ttggcatttt catgtttttc      120
tgctcatggg gtatctgggt gtcatttttc tcgcgttggc tgaccgatcc gacgcatggc      180
ctgggtatga cctcggccga acagggccaa atttatagca tcaactctct ggcaacgctg      240
gtgatcatgt ttgcgtacgg cgccattcag gaccaactgg gtatcaaacg taaactggtc      300
attttcgtga gtgccatcgc ggccctgggt ggtccgtttg ttcagttcgt ctatgcaccg      360

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CL5510WOPCT_SeqListing_ST25.txt

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atgctgaccg cgggcggcac cacgcgtttt attggtgtgc tgattggttc tatcgttctg      420
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aaatttggct tcgaatacgg tcagagtcgc gcctggggct cctttggtta tgcaattggt      540
gctctgtgtg cgggctttct gttcaacatc aatccgctgc tgaatTTTTg ggtcggtagc      600
atttgcgggc tgggtatgct gtgtgtctac gctttctggg tgccggcgaa aaaaaagaa      660
gaactgaaaa aagaagcgga tccgaacgca gctccgacca atccgtcatt taaagaaatg      720
atctcgggtg tgaaaatgcc gacgctgtgg gtgctgattg tttttatgct gttcaccaac      780
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tctgctatga tgggcgtggg tccgattatc atgaagaaaa ttggcgtccg taacagcctg      960
ctgctgggtg caaccgtgat gtttctgcgc attggcctgt gtggtgtttt ccacgatccg     1020
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gcgtaa                                           1086

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<210> 164
<211> 1176
<212> DNA
<213> Artificial Sequence

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<220>
<223> codon optimized CDS from Clostridium thermocellum

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<400> 164
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tccctgtttt acatgggtct ggctgtgttt ggtgttttca tgccgggtcta cctggaaggt      120
ctgggctatg ataacaccga catcggcacg tttctgagca ttagctcttt tgtcgggtctg      180
ttcgcacagc cgatctgggg cgtgattagc gatcgtgcca aatctaaaaa caatgtgctg      240
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tactatattt tcgcgggtgat ggtggtttac gcctttttcc aaaccccgat tacgccgatc      360
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atcctgggtc tggcagtgtt tattggctca gcttcgaaa ttatctttct ggttttcggc      780
gaccgtatta tcaaacgcct gggtattaaa tttaccctgt tcggtgcggc cgtcgtggca      840
gttgtccgtt gggcttcact gggctctgat aacaatattt ttgcagtgtt ggctctgcag      900
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gaaatgccgc	cggaactgaa	agcgagcggg	cagacgggtca	actctgtgat	cggctctgggc	1020
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caagtctttt	tcctgaatag	tgtgattggt	ctggcggtcca	ttgtgatctt	tggtgccatc	1140
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<210> 165
 <211> 1311
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon optimized CDS from Granulibacter bethesdensis

<400> 165	
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ggtcagccgc	cgtcggattc ccgtcagaaa cagggcgaaat ccgcgctgct ggataaactg 120
aactttttcc	tggcagatgt gcgtgacggg ctgggtccgt atctggcagt ttacctgctg 180
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aacaaaccgc	gtctgctggc tgttgcatgc ctgctgggtca ccctgagtac gctgctgctg 360
ccgtttatgt	ccggtctgcc gctggtgacc ctgacgcaaa gcatggcggc cgttgccggg 420
gcaattttcg	ccccgggtcat cgcagctatg accctgggtc tgggtgggcac ggatgggttt 480
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ctggcaaacg	gcgggtgaagc taacggcatg gatgggtgcag ctctgaaaga ccaggcatca 720
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ctgggcttcg	tgctgtacgc gctgctgatg ccggaaaccc gtcacctgta a 1311

<210> 166
 <211> 1371
 <212> DNA
 <213> Artificial Sequence

CL5510WOPCT_SeqListing_ST25.txt

<220>

<223> codon optimized CDS from *Serratia odorifera*

<400> 166

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atgctgaccc tgaccttcgt tatcaatatc gctatcccgg acgtgggagg ttttatctgg      60
ccgaaagtga atgtgaacaa caaagctgat attatccatc agggcatttc tcacgaaccg      120
cgtaacaaaa aatattacgt tctgctgagt ggtctgctgt ttttcttttt ctttacctgg      180
agcgcgtctt ttagtctgat ttctatctgg ctgaatcaga aaatcggcct gaaaggcacc      240
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tgcgcagtgg caggcaccac gctggtttct tgtttcctgc tgcgtggtga aaccccgga     1320
cgcgctccgc agtttcaaag tacgattaa tcatcggaac cgatccagta a                1371

```

<210> 167

<211> 1314

<212> DNA

<213> Artificial Sequence

<220>

<223> codon optimized CDS from *Streptomyces albus*

<400> 167

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ctgtcttggg gtctgttttc gatttggctg acgcaggata tcggcctgtc tccgggcccgt     180
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ctgggcctgg tggttggtag tgcttacctg gccatggcat ttgctgtggc ggttgccacc	420
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<210> 168
 <211> 1284
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon optimized CDS from Azotobacter vinelandii

<400> 168	
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tcgggcaccg aaacgggctt ttttttcgcg gccaacgcca ttgcagctct gttcatccag	180
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cacgatgtgg ttctgggcgc actggttggt gcagcttttc tggctttcgc gatgctggcg	360
ggcgtgggtg ttattgaatc atataccgaa cgtctgtcgc gccatgccgg ctttgaattt	420
ggcaccacgc gtatgtgggg ctccctgggt tgggcggccg caaccgggtg ggcagggtgc	480
gtgttcgata ttgaccgga tatcgccttt tacatgagct ctgctgcggg cctggcattc	540
ctgctgatcc tgagccgtct ggacatggat gcctttcgta accacgaaac ccgcgctggt	600
gaatctgcgc cggttcgcac ggcggatatt ctgcaactgc tgcgtctgcc gcgcttttgg	660

CL5510WOPCT_SeqListing_ST25.txt

gccttcagtc	tgtttctgac	cggcgtggca	ggtgtttata	tgatctacga	acagcaattc	720
ccggtgtatt	ttgcgagctt	tttcccgacc	ccggaagaag	gcacgcgcgc	ctatggttac	780
ctgaatagtt	cccaagtcct	ggtggaagct	ctgctgatgc	tggtcgcgcc	gtgggttgct	840
gcacgtaccg	gtgcaaaata	cggctctgctg	ctggcgggca	cgattatggt	tgtgcgcatc	900
ctgggcagtg	gtctggcttc	cgacgcgtgg	accattgccg	catgcaaaat	gctgcatgct	960
attgaagtgc	cgatcctgct	ggttgcggtc	ttcaaataca	tctgtgttaa	cttcgatgct	1020
cgtctgagcg	cgaccctgta	cctggtctct	tttcagttcg	cccagcaact	gacggcaatg	1080
ctgctgagcc	cggctgttgg	ctatggttac	gatcgcctgg	gctttgagag	tgtttatctg	1140
ctgctggctt	ccctggctcg	tgcgtgtctg	ctgctgagct	ggtctctgct	gcgtgccgac	1200
ccgtcatcga	aaaccacgcg	cgctgcggat	ggtgcaccgg	aactgccggc	cattgcacag	1260
gccgcaaadc	actatgaacc	gtaa				1284

<210> 169
 <211> 1278
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon optimized CDS from *Oenococcus oeni*

<400> 169						
atgattatga	tcaaccaatc	cgaaattaaa	accgccaaca	aaaaaaaaaga	cttctggggc	60
ttcccgttct	cgcacttcac	ctacttcttt	atctggcaga	ttatcaacgg	ttatctgacc	120
ctgtggatgg	aacaaattgg	ccatctgaat	ggtgcggaag	ccggcgtggt	tttcagtatg	180
atggccggtt	tttccctgat	tttcagccg	tcatttgga	tcattctgga	taaactgac	240
ttcaagaaaa	acctgatcct	gaccattagt	atcgcaggta	ttctgacg	cccgtatttc	300
caatggctgt	ttctgccgct	gatgaaaatc	aacagcacct	ttgtcgcgat	tatcacgggc	360
atctttctga	gtttcattct	gaatggcgg	gtctccgtga	ttgaacagta	tgttcaacgt	420
gcaagcctgg	ctaaccattt	tgaatacgg	cacagccgca	tgggcgggtc	tctggcaggc	480
atgtgcgcta	gcttcctggg	cggccaactg	tttctgtgga	gcccgaacag	catcttctgg	540
gcatgtacca	tttctgctat	gatcctgacg	ggtctgctgc	tgtttaacga	taaaattcac	600
atggaaaacg	caaactctgg	gggcggcacc	agctctcgtc	tgaacctgaa	acagatcagt	660
tccatcttca	aaatcaaaaa	cttctgggtc	ctgtcactgt	tttatattgg	cacggcgtcg	720
atctacgata	tcttcgacca	gcaattcatc	atctttttca	aatcattttt	cgacaccgca	780
tcgcagggta	cggcggccta	ttcctacatg	accacggcac	aaattggcat	cgaatttatt	840
ctgatgtttc	cgatgccgtg	gattatcaac	cgtatcgggtg	cacgcaatgg	cctgattgct	900
tatggcacca	tcctggcgat	tcgtattatc	ggcagtgtct	tgtccccgaa	cctgttttgg	960
gtgattctgc	tgcgcctgct	ggccgggtctg	gaaatgccgc	tgattctggt	tagcatcatg	1020
aaatacatct	ctggcgcctt	cgatctgcgc	ctgtatgcga	ccatctacgc	cctgtcatcg	1080

CL5510WOPCT_SeqListing_ST25.txt

aacttttgcta aacagattac cgaatttttc ctggcgaccg cggcgggcaa aatgtatgac	1140
tctatcggct tccatcacac gtacctgatt ctgggtgtta tcgtcgccat ttttaccatc	1200
ttcacggcac tgtttctgaa aaaagaaaac ccggtgcagg caggtgaacg tgatcgcgcg	1260
ggcaatccga aagcctaa	1278

<210> 170
 <211> 1290
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> codon optimized CDS from *Lactobacillus brevis*

<400> 170	
atggactccg caaaaaccga atcgaaacac ttctggggct tcccgctgtc gcatttctcc	60
tactttcttta tctggggccgt cgtgaatggc tatctgacct tgtggatgga acaggttgcc	120
catctgaacg gcacggaaag tgggtgccgtc ttttccatga tggcaggcat ttcactgac	180
tttcaaccga ttttcggtgt ggtttcggat aaactgctgt ttaagaaaaa cctgacctg	240
accattgcga tcgtgggcat tttcatcggc ccgtactttc agtggggttt catgccgatt	300
ctgcatatca gtgcgtttct ggtggccatt gttaccggca cgtttctgag tttcattctg	360
aacggcggtg tctccgtgat cgaacagtat gtgcaacgtg cgagcctggc caatggtttt	420
gaatacgcac actcacgcgt tggcgggttcg gtcgcagggt tcgtggctag cctggttgcg	480
ggtcgtatth tttctgtgaa accgaactct attttctggg cgtgcaccat cgcggccatt	540
atcctgacgt ttctgctgct gttctccgac aaagtgaacc tggataatgc ggcggcggcg	600
ggtgatacct cagactcgct ggatatgaaa acggctctga gtgtgtttta actgaaaaat	660
ctgtgggtcc tggccatttt ctatatgggc gcatccgctc tgtttgacgt tttcgatcag	720
caattcatca tctttttcaa aacctttttc gacacggcag ctgagggcac cctggtgtat	780
agctacatga gctctgcaca aacggctatt gaattttgcc tgatgtttcc gatgccgtgg	840
attatcaaca aaatcggctc tcgtaatggt ctgctgattt atggctttat cacctgtatt	900
cgcatcctgg gtagcgctct gtctccgaac tggatttggg ttgtcggctt ccgtctgctg	960
gcaggctctg aaatgccgct gctgctgacc tcaattatga aatataatgc gggcgccttt	1020
gacatccgcc tgtatgctac ggtgtacgca ctggcttcga atttcgcgaa acaagtttagc	1080
gtctttatth tctctaccgt cgcgggccgt atgtacgatg tgatcggtta tcaacacacc	1140
tacattatca tgggcattgt ggtgtttttc atcacgctgt ttgccgtgtt tttcctgaaa	1200
aaagaagacc cgattcaggc cgggtgaagt gaagatccga acgtgaaagc aaaagttgaa	1260
gcggccagtt ccaccgattc tcgcgaataa	1290

<210> 171
 <211> 1245
 <212> DNA
 <213> Artificial Sequence

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<220>

<223> codon optimized CDS from weissella paramesenteroides

<400> 171

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atggatcaga cgcagaatac gcagaaaaaa cacttttggg cgttcttcgg cacggatgtc      60
agctacttct tcatttggca gattgtgcag ggctttctgg tcctgtggct gaaacaggaa      120
gctgatctga gcggcggtca agcgggtttt gttttcagct ttctggcctt cgcattctctg      180
ttttaccagc cgggtgttcgg cattatcagc gacaaactgg tttttaagaa aaccctgctg      240
ctgtctatta cgatcgcggc cattctgata ggtccgtttt tccaatggct gttcattccg      300
ctgctgcatt ttagctctct gctgggcgca attatcggcg gtttcgctct ggcgtatgtc      360
ctgaacggcg gtgtggcggt tattgaaagt tacgtggaac gtgcctccct ggcaaattggc      420
tttgaatatg gtcacgctcg catgggcggg tcaatcggcg gtgcactggc atcgttcggt      480
gcaggctctg tctttgtgaa aaaccggttc ctgggtcttt ggatttgcag tctggcgggc      540
attatcctga cctgtctggt gatcttcggg gatcgtatta actttgctaa tgcagacgcg      600
gcggaagggt ctagttccgc accgctgaac gccaaaacca tcctgtctat cttcaaaatc      660
aaaaacttct ggatcctgag ctttttcttt atgggtacgt ctgcaattta tgatgtcttt      720
gaccagcaat tcccgggtgt ttaccagacc tttttcacga gtgcggccgc aggcaccgtg      780
gcatactccc gtctgctgac cacgcaaata gccctggaag cactgctgat gattccgatg      840
ccgtggatta tcaacaaaat cggcgctaaa aatgggtctga ttgcgtatgg tgttctgacc      900
ttcctgcgta tcacgctgag cgccattgca ccgaacttct ggtttctgac ctttgtgcgc      960
ctgctggcgt cattcgaaat gccgctgttt ctggtttcga ccatgaaata tatcgctggc     1020
gcgtttgatc tgcgtctgta tgccacgatt tacgccctgg cattcaattt tgcaaaacag     1080
atctcactgt tcatttttag caccgttgcc ggcgatctgt atgactccgt cggtttccat     1140
accacgtact ttatcctggc tgcgctgggt gcgctgggta cgattgttgc agtctttatg     1200
ctgaaaaaag aaaatccggc tcaggcgggt gaagtggcgg aataa                       1245

```

<210> 172

<211> 1278

<212> DNA

<213> Artificial Sequence

<220>

<223> codon optimized CDS from Mannheimia succiniciproducens

<400> 172

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atgctgatga cctcgcaaaa taaaatcaac gccgtgccgt cgaacaaaaa cttctacctg      60
aataaccgca actactggat cttctcaggt tatttctttg ttactttttt catcatggcg      120
acctgctatc cgtttctggg catttggtcg ggtgatatac acggcctgtc aggtgaagac      180
cgtggcacgg tgttcgcaat gatgtcgttt ttcgctctgt gttttcagcc ggttttcggc      240
tacgtcagcg ataaactggg tctgaaaaaa catctgctgt gggttctggg tatttctctg      300
ctgatctatg caccgttttt catttacatc tttgctccgc tgctgaaagt gaatgtttgg      360

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CL5510WOPCT_SeqListing_ST25.txt

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ctgggcagtc tgggtgggcgg tgcataatatt ggctttgttt tccaggcagg tgctccggcg      420
tccgaagcct atatcgaacg tgtttcacgt cgctcgaaat ttgaatacgg tcgtgtccgc      480
atgtttggca tggtcgggtg ggccatttgc gcaagcatcg ctggtgtcct gtatgcaacc      540
aaccggaatc tgggtgttttg gctgggcagc attgcttctc tgatcctgct gctgctgatt      600
gccctggcaa aaccggaaca gacctctacg gtgcaaatcg cggaaaaact gggcgccaac      660
aaaaatccgg ttaacctgcg ccaggctttt gcgctgctga aactgccgaa attctgggcg      720
ctgctggcct atgttatggg tattgctgtg gtctacgata tctttgacca gcaattcggc      780
aactttttca ataccttttt cgaaagccac gaacaaggca ttaaaatgtt tggttatgtc      840
accacggcgg gtgaactgct gaatgccctg attatgtttt tcgtgccgct gattatcaac      900
cgtatcggcg caaaaaatgc tctgctgatt gccggcacca tcatgagcgt gcgcattatc      960
ggcagctctt acgcgattga agcctggcat gtggttgtcc tgaaaacgct gcacatgttt     1020
gaagtcccgt tctatctggt gggctctgtt aaatacatcg cgaacgtctt tgaagtgcatt     1080
ttctcagcca ccatttatct ggttgcatgc cacttcgcta aacagatcgg caatatgctg     1140
gtgtcgccgc tggttggcgc gtggtatgat acctacgggt ttcaagacac gtacctgatt     1200
ctgggctgta tcgcggccgg ttttacgctg ctgagtgtgt tcaccctgac gggcaaaagt     1260
ctgagttccc agtcctaa                                     1278

```

```

<210> 173
<211> 1257
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> codon optimized CDS from Aggregatibacter aphrophilus

```

```

<400> 173
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tggctgggtg atatccacgg cctgaaaggt gaaaaaatcg gttacgtgtt tagtttcatc     180
tccctgtttg cgctgctgtt ccagccgatt ctgggctttc tgagcgacaa actgggtatc     240
cgtaaacatc tgctgtggct gctggcaatt ctgctgctgt tttatgctcc gtttttcatc     300
tacgttttcg ctccgctgct gaaaaccaac ctgtggctgg gtgtgattgc cggcgggtgca     360
tatatgggct ttgttttcca ggcgggtgcc ccggcaagtg aagcctatat tgaacgtatc     420
tcccgcctgg atggctttga atacggtcgt accgcctgt tcggcatgct gggttgggct     480
at ttg cgcga gtatcgccgg taacctgtac agctctcaac cgaatgccgt cttttggctg     540
ggctctgcta cggcgggtgg tctgctgggt ctgattttcc tggcgaaaac cgatagttcc     600
aacacggccc aggtcgtgga caaactgggt gtgaataaat caccgatcac cctgaaacaa     660
gcgctgaaac tgttttcgct gccgcgtttc tgggcactgc tgacgtatgt tgtcgggtgtg     720
gcttgtgttt acgatatttt tgaccagcaa ttcggcaact ttttcaacac ctttttcgaa     780

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CL5510WOPCT_SeqListing_ST25.txt

agcaaagaac agggcatgaa atttttcggg tatgtttacca cgggcgggtga actgctgaat 840
gccacgatca tgtttttcgt cccgctgctg attaaccgta tcggcgcaaa aaatgctctg 900
ctgattgcag gttcaatcat gtcgattcgc atcatgggct catcgtttgc gaccgaagcc 960
tggcatgtga ttgttctgaa aacgctgcac atgtttgaag ttccgttcta tctggtcggc 1020
gtgtttaaat acattgcgga tgtctttgaa gtgcgcttct ccgccaccat ctatctgggtg 1080
agctgccact tttctaaaca gattggtaac atgatcctga gcccggcagt tggcaccctg 1140
tatgacatgt acggttttca atctacgtac ttcattctgg gctgtatcgc tctgaccttt 1200
acgagcgttt ctgtcttcac cctgggttaat acgaaaaaac tgggtcaacaa tgcgtaa 1257

<210> 174
<211> 100
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 174
cgtctaccct tgttatacct cacaccgcaa ggagacgatc atgaccaata atcccccttc 60
agcacagatt aagcccggcg gtgtaggctg gagctgcttc 100

<210> 175
<211> 100
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 175
gcatcaggca atgaataccc aatgcgacca gcttcttata tcagaacagc cccaacgggtt 60
tatccgagta gtcaccagc catatgaata tcctccttag 100

<210> 176
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 176
atgaccaata atcccccttc ag 22

<210> 177
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 177
gcttcttata tcagaacagc c 21

CL5510WOPCT_SeqListing_ST25.txt