

SEQUENCE LISTING

<110> Evonik Degussa GmbH

<120> Method for producing L-amino acids

<130> 201600130

<160> 14

<170> PatentIn version 3.5

<210> 1

<211> 1719

<212> DNA

<213> Saccharomyces cerevisiae

<220>

<221> misc_feature

<222> (1)..(6)

<223> NdeI restriction site

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<221> CDS

<222> (4)..(1719)

<223> sequence of PDC1 of Sacharomyces cerevisiae optimized for the codon usage of Escherichia coli with a carboxy-terminal His6-tag

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<222> (1693)..(1698)

<223> XhoI restriction site

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cag gtt aat gtg aat acc gtt ttt ggt ctg cct ggc gat ttt aat ctg	96
Gln Val Asn Val Asn Thr Val Phe Gly Leu Pro Gly Asp Phe Asn Leu	
20 25 30	

agc ctg ctg gat aaa atc tat gaa gtt gaa ggt atg cgt tgg gca ggt	144
Ser Leu Leu Asp Lys Ile Tyr Glu Val Glu Gly Met Arg Trp Ala Gly	
35 40 45	

aat gca aat gaa ctg aat gca gcc tat gca gca gat ggt tat gca cgt	192
Asn Ala Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg	

50	55	60	
att aaa ggt atg agc tgc Ile Lys Gly Met Ser Cys 65	att att acc acc ttt Ile Ile Thr Thr Phe 70	ggt gtt ggt gaa ctg Gly Val Gly Glu Leu 75	240
agc gca ctg aat ggt att Ser Ala Leu Asn Gly Ile 80	gca ggt agc tat gca Ala Gly Ser Tyr Ala 85	gaa cat gtt ggt gtg Glu His Val Gly Val 90	288
ctg cat gtt gtt ggt gtt Leu His Val Val Gly Val 100	ccg agc att agc gca Pro Ser Ile Ser Ala 105	cag gca aaa cag ctg Gln Ala Lys Gln Leu 110	336
ctg ctg cat cat acc ctg Leu Leu His His Thr Leu 115	ggt aat ggt gat ttt Gly Asn Gly Asp Phe Thr 120	acc gtg ttt cat cgt Thr Val Phe His Arg 125	384
atg agc gca aat att agc Met Ser Ala Asn Ile Ser 130	gaa acc acc gca atg Glu Thr Thr Ala Met 135	att acc gat att gca Ile Thr Asp Ile Ala 140	432
acc gca ccg gca gaa att Thr Ala Pro Ala Glu Ile 145	gat cgt tgt att cgt Asp Arg Cys Ile Arg 150	acc acc tat gtt acc Thr Thr Tyr Val Thr 155	480
cag cgt ccg gtt tat ctg Gln Arg Pro Val Tyr Leu 160	ggt ctg cca gca aat Gly Leu Pro Ala Asn Leu 165	ctg gtt gat ctg aat Val Val Asp Leu Asn 170	528
gtt ccg gct aaa ctg ctg Val Pro Ala Lys Leu Leu 180	caa acc ccg att gat Gln Thr Pro Ile Asp 185	atg agc ctg aaa ccg Met Ser Leu Lys Pro 190	576
aat gat gca gaa agc gaa Asn Asp Ala Glu Ser Glu 195	aaa gaa gtg att gat Lys Glu Val Ile Asp 200	acc att ctg gcc ctg Thr Ile Leu Ala Leu 205	624
gtt aaa gat gca aaa aat Val Lys Asp Ala Lys Asn 210	ccg gtt att ctg gca Pro Val Ile Leu Ala 215	gat gcc tgt tgt agc Asp Ala Cys Cys Ser 220	672
cgt cat gat gtt aaa gca Arg His Asp Val Lys Ala 225	gaa acc aaa aaa ctg Glu Thr Lys Lys Leu 230	atc gac ctg acc cag Ile Asp Leu Thr Gln 235	720
ttt ccg gca ttt gtt acc Phe Pro Ala Phe Val Thr 240	ccg atg ggt aaa ggt Pro Met Gly Lys Gly 245	agc att gat gaa cag Ser Ile Asp Glu Gln 250	768

cat ccg cgt tat ggt ggt gtt tat gtt ggc acc ctg agc aaa ccg gaa	816
His Pro Arg Tyr Gly Gly Val Tyr Val Gly Thr Leu Ser Lys Pro Glu	
260 265 270	
gtt aaa gaa gca gtt gaa agc gca gat ctg att ctg agc gtt ggt gca	864
Val Lys Glu Ala Val Glu Ser Ala Asp Leu Ile Leu Ser Val Gly Ala	
275 280 285	
ctg ctg agt gat ttt aac acc ggt agc ttt tcg tat agc tac aaa acg	912
Leu Leu Ser Asp Phe Asn Thr Gly Ser Phe Ser Tyr Ser Tyr Lys Thr	
290 295 300	
aaa aac atc gtc gag ttt cat agc gat cac atg aaa att cgt aat gca	960
Lys Asn Ile Val Glu Phe His Ser Asp His Met Lys Ile Arg Asn Ala	
305 310 315	
acc ttt ccg ggt gtg cag atg aaa ttt gtt ctg caa aaa ctg ctg acc	1008
Thr Phe Pro Gly Val Gln Met Lys Phe Val Leu Gln Lys Leu Leu Thr	
320 325 330 335	
acc att gca gat gca gca aaa ggt tat aaa ccg gtt gca gtt ccg gca	1056
Thr Ile Ala Asp Ala Ala Lys Gly Tyr Lys Pro Val Ala Val Pro Ala	
340 345 350	
cgt aca ccg gca aat gca gcc gtt ccg gca tca aca ccg ctg aaa caa	1104
Arg Thr Pro Ala Asn Ala Ala Val Pro Ala Ser Thr Pro Leu Lys Gln	
355 360 365	
gaa tgg atg tgg aat cag ctg ggt aat ttt ctg caa gag ggt gat gtt	1152
Glu Trp Met Trp Asn Gln Leu Gly Asn Phe Leu Gln Glu Gly Asp Val	
370 375 380	
gtt att gca gaa acc ggc acc agc gca ttt ggt att aat cag acc acc	1200
Val Ile Ala Glu Thr Gly Thr Ser Ala Phe Gly Ile Asn Gln Thr Thr	
385 390 395	
ttt ccg aat aac acc tat ggt att agc cag gtt ctg tgg ggt agt att	1248
Phe Pro Asn Asn Thr Tyr Gly Ile Ser Gln Val Leu Trp Gly Ser Ile	
400 405 410 415	
ggt ttt acc acc ggt gca acc ctg ggt gca gca ttt gca gcc gaa gaa	1296
Gly Phe Thr Thr Gly Ala Thr Leu Gly Ala Ala Phe Ala Ala Glu Glu	
420 425 430	
atc gat ccg aaa aaa cgt gtg att ctg ttt att ggt gat ggt agc ctg	1344
Ile Asp Pro Lys Lys Arg Val Ile Leu Phe Ile Gly Asp Gly Ser Leu	
435 440 445	
caa ctg acc gtt caa gaa att agc acc atg att cgt tgg ggt ctg aaa	1392
Gln Leu Thr Val Gln Glu Ile Ser Thr Met Ile Arg Trp Gly Leu Lys	

450	455	460	
ccg tac ctg ttc gtt ctg aat aat gat ggc tat acc atc gag aaa ctg			1440
Pro Tyr Leu Phe Val Leu Asn Asn Asp Gly Tyr Thr Ile Glu Lys Leu			
465	470	475	
atc cac ggt ccg aaa gca cag tat aat gaa att cag ggt tgg gat cat			1488
Ile His Gly Pro Lys Ala Gln Tyr Asn Glu Ile Gln Gly Trp Asp His			
480	485	490	495
ctg tca ctg ctg ccg acc ttt ggc gca aaa gat tat gaa aca cat cgt			1536
Leu Ser Leu Leu Pro Thr Phe Gly Ala Lys Asp Tyr Glu Thr His Arg			
500	505	510	
gtt gca acc aca ggt gaa tgg gat aaa ctg acc cag gat aaa tcc ttt			1584
Val Ala Thr Thr Gly Glu Trp Asp Lys Leu Thr Gln Asp Lys Ser Phe			
515	520	525	
aat gat aac agc aaa atc cgc atg atc gaa att atg ctg ccg gtt ttt			1632
Asn Asp Asn Ser Lys Ile Arg Met Ile Glu Ile Met Leu Pro Val Phe			
530	535	540	
gat gca ccg cag aat ctg gtg gaa cag gcc aaa ctg acc gca gca acc			1680
Asp Ala Pro Gln Asn Leu Val Glu Gln Ala Lys Leu Thr Ala Ala Thr			
545	550	555	
aat gca aaa cag ctc gag cac cac cac cac cac cac tga			1719
Asn Ala Lys Gln Leu Glu His His His His His His			
560	565	570	

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 <212> PRT
 <213> *Saccharomyces cerevisiae*

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Phe Pro Gly Val Gln Met Lys Phe Val Leu Gln Lys Leu Leu Thr Thr
325 330 335

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

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

Trp Met Trp Asn Gln Leu Gly Asn Phe Leu Gln Glu Gly Asp Val Val
370 375 380

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

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

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

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

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

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

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

Ser Leu Leu Pro Thr Phe Gly Ala Lys Asp Tyr Glu Thr His Arg Val
500 505 510

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

Asp Asn Ser Lys Ile Arg Met Ile Glu Ile Met Leu Pro Val Phe Asp
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<220>
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<223> NdeI restriction site

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<222> (4)..(1932)
<223> sequence of AR010 of Sacharomyces cerevisiae optimized for the
codon usage of Escherichia coli with a carboxy-terminal His6-tag

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 <222> (1906)..(1911)
 <223> XhoI restriction site

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	1				5					10					15	

cac	ctg	gtt	agc	aat	cgt	agc	gca	acc	att	ccg	ttt	ggt	gaa	tat	atc	96
His	Leu	Val	Ser	Asn	Arg	Ser	Ala	Thr	Ile	Pro	Phe	Gly	Glu	Tyr	Ile	
			20						25					30		

ttt	aaa	cgc	ctg	ctg	agc	att	gat	acc	aaa	agc	gtg	ttt	ggt	gtt	ccg	144
Phe	Lys	Arg	Leu	Leu	Ser	Ile	Asp	Thr	Lys	Ser	Val	Phe	Gly	Val	Pro	
			35					40					45			

ggt	gat	ttt	aat	ctg	agc	ctg	ctg	gaa	tat	ctg	tat	agc	ccg	agc	gtt	192
Gly	Asp	Phe	Asn	Leu	Ser	Leu	Leu	Glu	Tyr	Leu	Tyr	Ser	Pro	Ser	Val	
		50					55					60				

gaa	agc	gca	ggt	ctg	cgt	tgg	gtt	ggc	acc	tgt	aat	gaa	ctg	aat	gca	240
Glu	Ser	Ala	Gly	Leu	Arg	Trp	Val	Gly	Thr	Cys	Asn	Glu	Leu	Asn	Ala	
	65					70				75						

gcc	tat	gca	gca	gat	ggt	tat	agc	cgt	tat	agc	aac	aaa	att	ggt	tgt	288
Ala	Tyr	Ala	Ala	Asp	Gly	Tyr	Ser	Arg	Tyr	Ser	Asn	Lys	Ile	Gly	Cys	
80					85					90					95	

ctg	att	acc	acc	tat	ggt	gtt	ggt	gaa	ctg	agc	gca	ctg	aat	ggt	att	336
Leu	Ile	Thr	Thr	Tyr	Gly	Val	Gly	Glu	Leu	Ser	Ala	Leu	Asn	Gly	Ile	
				100					105					110		

gca	ggt	agc	ttt	gca	gaa	aat	gtg	aaa	gtg	ctg	cat	att	gtt	ggt	gtg	384
Ala	Gly	Ser	Phe	Ala	Glu	Asn	Val	Lys	Val	Leu	His	Ile	Val	Gly	Val	
			115					120					125			

gcc	aaa	agt	att	gat	agc	cgt	agc	agc	aat	ttt	agc	gat	cgt	aat	ctg	432
Ala	Lys	Ser	Ile	Asp	Ser	Arg	Ser	Ser	Asn	Phe	Ser	Asp	Arg	Asn	Leu	
		130					135					140				

cat	cat	ctg	gtt	ccg	cag	ctg	cat	gat	agc	aac	ttt	aaa	ggt	ccg	aac	480
His	His	Leu	Val	Pro	Gln	Leu	His	Asp	Ser	Asn	Phe	Lys	Gly	Pro	Asn	
		145				150					155					

cat	aaa	gtg	tat	cac	gac	atg	gtt	aaa	gat	cgt	gtt	gca	tgt	agc	gtt	528
His	Lys	Val	Tyr	His	Asp	Met	Val	Lys	Asp	Arg	Val	Ala	Cys	Ser	Val	
160					165					170					175	

gca	tat	ctg	gaa	gat	att	gaa	acc	gca	tgt	gat	cag	gtg	gat	aat	gtg	576
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Ala Tyr Leu Glu Asp Ile Glu Thr Ala Cys Asp Gln Val Asp Asn Val	
180 185 190	
att cgc gat atc tat aaa tac agc aaa ccg ggt tat atc ttt gtg cct	624
Ile Arg Asp Ile Tyr Lys Tyr Ser Lys Pro Gly Tyr Ile Phe Val Pro	
195 200 205	
gcc gat ttt gca gat atg agc gtt acc tgt gat aat ctg gtt aat gtt	672
Ala Asp Phe Ala Asp Met Ser Val Thr Cys Asp Asn Leu Val Asn Val	
210 215 220	
ccg cgt att agc cag cag gat tgt att gtt tat ccg agc gaa aat cag	720
Pro Arg Ile Ser Gln Gln Asp Cys Ile Val Tyr Pro Ser Glu Asn Gln	
225 230 235	
ctg agc gac att att aac aaa atc acc agc tgg atc tat agc agc aaa	768
Leu Ser Asp Ile Ile Asn Lys Ile Thr Ser Trp Ile Tyr Ser Ser Lys	
240 245 250 255	
aca ccg gca att ctg ggt gat gtt ctg acc gat cgt tat ggt gtt agc	816
Thr Pro Ala Ile Leu Gly Asp Val Leu Thr Thr Asp Arg Tyr Gly Val Ser	
260 265 270	
aat ttt ctg aac aaa ctg att tgc aaa acc ggc atc tgg aat ttt tct	864
Asn Phe Leu Asn Lys Leu Ile Cys Lys Thr Gly Ile Trp Asn Phe Ser	
275 280 285	
acc gtt atg ggt aaa agc gtg atc gat gaa agc aat ccg acc tat atg	912
Thr Val Met Gly Lys Ser Val Ile Asp Glu Ser Asn Pro Thr Tyr Met	
290 295 300	
ggt cag tat aat ggt aaa gaa ggc ctg aaa cag gtc tat gaa cat ttt	960
Gly Gln Tyr Asn Gly Lys Glu Gly Leu Lys Gln Val Tyr Glu His Phe	
305 310 315	
gaa ctg tgt gat ctg gtg ctg cat ttt ggc gtt gac att aac gaa att	1008
Glu Leu Cys Asp Leu Val Leu His Phe Gly Val Asp Ile Asn Glu Ile	
320 325 330 335	
aac aac ggc cat tac acc ttc acc tat aaa ccg aat gca aaa atc atc	1056
Asn Asn Gly His Tyr Thr Phe Thr Tyr Lys Pro Asn Ala Lys Ile Ile	
340 345 350	
cag ttc cac ccg aac tat att cgt ctg gtt gat acc cgt cag ggt aat	1104
Gln Phe His Pro Asn Tyr Ile Arg Leu Val Asp Thr Arg Gln Gly Asn	
355 360 365	
gag cag atg ttt aaa ggt att aac ttt gca ccg atc ctg aaa gag ctg	1152
Glu Gln Met Phe Lys Gly Ile Asn Phe Ala Pro Ile Leu Lys Glu Leu	
370 375 380	

tat aaa cgt att gat gtg agc aaa ctg tcc ctg caa tat gat agt aat Tyr Lys Arg Ile Asp Val Ser Lys Leu Ser Leu Gln Tyr Asp Ser Asn 385 390 395	1200
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ggc cag agc agc att att acc cag gtt cat ctg caa aaa acg atg ccg Gly Gln Ser Ser Ile Ile Thr Gln Val His Leu Gln Lys Thr Met Pro 420 425 430	1296
aaa ttt ctg aat cca ggt gat gtt gtt gtt tgt gaa acc ggt agc ttt Lys Phe Leu Asn Pro Gly Asp Val Val Val Cys Glu Thr Gly Ser Phe 435 440 445	1344
cag ttt agc gtt cgt gat ttt gca ttt ccg agc cag ctg aaa tat atc Gln Phe Ser Val Arg Asp Phe Ala Phe Pro Ser Gln Leu Lys Tyr Ile 450 455 460	1392
agc cag ggt ttt ttt ctg agt att ggt atg gca ctg cct gcc gca ctg Ser Gln Gly Phe Phe Leu Ser Ile Gly Met Ala Leu Pro Ala Ala Leu 465 470 475	1440
ggc gtt ggt atc gca atg cag gat cat agc aat gca cat att aat ggt Gly Val Gly Ile Ala Met Gln Asp His Ser Asn Ala His Ile Asn Gly 480 485 490 495	1488
ggc aac gtg aaa gag gat tat aaa ccg cgt ctg att ctg ttt gaa ggt Gly Asn Val Lys Glu Asp Tyr Lys Pro Arg Leu Ile Leu Phe Glu Gly 500 505 510	1536
gat ggt gca gca cag atg acc att caa gaa ctg agc acc att ctg aaa Asp Gly Ala Ala Gln Met Thr Ile Gln Glu Leu Ser Thr Ile Leu Lys 515 520 525	1584
tgt aat att ccg ctg gaa gtg atc atc tgg aac aat aat ggt tat acg Cys Asn Ile Pro Leu Glu Val Ile Ile Trp Asn Asn Asn Gly Tyr Thr 530 535 540	1632
att gag cgt gca att atg ggt ccg acc cgt agc tat aat gat gtt atg Ile Glu Arg Ala Ile Met Gly Pro Thr Arg Ser Tyr Asn Asp Val Met 545 550 555	1680
agc tgg aaa tgg acc aaa ctg ttt gag gca ttt ggc gat ttt gat ggc Ser Trp Lys Trp Thr Lys Leu Phe Glu Ala Phe Gly Asp Phe Asp Gly 560 565 570 575	1728
aaa tat acc aat agc acc ctg att cag tgt ccg agt aaa ctg gca ctg	1776

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

aaa ctg gaa gaa ctg aaa aac agc aat aaa cgc agc ggt att gaa ctg 1824
Lys Leu Glu Glu Leu Lys Asn Ser Asn Lys Arg Ser Gly Ile Glu Leu
595 600 605

ctg gaa gtt aaa ctg ggc gaa ctg gat ttt ccg gaa caa ctg aaa tgc 1872
Leu Glu Val Lys Leu Gly Glu Leu Asp Phe Pro Glu Gln Leu Lys Cys
610 615 620

atg gtt gaa gca gca gcc ctg aaa cgt aat aaa ctc gag cac cac cac 1920
Met Val Glu Ala Ala Ala Leu Lys Arg Asn Lys Leu Glu His His His
625 630 635

cac cac cac tga 1932
His His His
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<212> PRT
<213> Saccharomyces cerevisiae

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35 40 45

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

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

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

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

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

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

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

Lys Val Tyr His Asp Met Val Lys Asp Arg Val Ala Cys Ser Val Ala
165 170 175

Tyr Leu Glu Asp Ile Glu Thr Ala Cys Asp Gln Val Asp Asn Val Ile
180 185 190

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

Asp Phe Ala Asp Met Ser Val Thr Cys Asp Asn Leu Val Asn Val Pro
210 215 220

Arg Ile Ser Gln Gln Asp Cys Ile Val Tyr Pro Ser Glu Asn Gln Leu
225 230 235 240

Ser Asp Ile Ile Asn Lys Ile Thr Ser Trp Ile Tyr Ser Ser Lys Thr
245 250 255

Pro Ala Ile Leu Gly Asp Val Leu Thr Asp Arg Tyr Gly Val Ser Asn
260 265 270

Phe Leu Asn Lys Leu Ile Cys Lys Thr Gly Ile Trp Asn Phe Ser Thr
275 280 285

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

290

295

300

Gln Tyr Asn Gly Lys Glu Gly Leu Lys Gln Val Tyr Glu His Phe Glu
 305 310 315 320

Leu Cys Asp Leu Val Leu His Phe Gly Val Asp Ile Asn Glu Ile Asn
 325 330 335

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

Phe His Pro Asn Tyr Ile Arg Leu Val Asp Thr Arg Gln Gly Asn Glu
 355 360 365

Gln Met Phe Lys Gly Ile Asn Phe Ala Pro Ile Leu Lys Glu Leu Tyr
 370 375 380

Lys Arg Ile Asp Val Ser Lys Leu Ser Leu Gln Tyr Asp Ser Asn Val
 385 390 395 400

Thr Gln Tyr Thr Asn Glu Thr Met Arg Leu Glu Asp Pro Thr Asn Gly
 405 410 415

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

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

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

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

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

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

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

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

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

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

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

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

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

Val Glu Ala Ala Ala Leu Lys Arg Asn Lys Leu Glu His His His His
625 630 635 640

His His

<210> 5
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<212> DNA
<213> Lactococcus lactis

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<222> (1)..(6)

<223> NdeI restriction site

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<222> (4)..(1671)

<223> sequence of kdcA of Lactococcus lactis optimized for the codon usage of Escherichia coli with a carboxy-terminal His6-tag

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1				5					10					15		

ggt	att	gaa	gaa	att	ttt	ggt	gtt	ccg	ggt	gat	tac	aac	ctg	caa	ttt	96
Gly	Ile	Glu	Glu	Ile	Phe	Gly	Val	Pro	Gly	Asp	Tyr	Asn	Leu	Gln	Phe	
				20					25					30		

ctg	gat	cag	att	atc	agc	cgt	gaa	gat	atg	aaa	tgg	att	ggc	aat	gcg	144
Leu	Asp	Gln	Ile	Ile	Ser	Arg	Glu	Asp	Met	Lys	Trp	Ile	Gly	Asn	Ala	
			35					40					45			

aat	gaa	ctg	aat	gca	agc	tat	atg	gca	gat	ggt	tat	gca	cgt	acc	aaa	192
Asn	Glu	Leu	Asn	Ala	Ser	Tyr	Met	Ala	Asp	Gly	Tyr	Ala	Arg	Thr	Lys	
		50					55					60				

aaa	gca	gca	gca	ttt	ctg	acc	acc	ttt	ggt	gtt	ggt	gaa	ctg	agc	gca	240
Lys	Ala	Ala	Ala	Phe	Leu	Thr	Thr	Phe	Gly	Val	Gly	Glu	Leu	Ser	Ala	
	65					70				75						

att	aat	ggt	ctg	gca	ggt	agc	tat	gca	gaa	aat	ctg	ccg	gtt	gtt	gaa	288
Ile	Asn	Gly	Leu	Ala	Gly	Ser	Tyr	Ala	Glu	Asn	Leu	Pro	Val	Val	Glu	
80					85					90					95	

att	gtt	ggt	agc	ccg	acc	agc	aaa	gtt	cag	aat	gat	ggt	aaa	ttt	gtg	336
Ile	Val	Gly	Ser	Pro	Thr	Ser	Lys	Val	Gln	Asn	Asp	Gly	Lys	Phe	Val	
				100					105					110		

cat	cat	acc	ctg	gcc	gat	ggt	gat	ttt	aaa	cac	ttt	atg	aaa	atg	cac	384
His	His	Thr	Leu	Ala	Asp	Gly	Asp	Phe	Lys	His	Phe	Met	Lys	Met	His	
			115					120					125			

gaa	ccg	gtt	acc	gca	gca	cgt	acc	ctg	ctg	acc	gca	gaa	aat	gca	acc	432
Glu	Pro	Val	Thr	Ala	Ala	Arg	Thr	Leu	Leu	Thr	Ala	Glu	Asn	Ala	Thr	
		130					135						140			

tat gaa att gat cgt gtt ctg agc cag ctg ctg aaa gaa cgt aaa ccg Tyr Glu Ile Asp Arg Val Leu Ser Gln Leu Leu Lys Glu Arg Lys Pro 145 150 155	480
gtg tat att aac ctg ccg gtg gat gtt gca gca gca aaa gca gaa aaa Val Tyr Ile Asn Leu Pro Val Asp Val Ala Ala Ala Lys Ala Glu Lys 160 165 170 175	528
ccg gca ctg agc ctg gaa aaa gaa agc agc acc acc aat acc acc gaa Pro Ala Leu Ser Leu Glu Lys Glu Ser Ser Thr Thr Asn Thr Thr Glu 180 185 190	576
cag gtt att ctg agc aaa atc gaa gaa agc ctg aaa aat gcc cag aaa Gln Val Ile Leu Ser Lys Ile Glu Glu Ser Leu Lys Asn Ala Gln Lys 195 200 205	624
ccg gtt gtt att gca ggt cat gaa gtt att agc ttt ggg ctg gaa aaa Pro Val Val Ile Ala Gly His Glu Val Ile Ser Phe Gly Leu Glu Lys 210 215 220	672
acc gtt acc cag ttt gtt agc gaa acc aaa ctg ccg att acc acc ctg Thr Val Thr Gln Phe Val Ser Glu Thr Lys Leu Pro Ile Thr Thr Leu 225 230 235	720
aat ttt ggt aaa agc gca gtt gat gaa agc ctg ccg agc ttt ctg ggt Asn Phe Gly Lys Ser Ala Val Asp Glu Ser Leu Pro Ser Phe Leu Gly 240 245 250 255	768
atc tat aat ggt aaa ctg tcc gag atc tcc ctg aaa aac ttt gtt gaa Ile Tyr Asn Gly Lys Leu Ser Glu Ile Ser Leu Lys Asn Phe Val Glu 260 265 270	816
agc gca gat ttc att ctg atg ctg ggt gtt aaa ctg acc gat agc agt Ser Ala Asp Phe Ile Leu Met Leu Gly Val Lys Leu Thr Asp Ser Ser 275 280 285	864
acc ggt gca ttt acc cat cat ctg gat gaa aac aaa atg atc agc ctg Thr Gly Ala Phe Thr His His Leu Asp Glu Asn Lys Met Ile Ser Leu 290 295 300	912
aac att gat gag ggc atc atc ttt aac aaa gtg gtg gaa gat ttt gat Asn Ile Asp Glu Gly Ile Ile Phe Asn Lys Val Val Glu Asp Phe Asp 305 310 315	960
ttt cgt gca gtt gtt agc agc ctg agc gaa ctg aaa ggt att gaa tat Phe Arg Ala Val Val Ser Ser Leu Ser Glu Leu Lys Gly Ile Glu Tyr 320 325 330 335	1008
gaa ggc cag tac atc gac aaa cag tat gaa gaa ttt att ccg agc agc Glu Gly Gln Tyr Ile Asp Lys Gln Tyr Glu Glu Phe Ile Pro Ser Ser 1056	1056

340	345	350	
gca ccg ctg agc cag gat cgc ctg tgg cag gca gtt gaa agt ctg acc Ala Pro Leu Ser Gln Asp Arg Leu Trp Gln Ala Val Glu Ser Leu Thr 355 360 365			1104
cag agc aat gaa acc att gtt gca gaa cag ggc acc agt ttt ttt ggt Gln Ser Asn Glu Thr Ile Val Ala Glu Gln Gly Thr Ser Phe Phe Gly 370 375 380			1152
gca agc acc att ttt ctg aaa agc aac agc cgt ttt att ggt cag ccg Ala Ser Thr Ile Phe Leu Lys Ser Asn Ser Arg Phe Ile Gly Gln Pro 385 390 395			1200
ctg tgg ggt agc att ggt tat acc ttt ccg gca gca ctg ggt agc cag Leu Trp Gly Ser Ile Gly Tyr Thr Phe Pro Ala Ala Leu Gly Ser Gln 400 405 410 415			1248
att gca gat aaa gaa agc cgt cat ctg ctg ttt att ggt gat ggt agc Ile Ala Asp Lys Glu Ser Arg His Leu Leu Phe Ile Gly Asp Gly Ser 420 425 430			1296
ctg caa ctg acc gtt caa gaa ctg ggt ctg agc att cgt gaa aaa ctg Leu Gln Leu Thr Val Gln Glu Leu Gly Leu Ser Ile Arg Glu Lys Leu 435 440 445			1344
aat ccg att tgc ttc atc att aac aac gat ggc tat acc gtg gaa cgt Asn Pro Ile Cys Phe Ile Ile Asn Asn Asp Gly Tyr Thr Val Glu Arg 450 455 460			1392
gaa att cat ggt ccg acc cag agt tat aat gat att ccg atg tgg aac Glu Ile His Gly Pro Thr Gln Ser Tyr Asn Asp Ile Pro Met Trp Asn 465 470 475			1440
tac tcg aaa ctg cct gaa acc ttt ggc gca acc gaa gat cgt gtg gtt Tyr Ser Lys Leu Pro Glu Thr Phe Gly Ala Thr Glu Asp Arg Val Val 480 485 490 495			1488
agc aaa att gtt cgt acc gaa aat gaa ttt gtg agc gtg atg aaa gaa Ser Lys Ile Val Arg Thr Glu Asn Glu Phe Val Ser Val Met Lys Glu 500 505 510			1536
gca cag gca gac gtt aat cgt atg tat tgg att gaa ctg gtg ctg gaa Ala Gln Ala Asp Val Asn Arg Met Tyr Trp Ile Glu Leu Val Leu Glu 515 520 525			1584
aaa gag gat gca ccg aaa ctg ctg aaa aaa atg ggt aaa ctg ttt gcc Lys Glu Asp Ala Pro Lys Leu Leu Lys Lys Met Gly Lys Leu Phe Ala 530 535 540			1632

gag cag aat aaa ctc gag cac cac cac cac cac tga
 Glu Gln Asn Lys Leu Glu His His His His His His
 545 550 555

1671

<210> 6
 <211> 555
 <212> PRT
 <213> Lactococcus lactis

<400> 6

Met Tyr Thr Val Gly Asp Tyr Leu Leu Asp Arg Leu His Glu Leu Gly
 1 5 10 15

Ile Glu Glu Ile Phe Gly Val Pro Gly Asp Tyr Asn Leu Gln Phe Leu
 20 25 30

Asp Gln Ile Ile Ser Arg Glu Asp Met Lys Trp Ile Gly Asn Ala Asn
 35 40 45

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

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

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

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

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

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

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

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

Ala Leu Ser Leu Glu Lys Glu Ser Ser Thr Thr Asn Thr Thr Glu Gln
180 185 190

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

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

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

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

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

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

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

Ile Asp Glu Gly Ile Ile Phe Asn Lys Val Val Glu Asp Phe Asp Phe
305 310 315 320

Arg Ala Val Val Ser Ser Leu Ser Glu Leu Lys Gly Ile Glu Tyr Glu
325 330 335

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

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

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

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

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

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

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

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

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

Ser Lys Leu Pro Glu Thr Phe Gly Ala Thr Glu Asp Arg Val Val Ser
485 490 495

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

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

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

Gln Asn Lys Leu Glu His His His His His His
545 550 555

<210> 7
 <211> 1207
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1203)
 <223> sequence of ybdL of Escherichia coli with an amino-terminal His6-tag

<220>
 <221> misc_feature
 <222> (37)..(42)
 <223> KasI restriction site

<220>
 <221> misc_feature
 <222> (1202)..(1207)
 <223> HindIII restriction site

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Met Ala Ser Arg Gly Ser His His His His His His Gly Ala Met Thr	
1 5 10 15	

aat aac cct ctg att cca caa agc aaa ctt cca caa ctt ggc acc act	96
Asn Asn Pro Leu Ile Pro Gln Ser Lys Leu Pro Gln Leu Gly Thr Thr	
20 25 30	

att ttc acc cag atg agc gcg ctg gcg cag caa cac cag gcg att aac	144
Ile Phe Thr Gln Met Ser Ala Leu Ala Gln Gln His Gln Ala Ile Asn	
35 40 45	

ctg tcg caa ggc ttt cct gat ttt gat ggt ccg cgc tat tta cag gag	192
Leu Ser Gln Gly Phe Pro Asp Phe Asp Gly Pro Arg Tyr Leu Gln Glu	
50 55 60	

cgg ctg gcg cac cac gtt gca cag ggg gca aac caa tac gcg ccc atg	240
Arg Leu Ala His His Val Ala Gln Gly Ala Asn Gln Tyr Ala Pro Met	
65 70 75 80	

acc ggc gtg cag gcc ttg cgc gag gcg att gct cag aaa acg gaa cgt	288
Thr Gly Val Gln Ala Leu Arg Glu Ala Ile Ala Gln Lys Thr Glu Arg	
85 90 95	

ttg tat ggc tat caa cca gat gcc gat agc gat atc acc gta acg gca	336
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Leu Tyr Gly Tyr Gln Pro Asp Ala Asp Ser Asp Ile Thr Val Thr Ala	
100 105 110	
ggg gcg acg gaa gcg tta tac gcg gcg att acc gca ctg gtg cgc aat	384
Gly Ala Thr Glu Ala Leu Tyr Ala Ala Ile Thr Ala Leu Val Arg Asn	
115 120 125	
ggc gat gaa gtg att tgt ttt gat ccc agc tat gac agt tac gcc ccc	432
Gly Asp Glu Val Ile Cys Phe Asp Pro Ser Tyr Asp Ser Tyr Ala Pro	
130 135 140	
gcc atc gcg ctt tct ggg gga ata gtg aag cgt atg gca ctg caa cca	480
Ala Ile Ala Leu Ser Gly Gly Ile Val Lys Arg Met Ala Leu Gln Pro	
145 150 155 160	
ccg cat ttt cgc gtt gac tgg cag gaa ttt gcc gca tta tta agc gag	528
Pro His Phe Arg Val Asp Trp Gln Glu Phe Ala Ala Leu Leu Ser Glu	
165 170 175	
cgc acc aga ctg gtg atc ctc aac act ccg cat aac ccc agt gca act	576
Arg Thr Arg Leu Val Ile Leu Asn Thr Pro His Asn Pro Ser Ala Thr	
180 185 190	
gtc tgg cag cag gct gat ttc gcc gct ttg tgg cag gcg atc gcc ggg	624
Val Trp Gln Gln Ala Asp Phe Ala Ala Leu Trp Gln Ala Ile Ala Gly	
195 200 205	
cac gag att ttt gtc att agc gat gaa gtc tac gag cac atc aac ttt	672
His Glu Ile Phe Val Ile Ser Asp Glu Val Tyr Glu His Ile Asn Phe	
210 215 220	
tca caa cag ggc cat gcc agt gtg ctg gcg cat ccg cag ctg cgt gag	720
Ser Gln Gln Gly His Ala Ser Val Leu Ala His Pro Gln Leu Arg Glu	
225 230 235 240	
cgg gca gtg gcg gtt tct tca ttt ggc aag acc tat cat atg acc ggc	768
Arg Ala Val Ala Val Ser Ser Phe Gly Lys Thr Tyr His Met Thr Gly	
245 250 255	
tgg aaa gtg ggt tat tgt gtt gcg cca gcg ccc atc agc gcc gaa att	816
Trp Lys Val Gly Tyr Cys Val Ala Pro Ala Pro Ile Ser Ala Glu Ile	
260 265 270	
cgc aag gta cat cag tat ctg acc ttt tcg gtg aat acc ccg gca cag	864
Arg Lys Val His Gln Tyr Leu Thr Phe Ser Val Asn Thr Pro Ala Gln	
275 280 285	
ctg gcg ctt gct gat atg cta cgt gca gaa cct gag cat tat ctt gcg	912
Leu Ala Leu Ala Asp Met Leu Arg Ala Glu Pro Glu His Tyr Leu Ala	
290 295 300	

tta ccg gac ttt tat cgc cag aag cgc gat att ctg gtg aat gct tta	960
Leu Pro Asp Phe Tyr Arg Gln Lys Arg Asp Ile Leu Val Asn Ala Leu	
305 310 315 320	

aat gaa agc cgg ctg gag att tta ccg tgt gaa ggt aca tac ttt ttg	1008
Asn Glu Ser Arg Leu Glu Ile Leu Pro Cys Glu Gly Thr Tyr Phe Leu	
325 330 335	

ctg gtg gat tac agc gcg gtt tct acc ctg gat gat gtt gag ttt tgc	1056
Leu Val Asp Tyr Ser Ala Val Ser Thr Leu Asp Asp Val Glu Phe Cys	
340 345 350	

cag tgg ctg acg cag gag cac ggc gta gcg gcg att ccg ctg tcg gtg	1104
Gln Trp Leu Thr Gln Glu His Gly Val Ala Ala Ile Pro Leu Ser Val	
355 360 365	

ttt tgc gcc gat ccc ttc cca cat aaa ctg att cgt ctc tgt ttt gcc	1152
Phe Cys Ala Asp Pro Phe Pro His Lys Leu Ile Arg Leu Cys Phe Ala	
370 375 380	

aag aag gaa tcg acg ttg ctg gca gca gct gaa cgc ctg cgc cag ctt	1200
Lys Lys Glu Ser Thr Leu Leu Ala Ala Ala Glu Arg Leu Arg Gln Leu	
385 390 395 400	

taa gctt	1207
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<210> 8
 <211> 400
 <212> PRT
 <213> Escherichia coli

<400> 8

Met Ala Ser Arg Gly Ser His His His His His His Gly Ala Met Thr
1 5 10 15

Asn Asn Pro Leu Ile Pro Gln Ser Lys Leu Pro Gln Leu Gly Thr Thr
20 25 30

Ile Phe Thr Gln Met Ser Ala Leu Ala Gln Gln His Gln Ala Ile Asn
35 40 45

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

Arg Leu Ala His His Val Ala Gln Gly Ala Asn Gln Tyr Ala Pro Met
65 70 75 80

Thr Gly Val Gln Ala Leu Arg Glu Ala Ile Ala Gln Lys Thr Glu Arg
85 90 95

Leu Tyr Gly Tyr Gln Pro Asp Ala Asp Ser Asp Ile Thr Val Thr Ala
100 105 110

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

Gly Asp Glu Val Ile Cys Phe Asp Pro Ser Tyr Asp Ser Tyr Ala Pro
130 135 140

Ala Ile Ala Leu Ser Gly Gly Ile Val Lys Arg Met Ala Leu Gln Pro
145 150 155 160

Pro His Phe Arg Val Asp Trp Gln Glu Phe Ala Ala Leu Leu Ser Glu
165 170 175

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

Val Trp Gln Gln Ala Asp Phe Ala Ala Leu Trp Gln Ala Ile Ala Gly
195 200 205

His Glu Ile Phe Val Ile Ser Asp Glu Val Tyr Glu His Ile Asn Phe
210 215 220

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

Arg Ala Val Ala Val Ser Ser Phe Gly Lys Thr Tyr His Met Thr Gly
245 250 255

Trp Lys Val Gly Tyr Cys Val Ala Pro Ala Pro Ile Ser Ala Glu Ile

260

265

270

Arg Lys Val His Gln Tyr Leu Thr Phe Ser Val Asn Thr Pro Ala Gln
 275 280 285

Leu Ala Leu Ala Asp Met Leu Arg Ala Glu Pro Glu His Tyr Leu Ala
 290 295 300

Leu Pro Asp Phe Tyr Arg Gln Lys Arg Asp Ile Leu Val Asn Ala Leu
 305 310 315 320

Asn Glu Ser Arg Leu Glu Ile Leu Pro Cys Glu Gly Thr Tyr Phe Leu
 325 330 335

Leu Val Asp Tyr Ser Ala Val Ser Thr Leu Asp Asp Val Glu Phe Cys
 340 345 350

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

Phe Cys Ala Asp Pro Phe Pro His Lys Leu Ile Arg Leu Cys Phe Ala
 370 375 380

Lys Lys Glu Ser Thr Leu Leu Ala Ala Ala Glu Arg Leu Arg Gln Leu
 385 390 395 400

<210> 9
 <211> 1549
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1545)
 <223> sequence of AR08 of *Saccharomyces cerevisiae* optimized for the
 codon usage of *Escherichia coli* with an amino-terminal His6-tag

<220>
 <221> misc_feature
 <222> (37)..(42)

<223> KasI restriction site

<220>

<221> misc_feature

<222> (1544)..(1549)

<223> HindIII restriction site

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Met Ala Ser Arg Gly Ser His His His His His His Gly Ala Met Thr	
1 5 10 15	

ctg ccg gaa agc aaa gat ttt agc tac ctg ttt tcc gat gaa acc aat	96
Leu Pro Glu Ser Lys Asp Phe Ser Tyr Leu Phe Ser Asp Glu Thr Asn	
20 25 30	

gca cgt aaa ccg agt ccg ctg aaa acc tgt att cat tta ttt cag gat	144
Ala Arg Lys Pro Ser Pro Leu Lys Thr Cys Ile His Leu Phe Gln Asp	
35 40 45	

ccg aac atc atc ttt ctg ggt ggt ggt ctg ccg ctg aaa gat tat ttt	192
Pro Asn Ile Ile Phe Leu Gly Gly Gly Leu Pro Leu Lys Asp Tyr Phe	
50 55 60	

ccg tgg gat aat ctg agc gtt gat agc ccg aaa ccg cct ttt ccg cag	240
Pro Trp Asp Asn Leu Ser Val Asp Ser Pro Lys Pro Pro Phe Pro Gln	
65 70 75 80	

ggt att ggt gca ccg att gat gaa cag aat tgc atc aaa tac acc gtg	288
Gly Ile Gly Ala Pro Ile Asp Glu Gln Asn Cys Ile Lys Tyr Thr Val	
85 90 95	

aac aaa gat tac gca gat aaa agc gca aat ccg agc aat gat att ccg	336
Asn Lys Asp Tyr Ala Asp Lys Ser Ala Asn Pro Ser Asn Asp Ile Pro	
100 105 110	

ctg agc cgt gca ctg cag tat ggt ttt agc gca ggt cag ccg gaa ctg	384
Leu Ser Arg Ala Leu Gln Tyr Gly Phe Ser Ala Gly Gln Pro Glu Leu	
115 120 125	

ctg aac ttt att cgt gat cat acc aaa atc atc cac gat ctg aaa tac	432
Leu Asn Phe Ile Arg Asp His Thr Lys Ile Ile His Asp Leu Lys Tyr	
130 135 140	

aaa gat tgg gat gtt ctg gca acc gca ggt aat acc aat gca tgg gaa	480
Lys Asp Trp Asp Val Leu Ala Thr Ala Gly Asn Thr Asn Ala Trp Glu	
145 150 155 160	

agc acc ctg cgt gtt ttt tgt aat cgt ggt gat gtt att ctg gtt gaa	528
Ser Thr Leu Arg Val Phe Cys Asn Arg Gly Asp Val Ile Leu Val Glu	

165	170	175	
gca cat agc ttt agc agc agc ctg gca agt gcc gaa gca cag ggt gtt Ala His Ser Phe Ser Ser Ser Leu Ala Ser Ala Glu Ala Gln Gly Val 180 185 190			576
att acc ttt ccg gtt ccg atc gat gca gat ggt att att ccg gaa aaa Ile Thr Phe Pro Val Pro Ile Asp Ala Asp Gly Ile Ile Pro Glu Lys 195 200 205			624
ctg gcc aaa gtg atg gaa aat tgg aca ccg ggt gct ccg aaa ccg aaa Leu Ala Lys Val Met Glu Asn Trp Thr Pro Gly Ala Pro Lys Pro Lys 210 215 220			672
ctg ctg tat acc att ccg aca ggt cag aat ccg acc ggc acc agc att Leu Leu Tyr Thr Ile Pro Thr Gly Gln Asn Pro Thr Gly Thr Ser Ile 225 230 235 240			720
gca gat cat cgt aaa gaa gcc atc tat aaa atc gcc cag aaa tac gat Ala Asp His Arg Lys Glu Ala Ile Tyr Lys Ile Ala Gln Lys Tyr Asp 245 250 255			768
ttc ctg atc gtt gaa gat gag ccg tat tat ttc ctg cag atg aac ccg Phe Leu Ile Val Glu Asp Glu Pro Tyr Tyr Phe Leu Gln Met Asn Pro 260 265 270			816
tat atc aaa gat ctg aaa gaa cgt gaa aaa gca cag agc agt ccg aaa Tyr Ile Lys Asp Leu Lys Glu Arg Glu Lys Ala Gln Ser Ser Pro Lys 275 280 285			864
cag gat cat gat gaa ttt ctg aaa agc ctg gcc aat acc ttt ctg agc Gln Asp His Asp Glu Phe Leu Lys Ser Leu Ala Asn Thr Phe Leu Ser 290 295 300			912
ctg gat acc gaa ggt cgt gtt att cgt atg gat agc ttt tca aaa gtt Leu Asp Thr Glu Gly Arg Val Ile Arg Met Asp Ser Phe Ser Lys Val 305 310 315 320			960
ctg gca ccg ggt aca cgt ctg ggt tgg att acc ggt agc agc aaa att Leu Ala Pro Gly Thr Arg Leu Gly Trp Ile Thr Gly Ser Ser Lys Ile 325 330 335			1008
ctg aaa ccg tat ctg agt ctg cat gaa atg acc att cag gca ccg gca Leu Lys Pro Tyr Leu Ser Leu His Glu Met Thr Ile Gln Ala Pro Ala 340 345 350			1056
ggt ttt acc cag gtt ctg gtt aat gca acc ctg agc cgt tgg ggt cag Gly Phe Thr Gln Val Leu Val Asn Ala Thr Leu Ser Arg Trp Gly Gln 355 360 365			1104

aaa ggc tat ctg gat tgg ctg ctg ggt ctg cgt cat gaa tat acc ctg Lys Gly Tyr Leu Asp Trp Leu Leu Gly Leu Arg His Glu Tyr Thr Leu 370 375 380	1152
aaa cgt gat tgt gca att gat gcc ctg tat aaa tac ctg ccg cag agt Lys Arg Asp Cys Ala Ile Asp Ala Leu Tyr Lys Tyr Leu Pro Gln Ser 385 390 395 400	1200
gat gca ttt gtt att aat ccg cct att gcc ggt atg ttc ttt acc gtt Asp Ala Phe Val Ile Asn Pro Pro Ile Ala Gly Met Phe Phe Thr Val 405 410 415	1248
aat att gat gca agc gtg cac ccg gaa ttc aaa acc aaa tat aac agc Asn Ile Asp Ala Ser Val His Pro Glu Phe Lys Thr Lys Tyr Asn Ser 420 425 430	1296
gat ccg tat cag ctg gaa cag agc ctg tat cat aaa gtt gtt gaa cgt Asp Pro Tyr Gln Leu Glu Gln Ser Leu Tyr His Lys Val Val Glu Arg 435 440 445	1344
ggg gtt ctg gtt gtt ccg ggt agc tgg ttt aaa agc gaa ggt gaa acc Gly Val Leu Val Val Pro Gly Ser Trp Phe Lys Ser Glu Gly Glu Thr 450 455 460	1392
gaa ccg cct cag cct gca gaa agt aaa gaa gtt agc aat ccg aat att Glu Pro Pro Gln Pro Ala Glu Ser Lys Glu Val Ser Asn Pro Asn Ile 465 470 475 480	1440
atc ttc ttc cgt ggc acc tat gca gca gtg agc cct gaa aaa ctg acc Ile Phe Phe Arg Gly Thr Tyr Ala Ala Val Ser Pro Glu Lys Leu Thr 485 490 495	1488
gaa ggc ctg aaa cgc ctg ggt gat acc ctg tat gaa gaa ttt ggt atc Glu Gly Leu Lys Arg Leu Gly Asp Thr Leu Tyr Glu Glu Phe Gly Ile 500 505 510	1536
agc aaa taa gctt Ser Lys	1549

<210> 10
 <211> 514
 <212> PRT
 <213> *Saccharomyces cerevisiae*

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

Ala Arg Lys Pro Ser Pro Leu Lys Thr Cys Ile His Leu Phe Gln Asp
35 40 45

Pro Asn Ile Ile Phe Leu Gly Gly Gly Leu Pro Leu Lys Asp Tyr Phe
50 55 60

Pro Trp Asp Asn Leu Ser Val Asp Ser Pro Lys Pro Pro Phe Pro Gln
65 70 75 80

Gly Ile Gly Ala Pro Ile Asp Glu Gln Asn Cys Ile Lys Tyr Thr Val
85 90 95

Asn Lys Asp Tyr Ala Asp Lys Ser Ala Asn Pro Ser Asn Asp Ile Pro
100 105 110

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

Leu Asn Phe Ile Arg Asp His Thr Lys Ile Ile His Asp Leu Lys Tyr
130 135 140

Lys Asp Trp Asp Val Leu Ala Thr Ala Gly Asn Thr Asn Ala Trp Glu
145 150 155 160

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

Ala His Ser Phe Ser Ser Ser Leu Ala Ser Ala Glu Ala Gln Gly Val
180 185 190

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

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

Leu Leu Tyr Thr Ile Pro Thr Gly Gln Asn Pro Thr Gly Thr Ser Ile
225 230 235 240

Ala Asp His Arg Lys Glu Ala Ile Tyr Lys Ile Ala Gln Lys Tyr Asp
245 250 255

Phe Leu Ile Val Glu Asp Glu Pro Tyr Tyr Phe Leu Gln Met Asn Pro
260 265 270

Tyr Ile Lys Asp Leu Lys Glu Arg Glu Lys Ala Gln Ser Ser Pro Lys
275 280 285

Gln Asp His Asp Glu Phe Leu Lys Ser Leu Ala Asn Thr Phe Leu Ser
290 295 300

Leu Asp Thr Glu Gly Arg Val Ile Arg Met Asp Ser Phe Ser Lys Val
305 310 315 320

Leu Ala Pro Gly Thr Arg Leu Gly Trp Ile Thr Gly Ser Ser Lys Ile
325 330 335

Leu Lys Pro Tyr Leu Ser Leu His Glu Met Thr Ile Gln Ala Pro Ala
340 345 350

Gly Phe Thr Gln Val Leu Val Asn Ala Thr Leu Ser Arg Trp Gly Gln
355 360 365

Lys Gly Tyr Leu Asp Trp Leu Leu Gly Leu Arg His Glu Tyr Thr Leu
370 375 380

Lys Arg Asp Cys Ala Ile Asp Ala Leu Tyr Lys Tyr Leu Pro Gln Ser
385 390 395 400

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

Asn Ile Asp Ala Ser Val His Pro Glu Phe Lys Thr Lys Tyr Asn Ser
420 425 430

Asp Pro Tyr Gln Leu Glu Gln Ser Leu Tyr His Lys Val Val Glu Arg
435 440 445

Gly Val Leu Val Val Pro Gly Ser Trp Phe Lys Ser Glu Gly Glu Thr
450 455 460

Glu Pro Pro Gln Pro Ala Glu Ser Lys Glu Val Ser Asn Pro Asn Ile
465 470 475 480

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

Glu Gly Leu Lys Arg Leu Gly Asp Thr Leu Tyr Glu Glu Phe Gly Ile
500 505 510

Ser Lys

<210> 11
<211> 1141
<212> DNA
<213> Bacillus sphaericus

<220>
<221> CDS
<222> (1)..(1137)
<223> sequence of leudh of Bacillus sphaericus optimized for the codon
usage of Escherichia coli with an amino-terminal His6-tag

<220>
<221> misc_feature
<222> (37)..(42)
<223> KasI restriction site

<220>
<221> misc_feature
<222> (1136)..(1141)

<223> HindIII restriction site

<400> 11

atg gct agc aga gga tcg cat cac cat cac cat cac ggc gcc atg gaa	48
Met Ala Ser Arg Gly Ser His His His His His His Gly Ala Met Glu	
1 5 10 15	
att ttc aaa tat atg gaa aaa tat gat tat gaa cag ctg gtg ttc tgt	96
Ile Phe Lys Tyr Met Glu Lys Tyr Asp Tyr Glu Gln Leu Val Phe Cys	
20 25 30	
cag gat gaa gca agc ggt ctg aaa gca gtt att gca att cat gat acc	144
Gln Asp Glu Ala Ser Gly Leu Lys Ala Val Ile Ala Ile His Asp Thr	
35 40 45	
acc ctg ggt ccg gca ctg ggt ggt gca cgt atg tgg acc tat gca agc	192
Thr Leu Gly Pro Ala Leu Gly Gly Ala Arg Met Trp Thr Tyr Ala Ser	
50 55 60	
gaa gaa aat gca att gaa gat gca ctg cgt ctg gca cgt ggt atg acc	240
Glu Glu Asn Ala Ile Glu Asp Ala Leu Arg Leu Ala Arg Gly Met Thr	
65 70 75 80	
tat aaa aac gca gca gca ggt ctg aat ctg ggt ggc ggt aaa acc gtt	288
Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys Thr Val	
85 90 95	
att att ggt gat ccg ttc aaa gat aaa aac gaa gaa atg ttt cgt gcc	336
Ile Ile Gly Asp Pro Phe Lys Asp Lys Asn Glu Glu Met Phe Arg Ala	
100 105 110	
ctg ggt cgt ttt att cag ggt ctg aat ggt cgt tat att acc gca gaa	384
Leu Gly Arg Phe Ile Gln Gly Leu Asn Gly Arg Tyr Ile Thr Ala Glu	
115 120 125	
gat gtt ggc acc acc gtt ctg gat atg gat ctg att cat gaa gaa acc	432
Asp Val Gly Thr Thr Val Leu Asp Met Asp Leu Ile His Glu Glu Thr	
130 135 140	
acc tat gtg acc ggt att agt ccg gca ttt ggt agc agc ggt aat ccg	480
Thr Tyr Val Thr Gly Ile Ser Pro Ala Phe Gly Ser Ser Gly Asn Pro	
145 150 155 160	
agt ccg gtt acc gcc tat ggt gtt tat cgt ggc atg aaa gca gca gca	528
Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met Lys Ala Ala Ala	
165 170 175	
aaa gaa gcc ttt ggt agc gat agc ctg gaa ggc ctg aaa gtt agc gtg	576
Lys Glu Ala Phe Gly Ser Asp Ser Leu Glu Gly Leu Lys Val Ser Val	
180 185 190	

cag ggt ctg ggt aat gtt gca tat aaa ctg tgt gaa tat ctg cac aac Gln Gly Leu Gly Asn Val Ala Tyr Lys Leu Cys Glu Tyr Leu His Asn 195 200 205	624
gaa ggt gca aaa ctg gtt gtt acc gat att aat cag gca gcc att gat Glu Gly Ala Lys Leu Val Val Thr Asp Ile Asn Gln Ala Ala Ile Asp 210 215 220	672
cgt gtg gtg aat gat ttt gat gca att gcc gtt gca ccg gat gaa att Arg Val Val Asn Asp Phe Asp Ala Ile Ala Val Ala Pro Asp Glu Ile 225 230 235 240	720
tat gca caa gaa gtg gat atc ttt agc ccg tgt gcg ctg ggt gca att Tyr Ala Gln Glu Val Asp Ile Phe Ser Pro Cys Ala Leu Gly Ala Ile 245 250 255	768
ctg aat gat gaa acc att ccg cag ctg aaa gca aaa gtt att gcc ggt Leu Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys Val Ile Ala Gly 260 265 270	816
agc gca aat aac caa ctg aaa gat agc cgt cat ggt gat tat ctg cat Ser Ala Asn Asn Gln Leu Lys Asp Ser Arg His Gly Asp Tyr Leu His 275 280 285	864
gag ctg ggt att gtt tat gct ccg gat tat gtt att aat gcc ggt ggt Glu Leu Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile Asn Ala Gly Gly 290 295 300	912
gtg att aat gtt gcc gat gaa ctg tat ggt tat aat cgt gaa cgt gcc Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn Arg Glu Arg Ala 305 310 315 320	960
atg aaa cgt gtg gat ggt att tat gat agc atc gag aaa atc ttt gcc Met Lys Arg Val Asp Gly Ile Tyr Asp Ser Ile Glu Lys Ile Phe Ala 325 330 335	1008
atc agc aaa cgt gat ggt att ccg acc tat gtt gca gca aat cgt ctg Ile Ser Lys Arg Asp Gly Ile Pro Thr Tyr Val Ala Ala Asn Arg Leu 340 345 350	1056
gcc gaa gaa cgt att gca cgt gtt gca aaa agc cgt agc cag ttt ctg Ala Glu Glu Arg Ile Ala Arg Val Ala Lys Ser Arg Ser Gln Phe Leu 355 360 365	1104
aaa aac gaa aaa aac att ctg aac ggt cgt taa gctt Lys Asn Glu Lys Asn Ile Leu Asn Gly Arg 370 375	1141

<210> 12
<211> 378
<212> PRT
<213> Bacillus sphaericus

<400> 12

Met Ala Ser Arg Gly Ser His His His His His His Gly Ala Met Glu
1 5 10 15

Ile Phe Lys Tyr Met Glu Lys Tyr Asp Tyr Glu Gln Leu Val Phe Cys
20 25 30

Gln Asp Glu Ala Ser Gly Leu Lys Ala Val Ile Ala Ile His Asp Thr
35 40 45

Thr Leu Gly Pro Ala Leu Gly Gly Ala Arg Met Trp Thr Tyr Ala Ser
50 55 60

Glu Glu Asn Ala Ile Glu Asp Ala Leu Arg Leu Ala Arg Gly Met Thr
65 70 75 80

Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys Thr Val
85 90 95

Ile Ile Gly Asp Pro Phe Lys Asp Lys Asn Glu Glu Met Phe Arg Ala
100 105 110

Leu Gly Arg Phe Ile Gln Gly Leu Asn Gly Arg Tyr Ile Thr Ala Glu
115 120 125

Asp Val Gly Thr Thr Val Leu Asp Met Asp Leu Ile His Glu Glu Thr
130 135 140

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

Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met Lys Ala Ala Ala
165 170 175

Lys Glu Ala Phe Gly Ser Asp Ser Leu Glu Gly Leu Lys Val Ser Val
180 185 190

Gln Gly Leu Gly Asn Val Ala Tyr Lys Leu Cys Glu Tyr Leu His Asn
195 200 205

Glu Gly Ala Lys Leu Val Val Thr Asp Ile Asn Gln Ala Ala Ile Asp
210 215 220

Arg Val Val Asn Asp Phe Asp Ala Ile Ala Val Ala Pro Asp Glu Ile
225 230 235 240

Tyr Ala Gln Glu Val Asp Ile Phe Ser Pro Cys Ala Leu Gly Ala Ile
245 250 255

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

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

Glu Leu Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile Asn Ala Gly Gly
290 295 300

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

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

Ile Ser Lys Arg Asp Gly Ile Pro Thr Tyr Val Ala Ala Asn Arg Leu
340 345 350

Ala Glu Glu Arg Ile Ala Arg Val Ala Lys Ser Arg Ser Gln Phe Leu
355 360 365

Lys Asn Glu Lys Asn Ile Leu Asn Gly Arg

<210> 13
 <211> 1147
 <212> DNA
 <213> Thermoactinomyces intermedius

<220>
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 <223> sequence of phedh of Thermoactinomyces intermedius optimized for the codon usage of Escherichia coli with an amino-terminal His6-tag

<220>
 <221> misc_feature
 <222> (37)..(42)
 <223> KasI restriction site

<220>
 <221> misc_feature
 <222> (1142)..(1147)
 <223> HindIII restriction site

<400> 13
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 Met Ala Ser Arg Gly Ser His His His His His His Gly Ala Met Arg
 1 5 10 15

gat gtt ttt gaa atg atg gat cgt tat ggt cac gaa cag gtg att ttt 96
 Asp Val Phe Glu Met Met Asp Arg Tyr Gly His Glu Gln Val Ile Phe
 20 25 30

tgt cgt cat ccg cag aca ggt ctg aaa gca att att gca ctg cat aat 144
 Cys Arg His Pro Gln Thr Gly Leu Lys Ala Ile Ile Ala Leu His Asn
 35 40 45

acc acc gca ggt ccg gca ctg ggt ggt tgt cgt atg att ccg tat gca 192
 Thr Thr Ala Gly Pro Ala Leu Gly Gly Cys Arg Met Ile Pro Tyr Ala
 50 55 60

agc acc gat gaa gca ctg gaa gat gtt ctg cgt ctg agc aaa ggt atg 240
 Ser Thr Asp Glu Ala Leu Glu Asp Val Leu Arg Leu Ser Lys Gly Met
 65 70 75 80

acc tat aaa tgt agc ctg gcc gat gtt gat ttt ggt ggt ggt aaa atg 288
 Thr Tyr Lys Cys Ser Leu Ala Asp Val Asp Phe Gly Gly Gly Lys Met
 85 90 95

gtg att att ggc gat ccg aaa aaa gac aaa agt ccg gaa ctg ttt cgt Val Ile Ile Gly Asp Pro Lys Lys Asp Lys Ser Pro Glu Leu Phe Arg 100 105 110	336
gtg att ggt cgt ttt gtt ggt ggt ctg aat ggt cgc ttt tat acc ggc Val Ile Gly Arg Phe Val Gly Gly Leu Asn Gly Arg Phe Tyr Thr Gly 115 120 125	384
acc gat atg ggc acc aat ccg gaa gat ttt gtt cat gca gca cgt gaa Thr Asp Met Gly Thr Asn Pro Glu Asp Phe Val His Ala Ala Arg Glu 130 135 140	432
agc aaa agt ttt gca ggt ctg ccg aaa agc tat ggt ggc aaa ggt gat Ser Lys Ser Phe Ala Gly Leu Pro Lys Ser Tyr Gly Gly Lys Gly Asp 145 150 155 160	480
acc agc att ccg acc gca ctg ggc gtt ttt cat ggt atg cgt gca acc Thr Ser Ile Pro Thr Ala Leu Gly Val Phe His Gly Met Arg Ala Thr 165 170 175	528
gca cgt ttt ctg tgg ggc acc gat cag ctg aaa ggt cgt gtt gtt gca Ala Arg Phe Leu Trp Gly Thr Asp Gln Leu Lys Gly Arg Val Val Ala 180 185 190	576
att cag ggt gtt ggt aaa gtt ggt gaa cgt ctg ctg cag ctg ctg gtt Ile Gln Gly Val Gly Lys Val Gly Glu Arg Leu Leu Gln Leu Leu Val 195 200 205	624
gaa gtt ggt gca tat tgt aaa att gcc gat att gat agc gtt cgt tgc Glu Val Gly Ala Tyr Cys Lys Ile Ala Asp Ile Asp Ser Val Arg Cys 210 215 220	672
gag caa ctg aaa gaa aaa tat ggt gat aaa gtg cag ctg gtt gat gtg Glu Gln Leu Lys Glu Lys Tyr Gly Asp Lys Val Gln Leu Val Asp Val 225 230 235 240	720
aac cgt att cat aaa gaa agc tgc gat atc ttt agc ccg tgt gca aaa Asn Arg Ile His Lys Glu Ser Cys Asp Ile Phe Ser Pro Cys Ala Lys 245 250 255	768
ggg ggt gtg gtt aat gat gat acc att gat gaa ttt cgt tgc ctg gca Gly Gly Val Val Asn Asp Asp Thr Ile Asp Glu Phe Arg Cys Leu Ala 260 265 270	816
att gtt ggt agc gca aat aat cag ctg gta gaa gat cgt cat ggt gca Ile Val Gly Ser Ala Asn Asn Gln Leu Val Glu Asp Arg His Gly Ala 275 280 285	864
ctg ctg cag aaa cgt agc att tgt tat gca ccg gat tat ctg gtt aat	912

Leu Leu Gln Lys Arg Ser Ile Cys Tyr Ala Pro Asp Tyr Leu Val Asn
 290 295 300

gca ggc ggt ctg att cag gtt gca gat gaa ctg gaa ggt ttt cat gaa 960
 Ala Gly Gly Leu Ile Gln Val Ala Asp Glu Leu Glu Gly Phe His Glu
 305 310 315 320

gaa cgt gtt ctg gca aaa acc gaa gcc att tat gat atg gtg ctg gat 1008
 Glu Arg Val Leu Ala Lys Thr Glu Ala Ile Tyr Asp Met Val Leu Asp
 325 330 335

att ttt cac cgt gcc aaa aac gaa aac att acc acc tgt gaa gca gcc 1056
 Ile Phe His Arg Ala Lys Asn Glu Asn Ile Thr Thr Cys Glu Ala Ala
 340 345 350

gat cgt att gtt atg gaa cgt ctg aaa aaa ctg acc gat att cgt cgt 1104
 Asp Arg Ile Val Met Glu Arg Leu Lys Lys Leu Thr Asp Ile Arg Arg
 355 360 365

att ctg ctg gaa gat ccg cgt aat agc gca cgt cgt taa gctt 1147
 Ile Leu Leu Glu Asp Pro Arg Asn Ser Ala Arg Arg
 370 375 380

<210> 14
 <211> 380
 <212> PRT
 <213> Thermoactinomyces intermedius

<400> 14

Met Ala Ser Arg Gly Ser His His His His His His Gly Ala Met Arg
 1 5 10 15

Asp Val Phe Glu Met Met Asp Arg Tyr Gly His Glu Gln Val Ile Phe
 20 25 30

Cys Arg His Pro Gln Thr Gly Leu Lys Ala Ile Ile Ala Leu His Asn
 35 40 45

Thr Thr Ala Gly Pro Ala Leu Gly Gly Cys Arg Met Ile Pro Tyr Ala
 50 55 60

Ser Thr Asp Glu Ala Leu Glu Asp Val Leu Arg Leu Ser Lys Gly Met
 65 70 75 80

Thr Tyr Lys Cys Ser Leu Ala Asp Val Asp Phe Gly Gly Gly Lys Met
85 90 95

Val Ile Ile Gly Asp Pro Lys Lys Asp Lys Ser Pro Glu Leu Phe Arg
100 105 110

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

Thr Asp Met Gly Thr Asn Pro Glu Asp Phe Val His Ala Ala Arg Glu
130 135 140

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

Thr Ser Ile Pro Thr Ala Leu Gly Val Phe His Gly Met Arg Ala Thr
165 170 175

Ala Arg Phe Leu Trp Gly Thr Asp Gln Leu Lys Gly Arg Val Val Ala
180 185 190

Ile Gln Gly Val Gly Lys Val Gly Glu Arg Leu Leu Gln Leu Leu Val
195 200 205

Glu Val Gly Ala Tyr Cys Lys Ile Ala Asp Ile Asp Ser Val Arg Cys
210 215 220

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

Asn Arg Ile His Lys Glu Ser Cys Asp Ile Phe Ser Pro Cys Ala Lys
245 250 255

Gly Gly Val Val Asn Asp Asp Thr Ile Asp Glu Phe Arg Cys Leu Ala
260 265 270

Ile Val Gly Ser Ala Asn Asn Gln Leu Val Glu Asp Arg His Gly Ala

275

280

285

Leu Leu Gln Lys Arg Ser Ile Cys Tyr Ala Pro Asp Tyr Leu Val Asn
290 295 300

Ala Gly Gly Leu Ile Gln Val Ala Asp Glu Leu Glu Gly Phe His Glu
305 310 315 320

Glu Arg Val Leu Ala Lys Thr Glu Ala Ile Tyr Asp Met Val Leu Asp
325 330 335

Ile Phe His Arg Ala Lys Asn Glu Asn Ile Thr Thr Cys Glu Ala Ala
340 345 350

Asp Arg Ile Val Met Glu Arg Leu Lys Lys Leu Thr Asp Ile Arg Arg
355 360 365

Ile Leu Leu Glu Asp Pro Arg Asn Ser Ala Arg Arg
370 375 380

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