

<110> CJ CheilJedang Corporation

<120> GLUTAMATE-CYSTEINE LIGASE VARIANT AND METHOD OF PRODUCING
GLUTATHIONE USING THE SAME

<130> OPA20226

<150> KR 10-2020-0036456

<151> 2020-03-25

<160> 29

<170> KoPatentIn 3.0

<210> 1

<211> 678

<212> PRT

<213> Saccharomyces cerevisiae

<400> 1

Met Gly Leu Leu Ala Leu Gly Thr Pro Leu Gln Trp Phe Glu Ser Arg

1 5 10 15

Thr Tyr Asn Glu His Ile Arg Asp Glu Gly Ile Glu Gln Leu Leu Tyr

20 25 30

Ile Phe Gln Ala Ala Gly Lys Arg Asp Asn Asp Pro Leu Phe Trp Gly

35 40 45

Asp Glu Leu Glu Tyr Met Val Val Asp Phe Asp Asp Lys Glu Arg Asn

50 55 60

Ser Met Leu Asp Val Cys His Asp Lys Ile Leu Thr Glu Leu Asn Met

65

70

75

80

Glu Asp Ser Ser Leu Cys Glu Ala Asn Asp Val Ser Phe His Pro Glu

85

90

95

Tyr Gly Arg Tyr Met Leu Glu Ala Thr Pro Ala Ser Pro Tyr Leu Asn

100

105

110

Tyr Val Gly Ser Tyr Val Glu Val Asn Met Gln Lys Arg Arg Ala Ile

115

120

125

Ala Glu Tyr Lys Leu Ser Glu Tyr Ala Arg Gln Asp Ser Lys Asn Asn

130

135

140

Leu His Val Gly Ser Arg Ser Val Pro Leu Thr Leu Thr Val Phe Pro

145

150

155

160

Arg Met Gly Cys Pro Asp Phe Ile Asn Ile Lys Asp Pro Trp Asn His

165

170

175

Lys Asn Ala Ala Ser Arg Ser Leu Phe Leu Pro Asp Glu Val Ile Asn

180

185

190

Arg His Val Arg Phe Pro Asn Leu Thr Ala Ser Ile Arg Thr Arg Arg

195

200

205

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

210

215

220

Pro Glu Thr Asp Asp Ser Ile Tyr Asp Arg Asp Trp Phe Leu Pro Glu

225

230

235

240

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

Ser Met Gly Phe Gly Met Gly Cys Ser Cys Leu Gln Val Thr Phe Gln
260 265 270

Ala Pro Asn Ile Asn Lys Ala Arg Tyr Leu Tyr Asp Ala Leu Val Asn
275 280 285

Phe Ala Pro Ile Met Leu Ala Phe Ser Ala Ala Ala Pro Ala Phe Lys
290 295 300

Gly Trp Leu Ala Asp Gln Asp Val Arg Trp Asn Val Ile Ser Gly Ala
305 310 315 320

Val Asp Asp Arg Thr Pro Lys Glu Arg Gly Val Ala Pro Leu Leu Pro
325 330 335

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

Lys Val Leu Glu Ile Pro Lys Ser Arg Tyr Ser Ser Val Asp Leu Phe
355 360 365

Leu Gly Gly Ser Lys Phe Phe Asn Arg Thr Tyr Asn Asp Thr Asn Val
370 375 380

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

Pro Leu Asp Tyr Asp Leu Ala Lys His Phe Ala His Leu Tyr Ile Arg

405	410	415	
Asp Pro Val Ser Thr Phe Glu Glu Leu Leu Asn Gln Asp Asn Lys Thr			
420	425	430	
Ser Ser Asn His Phe Glu Asn Ile Gln Ser Thr Asn Trp Gln Thr Leu			
435	440	445	
Arg Phe Lys Pro Pro Thr Gln Gln Ala Thr Pro Asp Lys Lys Asp Ser			
450	455	460	
Pro Gly Trp Arg Val Glu Phe Arg Pro Phe Glu Val Gln Leu Leu Asp			
465	470	475	480
Phe Glu Asn Ala Ala Tyr Ser Val Leu Ile Tyr Leu Ile Val Asp Ser			
485	490	495	
Ile Leu Thr Phe Ser Asp Asn Ile Asn Ala Tyr Ile His Met Ser Lys			
500	505	510	
Val Trp Glu Asn Met Lys Ile Ala His His Arg Asp Ala Ile Leu Phe			
515	520	525	
Glu Lys Phe His Trp Lys Lys Ser Phe Arg Asn Asp Thr Asp Val Glu			
530	535	540	
Thr Glu Asp Tyr Ser Ile Ser Glu Ile Phe His Asn Pro Glu Asn Gly			
545	550	555	560
Ile Phe Pro Gln Phe Val Thr Pro Ile Leu Cys Gln Lys Gly Phe Val			
565	570	575	

Thr Lys Asp Trp Lys Glu Leu Lys His Ser Ser Lys His Glu Arg Leu
580 585 590

Tyr Tyr Tyr Leu Lys Leu Ile Ser Asp Arg Ala Ser Gly Glu Leu Pro
595 600 605

Thr Thr Ala Lys Phe Phe Arg Asn Phe Val Leu Gln His Pro Asp Tyr
610 615 620

Lys His Asp Ser Lys Ile Ser Lys Ser Ile Asn Tyr Asp Leu Leu Ser
625 630 635 640

Thr Cys Asp Arg Leu Thr His Leu Asp Asp Ser Lys Gly Glu Leu Thr
645 650 655

Ser Phe Leu Gly Ala Glu Ile Ala Glu Tyr Val Lys Lys Asn Lys Pro
660 665 670

Ser Ile Glu Ser Lys Cys
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<210> 2

<211> 2037

<212> DNA

<213> Saccharomyces cerevisiae

<400> 2

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gacaatgacc ctctttttg gggagacgag ctgagtaca tggttgtaga tttgatgat	180
aaggagagaa attctatgct cgacgtttgc catgacaaga tactcactga gcttaatatg	240
gaggattcgt cctttgtga ggctaacgat gtgagtttc accctgagta tggccggtat	300
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aacatgcaaa aaagacgtgc cattgcagaa tataagctat ctgaatatgc gagacaagat	420
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acagcatcca tcaggaccag gcgtggtgaa aaagtttgca tgaatgttc catgtataaa	660
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gacaaagagg cgaaactggc ttccaaaccg gggttcattt atatggattc catgggtttt	780
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cctgctttta aagggtggct agccgaccaa gatgttcgtt ggaatgtgat atctggtgcg	960
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aacggatttg gaggcattgc caaagacgta caagataaag tccttgaaat accaaagtca	1080

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gacacaaatg tacctattaa tgaaaaagta ttaggacgac tactagagaa tgataaggcg	1200
ccactggact atgatcttgc taaacatttt gcgcattctt acataagaga tccagtatct	1260
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caaagtacaa attggcagac attacgtttt aaacccccca cacaacaagc aaccccgac	1380
aaaaaggatt ctctgggtg gagagtggaa ttcagacat ttgaagtgc actattagat	1440
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tccgataata ttaacgcata tattcatatg tccaaagtat gggaaaaat gaagatagcc	1560
catcacagag atgctatcct atttgaaaaa ttcatggga aaaaatcatt tcgcaacgac	1620
accgatgtgg aaactgaaga ttattctata agcgagattt tccataatcc agagaatgg	1680
atatttcctc aattgttac gccaatccta tgccaaaaag gggttgtaac caaagattgg	1740
aaagaattaa agcattctc caaacacgag agactatact attatttaa gctaattct	1800
gatagagcaa gcggtgaatt gccacaaca gcaaaattct ttagaaattt tgtactaaa	1860
catccagatt acaaacatga ttcaaaaatt tcaaagtcga tcaattatga ttgctttct	1920
acgtgtgata gactaccca ttagacgat tcaaaagggtg aattgacatc ctttttagga	1980
gctgaaattg cagaatatgt aaaaaaaaaat aagccttcaa tagaaagcaa atgttaa	2037

<210> 3
 <211> 678
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> S.cerevisiae GSH1 C86A

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 1 5 10 15

Thr Tyr Asn Glu His Ile Arg Asp Glu Gly Ile Glu Gln Leu Leu Tyr
 20 25 30

Ile Phe Gln Ala Ala Gly Lys Arg Asp Asn Asp Pro Leu Phe Trp Gly
 35 40 45

Asp Glu Leu Glu Tyr Met Val Val Asp Phe Asp Asp Lys Glu Arg Asn
 50 55 60

Ser Met Leu Asp Val Cys His Asp Lys Ile Leu Thr Glu Leu Asn Met
 65 70 75 80

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

Tyr Gly Arg Tyr Met Leu Glu Ala Thr Pro Ala Ser Pro Tyr Leu Asn
 100 105 110

Tyr Val Gly Ser Tyr Val Glu Val Asn Met Gln Lys Arg Arg Ala Ile

115

120

125

Ala Glu Tyr Lys Leu Ser Glu Tyr Ala Arg Gln Asp Ser Lys Asn Asn

130

135

140

Leu His Val Gly Ser Arg Ser Val Pro Leu Thr Leu Thr Val Phe Pro

145

150

155

160

Arg Met Gly Cys Pro Asp Phe Ile Asn Ile Lys Asp Pro Trp Asn His

165

170

175

Lys Asn Ala Ala Ser Arg Ser Leu Phe Leu Pro Asp Glu Val Ile Asn

180

185

190

Arg His Val Arg Phe Pro Asn Leu Thr Ala Ser Ile Arg Thr Arg Arg

195

200

205

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

210

215

220

Pro Glu Thr Asp Asp Ser Ile Tyr Asp Arg Asp Trp Phe Leu Pro Glu

225

230

235

240

Asp Lys Glu Ala Lys Leu Ala Ser Lys Pro Gly Phe Ile Tyr Met Asp

245

250

255

Ser Met Gly Phe Gly Met Gly Cys Ser Cys Leu Gln Val Thr Phe Gln

260

265

270

Ala Pro Asn Ile Asn Lys Ala Arg Tyr Leu Tyr Asp Ala Leu Val Asn

275

280

285

Phe Ala Pro Ile Met Leu Ala Phe Ser Ala Ala Ala Pro Ala Phe Lys

290

295

300

Gly Trp Leu Ala Asp Gln Asp Val Arg Trp Asn Val Ile Ser Gly Ala

305

310

315

320

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

325

330

335

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

340

345

350

Lys Val Leu Glu Ile Pro Lys Ser Arg Tyr Ser Ser Val Asp Leu Phe

355

360

365

Leu Gly Gly Ser Lys Phe Phe Asn Arg Thr Tyr Asn Asp Thr Asn Val

370

375

380

Pro Ile Asn Glu Lys Val Leu Gly Arg Leu Leu Glu Asn Asp Lys Ala

385

390

395

400

Pro Leu Asp Tyr Asp Leu Ala Lys His Phe Ala His Leu Tyr Ile Arg

405

410

415

Asp Pro Val Ser Thr Phe Glu Glu Leu Leu Asn Gln Asp Asn Lys Thr

420

425

430

Ser Ser Asn His Phe Glu Asn Ile Gln Ser Thr Asn Trp Gln Thr Leu

435

440

445

Arg Phe Lys Pro Pro Thr Gln Gln Ala Thr Pro Asp Lys Lys Asp Ser

450	455	460	
Pro Gly Trp Arg Val Glu Phe Arg Pro Phe Glu Val Gln Leu Leu Asp			
465	470	475	480
Phe Glu Asn Ala Ala Tyr Ser Val Leu Ile Tyr Leu Ile Val Asp Ser			
	485	490	495
Ile Leu Thr Phe Ser Asp Asn Ile Asn Ala Tyr Ile His Met Ser Lys			
	500	505	510
Val Trp Glu Asn Met Lys Ile Ala His His Arg Asp Ala Ile Leu Phe			
	515	520	525
Glu Lys Phe His Trp Lys Lys Ser Phe Arg Asn Asp Thr Asp Val Glu			
530	535	540	
Thr Glu Asp Tyr Ser Ile Ser Glu Ile Phe His Asn Pro Glu Asn Gly			
545	550	555	560
Ile Phe Pro Gln Phe Val Thr Pro Ile Leu Cys Gln Lys Gly Phe Val			
	565	570	575
Thr Lys Asp Trp Lys Glu Leu Lys His Ser Ser Lys His Glu Arg Leu			
	580	585	590
Tyr Tyr Tyr Leu Lys Leu Ile Ser Asp Arg Ala Ser Gly Glu Leu Pro			
595	600	605	
Thr Thr Ala Lys Phe Phe Arg Asn Phe Val Leu Gln His Pro Asp Tyr			
610	615	620	

Lys His Asp Ser Lys Ile Ser Lys Ser Ile Asn Tyr Asp Leu Leu Ser
625 630 635 640

Thr Cys Asp Arg Leu Thr His Leu Asp Asp Ser Lys Gly Glu Leu Thr
 645 650 655

Ser Phe Leu Gly Ala Glu Ile Ala Glu Tyr Val Lys Lys Asn Lys Pro
 660 665 670

Ser Ile Glu Ser Lys Cys
 675

<210> 4
<211> 678
<212> PRT
<213> Artificial Sequence

<220>
<223> S.cerevisiae GSH1 C86D

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Met Gly Leu Leu Ala Leu Gly Thr Pro Leu Gln Trp Phe Glu Ser Arg
 1 5 10 15

Thr Tyr Asn Glu His Ile Arg Asp Glu Gly Ile Glu Gln Leu Leu Tyr
 20 25 30

Ile Phe Gln Ala Ala Gly Lys Arg Asp Asn Asp Pro Leu Phe Trp Gly
 35 40 45

Asp Glu Leu Glu Tyr Met Val Val Asp Phe Asp Asp Lys Glu Arg Asn

50

55

60

Ser Met Leu Asp Val Cys His Asp Lys Ile Leu Thr Glu Leu Asn Met

65

70

75

80

Glu Asp Ser Ser Leu Asp Glu Ala Asn Asp Val Ser Phe His Pro Glu

85

90

95

Tyr Gly Arg Tyr Met Leu Glu Ala Thr Pro Ala Ser Pro Tyr Leu Asn

100

105

110

Tyr Val Gly Ser Tyr Val Glu Val Asn Met Gln Lys Arg Arg Ala Ile

115

120

125

Ala Glu Tyr Lys Leu Ser Glu Tyr Ala Arg Gln Asp Ser Lys Asn Asn

130

135

140

Leu His Val Gly Ser Arg Ser Val Pro Leu Thr Leu Thr Val Phe Pro

145

150

155

160

Arg Met Gly Cys Pro Asp Phe Ile Asn Ile Lys Asp Pro Trp Asn His

165

170

175

Lys Asn Ala Ala Ser Arg Ser Leu Phe Leu Pro Asp Glu Val Ile Asn

180

185

190

Arg His Val Arg Phe Pro Asn Leu Thr Ala Ser Ile Arg Thr Arg Arg

195

200

205

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

210

215

220

Pro Glu Thr Asp Asp Ser Ile Tyr Asp Arg Asp Trp Phe Leu Pro Glu
225 230 235 240

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

Ser Met Gly Phe Gly Met Gly Cys Ser Cys Leu Gln Val Thr Phe Gln
260 265 270

Ala Pro Asn Ile Asn Lys Ala Arg Tyr Leu Tyr Asp Ala Leu Val Asn
275 280 285

Phe Ala Pro Ile Met Leu Ala Phe Ser Ala Ala Ala Pro Ala Phe Lys
290 295 300

Gly Trp Leu Ala Asp Gln Asp Val Arg Trp Asn Val Ile Ser Gly Ala
305 310 315 320

Val Asp Asp Arg Thr Pro Lys Glu Arg Gly Val Ala Pro Leu Leu Pro
325 330 335

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

Lys Val Leu Glu Ile Pro Lys Ser Arg Tyr Ser Ser Val Asp Leu Phe
355 360 365

Leu Gly Gly Ser Lys Phe Phe Asn Arg Thr Tyr Asn Asp Thr Asn Val
370 375 380

Pro Ile Asn Glu Lys Val Leu Gly Arg Leu Leu Glu Asn Asp Lys Ala

385 390 395 400

Pro Leu Asp Tyr Asp Leu Ala Lys His Phe Ala His Leu Tyr Ile Arg

405 410 415

Asp Pro Val Ser Thr Phe Glu Glu Leu Leu Asn Gln Asp Asn Lys Thr

420 425 430

Ser Ser Asn His Phe Glu Asn Ile Gln Ser Thr Asn Trp Gln Thr Leu

435 440 445

Arg Phe Lys Pro Pro Thr Gln Gln Ala Thr Pro Asp Lys Lys Asp Ser

450 455 460

Pro Gly Trp Arg Val Glu Phe Arg Pro Phe Glu Val Gln Leu Leu Asp

465 470 475 480

Phe Glu Asn Ala Ala Tyr Ser Val Leu Ile Tyr Leu Ile Val Asp Ser

485 490 495

Ile Leu Thr Phe Ser Asp Asn Ile Asn Ala Tyr Ile His Met Ser Lys

500 505 510

Val Trp Glu Asn Met Lys Ile Ala His His Arg Asp Ala Ile Leu Phe

515 520 525

Glu Lys Phe His Trp Lys Lys Ser Phe Arg Asn Asp Thr Asp Val Glu

530 535 540

Thr Glu Asp Tyr Ser Ile Ser Glu Ile Phe His Asn Pro Glu Asn Gly

545 550 555 560

Ile Phe Pro Gln Phe Val Thr Pro Ile Leu Cys Gln Lys Gly Phe Val
565 570 575

Thr Lys Asp Trp Lys Glu Leu Lys His Ser Ser Lys His Glu Arg Leu
580 585 590

Tyr Tyr Tyr Leu Lys Leu Ile Ser Asp Arg Ala Ser Gly Glu Leu Pro
595 600 605

Thr Thr Ala Lys Phe Phe Arg Asn Phe Val Leu Gln His Pro Asp Tyr
610 615 620

Lys His Asp Ser Lys Ile Ser Lys Ser Ile Asn Tyr Asp Leu Leu Ser
625 630 635 640

Thr Cys Asp Arg Leu Thr His Leu Asp Asp Ser Lys Gly Glu Leu Thr
645 650 655

Ser Phe Leu Gly Ala Glu Ile Ala Glu Tyr Val Lys Lys Asn Lys Pro
660 665 670

Ser Ile Glu Ser Lys Cys
675

<210> 5

<211> 678

<212> PRT

<213> Artificial Sequence

<220>

<223> S.cerevisiae GSH1 C86E

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Thr Tyr Asn Glu His Ile Arg Asp Glu Gly Ile Glu Gln Leu Leu Tyr

20 25 30

Ile Phe Gln Ala Ala Gly Lys Arg Asp Asn Asp Pro Leu Phe Trp Gly

35 40 45

Asp Glu Leu Glu Tyr Met Val Val Asp Phe Asp Asp Lys Glu Arg Asn

50 55 60

Ser Met Leu Asp Val Cys His Asp Lys Ile Leu Thr Glu Leu Asn Met

65 70 75 80

Glu Asp Ser Ser Leu Glu Glu Ala Asn Asp Val Ser Phe His Pro Glu

85 90 95

Tyr Gly Arg Tyr Met Leu Glu Ala Thr Pro Ala Ser Pro Tyr Leu Asn

100 105 110

Tyr Val Gly Ser Tyr Val Glu Val Asn Met Gln Lys Arg Arg Ala Ile

115 120 125

Ala Glu Tyr Lys Leu Ser Glu Tyr Ala Arg Gln Asp Ser Lys Asn Asn

130 135 140

Leu His Val Gly Ser Arg Ser Val Pro Leu Thr Leu Thr Val Phe Pro

145 150 155 160

Arg Met Gly Cys Pro Asp Phe Ile Asn Ile Lys Asp Pro Trp Asn His
165 170 175

Lys Asn Ala Ala Ser Arg Ser Leu Phe Leu Pro Asp Glu Val Ile Asn
180 185 190

Arg His Val Arg Phe Pro Asn Leu Thr Ala Ser Ile Arg Thr Arg Arg
195 200 205

Gly Glu Lys Val Cys Met Asn Val Pro Met Tyr Lys Asp Ile Ala Thr
210 215 220

Pro Glu Thr Asp Asp Ser Ile Tyr Asp Arg Asp Trp Phe Leu Pro Glu
225 230 235 240

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

Ser Met Gly Phe Gly Met Gly Cys Ser Cys Leu Gln Val Thr Phe Gln
260 265 270

Ala Pro Asn Ile Asn Lys Ala Arg Tyr Leu Tyr Asp Ala Leu Val Asn
275 280 285

Phe Ala Pro Ile Met Leu Ala Phe Ser Ala Ala Ala Pro Ala Phe Lys
290 295 300

Gly Trp Leu Ala Asp Gln Asp Val Arg Trp Asn Val Ile Ser Gly Ala
305 310 315 320

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

	325	330	335
Lys Tyr Asn Lys Asn Gly Phe Gly Gly Ile Ala Lys Asp Val Gln Asp			
	340	345	350
Lys Val Leu Glu Ile Pro Lys Ser Arg Tyr Ser Ser Val Asp Leu Phe			
	355	360	365
Leu Gly Gly Ser Lys Phe Phe Asn Arg Thr Tyr Asn Asp Thr Asn Val			
	370	375	380
Pro Ile Asn Glu Lys Val Leu Gly Arg Leu Leu Glu Asn Asp Lys Ala			
385	390	395	400
Pro Leu Asp Tyr Asp Leu Ala Lys His Phe Ala His Leu Tyr Ile Arg			
	405	410	415
Asp Pro Val Ser Thr Phe Glu Glu Leu Leu Asn Gln Asp Asn Lys Thr			
	420	425	430
Ser Ser Asn His Phe Glu Asn Ile Gln Ser Thr Asn Trp Gln Thr Leu			
	435	440	445
Arg Phe Lys Pro Pro Thr Gln Gln Ala Thr Pro Asp Lys Lys Asp Ser			
	450	455	460
Pro Gly Trp Arg Val Glu Phe Arg Pro Phe Glu Val Gln Leu Leu Asp			
465	470	475	480
Phe Glu Asn Ala Ala Tyr Ser Val Leu Ile Tyr Leu Ile Val Asp Ser			
	485	490	495

Ile Leu Thr Phe Ser Asp Asn Ile Asn Ala Tyr Ile His Met Ser Lys

500

505

510

Val Trp Glu Asn Met Lys Ile Ala His His Arg Asp Ala Ile Leu Phe

515

520

525

Glu Lys Phe His Trp Lys Lys Ser Phe Arg Asn Asp Thr Asp Val Glu

530

535

540

Thr Glu Asp Tyr Ser Ile Ser Glu Ile Phe His Asn Pro Glu Asn Gly

545

550

555

560

Ile Phe Pro Gln Phe Val Thr Pro Ile Leu Cys Gln Lys Gly Phe Val

565

570

575

Thr Lys Asp Trp Lys Glu Leu Lys His Ser Ser Lys His Glu Arg Leu

580

585

590

Tyr Tyr Tyr Leu Lys Leu Ile Ser Asp Arg Ala Ser Gly Glu Leu Pro

595

600

605

Thr Thr Ala Lys Phe Phe Arg Asn Phe Val Leu Gln His Pro Asp Tyr

610

615

620

Lys His Asp Ser Lys Ile Ser Lys Ser Ile Asn Tyr Asp Leu Leu Ser

625

630

635

640

Thr Cys Asp Arg Leu Thr His Leu Asp Asp Ser Lys Gly Glu Leu Thr

645

650

655

Ser Phe Leu Gly Ala Glu Ile Ala Glu Tyr Val Lys Lys Asn Lys Pro

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665

670

Ser Ile Glu Ser Lys Cys

675

<210> 6

<211> 678

<212> PRT

<213> Artificial Sequence

<220>

<223> S.cerevisiae GSH1 C86F

<400> 6

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Thr Tyr Asn Glu His Ile Arg Asp Glu Gly Ile Glu Gln Leu Leu Tyr

20 25 30

Ile Phe Gln Ala Ala Gly Lys Arg Asp Asn Asp Pro Leu Phe Trp Gly

35 40 45

Asp Glu Leu Glu Tyr Met Val Val Asp Phe Asp Asp Lys Glu Arg Asn

50 55 60

Ser Met Leu Asp Val Cys His Asp Lys Ile Leu Thr Glu Leu Asn Met

65 70 75 80

Glu Asp Ser Ser Leu Phe Glu Ala Asn Asp Val Ser Phe His Pro Glu

85 90 95

Tyr Gly Arg Tyr Met Leu Glu Ala Thr Pro Ala Ser Pro Tyr Leu Asn

100

105

110

Tyr Val Gly Ser Tyr Val Glu Val Asn Met Gln Lys Arg Arg Ala Ile

115

120

125

Ala Glu Tyr Lys Leu Ser Glu Tyr Ala Arg Gln Asp Ser Lys Asn Asn

130

135

140

Leu His Val Gly Ser Arg Ser Val Pro Leu Thr Leu Thr Val Phe Pro

145

150

155

160

Arg Met Gly Cys Pro Asp Phe Ile Asn Ile Lys Asp Pro Trp Asn His

165

170

175

Lys Asn Ala Ala Ser Arg Ser Leu Phe Leu Pro Asp Glu Val Ile Asn

180

185

190

Arg His Val Arg Phe Pro Asn Leu Thr Ala Ser Ile Arg Thr Arg Arg

195

200

205

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

210

215

220

Pro Glu Thr Asp Asp Ser Ile Tyr Asp Arg Asp Trp Phe Leu Pro Glu

225

230

235

240

Asp Lys Glu Ala Lys Leu Ala Ser Lys Pro Gly Phe Ile Tyr Met Asp

245

250

255

Ser Met Gly Phe Gly Met Gly Cys Ser Cys Leu Gln Val Thr Phe Gln

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

Ser Ser Asn His Phe Glu Asn Ile Gln Ser Thr Asn Trp Gln Thr Leu

435

440

445

Arg Phe Lys Pro Pro Thr Gln Gln Ala Thr Pro Asp Lys Lys Asp Ser

450

455

460

Pro Gly Trp Arg Val Glu Phe Arg Pro Phe Glu Val Gln Leu Leu Asp

465

470

475

480

Phe Glu Asn Ala Ala Tyr Ser Val Leu Ile Tyr Leu Ile Val Asp Ser

485

490

495

Ile Leu Thr Phe Ser Asp Asn Ile Asn Ala Tyr Ile His Met Ser Lys

500

505

510

Val Trp Glu Asn Met Lys Ile Ala His His Arg Asp Ala Ile Leu Phe

515

520

525

Glu Lys Phe His Trp Lys Lys Ser Phe Arg Asn Asp Thr Asp Val Glu

530

535

540

Thr Glu Asp Tyr Ser Ile Ser Glu Ile Phe His Asn Pro Glu Asn Gly

545

550

555

560

Ile Phe Pro Gln Phe Val Thr Pro Ile Leu Cys Gln Lys Gly Phe Val

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570

575

Thr Lys Asp Trp Lys Glu Leu Lys His Ser Ser Lys His Glu Arg Leu

580

585

590

Tyr Tyr Tyr Leu Lys Leu Ile Ser Asp Arg Ala Ser Gly Glu Leu Pro

595

600

605

Thr Thr Ala Lys Phe Phe Arg Asn Phe Val Leu Gln His Pro Asp Tyr

610

615

620

Lys His Asp Ser Lys Ile Ser Lys Ser Ile Asn Tyr Asp Leu Leu Ser

625

630

635

640

Thr Cys Asp Arg Leu Thr His Leu Asp Asp Ser Lys Gly Glu Leu Thr

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Ser Phe Leu Gly Ala Glu Ile Ala Glu Tyr Val Lys Lys Asn Lys Pro

660

665

670

Ser Ile Glu Ser Lys Cys

675

<210> 7

<211> 678

<212> PRT

<213> Artificial Sequence

<220>

<223> S.cerevisiae GSH1 C86G

<400> 7

Met Gly Leu Leu Ala Leu Gly Thr Pro Leu Gln Trp Phe Glu Ser Arg

1

5

10

15

Thr Tyr Asn Glu His Ile Arg Asp Glu Gly Ile Glu Gln Leu Leu Tyr

20

25

30

Ile Phe Gln Ala Ala Gly Lys Arg Asp Asn Asp Pro Leu Phe Trp Gly

35

40

45

Asp Glu Leu Glu Tyr Met Val Val Asp Phe Asp Asp Lys Glu Arg Asn

50

55

60

Ser Met Leu Asp Val Cys His Asp Lys Ile Leu Thr Glu Leu Asn Met

65

70

75

80

Glu Asp Ser Ser Leu Gly Glu Ala Asn Asp Val Ser Phe His Pro Glu

85

90

95

Tyr Gly Arg Tyr Met Leu Glu Ala Thr Pro Ala Ser Pro Tyr Leu Asn

100

105

110

Tyr Val Gly Ser Tyr Val Glu Val Asn Met Gln Lys Arg Arg Ala Ile

115

120

125

Ala Glu Tyr Lys Leu Ser Glu Tyr Ala Arg Gln Asp Ser Lys Asn Asn

130

135

140

Leu His Val Gly Ser Arg Ser Val Pro Leu Thr Leu Thr Val Phe Pro

145

150

155

160

Arg Met Gly Cys Pro Asp Phe Ile Asn Ile Lys Asp Pro Trp Asn His

165

170

175

Lys Asn Ala Ala Ser Arg Ser Leu Phe Leu Pro Asp Glu Val Ile Asn

180

185

190

Arg His Val Arg Phe Pro Asn Leu Thr Ala Ser Ile Arg Thr Arg Arg

195	200	205	
Gly Glu Lys Val Cys Met Asn Val Pro Met Tyr Lys Asp Ile Ala Thr			
210	215	220	
Pro Glu Thr Asp Asp Ser Ile Tyr Asp Arg Asp Trp Phe Leu Pro Glu			
225	230	235	240
Asp Lys Glu Ala Lys Leu Ala Ser Lys Pro Gly Phe Ile Tyr Met Asp			
	245	250	255
Ser Met Gly Phe Gly Met Gly Cys Ser Cys Leu Gln Val Thr Phe Gln			
	260	265	270
Ala Pro Asn Ile Asn Lys Ala Arg Tyr Leu Tyr Asp Ala Leu Val Asn			
	275	280	285
Phe Ala Pro Ile Met Leu Ala Phe Ser Ala Ala Ala Pro Ala Phe Lys			
	290	295	300
Gly Trp Leu Ala Asp Gln Asp Val Arg Trp Asn Val Ile Ser Gly Ala			
305	310	315	320
Val Asp Asp Arg Thr Pro Lys Glu Arg Gly Val Ala Pro Leu Leu Pro			
	325	330	335
Lys Tyr Asn Lys Asn Gly Phe Gly Gly Ile Ala Lys Asp Val Gln Asp			
	340	345	350
Lys Val Leu Glu Ile Pro Lys Ser Arg Tyr Ser Ser Val Asp Leu Phe			
	355	360	365

Leu Gly Gly Ser Lys Phe Phe Asn Arg Thr Tyr Asn Asp Thr Asn Val

370

375

380

Pro Ile Asn Glu Lys Val Leu Gly Arg Leu Leu Glu Asn Asp Lys Ala

385

390

395

400

Pro Leu Asp Tyr Asp Leu Ala Lys His Phe Ala His Leu Tyr Ile Arg

405

410

415

Asp Pro Val Ser Thr Phe Glu Glu Leu Leu Asn Gln Asp Asn Lys Thr

420

425

430

Ser Ser Asn His Phe Glu Asn Ile Gln Ser Thr Asn Trp Gln Thr Leu

435

440

445

Arg Phe Lys Pro Pro Thr Gln Gln Ala Thr Pro Asp Lys Lys Asp Ser

450

455

460

Pro Gly Trp Arg Val Glu Phe Arg Pro Phe Glu Val Gln Leu Leu Asp

465

470

475

480

Phe Glu Asn Ala Ala Tyr Ser Val Leu Ile Tyr Leu Ile Val Asp Ser

485

490

495

Ile Leu Thr Phe Ser Asp Asn Ile Asn Ala Tyr Ile His Met Ser Lys

500

505

510

Val Trp Glu Asn Met Lys Ile Ala His His Arg Asp Ala Ile Leu Phe

515

520

525

Glu Lys Phe His Trp Lys Lys Ser Phe Arg Asn Asp Thr Asp Val Glu

530

535

540

Thr Glu Asp Tyr Ser Ile Ser Glu Ile Phe His Asn Pro Glu Asn Gly
545 550 555 560

Ile Phe Pro Gln Phe Val Thr Pro Ile Leu Cys Gln Lys Gly Phe Val
565 570 575

Thr Lys Asp Trp Lys Glu Leu Lys His Ser Ser Lys His Glu Arg Leu
580 585 590

Tyr Tyr Tyr Leu Lys Leu Ile Ser Asp Arg Ala Ser Gly Glu Leu Pro
595 600 605

Thr Thr Ala Lys Phe Phe Arg Asn Phe Val Leu Gln His Pro Asp Tyr
610 615 620

Lys His Asp Ser Lys Ile Ser Lys Ser Ile Asn Tyr Asp Leu Leu Ser
625 630 635 640

Thr Cys Asp Arg Leu Thr His Leu Asp Asp Ser Lys Gly Glu Leu Thr
645 650 655

Ser Phe Leu Gly Ala Glu Ile Ala Glu Tyr Val Lys Lys Asn Lys Pro
660 665 670

Ser Ile Glu Ser Lys Cys
675

<210> 8

<211> 678

<212> PRT

<213> Artificial Sequence

<220>

<223> S.cerevisiae GSH1 C86H

<400> 8

Met Gly Leu Leu Ala Leu Gly Thr Pro Leu Gln Trp Phe Glu Ser Arg

1 5 10 15

Thr Tyr Asn Glu His Ile Arg Asp Glu Gly Ile Glu Gln Leu Leu Tyr

20 25 30

Ile Phe Gln Ala Ala Gly Lys Arg Asp Asn Asp Pro Leu Phe Trp Gly

35 40 45

Asp Glu Leu Glu Tyr Met Val Val Asp Phe Asp Asp Lys Glu Arg Asn

50 55 60

Ser Met Leu Asp Val Cys His Asp Lys Ile Leu Thr Glu Leu Asn Met

65 70 75 80

Glu Asp Ser Ser Leu His Glu Ala Asn Asp Val Ser Phe His Pro Glu

85 90 95

Tyr Gly Arg Tyr Met Leu Glu Ala Thr Pro Ala Ser Pro Tyr Leu Asn

100 105 110

Tyr Val Gly Ser Tyr Val Glu Val Asn Met Gln Lys Arg Arg Ala Ile

115 120 125

Ala Glu Tyr Lys Leu Ser Glu Tyr Ala Arg Gln Asp Ser Lys Asn Asn

130	135	140	
Leu His Val Gly Ser Arg Ser Val Pro Leu Thr Leu Thr Val Phe Pro			
145	150	155	160
Arg Met Gly Cys Pro Asp Phe Ile Asn Ile Lys Asp Pro Trp Asn His			
	165	170	175
Lys Asn Ala Ala Ser Arg Ser Leu Phe Leu Pro Asp Glu Val Ile Asn			
	180	185	190
Arg His Val Arg Phe Pro Asn Leu Thr Ala Ser Ile Arg Thr Arg Arg			
	195	200	205
Gly Glu Lys Val Cys Met Asn Val Pro Met Tyr Lys Asp Ile Ala Thr			
	210	215	220
Pro Glu Thr Asp Asp Ser Ile Tyr Asp Arg Asp Trp Phe Leu Pro Glu			
225	230	235	240
Asp Lys Glu Ala Lys Leu Ala Ser Lys Pro Gly Phe Ile Tyr Met Asp			
	245	250	255
Ser Met Gly Phe Gly Met Gly Cys Ser Cys Leu Gln Val Thr Phe Gln			
	260	265	270
Ala Pro Asn Ile Asn Lys Ala Arg Tyr Leu Tyr Asp Ala Leu Val Asn			
	275	280	285
Phe Ala Pro Ile Met Leu Ala Phe Ser Ala Ala Ala Pro Ala Phe Lys			
290	295	300	

Gly Trp Leu Ala Asp Gln Asp Val Arg Trp Asn Val Ile Ser Gly Ala
305 310 315 320

Val Asp Asp Arg Thr Pro Lys Glu Arg Gly Val Ala Pro Leu Leu Pro
325 330 335

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

Lys Val Leu Glu Ile Pro Lys Ser Arg Tyr Ser Ser Val Asp Leu Phe
355 360 365

Leu Gly Gly Ser Lys Phe Phe Asn Arg Thr Tyr Asn Asp Thr Asn Val
370 375 380

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

Pro Leu Asp Tyr Asp Leu Ala Lys His Phe Ala His Leu Tyr Ile Arg
405 410 415

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

Ser Ser Asn His Phe Glu Asn Ile Gln Ser Thr Asn Trp Gln Thr Leu
435 440 445

Arg Phe Lys Pro Pro Thr Gln Gln Ala Thr Pro Asp Lys Lys Asp Ser
450 455 460

Pro Gly Trp Arg Val Glu Phe Arg Pro Phe Glu Val Gln Leu Leu Asp
465 470 475 480

Phe Glu Asn Ala Ala Tyr Ser Val Leu Ile Tyr Leu Ile Val Asp Ser
485 490 495

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

Val Trp Glu Asn Met Lys Ile Ala His His Arg Asp Ala Ile Leu Phe
515 520 525

Glu Lys Phe His Trp Lys Lys Ser Phe Arg Asn Asp Thr Asp Val Glu
530 535 540

Thr Glu Asp Tyr Ser Ile Ser Glu Ile Phe His Asn Pro Glu Asn Gly
545 550 555 560

Ile Phe Pro Gln Phe Val Thr Pro Ile Leu Cys Gln Lys Gly Phe Val
565 570 575

Thr Lys Asp Trp Lys Glu Leu Lys His Ser Ser Lys His Glu Arg Leu
580 585 590

Tyr Tyr Tyr Leu Lys Leu Ile Ser Asp Arg Ala Ser Gly Glu Leu Pro
595 600 605

Thr Thr Ala Lys Phe Phe Arg Asn Phe Val Leu Gln His Pro Asp Tyr
610 615 620

Lys His Asp Ser Lys Ile Ser Lys Ser Ile Asn Tyr Asp Leu Leu Ser
625 630 635 640

Thr Cys Asp Arg Leu Thr His Leu Asp Asp Ser Lys Gly Glu Leu Thr

645 650 655
 Ser Phe Leu Gly Ala Glu Ile Ala Glu Tyr Val Lys Lys Asn Lys Pro
 660 665 670
 Ser Ile Glu Ser Lys Cys
 675

<210> 9
 <211> 678
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> S.cerevisiae GSH1 C86I

<400> 9
 Met Gly Leu Leu Ala Leu Gly Thr Pro Leu Gln Trp Phe Glu Ser Arg
 1 5 10 15
 Thr Tyr Asn Glu His Ile Arg Asp Glu Gly Ile Glu Gln Leu Leu Tyr
 20 25 30
 Ile Phe Gln Ala Ala Gly Lys Arg Asp Asn Asp Pro Leu Phe Trp Gly
 35 40 45
 Asp Glu Leu Glu Tyr Met Val Val Asp Phe Asp Asp Lys Glu Arg Asn
 50 55 60
 Ser Met Leu Asp Val Cys His Asp Lys Ile Leu Thr Glu Leu Asn Met

65 70 75 80

Glu Asp Ser Ser Leu Ile Glu Ala Asn Asp Val Ser Phe His Pro Glu

85 90 95

Tyr Gly Arg Tyr Met Leu Glu Ala Thr Pro Ala Ser Pro Tyr Leu Asn

100 105 110

Tyr Val Gly Ser Tyr Val Glu Val Asn Met Gln Lys Arg Arg Ala Ile

115 120 125

Ala Glu Tyr Lys Leu Ser Glu Tyr Ala Arg Gln Asp Ser Lys Asn Asn

130 135 140

Leu His Val Gly Ser Arg Ser Val Pro Leu Thr Leu Thr Val Phe Pro

145 150 155 160

Arg Met Gly Cys Pro Asp Phe Ile Asn Ile Lys Asp Pro Trp Asn His

165 170 175

Lys Asn Ala Ala Ser Arg Ser Leu Phe Leu Pro Asp Glu Val Ile Asn

180 185 190

Arg His Val Arg Phe Pro Asn Leu Thr Ala Ser Ile Arg Thr Arg Arg

195 200 205

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

210 215 220

Pro Glu Thr Asp Asp Ser Ile Tyr Asp Arg Asp Trp Phe Leu Pro Glu

225 230 235 240

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

Ser Met Gly Phe Gly Met Gly Cys Ser Cys Leu Gln Val Thr Phe Gln
260 265 270

Ala Pro Asn Ile Asn Lys Ala Arg Tyr Leu Tyr Asp Ala Leu Val Asn
275 280 285

Phe Ala Pro Ile Met Leu Ala Phe Ser Ala Ala Ala Pro Ala Phe Lys
290 295 300

Gly Trp Leu Ala Asp Gln Asp Val Arg Trp Asn Val Ile Ser Gly Ala
305 310 315 320

Val Asp Asp Arg Thr Pro Lys Glu Arg Gly Val Ala Pro Leu Leu Pro
325 330 335

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

Lys Val Leu Glu Ile Pro Lys Ser Arg Tyr Ser Ser Val Asp Leu Phe
355 360 365

Leu Gly Gly Ser Lys Phe Phe Asn Arg Thr Tyr Asn Asp Thr Asn Val
370 375 380

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

Pro Leu Asp Tyr Asp Leu Ala Lys His Phe Ala His Leu Tyr Ile Arg
405 410 415

Asp Pro Val Ser Thr Phe Glu Glu Leu Leu Asn Gln Asp Asn Lys Thr

420

425

430

Ser Ser Asn His Phe Glu Asn Ile Gln Ser Thr Asn Trp Gln Thr Leu

435

440

445

Arg Phe Lys Pro Pro Thr Gln Gln Ala Thr Pro Asp Lys Lys Asp Ser

450

455

460

Pro Gly Trp Arg Val Glu Phe Arg Pro Phe Glu Val Gln Leu Leu Asp

465

470

475

480

Phe Glu Asn Ala Ala Tyr Ser Val Leu Ile Tyr Leu Ile Val Asp Ser

485

490

495

Ile Leu Thr Phe Ser Asp Asn Ile Asn Ala Tyr Ile His Met Ser Lys

500

505

510

Val Trp Glu Asn Met Lys Ile Ala His His Arg Asp Ala Ile Leu Phe

515

520

525

Glu Lys Phe His Trp Lys Lys Ser Phe Arg Asn Asp Thr Asp Val Glu

530

535

540

Thr Glu Asp Tyr Ser Ile Ser Glu Ile Phe His Asn Pro Glu Asn Gly

545

550

555

560

Ile Phe Pro Gln Phe Val Thr Pro Ile Leu Cys Gln Lys Gly Phe Val

565

570

575

Thr Lys Asp Trp Lys Glu Leu Lys His Ser Ser Lys His Glu Arg Leu

580 585 590
 Tyr Tyr Tyr Leu Lys Leu Ile Ser Asp Arg Ala Ser Gly Glu Leu Pro
 595 600 605
 Thr Thr Ala Lys Phe Phe Arg Asn Phe Val Leu Gln His Pro Asp Tyr
 610 615 620
 Lys His Asp Ser Lys Ile Ser Lys Ser Ile Asn Tyr Asp Leu Leu Ser
 625 630 635 640
 Thr Cys Asp Arg Leu Thr His Leu Asp Asp Ser Lys Gly Glu Leu Thr
 645 650 655
 Ser Phe Leu Gly Ala Glu Ile Ala Glu Tyr Val Lys Lys Asn Lys Pro
 660 665 670
 Ser Ile Glu Ser Lys Cys
 675

<210> 10
 <211> 678
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> S.cerevisiae GSH1 C86K

<400> 10
 Met Gly Leu Leu Ala Leu Gly Thr Pro Leu Gln Trp Phe Glu Ser Arg

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

Lys Asn Ala Ala Ser Arg Ser Leu Phe Leu Pro Asp Glu Val Ile Asn

180

185

190

Arg His Val Arg Phe Pro Asn Leu Thr Ala Ser Ile Arg Thr Arg Arg

195

200

205

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

210

215

220

Pro Glu Thr Asp Asp Ser Ile Tyr Asp Arg Asp Trp Phe Leu Pro Glu

225

230

235

240

Asp Lys Glu Ala Lys Leu Ala Ser Lys Pro Gly Phe Ile Tyr Met Asp

245

250

255

Ser Met Gly Phe Gly Met Gly Cys Ser Cys Leu Gln Val Thr Phe Gln

260

265

270

Ala Pro Asn Ile Asn Lys Ala Arg Tyr Leu Tyr Asp Ala Leu Val Asn

275

280

285

Phe Ala Pro Ile Met Leu Ala Phe Ser Ala Ala Ala Pro Ala Phe Lys

290

295

300

Gly Trp Leu Ala Asp Gln Asp Val Arg Trp Asn Val Ile Ser Gly Ala

305

310

315

320

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

325

330

335

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

340

345

350

Lys Val Leu Glu Ile Pro Lys Ser Arg Tyr Ser Ser Val Asp Leu Phe

355

360

365

Leu Gly Gly Ser Lys Phe Phe Asn Arg Thr Tyr Asn Asp Thr Asn Val

370

375

380

Pro Ile Asn Glu Lys Val Leu Gly Arg Leu Leu Glu Asn Asp Lys Ala

385

390

395

400

Pro Leu Asp Tyr Asp Leu Ala Lys His Phe Ala His Leu Tyr Ile Arg

405

410

415

Asp Pro Val Ser Thr Phe Glu Glu Leu Leu Asn Gln Asp Asn Lys Thr

420

425

430

Ser Ser Asn His Phe Glu Asn Ile Gln Ser Thr Asn Trp Gln Thr Leu

435

440

445

Arg Phe Lys Pro Pro Thr Gln Gln Ala Thr Pro Asp Lys Lys Asp Ser

450

455

460

Pro Gly Trp Arg Val Glu Phe Arg Pro Phe Glu Val Gln Leu Leu Asp

465

470

475

480

Phe Glu Asn Ala Ala Tyr Ser Val Leu Ile Tyr Leu Ile Val Asp Ser

485

490

495

Ile Leu Thr Phe Ser Asp Asn Ile Asn Ala Tyr Ile His Met Ser Lys

500

505

510

Val Trp Glu Asn Met Lys Ile Ala His His Arg Asp Ala Ile Leu Phe

515	520	525	
Glu Lys Phe His Trp Lys Lys Ser Phe Arg Asn Asp Thr Asp Val Glu			
530	535	540	
Thr Glu Asp Tyr Ser Ile Ser Glu Ile Phe His Asn Pro Glu Asn Gly			
545	550	555	560
Ile Phe Pro Gln Phe Val Thr Pro Ile Leu Cys Gln Lys Gly Phe Val			
	565	570	575
Thr Lys Asp Trp Lys Glu Leu Lys His Ser Ser Lys His Glu Arg Leu			
	580	585	590
Tyr Tyr Tyr Leu Lys Leu Ile Ser Asp Arg Ala Ser Gly Glu Leu Pro			
	595	600	605
Thr Thr Ala Lys Phe Phe Arg Asn Phe Val Leu Gln His Pro Asp Tyr			
	610	615	620
Lys His Asp Ser Lys Ile Ser Lys Ser Ile Asn Tyr Asp Leu Leu Ser			
625	630	635	640
Thr Cys Asp Arg Leu Thr His Leu Asp Asp Ser Lys Gly Glu Leu Thr			
	645	650	655
Ser Phe Leu Gly Ala Glu Ile Ala Glu Tyr Val Lys Lys Asn Lys Pro			
	660	665	670
Ser Ile Glu Ser Lys Cys			
	675		

<210> 11
 <211> 678
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> S.cerevisiae GSH1 C86L

<400> 11
 Met Gly Leu Leu Ala Leu Gly Thr Pro Leu Gln Trp Phe Glu Ser Arg
 1 5 10 15

Thr Tyr Asn Glu His Ile Arg Asp Glu Gly Ile Glu Gln Leu Leu Tyr
 20 25 30

Ile Phe Gln Ala Ala Gly Lys Arg Asp Asn Asp Pro Leu Phe Trp Gly
 35 40 45

Asp Glu Leu Glu Tyr Met Val Val Asp Phe Asp Asp Lys Glu Arg Asn
 50 55 60

Ser Met Leu Asp Val Cys His Asp Lys Ile Leu Thr Glu Leu Asn Met
 65 70 75 80

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

Tyr Gly Arg Tyr Met Leu Glu Ala Thr Pro Ala Ser Pro Tyr Leu Asn
 100 105 110

Tyr Val Gly Ser Tyr Val Glu Val Asn Met Gln Lys Arg Arg Ala Ile

115

120

125

Ala Glu Tyr Lys Leu Ser Glu Tyr Ala Arg Gln Asp Ser Lys Asn Asn

130

135

140

Leu His Val Gly Ser Arg Ser Val Pro Leu Thr Leu Thr Val Phe Pro

145

150

155

160

Arg Met Gly Cys Pro Asp Phe Ile Asn Ile Lys Asp Pro Trp Asn His

165

170

175

Lys Asn Ala Ala Ser Arg Ser Leu Phe Leu Pro Asp Glu Val Ile Asn

180

185

190

Arg His Val Arg Phe Pro Asn Leu Thr Ala Ser Ile Arg Thr Arg Arg

195

200

205

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

210

215

220

Pro Glu Thr Asp Asp Ser Ile Tyr Asp Arg Asp Trp Phe Leu Pro Glu

225

230

235

240

Asp Lys Glu Ala Lys Leu Ala Ser Lys Pro Gly Phe Ile Tyr Met Asp

245

250

255

Ser Met Gly Phe Gly Met Gly Cys Ser Cys Leu Gln Val Thr Phe Gln

260

265

270

Ala Pro Asn Ile Asn Lys Ala Arg Tyr Leu Tyr Asp Ala Leu Val Asn

275

280

285

Phe Ala Pro Ile Met Leu Ala Phe Ser Ala Ala Ala Pro Ala Phe Lys

290

295

300

Gly Trp Leu Ala Asp Gln Asp Val Arg Trp Asn Val Ile Ser Gly Ala

305

310

315

320

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

325

330

335

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

340

345

350

Lys Val Leu Glu Ile Pro Lys Ser Arg Tyr Ser Ser Val Asp Leu Phe

355

360

365

Leu Gly Gly Ser Lys Phe Phe Asn Arg Thr Tyr Asn Asp Thr Asn Val

370

375

380

Pro Ile Asn Glu Lys Val Leu Gly Arg Leu Leu Glu Asn Asp Lys Ala

385

390

395

400

Pro Leu Asp Tyr Asp Leu Ala Lys His Phe Ala His Leu Tyr Ile Arg

405

410

415

Asp Pro Val Ser Thr Phe Glu Glu Leu Leu Asn Gln Asp Asn Lys Thr

420

425

430

Ser Ser Asn His Phe Glu Asn Ile Gln Ser Thr Asn Trp Gln Thr Leu

435

440

445

Arg Phe Lys Pro Pro Thr Gln Gln Ala Thr Pro Asp Lys Lys Asp Ser

450	455	460	
Pro Gly Trp Arg Val Glu Phe Arg Pro Phe Glu Val Gln Leu Leu Asp			
465	470	475	480
Phe Glu Asn Ala Ala Tyr Ser Val Leu Ile Tyr Leu Ile Val Asp Ser			
	485	490	495
Ile Leu Thr Phe Ser Asp Asn Ile Asn Ala Tyr Ile His Met Ser Lys			
	500	505	510
Val Trp Glu Asn Met Lys Ile Ala His His Arg Asp Ala Ile Leu Phe			
	515	520	525
Glu Lys Phe His Trp Lys Lys Ser Phe Arg Asn Asp Thr Asp Val Glu			
530	535	540	
Thr Glu Asp Tyr Ser Ile Ser Glu Ile Phe His Asn Pro Glu Asn Gly			
545	550	555	560
Ile Phe Pro Gln Phe Val Thr Pro Ile Leu Cys Gln Lys Gly Phe Val			
	565	570	575
Thr Lys Asp Trp Lys Glu Leu Lys His Ser Ser Lys His Glu Arg Leu			
	580	585	590
Tyr Tyr Tyr Leu Lys Leu Ile Ser Asp Arg Ala Ser Gly Glu Leu Pro			
595	600	605	
Thr Thr Ala Lys Phe Phe Arg Asn Phe Val Leu Gln His Pro Asp Tyr			
610	615	620	

Lys His Asp Ser Lys Ile Ser Lys Ser Ile Asn Tyr Asp Leu Leu Ser
625 630 635 640

Thr Cys Asp Arg Leu Thr His Leu Asp Asp Ser Lys Gly Glu Leu Thr
 645 650 655

Ser Phe Leu Gly Ala Glu Ile Ala Glu Tyr Val Lys Lys Asn Lys Pro
 660 665 670

Ser Ile Glu Ser Lys Cys
 675

<210> 12

<211> 678

<212> PRT

<213> Artificial Sequence

<220>

<223> S.cerevisiae GSH1 C86M

<400> 12

Met Gly Leu Leu Ala Leu Gly Thr Pro Leu Gln Trp Phe Glu Ser Arg
 1 5 10 15

Thr Tyr Asn Glu His Ile Arg Asp Glu Gly Ile Glu Gln Leu Leu Tyr
 20 25 30

Ile Phe Gln Ala Ala Gly Lys Arg Asp Asn Asp Pro Leu Phe Trp Gly
 35 40 45

Asp Glu Leu Glu Tyr Met Val Val Asp Phe Asp Asp Lys Glu Arg Asn

50

55

60

Ser Met Leu Asp Val Cys His Asp Lys Ile Leu Thr Glu Leu Asn Met

65

70

75

80

Glu Asp Ser Ser Leu Met Glu Ala Asn Asp Val Ser Phe His Pro Glu

85

90

95

Tyr Gly Arg Tyr Met Leu Glu Ala Thr Pro Ala Ser Pro Tyr Leu Asn

100

105

110

Tyr Val Gly Ser Tyr Val Glu Val Asn Met Gln Lys Arg Arg Ala Ile

115

120

125

Ala Glu Tyr Lys Leu Ser Glu Tyr Ala Arg Gln Asp Ser Lys Asn Asn

130

135

140

Leu His Val Gly Ser Arg Ser Val Pro Leu Thr Leu Thr Val Phe Pro

145

150

155

160

Arg Met Gly Cys Pro Asp Phe Ile Asn Ile Lys Asp Pro Trp Asn His

165

170

175

Lys Asn Ala Ala Ser Arg Ser Leu Phe Leu Pro Asp Glu Val Ile Asn

180

185

190

Arg His Val Arg Phe Pro Asn Leu Thr Ala Ser Ile Arg Thr Arg Arg

195

200

205

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

210

215

220

Pro Glu Thr Asp Asp Ser Ile Tyr Asp Arg Asp Trp Phe Leu Pro Glu
225 230 235 240

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

Ser Met Gly Phe Gly Met Gly Cys Ser Cys Leu Gln Val Thr Phe Gln
260 265 270

Ala Pro Asn Ile Asn Lys Ala Arg Tyr Leu Tyr Asp Ala Leu Val Asn
275 280 285

Phe Ala Pro Ile Met Leu Ala Phe Ser Ala Ala Ala Pro Ala Phe Lys
290 295 300

Gly Trp Leu Ala Asp Gln Asp Val Arg Trp Asn Val Ile Ser Gly Ala
305 310 315 320

Val Asp Asp Arg Thr Pro Lys Glu Arg Gly Val Ala Pro Leu Leu Pro
325 330 335

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

Lys Val Leu Glu Ile Pro Lys Ser Arg Tyr Ser Ser Val Asp Leu Phe
355 360 365

Leu Gly Gly Ser Lys Phe Phe Asn Arg Thr Tyr Asn Asp Thr Asn Val
370 375 380

Pro Ile Asn Glu Lys Val Leu Gly Arg Leu Leu Glu Asn Asp Lys Ala

385 390 395 400

Pro Leu Asp Tyr Asp Leu Ala Lys His Phe Ala His Leu Tyr Ile Arg

405 410 415

Asp Pro Val Ser Thr Phe Glu Glu Leu Leu Asn Gln Asp Asn Lys Thr

420 425 430

Ser Ser Asn His Phe Glu Asn Ile Gln Ser Thr Asn Trp Gln Thr Leu

435 440 445

Arg Phe Lys Pro Pro Thr Gln Gln Ala Thr Pro Asp Lys Lys Asp Ser

450 455 460

Pro Gly Trp Arg Val Glu Phe Arg Pro Phe Glu Val Gln Leu Leu Asp

465 470 475 480

Phe Glu Asn Ala Ala Tyr Ser Val Leu Ile Tyr Leu Ile Val Asp Ser

485 490 495

Ile Leu Thr Phe Ser Asp Asn Ile Asn Ala Tyr Ile His Met Ser Lys

500 505 510

Val Trp Glu Asn Met Lys Ile Ala His His Arg Asp Ala Ile Leu Phe

515 520 525

Glu Lys Phe His Trp Lys Lys Ser Phe Arg Asn Asp Thr Asp Val Glu

530 535 540

Thr Glu Asp Tyr Ser Ile Ser Glu Ile Phe His Asn Pro Glu Asn Gly

545 550 555 560

Ile Phe Pro Gln Phe Val Thr Pro Ile Leu Cys Gln Lys Gly Phe Val
565 570 575

Thr Lys Asp Trp Lys Glu Leu Lys His Ser Ser Lys His Glu Arg Leu
580 585 590

Tyr Tyr Tyr Leu Lys Leu Ile Ser Asp Arg Ala Ser Gly Glu Leu Pro
595 600 605

Thr Thr Ala Lys Phe Phe Arg Asn Phe Val Leu Gln His Pro Asp Tyr
610 615 620

Lys His Asp Ser Lys Ile Ser Lys Ser Ile Asn Tyr Asp Leu Leu Ser
625 630 635 640

Thr Cys Asp Arg Leu Thr His Leu Asp Asp Ser Lys Gly Glu Leu Thr
645 650 655

Ser Phe Leu Gly Ala Glu Ile Ala Glu Tyr Val Lys Lys Asn Lys Pro
660 665 670

Ser Ile Glu Ser Lys Cys
675

<210> 13

<211> 678

<212> PRT

<213> Artificial Sequence

<220>

<223> S.cerevisiae GSH1 C86N

<400> 13

Met Gly Leu Leu Ala Leu Gly Thr Pro Leu Gln Trp Phe Glu Ser Arg

1 5 10 15

Thr Tyr Asn Glu His Ile Arg Asp Glu Gly Ile Glu Gln Leu Leu Tyr

20 25 30

Ile Phe Gln Ala Ala Gly Lys Arg Asp Asn Asp Pro Leu Phe Trp Gly

35 40 45

Asp Glu Leu Glu Tyr Met Val Val Asp Phe Asp Asp Lys Glu Arg Asn

50 55 60

Ser Met Leu Asp Val Cys His Asp Lys Ile Leu Thr Glu Leu Asn Met

65 70 75 80

Glu Asp Ser Ser Leu Asn Glu Ala Asn Asp Val Ser Phe His Pro Glu

85 90 95

Tyr Gly Arg Tyr Met Leu Glu Ala Thr Pro Ala Ser Pro Tyr Leu Asn

100 105 110

Tyr Val Gly Ser Tyr Val Glu Val Asn Met Gln Lys Arg Arg Ala Ile

115 120 125

Ala Glu Tyr Lys Leu Ser Glu Tyr Ala Arg Gln Asp Ser Lys Asn Asn

130 135 140

Leu His Val Gly Ser Arg Ser Val Pro Leu Thr Leu Thr Val Phe Pro

145 150 155 160

Arg Met Gly Cys Pro Asp Phe Ile Asn Ile Lys Asp Pro Trp Asn His
165 170 175

Lys Asn Ala Ala Ser Arg Ser Leu Phe Leu Pro Asp Glu Val Ile Asn
180 185 190

Arg His Val Arg Phe Pro Asn Leu Thr Ala Ser Ile Arg Thr Arg Arg
195 200 205

Gly Glu Lys Val Cys Met Asn Val Pro Met Tyr Lys Asp Ile Ala Thr
210 215 220

Pro Glu Thr Asp Asp Ser Ile Tyr Asp Arg Asp Trp Phe Leu Pro Glu
225 230 235 240

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

Ser Met Gly Phe Gly Met Gly Cys Ser Cys Leu Gln Val Thr Phe Gln
260 265 270

Ala Pro Asn Ile Asn Lys Ala Arg Tyr Leu Tyr Asp Ala Leu Val Asn
275 280 285

Phe Ala Pro Ile Met Leu Ala Phe Ser Ala Ala Ala Pro Ala Phe Lys
290 295 300

Gly Trp Leu Ala Asp Gln Asp Val Arg Trp Asn Val Ile Ser Gly Ala
305 310 315 320

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

	325	330	335
Lys Tyr Asn Lys Asn Gly Phe Gly Gly Ile Ala Lys Asp Val Gln Asp			
	340	345	350
Lys Val Leu Glu Ile Pro Lys Ser Arg Tyr Ser Ser Val Asp Leu Phe			
	355	360	365
Leu Gly Gly Ser Lys Phe Phe Asn Arg Thr Tyr Asn Asp Thr Asn Val			
	370	375	380
Pro Ile Asn Glu Lys Val Leu Gly Arg Leu Leu Glu Asn Asp Lys Ala			
385	390	395	400
Pro Leu Asp Tyr Asp Leu Ala Lys His Phe Ala His Leu Tyr Ile Arg			
	405	410	415
Asp Pro Val Ser Thr Phe Glu Glu Leu Leu Asn Gln Asp Asn Lys Thr			
	420	425	430
Ser Ser Asn His Phe Glu Asn Ile Gln Ser Thr Asn Trp Gln Thr Leu			
	435	440	445
Arg Phe Lys Pro Pro Thr Gln Gln Ala Thr Pro Asp Lys Lys Asp Ser			
	450	455	460
Pro Gly Trp Arg Val Glu Phe Arg Pro Phe Glu Val Gln Leu Leu Asp			
465	470	475	480
Phe Glu Asn Ala Ala Tyr Ser Val Leu Ile Tyr Leu Ile Val Asp Ser			
	485	490	495

Ile Leu Thr Phe Ser Asp Asn Ile Asn Ala Tyr Ile His Met Ser Lys

500

505

510

Val Trp Glu Asn Met Lys Ile Ala His His Arg Asp Ala Ile Leu Phe

515

520

525

Glu Lys Phe His Trp Lys Lys Ser Phe Arg Asn Asp Thr Asp Val Glu

530

535

540

Thr Glu Asp Tyr Ser Ile Ser Glu Ile Phe His Asn Pro Glu Asn Gly

545

550

555

560

Ile Phe Pro Gln Phe Val Thr Pro Ile Leu Cys Gln Lys Gly Phe Val

565

570

575

Thr Lys Asp Trp Lys Glu Leu Lys His Ser Ser Lys His Glu Arg Leu

580

585

590

Tyr Tyr Tyr Leu Lys Leu Ile Ser Asp Arg Ala Ser Gly Glu Leu Pro

595

600

605

Thr Thr Ala Lys Phe Phe Arg Asn Phe Val Leu Gln His Pro Asp Tyr

610

615

620

Lys His Asp Ser Lys Ile Ser Lys Ser Ile Asn Tyr Asp Leu Leu Ser

625

630

635

640

Thr Cys Asp Arg Leu Thr His Leu Asp Asp Ser Lys Gly Glu Leu Thr

645

650

655

Ser Phe Leu Gly Ala Glu Ile Ala Glu Tyr Val Lys Lys Asn Lys Pro

660

665

670

Ser Ile Glu Ser Lys Cys

675

<210> 14

<211> 678

<212> PRT

<213> Artificial Sequence

<220>

<223> S.cerevisiae GSH1 C86P

<400> 14

Met Gly Leu Leu Ala Leu Gly Thr Pro Leu Gln Trp Phe Glu Ser Arg

1 5 10 15

Thr Tyr Asn Glu His Ile Arg Asp Glu Gly Ile Glu Gln Leu Leu Tyr

20 25 30

Ile Phe Gln Ala Ala Gly Lys Arg Asp Asn Asp Pro Leu Phe Trp Gly

35 40 45

Asp Glu Leu Glu Tyr Met Val Val Asp Phe Asp Asp Lys Glu Arg Asn

50 55 60

Ser Met Leu Asp Val Cys His Asp Lys Ile Leu Thr Glu Leu Asn Met

65 70 75 80

Glu Asp Ser Ser Leu Pro Glu Ala Asn Asp Val Ser Phe His Pro Glu

85 90 95

Tyr Gly Arg Tyr Met Leu Glu Ala Thr Pro Ala Ser Pro Tyr Leu Asn

100

105

110

Tyr Val Gly Ser Tyr Val Glu Val Asn Met Gln Lys Arg Arg Ala Ile

115

120

125

Ala Glu Tyr Lys Leu Ser Glu Tyr Ala Arg Gln Asp Ser Lys Asn Asn

130

135

140

Leu His Val Gly Ser Arg Ser Val Pro Leu Thr Leu Thr Val Phe Pro

145

150

155

160

Arg Met Gly Cys Pro Asp Phe Ile Asn Ile Lys Asp Pro Trp Asn His

165

170

175

Lys Asn Ala Ala Ser Arg Ser Leu Phe Leu Pro Asp Glu Val Ile Asn

180

185

190

Arg His Val Arg Phe Pro Asn Leu Thr Ala Ser Ile Arg Thr Arg Arg

195

200

205

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

210

215

220

Pro Glu Thr Asp Asp Ser Ile Tyr Asp Arg Asp Trp Phe Leu Pro Glu

225

230

235

240

Asp Lys Glu Ala Lys Leu Ala Ser Lys Pro Gly Phe Ile Tyr Met Asp

245

250

255

Ser Met Gly Phe Gly Met Gly Cys Ser Cys Leu Gln Val Thr Phe Gln

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

Ser Ser Asn His Phe Glu Asn Ile Gln Ser Thr Asn Trp Gln Thr Leu

435

440

445

Arg Phe Lys Pro Pro Thr Gln Gln Ala Thr Pro Asp Lys Lys Asp Ser

450

455

460

Pro Gly Trp Arg Val Glu Phe Arg Pro Phe Glu Val Gln Leu Leu Asp

465

470

475

480

Phe Glu Asn Ala Ala Tyr Ser Val Leu Ile Tyr Leu Ile Val Asp Ser

485

490

495

Ile Leu Thr Phe Ser Asp Asn Ile Asn Ala Tyr Ile His Met Ser Lys

500

505

510

Val Trp Glu Asn Met Lys Ile Ala His His Arg Asp Ala Ile Leu Phe

515

520

525

Glu Lys Phe His Trp Lys Lys Ser Phe Arg Asn Asp Thr Asp Val Glu

530

535

540

Thr Glu Asp Tyr Ser Ile Ser Glu Ile Phe His Asn Pro Glu Asn Gly

545

550

555

560

Ile Phe Pro Gln Phe Val Thr Pro Ile Leu Cys Gln Lys Gly Phe Val

565

570

575

Thr Lys Asp Trp Lys Glu Leu Lys His Ser Ser Lys His Glu Arg Leu

580

585

590

Tyr Tyr Tyr Leu Lys Leu Ile Ser Asp Arg Ala Ser Gly Glu Leu Pro

595

600

605

Thr Thr Ala Lys Phe Phe Arg Asn Phe Val Leu Gln His Pro Asp Tyr

610

615

620

Lys His Asp Ser Lys Ile Ser Lys Ser Ile Asn Tyr Asp Leu Leu Ser

625

630

635

640

Thr Cys Asp Arg Leu Thr His Leu Asp Asp Ser Lys Gly Glu Leu Thr

645

650

655

Ser Phe Leu Gly Ala Glu Ile Ala Glu Tyr Val Lys Lys Asn Lys Pro

660

665

670

Ser Ile Glu Ser Lys Cys

675

<210> 15

<211> 678

<212> PRT

<213> Artificial Sequence

<220>

<223> S.cerevisiae GSH1 C86Q

<400> 15

Met Gly Leu Leu Ala Leu Gly Thr Pro Leu Gln Trp Phe Glu Ser Arg

1

5

10

15

Thr Tyr Asn Glu His Ile Arg Asp Glu Gly Ile Glu Gln Leu Leu Tyr

20

25

30

60

Ile Phe Gln Ala Ala Gly Lys Arg Asp Asn Asp Pro Leu Phe Trp Gly

35

40

45

Asp Glu Leu Glu Tyr Met Val Val Asp Phe Asp Asp Lys Glu Arg Asn

50

55

60

Ser Met Leu Asp Val Cys His Asp Lys Ile Leu Thr Glu Leu Asn Met

65

70

75

80

Glu Asp Ser Ser Leu Gln Glu Ala Asn Asp Val Ser Phe His Pro Glu

85

90

95

Tyr Gly Arg Tyr Met Leu Glu Ala Thr Pro Ala Ser Pro Tyr Leu Asn

100

105

110

Tyr Val Gly Ser Tyr Val Glu Val Asn Met Gln Lys Arg Arg Ala Ile

115

120

125

Ala Glu Tyr Lys Leu Ser Glu Tyr Ala Arg Gln Asp Ser Lys Asn Asn

130

135

140

Leu His Val Gly Ser Arg Ser Val Pro Leu Thr Leu Thr Val Phe Pro

145

150

155

160

Arg Met Gly Cys Pro Asp Phe Ile Asn Ile Lys Asp Pro Trp Asn His

165

170

175

Lys Asn Ala Ala Ser Arg Ser Leu Phe Leu Pro Asp Glu Val Ile Asn

180

185

190

Arg His Val Arg Phe Pro Asn Leu Thr Ala Ser Ile Arg Thr Arg Arg

195	200	205	
Gly Glu Lys Val Cys Met Asn Val Pro Met Tyr Lys Asp Ile Ala Thr			
210	215	220	
Pro Glu Thr Asp Asp Ser Ile Tyr Asp Arg Asp Trp Phe Leu Pro Glu			
225	230	235	240
Asp Lys Glu Ala Lys Leu Ala Ser Lys Pro Gly Phe Ile Tyr Met Asp			
	245	250	255
Ser Met Gly Phe Gly Met Gly Cys Ser Cys Leu Gln Val Thr Phe Gln			
	260	265	270
Ala Pro Asn Ile Asn Lys Ala Arg Tyr Leu Tyr Asp Ala Leu Val Asn			
	275	280	285
Phe Ala Pro Ile Met Leu Ala Phe Ser Ala Ala Ala Pro Ala Phe Lys			
	290	295	300
Gly Trp Leu Ala Asp Gln Asp Val Arg Trp Asn Val Ile Ser Gly Ala			
305	310	315	320
Val Asp Asp Arg Thr Pro Lys Glu Arg Gly Val Ala Pro Leu Leu Pro			
	325	330	335
Lys Tyr Asn Lys Asn Gly Phe Gly Gly Ile Ala Lys Asp Val Gln Asp			
	340	345	350
Lys Val Leu Glu Ile Pro Lys Ser Arg Tyr Ser Ser Val Asp Leu Phe			
	355	360	365

Leu Gly Gly Ser Lys Phe Phe Asn Arg Thr Tyr Asn Asp Thr Asn Val

370

375

380

Pro Ile Asn Glu Lys Val Leu Gly Arg Leu Leu Glu Asn Asp Lys Ala

385

390

395

400

Pro Leu Asp Tyr Asp Leu Ala Lys His Phe Ala His Leu Tyr Ile Arg

405

410

415

Asp Pro Val Ser Thr Phe Glu Glu Leu Leu Asn Gln Asp Asn Lys Thr

420

425

430

Ser Ser Asn His Phe Glu Asn Ile Gln Ser Thr Asn Trp Gln Thr Leu

435

440

445

Arg Phe Lys Pro Pro Thr Gln Gln Ala Thr Pro Asp Lys Lys Asp Ser

450

455

460

Pro Gly Trp Arg Val Glu Phe Arg Pro Phe Glu Val Gln Leu Leu Asp

465

470

475

480

Phe Glu Asn Ala Ala Tyr Ser Val Leu Ile Tyr Leu Ile Val Asp Ser

485

490

495

Ile Leu Thr Phe Ser Asp Asn Ile Asn Ala Tyr Ile His Met Ser Lys

500

505

510

Val Trp Glu Asn Met Lys Ile Ala His His Arg Asp Ala Ile Leu Phe

515

520

525

Glu Lys Phe His Trp Lys Lys Ser Phe Arg Asn Asp Thr Asp Val Glu

530

535

540

Thr Glu Asp Tyr Ser Ile Ser Glu Ile Phe His Asn Pro Glu Asn Gly
545 550 555 560

Ile Phe Pro Gln Phe Val Thr Pro Ile Leu Cys Gln Lys Gly Phe Val
565 570 575

Thr Lys Asp Trp Lys Glu Leu Lys His Ser Ser Lys His Glu Arg Leu
580 585 590

Tyr Tyr Tyr Leu Lys Leu Ile Ser Asp Arg Ala Ser Gly Glu Leu Pro
595 600 605

Thr Thr Ala Lys Phe Phe Arg Asn Phe Val Leu Gln His Pro Asp Tyr
610 615 620

Lys His Asp Ser Lys Ile Ser Lys Ser Ile Asn Tyr Asp Leu Leu Ser
625 630 635 640

Thr Cys Asp Arg Leu Thr His Leu Asp Asp Ser Lys Gly Glu Leu Thr
645 650 655

Ser Phe Leu Gly Ala Glu Ile Ala Glu Tyr Val Lys Lys Asn Lys Pro
660 665 670

Ser Ile Glu Ser Lys Cys
675

<210> 16
<211> 678
<212> PRT

<213> Artificial Sequence

<220>

<223> S.cerevisiae GSH1 C86R

<400> 16

Met Gly Leu Leu Ala Leu Gly Thr Pro Leu Gln Trp Phe Glu Ser Arg

1 5 10 15

Thr Tyr Asn Glu His Ile Arg Asp Glu Gly Ile Glu Gln Leu Leu Tyr

20 25 30

Ile Phe Gln Ala Ala Gly Lys Arg Asp Asn Asp Pro Leu Phe Trp Gly

35 40 45

Asp Glu Leu Glu Tyr Met Val Val Asp Phe Asp Asp Lys Glu Arg Asn

50 55 60

Ser Met Leu Asp Val Cys His Asp Lys Ile Leu Thr Glu Leu Asn Met

65 70 75 80

Glu Asp Ser Ser Leu Arg Glu Ala Asn Asp Val Ser Phe His Pro Glu

85 90 95

Tyr Gly Arg Tyr Met Leu Glu Ala Thr Pro Ala Ser Pro Tyr Leu Asn

100 105 110

Tyr Val Gly Ser Tyr Val Glu Val Asn Met Gln Lys Arg Arg Ala Ile

115 120 125

Ala Glu Tyr Lys Leu Ser Glu Tyr Ala Arg Gln Asp Ser Lys Asn Asn

130	135	140	
Leu His Val Gly Ser Arg Ser Val Pro Leu Thr Leu Thr Val Phe Pro			
145	150	155	160
Arg Met Gly Cys Pro Asp Phe Ile Asn Ile Lys Asp Pro Trp Asn His			
	165	170	175
Lys Asn Ala Ala Ser Arg Ser Leu Phe Leu Pro Asp Glu Val Ile Asn			
	180	185	190
Arg His Val Arg Phe Pro Asn Leu Thr Ala Ser Ile Arg Thr Arg Arg			
	195	200	205
Gly Glu Lys Val Cys Met Asn Val Pro Met Tyr Lys Asp Ile Ala Thr			
	210	215	220
Pro Glu Thr Asp Asp Ser Ile Tyr Asp Arg Asp Trp Phe Leu Pro Glu			
225	230	235	240
Asp Lys Glu Ala Lys Leu Ala Ser Lys Pro Gly Phe Ile Tyr Met Asp			
	245	250	255
Ser Met Gly Phe Gly Met Gly Cys Ser Cys Leu Gln Val Thr Phe Gln			
	260	265	270
Ala Pro Asn Ile Asn Lys Ala Arg Tyr Leu Tyr Asp Ala Leu Val Asn			
	275	280	285
Phe Ala Pro Ile Met Leu Ala Phe Ser Ala Ala Ala Pro Ala Phe Lys			
290	295	300	

Gly Trp Leu Ala Asp Gln Asp Val Arg Trp Asn Val Ile Ser Gly Ala
305 310 315 320

Val Asp Asp Arg Thr Pro Lys Glu Arg Gly Val Ala Pro Leu Leu Pro
325 330 335

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

Lys Val Leu Glu Ile Pro Lys Ser Arg Tyr Ser Ser Val Asp Leu Phe
355 360 365

Leu Gly Gly Ser Lys Phe Phe Asn Arg Thr Tyr Asn Asp Thr Asn Val
370 375 380

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

Pro Leu Asp Tyr Asp Leu Ala Lys His Phe Ala His Leu Tyr Ile Arg
405 410 415

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

Ser Ser Asn His Phe Glu Asn Ile Gln Ser Thr Asn Trp Gln Thr Leu
435 440 445

Arg Phe Lys Pro Pro Thr Gln Gln Ala Thr Pro Asp Lys Lys Asp Ser
450 455 460

Pro Gly Trp Arg Val Glu Phe Arg Pro Phe Glu Val Gln Leu Leu Asp
465 470 475 480

Phe Glu Asn Ala Ala Tyr Ser Val Leu Ile Tyr Leu Ile Val Asp Ser
485 490 495

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

Val Trp Glu Asn Met Lys Ile Ala His His Arg Asp Ala Ile Leu Phe
515 520 525

Glu Lys Phe His Trp Lys Lys Ser Phe Arg Asn Asp Thr Asp Val Glu
530 535 540

Thr Glu Asp Tyr Ser Ile Ser Glu Ile Phe His Asn Pro Glu Asn Gly
545 550 555 560

Ile Phe Pro Gln Phe Val Thr Pro Ile Leu Cys Gln Lys Gly Phe Val
565 570 575

Thr Lys Asp Trp Lys Glu Leu Lys His Ser Ser Lys His Glu Arg Leu
580 585 590

Tyr Tyr Tyr Leu Lys Leu Ile Ser Asp Arg Ala Ser Gly Glu Leu Pro
595 600 605

Thr Thr Ala Lys Phe Phe Arg Asn Phe Val Leu Gln His Pro Asp Tyr
610 615 620

Lys His Asp Ser Lys Ile Ser Lys Ser Ile Asn Tyr Asp Leu Leu Ser
625 630 635 640

Thr Cys Asp Arg Leu Thr His Leu Asp Asp Ser Lys Gly Glu Leu Thr

645	650	655
Ser Phe Leu Gly Ala Glu Ile Ala Glu Tyr Val Lys Lys Asn Lys Pro		
660	665	670

Ser Ile Glu Ser Lys Cys
675

<210> 17
<211> 678
<212> PRT
<213> Artificial Sequence

<220>
<223> S.cerevisiae GSH1 C86S

<400> 17
Met Gly Leu Leu Ala Leu Gly Thr Pro Leu Gln Trp Phe Glu Ser Arg
1 5 10 15

Thr Tyr Asn Glu His Ile Arg Asp Glu Gly Ile Glu Gln Leu Leu Tyr
20 25 30

Ile Phe Gln Ala Ala Gly Lys Arg Asp Asn Asp Pro Leu Phe Trp Gly
35 40 45

Asp Glu Leu Glu Tyr Met Val Val Asp Phe Asp Asp Lys Glu Arg Asn
50 55 60

Ser Met Leu Asp Val Cys His Asp Lys Ile Leu Thr Glu Leu Asn Met

65 70 75 80

Glu Asp Ser Ser Leu Ser Glu Ala Asn Asp Val Ser Phe His Pro Glu

85 90 95

Tyr Gly Arg Tyr Met Leu Glu Ala Thr Pro Ala Ser Pro Tyr Leu Asn

100 105 110

Tyr Val Gly Ser Tyr Val Glu Val Asn Met Gln Lys Arg Arg Ala Ile

115 120 125

Ala Glu Tyr Lys Leu Ser Glu Tyr Ala Arg Gln Asp Ser Lys Asn Asn

130 135 140

Leu His Val Gly Ser Arg Ser Val Pro Leu Thr Leu Thr Val Phe Pro

145 150 155 160

Arg Met Gly Cys Pro Asp Phe Ile Asn Ile Lys Asp Pro Trp Asn His

165 170 175

Lys Asn Ala Ala Ser Arg Ser Leu Phe Leu Pro Asp Glu Val Ile Asn

180 185 190

Arg His Val Arg Phe Pro Asn Leu Thr Ala Ser Ile Arg Thr Arg Arg

195 200 205

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

210 215 220

Pro Glu Thr Asp Asp Ser Ile Tyr Asp Arg Asp Trp Phe Leu Pro Glu

225 230 235 240

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

Ser Met Gly Phe Gly Met Gly Cys Ser Cys Leu Gln Val Thr Phe Gln
260 265 270

Ala Pro Asn Ile Asn Lys Ala Arg Tyr Leu Tyr Asp Ala Leu Val Asn
275 280 285

Phe Ala Pro Ile Met Leu Ala Phe Ser Ala Ala Ala Pro Ala Phe Lys
290 295 300

Gly Trp Leu Ala Asp Gln Asp Val Arg Trp Asn Val Ile Ser Gly Ala
305 310 315 320

Val Asp Asp Arg Thr Pro Lys Glu Arg Gly Val Ala Pro Leu Leu Pro
325 330 335

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

Lys Val Leu Glu Ile Pro Lys Ser Arg Tyr Ser Ser Val Asp Leu Phe
355 360 365

Leu Gly Gly Ser Lys Phe Phe Asn Arg Thr Tyr Asn Asp Thr Asn Val
370 375 380

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

Pro Leu Asp Tyr Asp Leu Ala Lys His Phe Ala His Leu Tyr Ile Arg
405 410 415

Asp Pro Val Ser Thr Phe Glu Glu Leu Leu Asn Gln Asp Asn Lys Thr

420

425

430

Ser Ser Asn His Phe Glu Asn Ile Gln Ser Thr Asn Trp Gln Thr Leu

435

440

445

Arg Phe Lys Pro Pro Thr Gln Gln Ala Thr Pro Asp Lys Lys Asp Ser

450

455

460

Pro Gly Trp Arg Val Glu Phe Arg Pro Phe Glu Val Gln Leu Leu Asp

465

470

475

480

Phe Glu Asn Ala Ala Tyr Ser Val Leu Ile Tyr Leu Ile Val Asp Ser

485

490

495

Ile Leu Thr Phe Ser Asp Asn Ile Asn Ala Tyr Ile His Met Ser Lys

500

505

510

Val Trp Glu Asn Met Lys Ile Ala His His Arg Asp Ala Ile Leu Phe

515

520

525

Glu Lys Phe His Trp Lys Lys Ser Phe Arg Asn Asp Thr Asp Val Glu

530

535

540

Thr Glu Asp Tyr Ser Ile Ser Glu Ile Phe His Asn Pro Glu Asn Gly

545

550

555

560

Ile Phe Pro Gln Phe Val Thr Pro Ile Leu Cys Gln Lys Gly Phe Val

565

570

575

Thr Lys Asp Trp Lys Glu Leu Lys His Ser Ser Lys His Glu Arg Leu

580 585 590
 Tyr Tyr Tyr Leu Lys Leu Ile Ser Asp Arg Ala Ser Gly Glu Leu Pro
 595 600 605
 Thr Thr Ala Lys Phe Phe Arg Asn Phe Val Leu Gln His Pro Asp Tyr
 610 615 620
 Lys His Asp Ser Lys Ile Ser Lys Ser Ile Asn Tyr Asp Leu Leu Ser
 625 630 635 640
 Thr Cys Asp Arg Leu Thr His Leu Asp Asp Ser Lys Gly Glu Leu Thr
 645 650 655
 Ser Phe Leu Gly Ala Glu Ile Ala Glu Tyr Val Lys Lys Asn Lys Pro
 660 665 670
 Ser Ile Glu Ser Lys Cys
 675

<210> 18
 <211> 678
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> S.cerevisiae GSH1 C86T

<400> 18
 Met Gly Leu Leu Ala Leu Gly Thr Pro Leu Gln Trp Phe Glu Ser Arg

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

Lys Asn Ala Ala Ser Arg Ser Leu Phe Leu Pro Asp Glu Val Ile Asn

180

185

190

Arg His Val Arg Phe Pro Asn Leu Thr Ala Ser Ile Arg Thr Arg Arg

195

200

205

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

210

215

220

Pro Glu Thr Asp Asp Ser Ile Tyr Asp Arg Asp Trp Phe Leu Pro Glu

225

230

235

240

Asp Lys Glu Ala Lys Leu Ala Ser Lys Pro Gly Phe Ile Tyr Met Asp

245

250

255

Ser Met Gly Phe Gly Met Gly Cys Ser Cys Leu Gln Val Thr Phe Gln

260

265

270

Ala Pro Asn Ile Asn Lys Ala Arg Tyr Leu Tyr Asp Ala Leu Val Asn

275

280

285

Phe Ala Pro Ile Met Leu Ala Phe Ser Ala Ala Ala Pro Ala Phe Lys

290

295

300

Gly Trp Leu Ala Asp Gln Asp Val Arg Trp Asn Val Ile Ser Gly Ala

305

310

315

320

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

325

330

335

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

340

345

350

Lys Val Leu Glu Ile Pro Lys Ser Arg Tyr Ser Ser Val Asp Leu Phe

355

360

365

Leu Gly Gly Ser Lys Phe Phe Asn Arg Thr Tyr Asn Asp Thr Asn Val

370

375

380

Pro Ile Asn Glu Lys Val Leu Gly Arg Leu Leu Glu Asn Asp Lys Ala

385

390

395

400

Pro Leu Asp Tyr Asp Leu Ala Lys His Phe Ala His Leu Tyr Ile Arg

405

410

415

Asp Pro Val Ser Thr Phe Glu Glu Leu Leu Asn Gln Asp Asn Lys Thr

420

425

430

Ser Ser Asn His Phe Glu Asn Ile Gln Ser Thr Asn Trp Gln Thr Leu

435

440

445

Arg Phe Lys Pro Pro Thr Gln Gln Ala Thr Pro Asp Lys Lys Asp Ser

450

455

460

Pro Gly Trp Arg Val Glu Phe Arg Pro Phe Glu Val Gln Leu Leu Asp

465

470

475

480

Phe Glu Asn Ala Ala Tyr Ser Val Leu Ile Tyr Leu Ile Val Asp Ser

485

490

495

Ile Leu Thr Phe Ser Asp Asn Ile Asn Ala Tyr Ile His Met Ser Lys

500

505

510

Val Trp Glu Asn Met Lys Ile Ala His His Arg Asp Ala Ile Leu Phe

515	520	525	
Glu Lys Phe His Trp Lys Lys Ser Phe Arg Asn Asp Thr Asp Val Glu			
530	535	540	
Thr Glu Asp Tyr Ser Ile Ser Glu Ile Phe His Asn Pro Glu Asn Gly			
545	550	555	560
Ile Phe Pro Gln Phe Val Thr Pro Ile Leu Cys Gln Lys Gly Phe Val			
	565	570	575
Thr Lys Asp Trp Lys Glu Leu Lys His Ser Ser Lys His Glu Arg Leu			
	580	585	590
Tyr Tyr Tyr Leu Lys Leu Ile Ser Asp Arg Ala Ser Gly Glu Leu Pro			
	595	600	605
Thr Thr Ala Lys Phe Phe Arg Asn Phe Val Leu Gln His Pro Asp Tyr			
	610	615	620
Lys His Asp Ser Lys Ile Ser Lys Ser Ile Asn Tyr Asp Leu Leu Ser			
625	630	635	640
Thr Cys Asp Arg Leu Thr His Leu Asp Asp Ser Lys Gly Glu Leu Thr			
	645	650	655
Ser Phe Leu Gly Ala Glu Ile Ala Glu Tyr Val Lys Lys Asn Lys Pro			
	660	665	670
Ser Ile Glu Ser Lys Cys			
	675		

<210> 19
 <211> 678
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> S.cerevisiae GSH1 C86V

<400> 19
 Met Gly Leu Leu Ala Leu Gly Thr Pro Leu Gln Trp Phe Glu Ser Arg
 1 5 10 15

Thr Tyr Asn Glu His Ile Arg Asp Glu Gly Ile Glu Gln Leu Leu Tyr
 20 25 30

Ile Phe Gln Ala Ala Gly Lys Arg Asp Asn Asp Pro Leu Phe Trp Gly
 35 40 45

Asp Glu Leu Glu Tyr Met Val Val Asp Phe Asp Asp Lys Glu Arg Asn
 50 55 60

Ser Met Leu Asp Val Cys His Asp Lys Ile Leu Thr Glu Leu Asn Met
 65 70 75 80

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

Tyr Gly Arg Tyr Met Leu Glu Ala Thr Pro Ala Ser Pro Tyr Leu Asn
 100 105 110

Tyr Val Gly Ser Tyr Val Glu Val Asn Met Gln Lys Arg Arg Ala Ile

115

120

125

Ala Glu Tyr Lys Leu Ser Glu Tyr Ala Arg Gln Asp Ser Lys Asn Asn

130

135

140

Leu His Val Gly Ser Arg Ser Val Pro Leu Thr Leu Thr Val Phe Pro

145

150

155

160

Arg Met Gly Cys Pro Asp Phe Ile Asn Ile Lys Asp Pro Trp Asn His

165

170

175

Lys Asn Ala Ala Ser Arg Ser Leu Phe Leu Pro Asp Glu Val Ile Asn

180

185

190

Arg His Val Arg Phe Pro Asn Leu Thr Ala Ser Ile Arg Thr Arg Arg

195

200

205

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

210

215

220

Pro Glu Thr Asp Asp Ser Ile Tyr Asp Arg Asp Trp Phe Leu Pro Glu

225

230

235

240

Asp Lys Glu Ala Lys Leu Ala Ser Lys Pro Gly Phe Ile Tyr Met Asp

245

250

255

Ser Met Gly Phe Gly Met Gly Cys Ser Cys Leu Gln Val Thr Phe Gln

260

265

270

Ala Pro Asn Ile Asn Lys Ala Arg Tyr Leu Tyr Asp Ala Leu Val Asn

275

280

285

Phe Ala Pro Ile Met Leu Ala Phe Ser Ala Ala Ala Pro Ala Phe Lys

290

295

300

Gly Trp Leu Ala Asp Gln Asp Val Arg Trp Asn Val Ile Ser Gly Ala

305

310

315

320

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

325

330

335

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

340

345

350

Lys Val Leu Glu Ile Pro Lys Ser Arg Tyr Ser Ser Val Asp Leu Phe

355

360

365

Leu Gly Gly Ser Lys Phe Phe Asn Arg Thr Tyr Asn Asp Thr Asn Val

370

375

380

Pro Ile Asn Glu Lys Val Leu Gly Arg Leu Leu Glu Asn Asp Lys Ala

385

390

395

400

Pro Leu Asp Tyr Asp Leu Ala Lys His Phe Ala His Leu Tyr Ile Arg

405

410

415

Asp Pro Val Ser Thr Phe Glu Glu Leu Leu Asn Gln Asp Asn Lys Thr

420

425

430

Ser Ser Asn His Phe Glu Asn Ile Gln Ser Thr Asn Trp Gln Thr Leu

435

440

445

Arg Phe Lys Pro Pro Thr Gln Gln Ala Thr Pro Asp Lys Lys Asp Ser

450	455	460	
Pro Gly Trp Arg Val Glu Phe Arg Pro Phe Glu Val Gln Leu Leu Asp			
465	470	475	480
Phe Glu Asn Ala Ala Tyr Ser Val Leu Ile Tyr Leu Ile Val Asp Ser			
	485	490	495
Ile Leu Thr Phe Ser Asp Asn Ile Asn Ala Tyr Ile His Met Ser Lys			
	500	505	510
Val Trp Glu Asn Met Lys Ile Ala His His Arg Asp Ala Ile Leu Phe			
	515	520	525
Glu Lys Phe His Trp Lys Lys Ser Phe Arg Asn Asp Thr Asp Val Glu			
530	535	540	
Thr Glu Asp Tyr Ser Ile Ser Glu Ile Phe His Asn Pro Glu Asn Gly			
545	550	555	560
Ile Phe Pro Gln Phe Val Thr Pro Ile Leu Cys Gln Lys Gly Phe Val			
	565	570	575
Thr Lys Asp Trp Lys Glu Leu Lys His Ser Ser Lys His Glu Arg Leu			
	580	585	590
Tyr Tyr Tyr Leu Lys Leu Ile Ser Asp Arg Ala Ser Gly Glu Leu Pro			
595	600	605	
Thr Thr Ala Lys Phe Phe Arg Asn Phe Val Leu Gln His Pro Asp Tyr			
610	615	620	

Lys His Asp Ser Lys Ile Ser Lys Ser Ile Asn Tyr Asp Leu Leu Ser
625 630 635 640

Thr Cys Asp Arg Leu Thr His Leu Asp Asp Ser Lys Gly Glu Leu Thr
645 650 655

Ser Phe Leu Gly Ala Glu Ile Ala Glu Tyr Val Lys Lys Asn Lys Pro
660 665 670

Ser Ile Glu Ser Lys Cys
675

<210> 20

<211> 678

<212> PRT

<213> Artificial Sequence

<220>

<223> S.cerevisiae GSH1 C86W

<400> 20

Met Gly Leu Leu Ala Leu Gly Thr Pro Leu Gln Trp Phe Glu Ser Arg
1 5 10 15

Thr Tyr Asn Glu His Ile Arg Asp Glu Gly Ile Glu Gln Leu Leu Tyr
20 25 30

Ile Phe Gln Ala Ala Gly Lys Arg Asp Asn Asp Pro Leu Phe Trp Gly
35 40 45

Asp Glu Leu Glu Tyr Met Val Val Asp Phe Asp Asp Lys Glu Arg Asn

50

55

60

Ser Met Leu Asp Val Cys His Asp Lys Ile Leu Thr Glu Leu Asn Met

65

70

75

80

Glu Asp Ser Ser Leu Trp Glu Ala Asn Asp Val Ser Phe His Pro Glu

85

90

95

Tyr Gly Arg Tyr Met Leu Glu Ala Thr Pro Ala Ser Pro Tyr Leu Asn

100

105

110

Tyr Val Gly Ser Tyr Val Glu Val Asn Met Gln Lys Arg Arg Ala Ile

115

120

125

Ala Glu Tyr Lys Leu Ser Glu Tyr Ala Arg Gln Asp Ser Lys Asn Asn

130

135

140

Leu His Val Gly Ser Arg Ser Val Pro Leu Thr Leu Thr Val Phe Pro

145

150

155

160

Arg Met Gly Cys Pro Asp Phe Ile Asn Ile Lys Asp Pro Trp Asn His

165

170

175

Lys Asn Ala Ala Ser Arg Ser Leu Phe Leu Pro Asp Glu Val Ile Asn

180

185

190

Arg His Val Arg Phe Pro Asn Leu Thr Ala Ser Ile Arg Thr Arg Arg

195

200

205

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

210

215

220

Pro Glu Thr Asp Asp Ser Ile Tyr Asp Arg Asp Trp Phe Leu Pro Glu
225 230 235 240

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

Ser Met Gly Phe Gly Met Gly Cys Ser Cys Leu Gln Val Thr Phe Gln
260 265 270

Ala Pro Asn Ile Asn Lys Ala Arg Tyr Leu Tyr Asp Ala Leu Val Asn
275 280 285

Phe Ala Pro Ile Met Leu Ala Phe Ser Ala Ala Ala Pro Ala Phe Lys
290 295 300

Gly Trp Leu Ala Asp Gln Asp Val Arg Trp Asn Val Ile Ser Gly Ala
305 310 315 320

Val Asp Asp Arg Thr Pro Lys Glu Arg Gly Val Ala Pro Leu Leu Pro
325 330 335

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

Lys Val Leu Glu Ile Pro Lys Ser Arg Tyr Ser Ser Val Asp Leu Phe
355 360 365

Leu Gly Gly Ser Lys Phe Phe Asn Arg Thr Tyr Asn Asp Thr Asn Val
370 375 380

Pro Ile Asn Glu Lys Val Leu Gly Arg Leu Leu Glu Asn Asp Lys Ala

385 390 395 400

Pro Leu Asp Tyr Asp Leu Ala Lys His Phe Ala His Leu Tyr Ile Arg

405 410 415

Asp Pro Val Ser Thr Phe Glu Glu Leu Leu Asn Gln Asp Asn Lys Thr

420 425 430

Ser Ser Asn His Phe Glu Asn Ile Gln Ser Thr Asn Trp Gln Thr Leu

435 440 445

Arg Phe Lys Pro Pro Thr Gln Gln Ala Thr Pro Asp Lys Lys Asp Ser

450 455 460

Pro Gly Trp Arg Val Glu Phe Arg Pro Phe Glu Val Gln Leu Leu Asp

465 470 475 480

Phe Glu Asn Ala Ala Tyr Ser Val Leu Ile Tyr Leu Ile Val Asp Ser

485 490 495

Ile Leu Thr Phe Ser Asp Asn Ile Asn Ala Tyr Ile His Met Ser Lys

500 505 510

Val Trp Glu Asn Met Lys Ile Ala His His Arg Asp Ala Ile Leu Phe

515 520 525

Glu Lys Phe His Trp Lys Lys Ser Phe Arg Asn Asp Thr Asp Val Glu

530 535 540

Thr Glu Asp Tyr Ser Ile Ser Glu Ile Phe His Asn Pro Glu Asn Gly

545 550 555 560

Ile Phe Pro Gln Phe Val Thr Pro Ile Leu Cys Gln Lys Gly Phe Val
565 570 575

Thr Lys Asp Trp Lys Glu Leu Lys His Ser Ser Lys His Glu Arg Leu
580 585 590

Tyr Tyr Tyr Leu Lys Leu Ile Ser Asp Arg Ala Ser Gly Glu Leu Pro
595 600 605

Thr Thr Ala Lys Phe Phe Arg Asn Phe Val Leu Gln His Pro Asp Tyr
610 615 620

Lys His Asp Ser Lys Ile Ser Lys Ser Ile Asn Tyr Asp Leu Leu Ser
625 630 635 640

Thr Cys Asp Arg Leu Thr His Leu Asp Asp Ser Lys Gly Glu Leu Thr
645 650 655

Ser Phe Leu Gly Ala Glu Ile Ala Glu Tyr Val Lys Lys Asn Lys Pro
660 665 670

Ser Ile Glu Ser Lys Cys
675

<210> 21

<211> 678

<212> PRT

<213> Artificial Sequence

<220>

<223> S.cerevisiae GSH1 C86Y

<400> 21

Met Gly Leu Leu Ala Leu Gly Thr Pro Leu Gln Trp Phe Glu Ser Arg

1 5 10 15

Thr Tyr Asn Glu His Ile Arg Asp Glu Gly Ile Glu Gln Leu Leu Tyr

20 25 30

Ile Phe Gln Ala Ala Gly Lys Arg Asp Asn Asp Pro Leu Phe Trp Gly

35 40 45

Asp Glu Leu Glu Tyr Met Val Val Asp Phe Asp Asp Lys Glu Arg Asn

50 55 60

Ser Met Leu Asp Val Cys His Asp Lys Ile Leu Thr Glu Leu Asn Met

65 70 75 80

Glu Asp Ser Ser Leu Tyr Glu Ala Asn Asp Val Ser Phe His Pro Glu

85 90 95

Tyr Gly Arg Tyr Met Leu Glu Ala Thr Pro Ala Ser Pro Tyr Leu Asn

100 105 110

Tyr Val Gly Ser Tyr Val Glu Val Asn Met Gln Lys Arg Arg Ala Ile

115 120 125

Ala Glu Tyr Lys Leu Ser Glu Tyr Ala Arg Gln Asp Ser Lys Asn Asn

130 135 140

Leu His Val Gly Ser Arg Ser Val Pro Leu Thr Leu Thr Val Phe Pro

145 150 155 160

Arg Met Gly Cys Pro Asp Phe Ile Asn Ile Lys Asp Pro Trp Asn His
165 170 175

Lys Asn Ala Ala Ser Arg Ser Leu Phe Leu Pro Asp Glu Val Ile Asn
180 185 190

Arg His Val Arg Phe Pro Asn Leu Thr Ala Ser Ile Arg Thr Arg Arg
195 200 205

Gly Glu Lys Val Cys Met Asn Val Pro Met Tyr Lys Asp Ile Ala Thr
210 215 220

Pro Glu Thr Asp Asp Ser Ile Tyr Asp Arg Asp Trp Phe Leu Pro Glu
225 230 235 240

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

Ser Met Gly Phe Gly Met Gly Cys Ser Cys Leu Gln Val Thr Phe Gln
260 265 270

Ala Pro Asn Ile Asn Lys Ala Arg Tyr Leu Tyr Asp Ala Leu Val Asn
275 280 285

Phe Ala Pro Ile Met Leu Ala Phe Ser Ala Ala Ala Pro Ala Phe Lys
290 295 300

Gly Trp Leu Ala Asp Gln Asp Val Arg Trp Asn Val Ile Ser Gly Ala
305 310 315 320

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

	325	330	335
Lys Tyr Asn Lys Asn Gly Phe Gly Gly Ile Ala Lys Asp Val Gln Asp			
	340	345	350
Lys Val Leu Glu Ile Pro Lys Ser Arg Tyr Ser Ser Val Asp Leu Phe			
	355	360	365
Leu Gly Gly Ser Lys Phe Phe Asn Arg Thr Tyr Asn Asp Thr Asn Val			
	370	375	380
Pro Ile Asn Glu Lys Val Leu Gly Arg Leu Leu Glu Asn Asp Lys Ala			
385	390	395	400
Pro Leu Asp Tyr Asp Leu Ala Lys His Phe Ala His Leu Tyr Ile Arg			
	405	410	415
Asp Pro Val Ser Thr Phe Glu Glu Leu Leu Asn Gln Asp Asn Lys Thr			
	420	425	430
Ser Ser Asn His Phe Glu Asn Ile Gln Ser Thr Asn Trp Gln Thr Leu			
	435	440	445
Arg Phe Lys Pro Pro Thr Gln Gln Ala Thr Pro Asp Lys Lys Asp Ser			
	450	455	460
Pro Gly Trp Arg Val Glu Phe Arg Pro Phe Glu Val Gln Leu Leu Asp			
465	470	475	480
Phe Glu Asn Ala Ala Tyr Ser Val Leu Ile Tyr Leu Ile Val Asp Ser			
	485	490	495

Ile Leu Thr Phe Ser Asp Asn Ile Asn Ala Tyr Ile His Met Ser Lys

500

505

510

Val Trp Glu Asn Met Lys Ile Ala His His Arg Asp Ala Ile Leu Phe

515

520

525

Glu Lys Phe His Trp Lys Lys Ser Phe Arg Asn Asp Thr Asp Val Glu

530

535

540

Thr Glu Asp Tyr Ser Ile Ser Glu Ile Phe His Asn Pro Glu Asn Gly

545

550

555

560

Ile Phe Pro Gln Phe Val Thr Pro Ile Leu Cys Gln Lys Gly Phe Val

565

570

575

Thr Lys Asp Trp Lys Glu Leu Lys His Ser Ser Lys His Glu Arg Leu

580

585

590

Tyr Tyr Tyr Leu Lys Leu Ile Ser Asp Arg Ala Ser Gly Glu Leu Pro

595

600

605

Thr Thr Ala Lys Phe Phe Arg Asn Phe Val Leu Gln His Pro Asp Tyr

610

615

620

Lys His Asp Ser Lys Ile Ser Lys Ser Ile Asn Tyr Asp Leu Leu Ser

625

630

635

640

Thr Cys Asp Arg Leu Thr His Leu Asp Asp Ser Lys Gly Glu Leu Thr

645

650

655

Ser Phe Leu Gly Ala Glu Ile Ala Glu Tyr Val Lys Lys Asn Lys Pro

660

665

670

Ser Ile Glu Ser Lys Cys

675

<210> 22

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> F_BamHI_GSH1

<400> 22

ggtaggatcc atgggactct tagcttggg cac

33

<210> 23

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> R_GSH1_C86R

<400> 23

ttagcctccc taagggacga atcct

25

<210> 24

<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> F_GSH1_C86R

<400> 24

cgtcccttag ggaggctaac gatgt

25

<210> 25
<211> 35
<212> DNA
<213> Artificial Sequence

<220>

<223> R_XhoI_GSH1

<400> 25

atgactcgag ttaacatttg cttctattg aaggc

35

<210> 26
<211> 33
<212> DNA
<213> Artificial Sequence

<220>

<223> F_SpeI_GSH1_DW

<400> 26
tagaactagt actccttta ttctggtgt gaa 33

<210> 27
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> R_Ncol_GSH1_DW

<400> 27
gctgccatgg gaatagtgtg aaccgataac tgtgt 35

<210> 28
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> R_AL killer

<400> 28
gagcaatgaa cccaataacg aaatctt 27

<210> 29
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> F_BR killer

<400> 29
cttgacgttc gttcgactga tgag

24