

SEQUENCE LISTING

<110> Temasek Life Sciences Laboratory Limited

<120> Methods For Tuning Carotenoid Production Levels And Compositions
In Rhodosporidium And Rhodotorula Genera

<130> 2577-244PCT

<150> US 62/091,913

<151> 2014-12-15

<160> 118

<170> PatentIn version 3.5

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<211> 1684

<212> DNA

<213> Rhodosporidium toruloides

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

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Phe Pro Pro Leu Arg Asp Phe Leu Pro Ile Leu Leu Asn Ser Pro Asp
260 265 270

Ala Ala Gln Arg Gln Arg Ile Glu Asp Leu Gln Ala Ala Ile Glu Ile
275 280 285

Leu Ser Ile His Ser Lys Ser Phe Ser Thr Ala Ser Gln Val Phe Glu
290 295 300

Gly Arg Leu Arg Leu Asp Leu Leu Ser Leu Tyr Ala Trp Cys Arg Val
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Cys Asp Asp Leu Ile Asp Asn Ala Ser Thr Val Ala Ala Ala Glu Ser
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595 600 605

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Page 13 of 97

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aaa gcc tga Lys Ala	1121

<210> 6
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 <212> PRT
 <213> Rhodosporidium toruloides

<400> 6

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 35 40 45

Ala Phe Asn Gln Trp Met Gly Val Ala Asp Val Asp Leu Glu Ile Val
 50 55 60

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

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

Leu Ala Phe Gln Glu Leu Gln Arg Ile His Pro Arg Pro Gly Ile Lys
 115 120 125

Val Glu Glu Met Val Thr Glu Glu Leu Leu Asn Leu His Arg Gly Gln
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Gly Met Asp Leu Phe Trp Arg Glu Asn Leu Ile Cys Pro Thr Glu Pro
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Glu Tyr Ile Asp Met Val Asn Asn Lys Thr Gly Gly Leu Phe Arg Ile
 165 170 175

Ala Ile Lys Leu Met Met Ala Ala Ser Pro Ala Pro Pro Arg Asp Tyr
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Val Pro Leu Ala Asn Leu Ile Gly Ile Ile Phe Gln Ile Arg Asp Asp
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Tyr Val Asn Leu Gln Ser Val Glu Tyr Ala Asn Asn Lys Gly Tyr Cys
210 215 220

Glu Asp Phe Ser Glu Gly Lys Phe Ser Phe Pro Ile Val His Ser Ile
225 230 235 240

Arg Ser Asp Thr Ser Asn Arg Gln Ile Leu Asn Ile Leu Arg Glu Arg
245 250 255

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

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

Gln Gln Ala Arg Asp Glu Val Ala Arg Leu Gly Gly Asn Arg Gly Val
290 295 300

Glu Ala Ile Leu Asp Lys Leu Val Leu Glu Glu Pro Gln Val Lys Val
305 310 315 320

Asn Gly Val Glu Gly Glu Ala Met Glu Arg Lys Leu Glu Glu Val Val
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Lys Ser Lys Pro Val Lys Ala Val Thr Asn Gly Val Asn Gly Val His
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Ala His Ala Leu Pro Lys Ala
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<212> DNA
<213> Rhodosporidium toruloides

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<210> 8

<211> 2334

<212> DNA

<213> Rhodosporidium toruloides

<400> 8

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<210> 9

<211> 1546

<212> DNA

<213> Rhodosporidium toruloides

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 <211> 2079
 <212> DNA
 <213> Rhodosporidium toruloides

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<210> 11
<211> 1911
<212> DNA
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<220>
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gtg cga gag gag cgc acg ctc gag gag tgc gct tgc gaa ggt cag ctc      96
Val Arg Glu Glu Arg Thr Leu Glu Glu Cys Ala Cys Glu Gly Gln Leu
          20         25         30

ccg caa gag ctc gtc ggc ggg atg tac gtg cgg aat ggg ggt gag cct      144
Pro Gln Glu Leu Val Gly Gly Met Tyr Val Arg Asn Gly Gly Glu Pro
          35         40         45

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gcg ctg gca gag ttg cga gga gac gac tcc gca gac gga cct gcc tac	192
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cac tgg ttc gac ggt gac ggc atg ctg acg ggc gtg tac ttc aag ccc	240
His Trp Phe Asp Gly Asp Gly Met Leu Thr Gly Val Tyr Phe Lys Pro	
65 70 75 80	
gtc ccc tcc tcc tcg ccc ttc gac ccg aac ccg cgt atc gcc ccg ctc	288
Val Pro Ser Ser Ser Pro Phe Asp Pro Asn Pro Arg Ile Ala Pro Leu	
85 90 95	
ttc gtc aac aaa tac gtc ctc acc gac gtc ttc ctc gcc tcg aaa gcg	336
Phe Val Asn Lys Tyr Val Leu Thr Asp Val Phe Leu Ala Ser Lys Ala	
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ctc ggc gtc aca cat ccc atc cta ccc tcc atc gcc aca ctc ctc ggc	384
Leu Gly Val Thr His Pro Ile Leu Pro Ser Ile Ala Thr Leu Leu Gly	
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Ser Ile Trp Ser Leu His Leu Ile Leu Tyr Ser Val Phe Arg Ala Leu	
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145 150 155 160	
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Ser Val Ala Asn Thr Ser Val Leu Trp His Asp Gly Arg Ala Leu Ala	
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Ser Cys Glu Ser Gly Pro Leu Thr Trp Val Thr Leu Pro Glu Leu Asp	
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Thr Val Gly Phe Trp Ser Leu Glu Gly Asp Asn Gly Glu Lys Gly Leu	
195 200 205	
cga gag cag ggt ggc atg ctc ggc tgg atg aag gag tgg acg acg gcg	672
Arg Glu Gln Gly Gly Met Leu Gly Trp Met Lys Glu Trp Thr Thr Ala	
210 215 220	
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His Pro Lys Arg Asp Pro His Thr Gly Glu Leu Met Leu Phe His Met	
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Ser Phe Leu Pro Pro Tyr Leu His Tyr Ser Val Ile Pro Ser Thr His	
245 250 255	
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Ala Pro Pro Pro Ser Ala Arg Ser Glu Lys Ala Ala Pro Thr Pro Arg	

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Met	Ala	Ala	Ser	Arg	Thr	His	Ser	Ile	Leu	Leu	Asp	Met	Pro	Leu	Ser		
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Pro	Ser	Lys	Pro	Ala	Arg	Phe	Gly	Val	Leu	Pro	Arg	His	Lys	Pro	Thr		
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Phe	Ala	Tyr	Asp	Glu	Pro	Pro	Ser	Thr	Ser	His	Asp	Glu	Val	Glu	Ala		
		355				360					365						
gtc	aac	ctc	gtc	tgc	tgc	cgc	ctc	aac	tct	ccc	cgc	ctc	atc	tac	tcc	1152	
Val	Asn	Leu	Val	Cys	Cys	Arg	Leu	Asn	Ser	Pro	Arg	Leu	Ile	Tyr	Ser		
	370					375					380						
gcc	ggt	aac	ctc	gtc	ctc	ccc	gag	tct	caa	tcc	ctc	cca	gca	ggc	gcc	1200	
Ala	Gly	Asn	Leu	Val	Leu	Pro	Glu	Ser	Gln	Ser	Leu	Pro	Ala	Gly	Ala		
385					390					395				400			
aaa	gag	tcc	tgc	gag	ctc	tac	tac	tac	cgc	ttc	ccc	tct	tcc	tcc	tcc	1248	
Lys	Glu	Ser	Cys	Glu	Leu	Tyr	Tyr	Tyr	Arg	Phe	Pro	Ser	Ser	Ser	Ser		
				405					410					415			
gcc	tcc	gtc	acc	ctc	gaa	ccg	tcg	cac	gcc	ttc	ccc	ctc	gcc	gcg	att	1296	
Ala	Ser	Val	Thr	Leu	Glu	Pro	Ser	His	Ala	Phe	Pro	Leu	Ala	Ala	Ile		
			420					425					430				
ccc	ttc	gag	ttc	ccg	acc	gta	ccg	cag	gac	cgc	gcg	gtc	ggc	ccg	tcg	1344	
Pro	Phe	Glu	Phe	Pro	Thr	Val	Pro	Gln	Asp	Arg	Ala	Val	Gly	Pro	Ser		
		435				440						445					
aag	tac	gtc	tat	ggg	tgc	tcg	gtg	aag	cac	ggg	tcg	ttc	gat	gcg	gcg	1392	
Lys	Tyr	Val	Tyr	Gly	Cys	Ser	Val	Lys	His	Gly	Ser	Phe	Asp	Ala	Ala		
	450					455				460							
ctt	ggg	tcg	gcg	gcg	aag	atc	gac	tgc	ctc	gtc	aag	gtc	aac	gtc	gac	1440	
Leu	Gly	Ser	Ala	Ala	Lys	Ile	Asp	Cys	Leu	Val	Lys	Val	Asn	Val	Asp		
465					470					475				480			

ttg ctc gtc cgg cag ggc aag aag cgc aac gag gcg ggc gag gga cag	1488
Leu Leu Val Arg Gln Gly Lys Lys Arg Asn Glu Ala Gly Glu Gly Gln	
485 490 495	
tcg gag cga ccg gtc gac gag cga gga atc ctc gac gtg att gcc cag	1536
Ser Glu Arg Pro Val Asp Glu Arg Gly Ile Leu Asp Val Ile Ala Gln	
500 505 510	
cag acg ccg aga cga ggg gac cgc acc tct tcg gac gac gac gag ccg	1584
Gln Thr Pro Arg Arg Gly Asp Arg Thr Ser Ser Asp Asp Asp Glu Pro	
515 520 525	
atc cgg atc ttc gag ctc cct ccg ctg cac tac gca cag gag agc tcg	1632
Ile Arg Ile Phe Glu Leu Pro Pro Leu His Tyr Ala Gln Glu Ser Ser	
530 535 540	
ttc gtc cct cgc caa aac ccc cgg tca gaa gac gac ggc tac ctc ctc	1680
Phe Val Pro Arg Gln Asn Pro Arg Ser Glu Asp Asp Gly Tyr Leu Leu	
545 550 555 560	
acc tac gtc ttt gac gaa cgc caa ctc gac ccc tcg acc ggt cgc gct	1728
Thr Tyr Val Phe Asp Glu Arg Gln Leu Asp Pro Ser Thr Gly Arg Ala	
565 570 575	
gtc gaa ggc gct aag agc gag ttg tgg gtc atc gat gcg tgg acg atg	1776
Val Glu Gly Ala Lys Ser Glu Leu Trp Val Ile Asp Ala Trp Thr Met	
580 585 590	
aag gac gtt gtg tgc agg gtc aag ttg ccg cag agg gtg ccg tac ggg	1824
Lys Asp Val Val Cys Arg Val Lys Leu Pro Gln Arg Val Pro Tyr Gly	
595 600 605	
ttg cac ggg cat tgg ttc tcg agg gaa gag atc gag gag cag cgc agg	1872
Leu His Gly His Trp Phe Ser Arg Glu Glu Ile Glu Glu Gln Arg Arg	
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gct ccc tca gtc cgc tcg cgt cct ccg cca aag tcc tag	1911
Ala Pro Ser Val Arg Ser Arg Pro Pro Pro Lys Ser	
625 630 635	

<210> 12
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 <212> PRT
 <213> Rhodosporidium toruloides

<400> 12

Met Gly Thr Lys Pro Arg His Thr Tyr Lys Gln Gly Asn Tyr Leu Pro
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Pro Gln Glu Leu Val Gly Gly Met Tyr Val Arg Asn Gly Gly Glu Pro
35 40 45

Ala Leu Ala Glu Leu Arg Gly Asp Asp Ser Ala Asp Gly Pro Ala Tyr
50 55 60

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

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

Phe Val Asn Lys Tyr Val Leu Thr Asp Val Phe Leu Ala Ser Lys Ala
100 105 110

Leu Gly Val Thr His Pro Ile Leu Pro Ser Ile Ala Thr Leu Leu Gly
115 120 125

Ser Ile Trp Ser Leu His Leu Ile Leu Tyr Ser Val Phe Arg Ala Leu
130 135 140

Phe Leu Ala Phe Cys Ser Phe Phe Thr Glu Ser Pro Leu Arg His Leu
145 150 155 160

Ser Val Ala Asn Thr Ser Val Leu Trp His Asp Gly Arg Ala Leu Ala
165 170 175

Ser Cys Glu Ser Gly Pro Leu Thr Trp Val Thr Leu Pro Glu Leu Asp
180 185 190

Thr Val Gly Phe Trp Ser Leu Glu Gly Asp Asn Gly Glu Lys Gly Leu
195 200 205

Arg Glu Gln Gly Gly Met Leu Gly Trp Met Lys Glu Trp Thr Thr Ala
210 215 220

His Pro Lys Arg Asp Pro His Thr Gly Glu Leu Met Leu Phe His Met
225 230 235 240

Ser Phe Leu Pro Pro Tyr Leu His Tyr Ser Val Ile Pro Ser Thr His
245 250 255

Ala Pro Pro Pro Ser Ala Arg Ser Glu Lys Ala Ala Pro Thr Pro Arg
260 265 270

Ile Leu Ala Ala Pro Val Pro Ile Ala Ala Pro Arg Met Met His Asp
275 280 285

Met Ala Ala Ser Arg Thr His Ser Ile Leu Leu Asp Met Pro Leu Ser
290 295 300

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

Pro Ser Lys Pro Ala Arg Phe Gly Val Leu Pro Arg His Lys Pro Thr
325 330 335

Leu Val Lys Trp Tyr Ile Ala Pro Ala Cys Ile Ile Phe His Thr Ala
340 345 350

Phe Ala Tyr Asp Glu Pro Pro Ser Thr Ser His Asp Glu Val Glu Ala
355 360 365

Val Asn Leu Val Cys Cys Arg Leu Asn Ser Pro Arg Leu Ile Tyr Ser
370 375 380

Ala Gly Asn Leu Val Leu Pro Glu Ser Gln Ser Leu Pro Ala Gly Ala
385 390 395 400

Lys Glu Ser Cys Glu Leu Tyr Tyr Tyr Arg Phe Pro Ser Ser Ser Ser
405 410 415

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

Pro Phe Glu Phe Pro Thr Val Pro Gln Asp Arg Ala Val Gly Pro Ser
435 440 445

Lys Tyr Val Tyr Gly Cys Ser Val Lys His Gly Ser Phe Asp Ala Ala
450 455 460

Leu Gly Ser Ala Ala Lys Ile Asp Cys Leu Val Lys Val Asn Val Asp
465 470 475 480

Leu Leu Val Arg Gln Gly Lys Lys Arg Asn Glu Ala Gly Glu Gly Gln
485 490 495

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

Gln Thr Pro Arg Arg Gly Asp Arg Thr Ser Ser Asp Asp Asp Glu Pro
515 520 525

Ile Arg Ile Phe Glu Leu Pro Pro Leu His Tyr Ala Gln Glu Ser Ser
530 535 540

Phe Val Pro Arg Gln Asn Pro Arg Ser Glu Asp Asp Gly Tyr Leu Leu
545 550 555 560

Thr Tyr Val Phe Asp Glu Arg Gln Leu Asp Pro Ser Thr Gly Arg Ala
565 570 575

Val Glu Gly Ala Lys Ser Glu Leu Trp Val Ile Asp Ala Trp Thr Met
580 585 590

Lys Asp Val Val Cys Arg Val Lys Leu Pro Gln Arg Val Pro Tyr Gly
595 600 605

Leu His Gly His Trp Phe Ser Arg Glu Glu Ile Glu Glu Gln Arg Arg
610 615 620

Ala Pro Ser Val Arg Ser Arg Pro Pro Pro Lys Ser
625 630 635

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<211> 793
<212> DNA
<213> Rhodosporidium toruloides

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cttccgaaag ctgcgcacag tgcattcagt tacgtacacg cccgtacact ccctcttgcg      180
cggtcgaggg ctcaccaact cttcatcagt tctccccaca tcctcgaact ttattcgccg      240
caaacgctct ctatccgcct gactgagggg caggatgttc cgacagagct catcataccg      300
ctcgatgcag ctggaaaagc gccgacgggc ttgctcggcc gactggacag gcttgagcgg      360
gcgatgggac tggaaatgcg aactgtaagg ctgtcgtggc ctgcttcggg gcgtacagct      420
tactgtctcc tcttggttg aaccagctaa cctcgtagcc gcacagcacc cgaccacctt      480
ccacctctcg acccaccgcg ctccctcatc ctgcctgac cttccctcc ctcacctct      540
catctccgcc actccatcct tcgtctcccc ctctgtgac caaacctct acgtcccctt      600
caccatcctt ctcgaaccaa tccacttcgg cggcgtgccg gaatcgacgc tgccgtttgt      660
tctggtactg gttgggttg tgggagtgat gggagtgagt ggagtggcgg gagggatggg      720
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<210> 14
<211> 675
<212> DNA
<213> Rhodosporidium toruloides

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<220>
<221> CDS
<222> (1)..(675)

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1          5          10          15

gca acc ctc aca ccc ctc gca ctc gga aac acc gaa atc ctc gtc tca      96
Ala Thr Leu Thr Pro Leu Ala Leu Gly Asn Thr Glu Ile Leu Val Ser
          20          25          30

cgc ttg ccg ttc gag ctt gcg gat ctt ccg aaa gct gcg cac agt gca      144
Arg Leu Pro Phe Glu Leu Ala Asp Leu Pro Lys Ala Ala His Ser Ala
          35          40          45

tca gtt tct ccc cac atc ctc gaa ctt tat tcg ccg caa acg ctc tct      192
Ser Val Ser Pro His Ile Leu Glu Leu Tyr Ser Pro Gln Thr Leu Ser
          50          55          60

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atc	cgc	ctg	act	gag	ggt	cag	gat	gtt	ccg	aca	gag	ctc	atc	ata	ccg	240
Ile	Arg	Leu	Thr	Glu	Gly	Gln	Asp	Val	Pro	Thr	Glu	Leu	Ile	Ile	Pro	
65					70					75					80	

ctc	gat	gca	gct	gga	aaa	gcg	ccg	acg	ggc	ttg	ctc	ggc	cga	ctg	gac	288
Leu	Asp	Ala	Ala	Gly	Lys	Ala	Pro	Thr	Gly	Leu	Leu	Gly	Arg	Leu	Asp	
				85					90					95		

agg	ctt	gag	cgg	gcg	atg	gga	ctg	gaa	atg	cga	act	gta	agg	ctg	tcg	336
Arg	Leu	Glu	Arg	Ala	Met	Gly	Leu	Glu	Met	Arg	Thr	Val	Arg	Leu	Ser	
			100					105					110			

tgg	cct	gct	tcg	cac	ccg	acc	acc	ttc	cac	ctc	tcg	acc	cac	cgc	gct	384
Trp	Pro	Ala	Ser	His	Pro	Thr	Thr	Phe	His	Leu	Ser	Thr	His	Arg	Ala	
		115					120					125				

ccc	tca	tcc	tcg	cct	gac	cct	tcc	ctc	cct	cac	ctc	ctc	atc	tcc	gcc	432
Pro	Ser	Ser	Ser	Pro	Asp	Pro	Ser	Leu	Pro	His	Leu	Leu	Ile	Ser	Ala	
		130				135					140					

act	cca	tcc	ttc	gtc	tcc	ccc	tcc	tgt	gac	caa	acc	ctc	tac	gtc	ccc	480
Thr	Pro	Ser	Phe	Val	Ser	Pro	Ser	Cys	Asp	Gln	Thr	Leu	Tyr	Val	Pro	
145					150					155					160	

ttc	acc	atc	ctt	ctc	gaa	cca	atc	cac	ttc	ggc	ggc	gtg	ccg	gaa	tcg	528
Phe	Thr	Ile	Leu	Leu	Glu	Pro	Ile	His	Phe	Gly	Gly	Val	Pro	Glu	Ser	
				165					170					175		

acg	ctg	ccg	ttt	gtt	ctg	gta	ctg	gtt	ggg	ttg	gtg	gga	gtg	atg	gga	576
Thr	Leu	Pro	Phe	Val	Leu	Val	Leu	Val	Gly	Leu	Val	Gly	Val	Met	Gly	
			180					185					190			

gtg	agt	gga	gtg	gcg	gga	ggg	atg	ggg	agg	tgg	ttg	gag	gag	ctg	gca	624
Val	Ser	Gly	Val	Ala	Gly	Gly	Met	Gly	Arg	Trp	Leu	Glu	Glu	Leu	Ala	
		195					200					205				

gag	gcc	gat	tgg	aag	ctt	ggt	cgg	gcg	gga	gaa	gac	gag	aag	gcg	gat	672
Glu	Ala	Asp	Trp	Lys	Leu	Gly	Arg	Ala	Gly	Glu	Asp	Glu	Lys	Ala	Asp	
	210					215					220					

tga																675
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<210> 15
 <211> 224
 <212> PRT
 <213> Rhodosporidium toruloides

<400> 15

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

Arg Leu Pro Phe Glu Leu Ala Asp Leu Pro Lys Ala Ala His Ser Ala
35 40 45

Ser Val Ser Pro His Ile Leu Glu Leu Tyr Ser Pro Gln Thr Leu Ser
50 55 60

Ile Arg Leu Thr Glu Gly Gln Asp Val Pro Thr Glu Leu Ile Ile Pro
65 70 75 80

Leu Asp Ala Ala Gly Lys Ala Pro Thr Gly Leu Leu Gly Arg Leu Asp
85 90 95

Arg Leu Glu Arg Ala Met Gly Leu Glu Met Arg Thr Val Arg Leu Ser
100 105 110

Trp Pro Ala Ser His Pro Thr Thr Phe His Leu Ser Thr His Arg Ala
115 120 125

Pro Ser Ser Ser Pro Asp Pro Ser Leu Pro His Leu Leu Ile Ser Ala
130 135 140

Thr Pro Ser Phe Val Ser Pro Ser Cys Asp Gln Thr Leu Tyr Val Pro
145 150 155 160

Phe Thr Ile Leu Leu Glu Pro Ile His Phe Gly Gly Val Pro Glu Ser
165 170 175

Thr Leu Pro Phe Val Leu Val Leu Val Gly Leu Val Gly Val Met Gly
180 185 190

Val Ser Gly Val Ala Gly Gly Met Gly Arg Trp Leu Glu Glu Leu Ala
195 200 205

Glu Ala Asp Trp Lys Leu Gly Arg Ala Gly Glu Asp Glu Lys Ala Asp
210 215 220

<210> 16
<211> 2565

<212> DNA

<213> *Rhodosporidium toruloides*

<400> 16

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caggcgggac gaggggatcg tgggtgcagcg cgcgcctggg gaggattcgc tggacatcgg	180
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<210> 17
 <211> 1628
 <212> DNA
 <213> Rhodosporidium toruloides

<220>
 <221> CDS
 <222> (28)..(1542)

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1 5	
gac agc atc ccc cag gct tac gac acc gtc acc aag gcg ttc ttg tcg	102
Asp Ser Ile Pro Gln Ala Tyr Asp Thr Val Thr Lys Ala Phe Leu Ser	

10	15	20	25	
gga aag act agg ccc atc gcc tgg cgc aag gcg cag atc aag aaa ctc Gly Lys Thr Arg Pro Ile Ala Trp Arg Lys Ala Gln Ile Lys Lys Leu	30	35	40	150
ggg ttc ctt gtc caa gac aac gaa gac gcc ttc gtc cgc gct ctc gag Gly Phe Leu Val Gln Asp Asn Glu Asp Ala Phe Val Arg Ala Leu Glu	45	50	55	198
caa gac ttt ggc cgt ccc gct ttc gag aca atc aca gcc gag atc aac Gln Asp Phe Gly Arg Pro Ala Phe Glu Thr Ile Thr Ala Glu Ile Asn	60	65	70	246
ccc gtc aag gct gag att aac gag gtc tac gac cac ctc gag aag tgg Pro Val Lys Ala Glu Ile Asn Glu Val Tyr Asp His Leu Glu Lys Trp	75	80	85	294
gcc aag ccg agg cgc gtc aag act tcg gcg acg tgg tac gct acc aag Ala Lys Pro Arg Arg Val Lys Thr Ser Ala Thr Trp Tyr Ala Thr Lys	90	95	100	342
ccg acg gtc tac tcg gag cct aag ggt gtc acg ctc gtt atc ggg acg Pro Thr Val Tyr Ser Glu Pro Lys Gly Val Thr Leu Val Ile Gly Thr	110	115	120	390
tgg aac tac ccg atc acg ctc ctc ctc gtc ccg ctt ctc ggc gcc atc Trp Asn Tyr Pro Ile Thr Leu Leu Leu Val Pro Leu Leu Gly Ala Ile	125	130	135	438
tct gcc ggc tgc acc gcg ctc gtc aag ccc gct gag caa gcc cct cac Ser Ala Gly Cys Thr Ala Leu Val Lys Pro Ala Glu Gln Ala Pro His	140	145	150	486
gtc gcc gcg ctc gtc gcc gac ctc ctg ccc aag tac ctc gac ccc acc Val Ala Ala Leu Val Ala Asp Leu Leu Pro Lys Tyr Leu Asp Pro Thr	155	160	165	534
gcc ttc atc tgc atc aac ggc gcc atc cct caa gcg acc gct ctc ctc Ala Phe Ile Cys Ile Asn Gly Ala Ile Pro Gln Ala Thr Ala Leu Leu	170	175	180	582
aaa ctc aag ttc gat cac atc ttc tac acc ggt tcg gga acg gtc ggc Lys Leu Lys Phe Asp His Ile Phe Tyr Thr Gly Ser Gly Thr Val Gly	190	195	200	630
aag atc gtt gcg cgt gcg gcg gcg gag cac ctt tgc ccg gtt acg ctt Lys Ile Val Ala Arg Ala Ala Ala Glu His Leu Cys Pro Val Thr Leu	205	210	215	678
gag ttg ggg gga aag agt ccg gcg gtt gtg ctg gat gat gcg gat att Glu Leu Gly Gly Lys Ser Pro Ala Val Val Leu Asp Asp Ala Asp Ile	220	225	230	726

gag gtt gtg gcg agg agg atc gtt tgg gcc aag ttt acc aac gct ggg Glu Val Val Ala Arg Arg Ile Val Trp Ala Lys Phe Thr Asn Ala Gly 235 240 245	774
cag atc tgc atc tcg aca gac tac gtc ctc acg acc ccg cag acc gag Gln Ile Cys Ile Ser Thr Asp Tyr Val Leu Thr Thr Pro Gln Thr Glu 250 255 260 265	822
ccc aag ctc ctc gaa gcc ctc aag cgc gct ctc gcc gcc ttc tcc gcc Pro Lys Leu Leu Glu Ala Leu Lys Arg Ala Leu Ala Ala Phe Ser Ala 270 275 280	870
aac ccc gcc gcc tcc tcc tcc tcg gaa aag tcg tca acc tcg ctc gtg Asn Pro Ala Ala Ser Ser Ser Ser Glu Lys Ser Ser Thr Ser Leu Val 285 290 295	918
cac aac ccg aac tac tcg cgc atc atc aac cag aac cac tac aac cgc His Asn Pro Asn Tyr Ser Arg Ile Ile Asn Gln Asn His Tyr Asn Arg 300 305 310	966
gtt tcg aag ttg ctt gat gcg act aag ggc gag gtg gtt gtt gga ggc Val Ser Lys Leu Leu Asp Ala Thr Lys Gly Glu Val Val Val Gly Gly 315 320 325	1014
ggg agg gac gag aag gag cgc aag att gag gtt acg att gtg agg ggc Gly Arg Asp Glu Lys Glu Arg Lys Ile Glu Val Thr Ile Val Arg Gly 330 335 340 345	1062
gtc aag ccg gat gac tcg ctc atg tcg gag gag att ttc ggc ccc gtc Val Lys Pro Asp Asp Ser Leu Met Ser Glu Glu Ile Phe Gly Pro Val 350 355 360	1110
ctc ccg atc atg acc ctc cca acg ctc gac gac atg gtc aag ttc atc Leu Pro Ile Met Thr Leu Pro Thr Leu Asp Asp Met Val Lys Phe Ile 365 370 375	1158
cag tcg cgc gac acc cct ctc gcg ctc tac gtc ttc acg cag agc aag Gln Ser Arg Asp Thr Pro Leu Ala Leu Tyr Val Phe Thr Gln Ser Lys 380 385 390	1206
aag aac cgc gac ttc atc ttt gag cgc act cgc tcg gga gga ttc gtc Lys Asn Arg Asp Phe Ile Phe Glu Arg Thr Arg Ser Gly Gly Phe Val 395 400 405	1254
cag aac gat gtg ctc gtt cag ttc atg atc cct ggg ctg ccg ttc ggc Gln Asn Asp Val Leu Val Gln Phe Met Ile Pro Gly Leu Pro Phe Gly 410 415 420 425	1302
ggt acg ggc gcg gcg ggt tac gga aac tac cac ggc agg cgc acc ttc Gly Thr Gly Ala Ala Gly Tyr Gly Asn Tyr His Gly Arg Arg Thr Phe 430 435 440	1350
gac acg ttc tcg cac gag cgc gcg tcg gcc aat gtc ccc acc tgg atg Asp Thr Phe Ser His Glu Arg Ala Ser Ala Asn Val Pro Thr Trp Met	1398

445	450	455	
gac atg atc atg gcg tcg cgg tac cct ccc tac acc cag aag aag ctg			1446
Asp Met Ile Met Ala Ser Arg Tyr Pro Pro Tyr Thr Gln Lys Lys Leu			
460	465	470	
aag atg ctc ctg ttc gcg acc aag gcg gtg atc aag aag ccc agc aag			1494
Lys Met Leu Leu Phe Ala Thr Lys Ala Val Ile Lys Lys Pro Ser Lys			
475	480	485	
ttt ggc tcg atc tcg cgc ttg ctc aag aag ttg acg gga cag gcg tga			1542
Phe Gly Ser Ile Ser Arg Leu Leu Lys Lys Leu Thr Gly Gln Ala			
490	495	500	
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accctctcct caccctctcc caatca			1628

<210> 18
 <211> 504
 <212> PRT
 <213> Rhodosporidium toruloides

<400> 18

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

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

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

Phe	Glu	Thr	Ile	Thr	Ala	Glu	Ile	Asn	Pro	Val	Lys	Ala	Glu	Ile	Asn
65					70				75					80	

Glu	Val	Tyr	Asp	His	Leu	Glu	Lys	Trp	Ala	Lys	Pro	Arg	Arg	Val	Lys
			85					90						95	

Thr	Ser	Ala	Thr	Trp	Tyr	Ala	Thr	Lys	Pro	Thr	Val	Tyr	Ser	Glu	Pro
		100					105					110			

Lys Gly Val Thr Leu Val Ile Gly Thr Trp Asn Tyr Pro Ile Thr Leu
115 120 125

Leu Leu Val Pro Leu Leu Gly Ala Ile Ser Ala Gly Cys Thr Ala Leu
130 135 140

Val Lys Pro Ala Glu Gln Ala Pro His Val Ala Ala Leu Val Ala Asp
145 150 155 160

Leu Leu Pro Lys Tyr Leu Asp Pro Thr Ala Phe Ile Cys Ile Asn Gly
165 170 175

Ala Ile Pro Gln Ala Thr Ala Leu Leu Lys Leu Lys Phe Asp His Ile
180 185 190

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

Ala Glu His Leu Cys Pro Val Thr Leu Glu Leu Gly Gly Lys Ser Pro
210 215 220

Ala Val Val Leu Asp Asp Ala Asp Ile Glu Val Val Ala Arg Arg Ile
225 230 235 240

Val Trp Ala Lys Phe Thr Asn Ala Gly Gln Ile Cys Ile Ser Thr Asp
245 250 255

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

Lys Arg Ala Leu Ala Ala Phe Ser Ala Asn Pro Ala Ala Ser Ser Ser
275 280 285

Ser Glu Lys Ser Ser Thr Ser Leu Val His Asn Pro Asn Tyr Ser Arg
290 295 300

Ile Ile Asn Gln Asn His Tyr Asn Arg Val Ser Lys Leu Leu Asp Ala
305 310 315 320

Thr Lys Gly Glu Val Val Val Gly Gly Gly Arg Asp Glu Lys Glu Arg
325 330 335

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

Met Ser Glu Glu Ile Phe Gly Pro Val Leu Pro Ile Met Thr Leu Pro
355 360 365

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

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

Glu Arg Thr Arg Ser Gly Gly Phe Val Gln Asn Asp Val Leu Val Gln
405 410 415

Phe Met Ile Pro Gly Leu Pro Phe Gly Gly Thr Gly Ala Ala Gly Tyr
420 425 430

Gly Asn Tyr His Gly Arg Arg Thr Phe Asp Thr Phe Ser His Glu Arg
435 440 445

Ala Ser Ala Asn Val Pro Thr Trp Met Asp Met Ile Met Ala Ser Arg
450 455 460

Tyr Pro Pro Tyr Thr Gln Lys Lys Leu Lys Met Leu Leu Phe Ala Thr
465 470 475 480

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

Leu Lys Lys Leu Thr Gly Gln Ala
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<210> 19

<211> 3136

<212> DNA

<213> Rhodosporidium toruloides

<400> 19

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aacgagcgac ttgcgcgacac cgtcccgac ctcgaccgt ctggcggagg agtgcgtccg	180
gcgatgtctc ctcgagatcg gtcgcctgcc agctctcgtg gctcgcagga cgacagctcg	240
tcgacattgt cggatcgtgg gcgacagcgc aggcgttcgg caagctcgga acggtcggat	300
cagcctgaag aagcggagaa gactgcggat ccacctcagg cttcaggtgc gtccggctcg	360
ctctcctgac gctcgcgccg ctcccagacg ttgggtactga ctgtgtggtc atcgcgtcga	420
caggcctggc gcatcccgct tctcccagg cacctcatcc gatcgccagg tcctcctccg	480
ccaccacgtc tgtccccgcg ctttctgctt ccgtgcgcgc cgatcgctc gaccaccagc	540
ttcagaccac gtctccagat tgccccgcc catctcgcgc gcgccgcgtc gctcgtgtct	600
ctccaattc ccgcaacgag cgccccgtgc cgtccgccat cccttcctcc aacttctccg	660
cccaccatcg accagcccac ggtctgcgtc gacaatcctc cctccctcca tcgagccgcc	720
gcgcgagggc gagctcgctg agcccgccgt cgacctcgtc aggtctcgct tcttcctcgt	780
accgtccgtc ccggcacctg gatcctgacc agcattggct ttcagaggac gaggcgcacg	840
acgccgtcag ggttgcggtat cggccgcgtc ggccacggcg gacgaggtcg agcaggagcg	900
acgactcgga aggtcccgag cgcgacagcc ccaagctcct cgccgcgtcg ggccttggcg	960
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cgatcgagac ggcgtcgatg acgaccacga ccgccttcac cttactccg cccgccgtcg	1260
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ccatgttgcg cgtcacgagc tgtcagatgc tcgaggacgg ccgcctcatc ctcgagacga	2460
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tgcatatctg cctcgacttc ctaccacgc tgcgcgctag ctccggcgccg tggattatcg	2760
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<210> 20
 <211> 2889
 <212> DNA

<213> Rhodosporidium toruloides

<220>

<221> CDS

<222> (85)..(2889)

<400> 20

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ctgccacgat ctgagcaacc acgc atg tcg act cta gcc atc aga ccc gac 111

Met Ser Thr Leu Ala Ile Arg Pro Asp

1 5

gaa cca ccg aac gag cga ctt cgc gac acc gtc ccc gac ctc gac ccg 159

Glu Pro Pro Asn Glu Arg Leu Arg Asp Thr Val Pro Asp Leu Asp Pro

10 15 20 25

tct ggc gga gga gtg cgt ccg gcg atg tct cct cga gat cgg tcg cct 207

Ser Gly Gly Gly Val Arg Pro Ala Met Ser Pro Arg Asp Arg Ser Pro

30 35 40

gcc agc tct cgt ggc tcg cag gac gac agc tcg tcg aca ttg tcg gat 255

Ala Ser Ser Arg Gly Ser Gln Asp Asp Ser Ser Ser Thr Leu Ser Asp

45 50 55

cgt ggg cga cag cgc agg cgt tcg gca agc tcg gaa cgg tcg gat cag 303

Arg Gly Arg Gln Arg Arg Arg Ser Ala Ser Ser Glu Arg Ser Asp Gln

60 65 70

cct gaa gaa gcg gag aag act gcg gat cca cct cag gct tca ggc ctg 351

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

75 80 85

gcg cat ccc gct tct ccc gag gca cct cat ccg atc gcc agg tcc tcc 399

Ala His Pro Ala Ser Pro Glu Ala Pro His Pro Ile Ala Arg Ser Ser

90 95 100 105

tcc gcc acc acg tct gtc ccc gcg cct tct gct tcc gtg cgc gcc gat 447

Ser Ala Thr Thr Ser Val Pro Ala Pro Ser Ala Ser Val Arg Ala Asp

110 115 120

cgc ctc gac cac cag ctt cag acc acg tct cca gat tgc ccc gcc cca 495

Arg Leu Asp His Gln Leu Gln Thr Thr Ser Pro Asp Cys Pro Ala Pro

125 130 135

tct cgc atg cgc cgc gtc gct cgt gtc tct ccc aat tcc cgc aac gag 543

Ser Arg Met Arg Arg Val Ala Arg Val Ser Pro Asn Ser Arg Asn Glu

140 145 150

cgc ccc gtg ccg tcc gcc atc cct tcc tcc aac ttc tcc gcc cac cat 591

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

155 160 165

cga cca gcc cac ggt ctg cgt cga caa tcc tcc ctc cct cca tcg agc	639
Arg Pro Ala His Gly Leu Arg Arg Gln Ser Ser Leu Pro Pro Ser Ser	
170 175 180 185	
cgc cgc gcg agg gcg agc tcg ctg agc ccg ccg tcg acc tcg tca ggt	687
Arg Arg Ala Arg Ala Ser Ser Leu Ser Pro Pro Ser Thr Ser Ser Gly	
190 195 200	
ctc gct tct tcc tcg tac cgt ccg tcc cgg cac ctg gat cct gac cag	735
Leu Ala Ser Ser Ser Tyr Arg Pro Ser Arg His Leu Asp Pro Asp Gln	
205 210 215	
cat tgg ctt tca gag gac gag gcg cac gac gcc gtc agg gtt gcg gat	783
His Trp Leu Ser Glu Asp Glu Ala His Asp Ala Val Arg Val Ala Asp	
220 225 230	
cgg ccg cgt cgg cca ccg ccg acg agg tcg agc agg agc gac gac tcg	831
Arg Pro Arg Arg Pro Arg Arg Thr Arg Ser Ser Arg Ser Asp Asp Ser	
235 240 245	
gaa ggt ccc gag cgc gac agc ccc aag ctc ctc gcc gcg tcg ggc ctt	879
Glu Gly Pro Glu Arg Asp Ser Pro Lys Leu Leu Ala Ala Ser Gly Leu	
250 255 260 265	
ggc gaa gac ccg acg tcg gct cac cac atc cac aac cga ccc tcc aag	927
Gly Glu Asp Pro Thr Ser Ala His His Ile His Asn Arg Pro Ser Lys	
270 275 280	
gcg ttc aga ccg tcg gcg acg ccg ccg atg gca gag ttg acg gac ggg	975
Ala Phe Arg Pro Ser Ala Thr Pro Pro Met Ala Glu Leu Thr Asp Gly	
285 290 295	
cga tcg ctg tac gct gtc gtc ccg gac ctc gct cgc ctc ctc tgc	1023
Arg Ser Leu Tyr Ala Val Val Pro Asp Leu Ala Arg Leu Leu Leu Cys	
300 305 310	
ccg tcc tgc cac cgc ctc tac acc gat ccc gcc aca ctc gcc tgc ggt	1071
Pro Ser Cys His Arg Leu Tyr Thr Asp Pro Ala Thr Leu Ala Cys Gly	
315 320 325	
cac tcg cgc tgc ctc gtc tgc tcg gga gcg tca gat acc ctc gcc acc	1119
His Ser Arg Cys Leu Val Cys Ser Gly Ala Ser Asp Thr Leu Ala Thr	
330 335 340 345	
ccg ccg atc gag acg gcg tcg atg acg acc acg acc gcc ttc acc ttc	1167
Pro Pro Ile Glu Thr Ala Ser Met Thr Thr Thr Thr Ala Phe Thr Phe	
350 355 360	
act ccg ccc gcc gtc gcg ccg cat acg gcc ggc atc gcc tcg cct ctc	1215
Thr Pro Pro Ala Val Ala Arg His Thr Ala Gly Ile Ala Ser Pro Leu	
365 370 375	
cct tcg ccc ccc gtc gtc gca cac ctc gac aac aac cag ctg tat cgc	1263
Pro Ser Pro Pro Val Val Ala His Leu Asp Asn Asn Gln Leu Tyr Arg	

380	385	390	
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gct cag acg cac atc ccc gtc gat ctt ccc aat ctc acc tgc ccc gac Ala Gln Thr His Ile Pro Val Asp Leu Pro Asn Leu Thr Cys Pro Asp 410 415 420 425			1359
tcg tcg tgc gac tac aac ttc tcg cac ctc atc gtc ccc cac ctc ccg Ser Ser Cys Asp Tyr Asn Phe Ser His Leu Ile Val Pro His Leu Pro 430 435 440			1407
ctt cat gtc gac tac acc ctg cgc aag gtc agc gag atg ctg cag aag Leu His Val Asp Tyr Thr Leu Arg Lys Val Ser Glu Met Leu Gln Lys 445 450 455			1455
gct gtg cct gga ctg gca gca tgg gcg acg cgt ctt gcg tcg aag aac Ala Val Pro Gly Leu Ala Ala Trp Ala Thr Arg Leu Ala Ser Lys Asn 460 465 470			1503
gac ccg cat ctc gcg ccg ttg ttc tcg gat gtg cga ttg gcg agt gag Asp Pro His Leu Ala Pro Leu Phe Ser Asp Val Arg Leu Ala Ser Glu 475 480 485			1551
gcg ccg acc gat gtc gag gag aac ggc gag cag ccg atg gtc gag ggc Ala Pro Thr Asp Val Glu Glu Asn Gly Glu Gln Pro Met Val Glu Gly 490 495 500 505			1599
gac gtc cag cct ggt gcg gta tcg cgc acg agc agc ggc agc agt ggc Asp Val Gln Pro Gly Ala Val Ser Arg Thr Ser Ser Gly Ser Ser Gly 510 515 520			1647
ggc ggc gac gag gag acg atc gaa ggg cac gac gac agc aag cgg gcg Gly Gly Asp Glu Glu Thr Ile Glu Gly His Asp Asp Ser Lys Arg Ala 525 530 535			1695
cac aag tcg cgc aag tcg tgg cag gcg agc aag aag acg cga acg gtg His Lys Ser Arg Lys Ser Trp Gln Ala Ser Lys Lys Thr Arg Thr Val 540 545 550			1743
tcg ttc agc gac gtc tcg atg gct tcg cct gcc gtc ggt cca tct cgc Ser Phe Ser Asp Val Ser Met Ala Ser Pro Ala Val Gly Pro Ser Arg 555 560 565			1791
acg tcg acg ccg acg ccg cac gcc gca caa cga gac gac aag cac ctc Thr Ser Thr Pro Thr Pro His Ala Ala Gln Arg Asp Asp Lys His Leu 570 575 580 585			1839
gac atc gct ggc ttg tcg ccg tcg ttc ctc acc gac ctg cac aac gag Asp Ile Ala Gly Leu Ser Pro Ser Phe Leu Thr Asp Leu His Asn Glu 590 595 600			1887

tgc gag tgt caa gtg tgc ttc cag ctc ttc cac gag ccg gtc acc tcg Cys Glu Cys Gln Val Cys Phe Gln Leu Phe His Glu Pro Val Thr Ser	1935
605 610 615	
cct tgc ggc cac tcg ttc tgc cga caa tgc ctc gcc cgc tcg tac gat Pro Cys Gly His Ser Phe Cys Arg Gln Cys Leu Ala Arg Ser Tyr Asp	1983
620 625 630	
cac tcc gac aag tgc cct ctc tgc cgc gcc gac ctc ccg ccc ctc gcc His Ser Asp Lys Cys Pro Leu Cys Arg Ala Asp Leu Pro Pro Leu Ala	2031
635 640 645	
tac ttc cgc tgg caa cga ccc aac atc gcg ctc acc aag att atc gag Tyr Phe Arg Trp Gln Arg Pro Asn Ile Ala Leu Thr Lys Ile Ile Glu	2079
650 655 660 665	
acc gct ctc cct caa caa gcc gct gag cgc gcc gcg acc gtc aag gag Thr Ala Leu Pro Gln Gln Ala Ala Glu Arg Ala Ala Thr Val Lys Glu	2127
670 675 680	
gaa gaa ctt gcg ctg ctt gcg tcg gtc ccc gtg ttc gtc tgt acg acc Glu Glu Leu Ala Leu Leu Ala Ser Val Pro Val Phe Val Cys Thr Thr	2175
685 690 695	
gca tgg cca ggc atc aag tgc ttc ctg cac atc ttc gag cct cgg tat Ala Trp Pro Gly Ile Lys Cys Phe Leu His Ile Phe Glu Pro Arg Tyr	2223
700 705 710	
cgc ctc atg gtc cgc cgc gtg ctc gag acg ccc gaa cgt tcg ttc ggc Arg Leu Met Val Arg Arg Val Leu Glu Thr Pro Glu Arg Ser Phe Gly	2271
715 720 725	
atg gtc ctt cct ctc cgc agc gcc gga ccc gac gct gtc aac gag tat Met Val Leu Pro Leu Arg Ser Ala Gly Pro Asp Ala Val Asn Glu Tyr	2319
730 735 740 745	
ggc acc atg ttg cgc gtc acg agc tgt cag atg ctc gag gac ggc cgc Gly Thr Met Leu Arg Val Thr Ser Cys Gln Met Leu Glu Asp Gly Arg	2367
750 755 760	
ctc atc ctc gag acg atc ggg acg tac cgc ttc cgc ctc ctc gag cgc Leu Ile Leu Glu Thr Ile Gly Thr Tyr Arg Phe Arg Leu Leu Glu Arg	2415
765 770 775	
agc atg gtc gac ggg tac aac gtc ggc aag gtc gaa cgt gtc gac gac Ser Met Val Asp Gly Tyr Asn Val Gly Lys Val Glu Arg Val Asp Asp	2463
780 785 790	
gtc tcg ccg gaa caa gaa gcg gag ctt gag cgg gtc gcg ctc gcg agg Val Ser Pro Glu Gln Glu Ala Glu Leu Glu Arg Val Ala Leu Ala Arg	2511
795 800 805	
aac gat acc ctc caa gac gag tac gcc gac cct gaa cca gtc gga ccg Asn Asp Thr Leu Gln Asp Glu Tyr Ala Asp Pro Glu Pro Val Gly Pro	2559

810	815	820	825	
gac agc gtg ccc ctc tcg aga ccg ccc atg acc ggc aac gtc gag ttg				2607
Asp Ser Val Pro Leu Ser Arg Pro Pro Met Thr Gly Asn Val Glu Leu				
	830	835	840	
tcg acc gac cag ctc atg cag atc tgc ctc gac ttc ctc acc acg ctg				2655
Ser Thr Asp Gln Leu Met Gln Ile Cys Leu Asp Phe Leu Thr Thr Leu				
	845	850	855	
cgc gct agc tcg gcg ccg tgg att atc gag cgg ctg aac cgg acg gtc				2703
Arg Ala Ser Ser Ala Pro Trp Ile Ile Glu Arg Leu Asn Arg Thr Val				
	860	865	870	
ggc gag gtg ccc aac aac ccg cac gac ttc agc tgg ttc gcc gcc gag				2751
Gly Glu Val Pro Asn Asn Pro His Asp Phe Ser Trp Phe Ala Ala Glu				
	875	880	885	
gtc ttc ccc gtc gaa gat cac gtc aag gtc acg ctt ctc cag atc acg				2799
Val Phe Pro Val Glu Asp His Val Lys Val Thr Leu Leu Gln Ile Thr				
	890	895	900	905
agt gtc cgc gaa cga ctg cgc ttg atc gtc ttc tgg atc gag cag ttc				2847
Ser Val Arg Glu Arg Leu Arg Leu Ile Val Phe Trp Ile Glu Gln Phe				
	910	915	920	
agg tcg tcg tgg tgg tac tcc cga ggc tgc aac atc gcc tag				2889
Arg Ser Ser Trp Trp Tyr Ser Arg Gly Cys Asn Ile Ala				
	925	930		

<210> 21
 <211> 934
 <212> PRT
 <213> Rhodosporidium toruloides

<400> 21

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

Ala Met Ser Pro Arg Asp Arg Ser Pro Ala Ser Ser Arg Gly Ser Gln
35 40 45

Asp Asp Ser Ser Ser Thr Leu Ser Asp Arg Gly Arg Gln Arg Arg Arg
50 55 60

Ser Ala Ser Ser Glu Arg Ser Asp Gln Pro Glu Glu Ala Glu Lys Thr
65 70 75 80

Ala Asp Pro Pro Gln Ala Ser Gly Leu Ala His Pro Ala Ser Pro Glu
85 90 95

Ala Pro His Pro Ile Ala Arg Ser Ser Ala Thr Thr Ser Val Pro
100 105 110

Ala Pro Ser Ala Ser Val Arg Ala Asp Arg Leu Asp His Gln Leu Gln
115 120 125

Thr Thr Ser Pro Asp Cys Pro Ala Pro Ser Arg Met Arg Arg Val Ala
130 135 140

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

Pro Ser Ser Asn Phe Ser Ala His His Arg Pro Ala His Gly Leu Arg
165 170 175

Arg Gln Ser Ser Leu Pro Pro Ser Ser Arg Arg Ala Arg Ala Ser Ser
180 185 190

Leu Ser Pro Pro Ser Thr Ser Ser Gly Leu Ala Ser Ser Ser Tyr Arg
195 200 205

Pro Ser Arg His Leu Asp Pro Asp Gln His Trp Leu Ser Glu Asp Glu
210 215 220

Ala His Asp Ala Val Arg Val Ala Asp Arg Pro Arg Arg Pro Arg Arg
225 230 235 240

Thr Arg Ser Ser Arg Ser Asp Asp Ser Glu Gly Pro Glu Arg Asp Ser
245 250 255

Pro Lys Leu Leu Ala Ala Ser Gly Leu Gly Glu Asp Pro Thr Ser Ala
260 265 270

His His Ile His Asn Arg Pro Ser Lys Ala Phe Arg Pro Ser Ala Thr
275 280 285

Pro Pro Met Ala Glu Leu Thr Asp Gly Arg Ser Leu Tyr Ala Val Val
290 295 300

Pro Asp Leu Ala Arg Leu Leu Leu Cys Pro Ser Cys His Arg Leu Tyr
305 310 315 320

Thr Asp Pro Ala Thr Leu Ala Cys Gly His Ser Arg Cys Leu Val Cys
325 330 335

Ser Gly Ala Ser Asp Thr Leu Ala Thr Pro Pro Ile Glu Thr Ala Ser
340 345 350

Met Thr Thr Thr Thr Ala Phe Thr Phe Thr Pro Pro Ala Val Ala Arg
355 360 365

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

His Leu Asp Asn Asn Gln Leu Tyr Arg Thr Leu Ser Ala Thr Ser Thr
385 390 395 400

Thr Ser Thr Pro Ser Val Ala Ser Thr Ala Gln Thr His Ile Pro Val
405 410 415

Asp Leu Pro Asn Leu Thr Cys Pro Asp Ser Ser Cys Asp Tyr Asn Phe
420 425 430

Ser His Leu Ile Val Pro His Leu Pro Leu His Val Asp Tyr Thr Leu
435 440 445

Arg Lys Val Ser Glu Met Leu Gln Lys Ala Val Pro Gly Leu Ala Ala
450 455 460

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

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

Asn Gly Glu Gln Pro Met Val Glu Gly Asp Val Gln Pro Gly Ala Val
500 505 510

Ser Arg Thr Ser Ser Gly Ser Ser Gly Gly Gly Asp Glu Glu Thr Ile
515 520 525

Glu Gly His Asp Asp Ser Lys Arg Ala His Lys Ser Arg Lys Ser Trp
530 535 540

Gln Ala Ser Lys Lys Thr Arg Thr Val Ser Phe Ser Asp Val Ser Met
545 550 555 560

Ala Ser Pro Ala Val Gly Pro Ser Arg Thr Ser Thr Pro Thr Pro His
565 570 575

Ala Ala Gln Arg Asp Asp Lys His Leu Asp Ile Ala Gly Leu Ser Pro
580 585 590

Ser Phe Leu Thr Asp Leu His Asn Glu Cys Glu Cys Gln Val Cys Phe
595 600 605

Gln Leu Phe His Glu Pro Val Thr Ser Pro Cys Gly His Ser Phe Cys
610 615 620

Arg Gln Cys Leu Ala Arg Ser Tyr Asp His Ser Asp Lys Cys Pro Leu
625 630 635 640

Cys Arg Ala Asp Leu Pro Pro Leu Ala Tyr Phe Arg Trp Gln Arg Pro
645 650 655

Asn Ile Ala Leu Thr Lys Ile Ile Glu Thr Ala Leu Pro Gln Gln Ala
660 665 670

Ala Glu Arg Ala Ala Thr Val Lys Glu Glu Glu Leu Ala Leu Leu Ala
675 680 685

Ser Val Pro Val Phe Val Cys Thr Thr Ala Trp Pro Gly Ile Lys Cys
690 695 700

Phe Leu His Ile Phe Glu Pro Arg Tyr Arg Leu Met Val Arg Arg Val
705 710 715 720

Leu Glu Thr Pro Glu Arg Ser Phe Gly Met Val Leu Pro Leu Arg Ser
725 730 735

Ala Gly Pro Asp Ala Val Asn Glu Tyr Gly Thr Met Leu Arg Val Thr
740 745 750

Ser Cys Gln Met Leu Glu Asp Gly Arg Leu Ile Leu Glu Thr Ile Gly
755 760 765

Thr Tyr Arg Phe Arg Leu Leu Glu Arg Ser Met Val Asp Gly Tyr Asn
770 775 780

Val Gly Lys Val Glu Arg Val Asp Asp Val Ser Pro Glu Gln Glu Ala
785 790 795 800

Glu Leu Glu Arg Val Ala Leu Ala Arg Asn Asp Thr Leu Gln Asp Glu
805 810 815

Tyr Ala Asp Pro Glu Pro Val Gly Pro Asp Ser Val Pro Leu Ser Arg
820 825 830

Pro Pro Met Thr Gly Asn Val Glu Leu Ser Thr Asp Gln Leu Met Gln
835 840 845

Ile Cys Leu Asp Phe Leu Thr Thr Leu Arg Ala Ser Ser Ala Pro Trp
850 855 860

Ile Ile Glu Arg Leu Asn Arg Thr Val Gly Glu Val Pro Asn Asn Pro
865 870 875 880

His Asp Phe Ser Trp Phe Ala Ala Glu Val Phe Pro Val Glu Asp His
885 890 895

Val Lys Val Thr Leu Leu Gln Ile Thr Ser Val Arg Glu Arg Leu Arg
900 905 910

Leu Ile Val Phe Trp Ile Glu Gln Phe Arg Ser Ser Trp Trp Tyr Ser
915 920 925

Arg Gly Cys Asn Ile Ala
930

<210> 22
<211> 2357
<212> DNA
<213> Rhodosporidium toruloides

<400> 22
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gttggtgctgg atctcggctc gcggatatgg aaggtcgggt tcagcgggga gccgcagccg 420
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gaggagctca tagaggagat caagacgcgg ctgtgttttg tcggtgagga ggtcccgtc 1320

gatgcgagcc ggggcgagag ggaggcgtcc gcgttcagcg gatcggccat gagcgtcgac	1380
actgcatcag cacgcgacaa ctttgacgac ctttccgacc ccgacaacgc actactaaag	1440
gagctttact cccgcttcgc cgcgacatcg accgccaaac ccgtttcctt ccggataccc	1500
aacttgtccc aacctgcat cgcgaaagggt acaggctgag ggtggatcca ggtgcccggc	1560
tggatcaggg agcgcgccgc cgagggtgtg tgggaggagg atggtgatgg agacgagcgt	1620
gggcttgccg ccgttgctct tgactgccta ttgaagggtgc gcaagctgac cacttcgctc	1680
gagcgaagta gctgacactg caccggttcc cccagctccc ccttgacctt cgaaagccga	1740
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cgcctctgcc agcagcatcc gtcgaacctc cttcttccga ccctgccgga cccatgtcga	1920
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gaaagcatgc cctcgcgact cgactgcaca acctgcggca ttgcctcga tacgccccgc	2040
ttgtccctct cgctcgacac ctcgccatct tgaaccaccc atctccgaac tcctcggcat	2100
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ctgagattgc gagggagcag tgggatgcag gggtgcggtt tgcggaggca gaagaggcgg	2280
agggagagga aggagaggag tttgaggagc gggaagtgat ccggccggct ctgccggact	2340
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<210> 23
 <211> 2046
 <212> DNA
 <213> Rhodosporidium toruloides

<220>
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atcagcctcc cgcgagcgct agcaggctct cttagccgcc tcacgcctac ctgcga	117
atg tcc tcc cca cct cgc ttc gcg ccc ggt tcg acc tcg ccc acg cag	165
Met Ser Ser Pro Pro Arg Phe Ala Pro Gly Ser Thr Ser Pro Thr Gln	

1	5	10	15	
tcg agg ccg cgt gcg acg cac agc agc cca aca caa ggt ccc ttc gca				213
Ser Arg Pro Arg Ala Thr His Ser Ser Pro Thr Gln Gly Pro Phe Ala	20	25	30	
acg cct gcg cgc cca ggt gcg agc tca gcg gcg cac caa ccc gat cct				261
Thr Pro Ala Arg Pro Gly Ala Ser Ser Ala Ala His Gln Pro Asp Pro	35	40	45	
tca acc tcg aca gca ggc gcc gcc tcc ctc ctc acg tct tct cct cac				309
Ser Thr Ser Thr Ala Gly Ala Ala Ser Leu Leu Thr Ser Ser Pro His	50	55	60	
tac acg act tcg ctg cgc tct cga cac tcg ctt tac ggc acg gaa gac				357
Tyr Thr Thr Ser Leu Arg Ser Arg His Ser Leu Tyr Gly Thr Glu Asp	65	70	75	80
cgt gtt gtg ctg gat ctc ggc tcg cgg ata tgg aag gtc ggg ttc agc				405
Arg Val Val Leu Asp Leu Gly Ser Arg Ile Trp Lys Val Gly Phe Ser	85	90	95	
ggg gag ccg cag ccg cgc gag tgc cgg agc gtc gtg agc gag ttg gcg				453
Gly Glu Pro Gln Pro Arg Glu Cys Arg Ser Val Val Ser Glu Leu Ala	100	105	110	
cat gag cgg gct ggg cga aga gca ggg ccg tcc ata ggc gcg aga ggg				501
His Glu Arg Ala Gly Arg Arg Ala Gly Pro Ser Ile Gly Ala Arg Gly	115	120	125	
gac gac gac gaa gag gac tgc ttt tgg gcg ctc gag aag gcc gag ccg				549
Asp Asp Asp Glu Glu Asp Cys Phe Trp Ala Leu Glu Lys Ala Glu Pro	130	135	140	
agc gag gag gag tgg ttg att cgc gag gag agg gtg aag cga tta ctg				597
Ser Glu Glu Glu Trp Leu Ile Arg Glu Glu Arg Val Lys Arg Leu Leu	145	150	155	160
cgc aag atc tgg ttc gaa aac ctc atg atc gac ccg aag acg cgc aaa				645
Arg Lys Ile Trp Phe Glu Asn Leu Met Ile Asp Pro Lys Thr Arg Lys	165	170	175	
gtc atc gtc gtg gag aac cca ctg ctg tcg acg cgc gtg aag gag atg				693
Val Ile Val Val Glu Asn Pro Leu Leu Ser Thr Arg Val Lys Glu Met	180	185	190	
atc gcg cgg gtc ttg ttc gac aac ttg cag atc ccg tcg ctc agc ttc				741
Ile Ala Arg Val Leu Phe Asp Asn Leu Gln Ile Pro Ser Leu Ser Phe	195	200	205	
gct tcc gcc ccc ttg ctc gcc ttg atg gcg gcc ggc aca gtg acc ggt				789
Ala Ser Ala Pro Leu Leu Ala Leu Met Ala Ala Gly Thr Val Thr Gly	210	215	220	

ctt gtc gtc gac gtc gga aac ctc gag acg acc gtt ctt ccc gtc ttt Leu Val Val Asp Val Gly Asn Leu Glu Thr Thr Val Leu Pro Val Phe 225 230 235 240	837
cac gct cgc ccg ctc ttt ccc tcc ctc acc aca act cct cgc gcg ggc His Ala Arg Pro Leu Phe Pro Ser Leu Thr Thr Thr Pro Arg Ala Gly 245 250 255	885
tct cgc ctg aac cgc cgc ctc cgc tct ctc ctc ctc gca ttc ggc tca Ser Arg Leu Asn Arg Arg Leu Arg Ser Leu Leu Leu Ala Phe Gly Ser 260 265 270	933
tac gca cct cct ccc tcc tcc ctc aac tcc atg acg cct ccc gct atc Tyr Ala Pro Pro Pro Ser Ser Leu Asn Ser Met Thr Pro Pro Ala Ile 275 280 285	981
gga cgg ata ccg aag gag ctc ttg acg gag gag ctc ata gag gag atc Gly Arg Ile Pro Lys Glu Leu Leu Thr Glu Glu Leu Ile Glu Glu Ile 290 295 300	1029
aag acg cgg ctg tgt ttt gtc ggt gag gag gtc ccg ctc gat gcg agc Lys Thr Arg Leu Cys Phe Val Gly Glu Glu Val Pro Leu Asp Ala Ser 305 310 315 320	1077
cgg ggc gag agg gag gcg tcc gcg ttc agc gga tcg gcc atg agc gtc Arg Gly Glu Arg Glu Ala Ser Ala Phe Ser Gly Ser Ala Met Ser Val 325 330 335	1125
gac act gca tca gca cgc gac aac ttt gac gac cct tcc gac ccc gac Asp Thr Ala Ser Ala Arg Asp Asn Phe Asp Asp Pro Ser Asp Pro Asp 340 345 350	1173
aac gca cta cta aag gag ctt tac tcc cgc ttc gcc gcg aca tcg acc Asn Ala Leu Leu Lys Glu Leu Tyr Ser Arg Phe Ala Ala Thr Ser Thr 355 360 365	1221
gcc aaa ccc gtt tcc ttc cgg ata ccc aac ttg tcc caa cct gcg atc Ala Lys Pro Val Ser Phe Arg Ile Pro Asn Leu Ser Gln Pro Ala Ile 370 375 380	1269
gcg aac ggt aca ggt cga ggg tgg atc cag gtg ccc ggc tgg atc agg Ala Asn Gly Thr Gly Arg Gly Trp Ile Gln Val Pro Gly Trp Ile Arg 385 390 395 400	1317
gag cgc gcc gcc gag gtg ttg tgg gag gag gat ggt gat gga gac gag Glu Arg Ala Ala Glu Val Leu Trp Glu Glu Asp Gly Asp Gly Asp Glu 405 410 415	1365
cgt ggg ctt gcc gcc gtt gtc ctt gac tgc cta ttg aag ctc ccc ctt Arg Gly Leu Ala Ala Val Val Leu Asp Cys Leu Leu Lys Leu Pro Leu 420 425 430	1413
gac ctt cga aag ccg atg gcc tcg tca atc ctc ctc acg ggc ggc acc Asp Leu Arg Lys Pro Met Ala Ser Ser Ile Leu Leu Thr Gly Gly Thr 440 445 450	1461

435	440	445	
gcc atg ctc ccc ggc ttc ttc cca cgc ttc aag gcc gct ctt ctt gcc Ala Met Leu Pro Gly Phe Phe Pro Arg Phe Lys Ala Ala Leu Leu Ala 450 455 460			1509
cag ctc gac cgc tcg cat cct cct tcc cct ccg cct tcc ccg cct ctg Gln Leu Asp Arg Ser His Pro Pro Ser Pro Pro Pro Ser Pro Pro Leu 465 470 475 480			1557
cca gca gca tcc gtc gaa cct cct tct tcc gac cct gcc gga ccc atg Pro Ala Ala Ser Val Glu Pro Pro Ser Ser Asp Pro Ala Gly Pro Met 485 490 495			1605
tcg acg gac acg gcg gca tcg cct gcg ccc tct cgc tcg agc gaa gtc Ser Thr Asp Thr Ala Ala Ser Pro Ala Pro Ser Arg Ser Ser Glu Val 500 505 510			1653
aat gcg aag cgg cgg cga aag cat gcc ctc gcg act cga ctg cac aac Asn Ala Lys Arg Arg Arg Lys His Ala Leu Ala Thr Arg Leu His Asn 515 520 525			1701
ctg cgg cat tcg cct cga tac gcc ccg ctt gtc cct ctc gct cga cac Leu Arg His Ser Pro Arg Tyr Ala Pro Leu Val Pro Leu Ala Arg His 530 535 540			1749
ctc gcc atc ttg aac cac cca tct ccg aac tcc tcg gca tcg tcg acg Leu Ala Ile Leu Asn His Pro Ser Pro Asn Ser Ser Ala Ser Ser Thr 545 550 555 560			1797
gcg ccc tca tca acc ctc gct cga cag cgc gaa ggt tcg gct ccg tct Ala Pro Ser Ser Thr Leu Ala Arg Gln Arg Glu Gly Ser Ala Pro Ser 565 570 575			1845
ttc tcg ccc gcc ttg caa agc tgg atc ggc ggc agc ctc gca gga gcg Phe Ser Pro Ala Leu Gln Ser Trp Ile Gly Gly Ser Leu Ala Gly Ala 580 585 590			1893
ctc aag acg ggc ggg cct gag att gcg agg gag cag tgg gat gca ggg Leu Lys Thr Gly Gly Pro Glu Ile Ala Arg Glu Gln Trp Asp Ala Gly 595 600 605			1941
ttg cgg ttt gcg gag gca gaa gag gcg gag gga gag gaa gga gag gag Leu Arg Phe Ala Glu Ala Glu Glu Ala Glu Gly Glu Glu Gly Glu Glu 610 615 620			1989
ttt gag gag cgg gaa gtg atc cgg ccg gct ctg ccg gac tgg acg agg Phe Glu Glu Arg Glu Val Ile Arg Pro Ala Leu Pro Asp Trp Thr Arg 625 630 635 640			2037
atc gcg tag Ile Ala			2046

<210> 24
 <211> 642
 <212> PRT
 <213> Rhodosporidium toruloides

<400> 24

Met Ser Ser Pro Pro Arg Phe Ala Pro Gly Ser Thr Ser Pro Thr Gln
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Ser Arg Pro Arg Ala Thr His Ser Ser Pro Thr Gln Gly Pro Phe Ala
 20 25 30

Thr Pro Ala Arg Pro Gly Ala Ser Ser Ala Ala His Gln Pro Asp Pro
 35 40 45

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

Tyr Thr Thr Ser Leu Arg Ser Arg His Ser Leu Tyr Gly Thr Glu Asp
 65 70 75 80

Arg Val Val Leu Asp Leu Gly Ser Arg Ile Trp Lys Val Gly Phe Ser
 85 90 95

Gly Glu Pro Gln Pro Arg Glu Cys Arg Ser Val Val Ser Glu Leu Ala
 100 105 110

His Glu Arg Ala Gly Arg Arg Ala Gly Pro Ser Ile Gly Ala Arg Gly
 115 120 125

Asp Asp Asp Glu Glu Asp Cys Phe Trp Ala Leu Glu Lys Ala Glu Pro
 130 135 140

Ser Glu Glu Glu Trp Leu Ile Arg Glu Glu Arg Val Lys Arg Leu Leu
 145 150 155 160

Arg Lys Ile Trp Phe Glu Asn Leu Met Ile Asp Pro Lys Thr Arg Lys
 165 170 175

Val Ile Val Val Glu Asn Pro Leu Leu Ser Thr Arg Val Lys Glu Met
 180 185 190

Ile Ala Arg Val Leu Phe Asp Asn Leu Gln Ile Pro Ser Leu Ser Phe
195 200 205

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

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

His Ala Arg Pro Leu Phe Pro Ser Leu Thr Thr Thr Pro Arg Ala Gly
245 250 255

Ser Arg Leu Asn Arg Arg Leu Arg Ser Leu Leu Leu Ala Phe Gly Ser
260 265 270

Tyr Ala Pro Pro Pro Ser Ser Leu Asn Ser Met Thr Pro Pro Ala Ile
275 280 285

Gly Arg Ile Pro Lys Glu Leu Leu Thr Glu Glu Leu Ile Glu Glu Ile
290 295 300

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

Arg Gly Glu Arg Glu Ala Ser Ala Phe Ser Gly Ser Ala Met Ser Val
325 330 335

Asp Thr Ala Ser Ala Arg Asp Asn Phe Asp Asp Pro Ser Asp Pro Asp
340 345 350

Asn Ala Leu Leu Lys Glu Leu Tyr Ser Arg Phe Ala Ala Thr Ser Thr
355 360 365

Ala Lys Pro Val Ser Phe Arg Ile Pro Asn Leu Ser Gln Pro Ala Ile
370 375 380

Ala Asn Gly Thr Gly Arg Gly Trp Ile Gln Val Pro Gly Trp Ile Arg
385 390 395 400

Glu Arg Ala Ala Glu Val Leu Trp Glu Glu Asp Gly Asp Gly Asp Glu
405 410 415

Arg Gly Leu Ala Ala Val Val Leu Asp Cys Leu Leu Lys Leu Pro Leu
420 425 430

Asp Leu Arg Lys Pro Met Ala Ser Ser Ile Leu Leu Thr Gly Gly Thr
435 440 445

Ala Met Leu Pro Gly Phe Phe Pro Arg Phe Lys Ala Ala Leu Leu Ala
450 455 460

Gln Leu Asp Arg Ser His Pro Pro Ser Pro Pro Pro Ser Pro Pro Leu
465 470 475 480

Pro Ala Ala Ser Val Glu Pro Pro Ser Ser Asp Pro Ala Gly Pro Met
485 490 495

Ser Thr Asp Thr Ala Ala Ser Pro Ala Pro Ser Arg Ser Ser Glu Val
500 505 510

Asn Ala Lys Arg Arg Arg Lys His Ala Leu Ala Thr Arg Leu His Asn
515 520 525

Leu Arg His Ser Pro Arg Tyr Ala Pro Leu Val Pro Leu Ala Arg His
530 535 540

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

Ala Pro Ser Ser Thr Leu Ala Arg Gln Arg Glu Gly Ser Ala Pro Ser
565 570 575

Phe Ser Pro Ala Leu Gln Ser Trp Ile Gly Gly Ser Leu Ala Gly Ala
580 585 590

Leu Lys Thr Gly Gly Pro Glu Ile Ala Arg Glu Gln Trp Asp Ala Gly
595 600 605

Leu Arg Phe Ala Glu Ala Glu Glu Ala Glu Gly Glu Glu Gly Glu Glu
610 615 620

Phe Glu Glu Arg Glu Val Ile Arg Pro Ala Leu Pro Asp Trp Thr Arg
625 630 635 640

Ile Ala

<210> 25
<211> 45
<212> PRT
<213> Aspergillus fumigatus Af293

<400> 25

Leu Ile Gln Cys Ser His Cys Leu Arg Pro Leu Arg Ser Pro Leu Arg
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Leu Pro Cys Gly Asn Thr Phe Cys Arg Ala Cys Leu Pro Pro Leu Tyr
20 25 30

Glu Arg Lys Gly Ile Thr Tyr Pro Ala Asp Glu Gly Arg
35 40 45

<210> 26
<211> 44
<212> PRT
<213> Blakeslea trispora

<400> 26

Ser Thr Glu Cys Pro Ile Cys Cys Ser Arg Phe Asn Asn Pro Thr Thr
1 5 10 15

Thr Pro Cys Gly His Thr Phe Cys Arg Asn Cys Leu Ile Arg Ser Leu
20 25 30

Asp His Gln Arg Ser Cys Pro Phe Cys Arg Asp Asn
35 40

<210> 27
<211> 45
<212> PRT
<213> Fusarium fujikuroi

<400> 27

Leu Phe Gln Cys Gln Ile Cys Ser Leu Pro Leu Asp Glu Pro Ile Ser
 1 5 10 15

Leu Pro Cys Gly Lys Ser Leu Cys Arg Arg Cys Leu Pro Gly Thr His
 20 25 30

Met Arg Ala Asn Ile Thr Tyr Pro Ala Ala Pro Glu Arg
 35 40 45

<210> 28
 <211> 44
 <212> PRT
 <213> Mucor circinelloides

<400> 28

Pro Thr Glu Cys Pro Ile Cys Cys Thr Arg Phe Thr Asn Ala Thr Thr
 1 5 10 15

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

Asp His Gln Arg Ser Cys Pro Phe Cys Arg Asp Ser
 35 40

<210> 29
 <211> 47
 <212> PRT
 <213> Phycomyces blakesleeanus

<400> 29

Thr Ser His Gly Val Glu Arg Arg Ile Arg Glu Lys Asp Pro Thr Leu
 1 5 10 15

Leu Thr Phe Gly Pro Asp Pro Cys Lys Thr Ile Phe Gly Arg Ile Gln
 20 25 30

Ser Val Tyr His His Ile Ser Lys Phe Gly Ala Asn Ala Gln Ile
 35 40 45

<210> 30
 <211> 64
 <212> PRT

<213> Rhodosporidium toruloides

<400> 30

Leu Leu Leu Cys Pro Ser Cys His Arg Leu Tyr Thr Asp Pro Ala Thr
1 5 10 15

Leu Ala Cys Gly His Ser Arg Cys Leu Val Cys Ser Gly Ala Ser Asp
20 25 30

Thr Leu Ala Thr Pro Pro Ile Glu Thr Ala Ser Met Thr Thr Thr Thr
35 40 45

Ala Phe Thr Phe Thr Pro Pro Ala Val Ala Arg His Thr Ala Gly Ile
50 55 60

<210> 31

<211> 74

<212> PRT

<213> Ustilago maydis 521

<400> 31

Tyr Ala Ser Ser Pro Leu Pro Arg Ser Pro His Gln Arg Pro Ser Leu
1 5 10 15

Pro Ala Ser Ser Gly Ala Ser Val Ala Ser Pro Arg Ser His His Ala
20 25 30

Arg Val Arg Arg Thr Ala Ala Ala Ser Ser Val Leu Ser Thr Ser Ile
35 40 45

Arg Pro Ser Thr Gly Ser Arg Ala Arg Ala Ala Thr Arg Arg Arg Arg
50 55 60

Arg Ser Pro Leu Asp Arg Ser Ser Val Arg
65 70

<210> 32

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 32
tttactagtg gacggcttgt tctctcctg 29

<210> 33
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 33
tttccatggt gaggatctg gtgttggtc 29

<210> 34
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 34
tttactagtg gacggcttgt tctctcctg 29

<210> 35
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<400> 35
tttccatggt gaggatctg gtgttggtc 29

<210> 36
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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<400> 36
ggaactcatc cgctcgatcg 20

<210> 37

<211> 20
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 <213> Artificial Sequence

 <220>
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 <400> 37
 caggccttcg ccatcggatt 20

<210> 38
 <211> 20
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 <213> Artificial Sequence

 <220>
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 <400> 38
 tcctcttccg actgggacaa 20

<210> 39
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 <220>
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 <400> 39
 cccaaacaac accgagagga 20

<210> 40
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 <212> DNA
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 <220>
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 <400> 40
 aaacactgat agtttttgga aggggtgacgc acctc 35

<210> 41
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
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<400> 41
tcgagctcgg taccaggag gagaagaagg tgatgg 36

<210> 42
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 42
tcgctggatt ggtacgacaa c 21

<210> 43
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 43
ccaccagtga ccatctcttc g 21

<210> 44
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 44
aaaggtaccg acttgccga gcgagagac 29

<210> 45
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 45
aaaaagctta gactccagaa cccgaccgta 30

<210> 46

<211> 28
 <212> DNA
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 <223> synthetic oligonucleotide

 <400> 46
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 <210> 47
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 <210> 48
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 <212> DNA
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 <210> 49
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 <400> 49
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 <210> 50
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 <212> DNA
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 <220>
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<400> 50
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<210> 51
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 51
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<210> 52
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 52
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<210> 53
<211> 30
<212> DNA
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<223> synthetic oligonucleotide

<400> 53
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<210> 54
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

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 <400> 93
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 <210> 94
 <211> 597
 <212> DNA
 <213> Ustilago maydis

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 <213> Rhodosporidium toruloides

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 <211> 888
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 <213> *Aspergillus nidulans*

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 <213> *Aspergillus niger*

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 <211> 388
 <212> DNA
 <213> Ashibia gossipii

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 <213> Rhodoturula grammis

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 <212> DNA
 <213> Sporobolomyces roseus

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<210> 103

<211> 944

<212> DNA

<213> Rhodotorula glutinis ATCC 204091

<400> 103

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<210> 104
 <211> 1462
 <212> DNA
 <213> Rhodotorula graminis strain WP1

<400> 104	
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acccttgtgt aggcgtaggt ca	1462

<210> 105
 <211> 1315
 <212> DNA
 <213> Rhodotorula glutinis ATCC 204091

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gagtacgtcg acgggctcac tacagctagc aacagcaagg ctaccacgcc agctacacgc	1260
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<210> 106

<211> 1497

<212> DNA

<213> Rhodotorula glutinis ATCC 204091

<400> 106

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<210> 107
 <211> 1594
 <212> DNA
 <213> Rhodotorula glutinis ATCC 204091

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<210> 108
 <211> 1396
 <212> DNA
 <213> Rhodotorula glutinis ATCC 204091

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cccagaccgc cccaacaca atacagacga gatcgatagt tgccccagtc acagcgagcg	720
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<210> 109
 <211> 1468
 <212> DNA
 <213> Rhodotorula graminis strain WP1

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<210> 110

<211> 1520

<212> DNA

<213> Rhodotorula graminis strain WP1

<400> 110

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<210> 111
 <211> 1210
 <212> DNA
 <213> Rhodotorula graminis strain WP1

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 <212> DNA
 <213> Rhodotorula graminis strain WP1

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<210> 113
 <211> 1634
 <212> DNA
 <213> Rhodotorula glutinis ATCC 204091

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 <212> DNA
 <213> Rhodosporidium toruloides

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<210> 115
 <211> 660
 <212> DNA
 <213> Ustilago maydis

<400> 115	
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<210> 116

<211> 951

<212> DNA

<213> Rhodotorula graminis strain WP1

<400> 116

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<210> 117
 <211> 2136
 <212> DNA
 <213> *Rhodotorula glutinis* ATCC 204091

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 <212> DNA
 <213> Sporobolomyces roseus

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