

Sequences

- <110> Spicer Consulting Ltd
- 5 <120> METHODS OF MODIFYING ALGAL CELL GENOMES
- <130> GB1214645.2
- <160> 39
- 10 <210> 1
<211> 188
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<213> *Chlamydomonas reinhardtii*
- 15 <220>
<223> RbcS2 (ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit
2) 3'untranslated region
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gatggaagat actgctctca agtgctgaag cggtagctta gctccccgtt tcgtgctgat 120
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ctccgttg 188
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- 30 <220>
<223> Beta-2-tubulin (TUB2) 3'untranslated region
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tgaccgtgac tgaccctgga caaagggtcc ctgactgaag acaacttgac atgtgattgc 120
catttgacgc tttggtgtgg aggcggattg tgagatggga ggggggcca ttgccttcgt 180
gaccataacg acatcgaatt tcatacatgt gaacagttca gcatggacat tcatctcgtc 240
ggattagctc ttgtgtgata ggccatagca gctggactgt tgtgggctct cgatctgcgt 300
- 40 agctactggc tgtgattgtg cttcaggcgg caggggcagg taactgccct gaacgtaaag 360
gtgcagcagc agacagcgga tgtgcagaac gaatagcgca gtggataagg ttgatgggtg 420
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- 45 <210> 3
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 5 <222> (1)..(36)
 <223> consensus intron splice acceptor sequence

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 10 <222> 37
 <223> start of next exon

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 15 cagcatctaa ccctgcgtcg cttttttttt ttccagg 37

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 ctaaccctgc gtcgcttttt tttttttcag g 31

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 40 <212> DNA
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 <223> Hsp70A proximal promoter
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ggctatgagg gcgggggaag ctctggaagg gccgcgatgg ggcgcgcggc gtccagaagg 120

cgccatacgg cccgctggcg gcacccatcc ggtataaaaag cccgcgaccc cgaacggtga 180

cctccacttt cagcgacaaa cgagcactta tacatacgcg actattctgc cgctatacat 240

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<213> *Chlamydomonas reinhardtii*

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<223> RbcS2 (ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit
5 2) proximal promoter

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atccggaagc cccctggccc acaaaggcta ggcgccaatg caagcagttc gcatgcagcc 120
10 cctggagcgg tgccctcctg ataaaccggc cagggggcct atgttcttta cttttttaca 180
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<223> Beta-2-tubulin (TUB2) proximal promoter

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25 ttcaaacacc tagatcacta ccacttctac acaggccact cgagcttggtg atcgca 176

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30 <213> Artificial Sequence

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<223> consensus intron splice donor sequence

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40 <220>
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45 <400> 8
magttragt 9

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50 <212> DNA

<213> *Streptomyces actinophage* R4
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 <223> R4 attB site in direct orientation
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 10 <211> 50
 <212> DNA
 <213> *Streptomyces actinophage* R4
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 15 <223> attB site in reverse (inverted) orientation
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 tgtctgccgg tgcccttcta ccactgcttc ggcattgtca tgggcaactc 50
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 20 <211> 33
 <212> DNA
 <213> *Zygosaccharomyces bisporus*
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 25 <223> B3 recombinase recognition target sequence
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 ggttgcttaa gaataagtaa ttcttaagca acc 33
 30 <210> 12
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 <213> *Saccharomyces cerevisiae* 2 micron plasmid
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 <223> FRT WT
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 <213> *Streptomyces actinophage* TG1

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 <213> *Streptomyces actinophage* TG1
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35 gtccagccca acagtgttag tctttgctct taccagttg ggcgggata 49

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 <213> *Zygosaccharomyces bailii*

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25	<213> <i>Kluyveromyces lactis</i>	
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 5 <223> 2A peptide consensus sequence

 <220>
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 10 <223> can be Val or Ile

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 15
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 <213> *Thosea asigna*

 20
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 <223> Thoseaasigna virus 2A peptide

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 25 Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro
 5 10 15

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 30 <212> PRT
 <213> *Streptomyces actinophage R4*

 <220>
 <223> (sre)R4 recombinase

 35
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 Ser Leu Asp Arg Thr Gly Glu Glu Leu Gly Val Glu Arg Gln Glu Glu
 20 25 30
 Ser Cys Arg Glu Leu Cys Lys Ser Leu Gly Met Glu Val Gly Gln Val
 35 40 45
 Trp Val Asp Asn Asp Leu Ser Ala Thr Lys Lys Asn Val Val Arg Pro
 50 55 60
 45 Asp Phe Glu Ala Met Ile Ala Ser Asn Pro Gln Ala Ile Val Cys Trp
 65 70 75 80
 His Thr Asp Arg Leu Ile Arg Val Thr Arg Asp Leu Glu Arg Val Ile
 85 90 95
 Asp Leu Gly Val Asn Val His Ala Val Met Ala Gly His Leu Asp Leu
 100 105 110
 50 Ser Thr Pro Ala Gly Arg Ala Val Ala Arg Thr Val Thr Ala Trp Ala
 115 120 125
 Thr Tyr Glu Gly Glu Gln Lys Ala Glu Arg Gln Lys Leu Ala Asn Ile

	130		135		140	
	Gln Asn Ala Arg Ala Gly Lys Pro Tyr Thr Pro Gly Ile Arg Pro Phe					
	145		150		155	160
5	Gly Tyr Gly Asp Asp His Met Thr Ile Val Thr Ala Glu Ala Asp Ala					
		165		170		175
	Ile Arg Asp Gly Ala Lys Met Ile Leu Asp Gly Trp Ser Leu Ser Ala					
		180		185		190
	Val Ala Arg Tyr Trp Glu Glu Leu Lys Leu Gln Ser Pro Arg Ser Met					
		195		200		205
10	Ala Ala Gly Gly Lys Gly Trp Ser Leu Arg Gly Val Lys Lys Val Leu					
		210		215		220
	Thr Ser Pro Arg Tyr Val Gly Arg Ser Ser Tyr Leu Gly Glu Val Val					
		225		230		235
	Gly Asp Ala Gln Trp Pro Pro Ile Leu Asp Pro Asp Val Tyr Tyr Gly					
		245		250		255
15	Val Val Ala Ile Leu Asn Asn Pro Asp Arg Phe Ser Gly Gly Pro Arg					
		260		265		270
	Thr Gly Arg Thr Pro Gly Thr Leu Leu Ala Gly Ile Ala Leu Cys Gly					
		275		280		285
20	Glu Cys Gly Lys Thr Val Ser Gly Arg Gly Tyr Arg Gly Val Leu Val					
		290		295		300
	Tyr Gly Cys Lys Asp Thr His Thr Arg Thr Pro Arg Ser Ile Ala Asp					
		305		310		315
	Gly Arg Ala Ser Ser Ser Thr Leu Ala Arg Leu Met Phe Pro Asp Phe					
		325		330		335
25	Leu Pro Gly Leu Leu Ala Ser Gly Gln Ala Glu Asp Gly Gln Ser Ala					
		340		345		350
	Ala Ser Lys His Ser Glu Ala Gln Thr Leu Arg Glu Arg Leu Asp Gly					
		355		360		365
30	Leu Ala Thr Ala Tyr Ala Glu Gly Ala Ile Ser Leu Ser Gln Met Thr					
		370		375		380
	Ala Gly Ser Glu Ala Leu Arg Lys Lys Leu Glu Val Ile Glu Ala Asp					
		385		390		395
	Leu Val Gly Ser Ala Gly Ile Pro Pro Phe Asp Pro Val Ala Gly Val					
		405		410		415
35	Ala Gly Leu Ile Ser Gly Trp Pro Thr Thr Pro Leu Pro Thr Arg Arg					
		420		425		430
	Ala Trp Val Asp Phe Cys Leu Val Val Thr Leu Asn Thr Gln Lys Gly					
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40	Arg His Ala Ser Ser Met Thr Val Asp Asp His Val Thr Ile Glu Trp					
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	Arg Asp Val Ala Glu					
	465					
45	<210> 25					
	<211> 567					
	<212> PRT					
	<213> <i>Zygosaccharomyces bisporus</i>					
50	<220>					

<223> B3 recombinase

<400> 25

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				20					25					30		
	Lys	Leu	Ser	Gly	Ile	Ile	Thr	Met	Ala	Ile	Leu	Lys	Ala	Ile	Lys	Ala
			35					40					45			
10	Leu	Thr	Glu	Val	Lys	Lys	Thr	Thr	Phe	Asn	Lys	Tyr	Lys	Thr	Thr	Ile
		50					55					60				
	Lys	Gln	Gly	Leu	Gln	Tyr	Asp	Val	Gly	Ser	Ser	Thr	Ile	Ser	Phe	Val
	65					70				75					80	
15	Tyr	His	Leu	Lys	Asp	Cys	Asp	Glu	Leu	Ser	Arg	Gly	Leu	Ser	Asp	Ala
					85					90					95	
	Phe	Glu	Pro	Tyr	Lys	Phe	Lys	Ile	Lys	Ser	Asn	Lys	Glu	Ala	Thr	Ser
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	Phe	Lys	Thr	Leu	Phe	Arg	Gly	Pro	Ser	Phe	Gly	Ser	Gln	Lys	Asn	Trp
			115				120						125			
20	Arg	Lys	Lys	Glu	Val	Asp	Arg	Glu	Val	Asp	Asn	Leu	Phe	His	Ser	Thr
		130					135					140				
	Glu	Thr	Asp	Glu	Ser	Ile	Phe	Lys	Phe	Ile	Leu	Asn	Thr	Leu	Asp	Ser
	145					150				155					160	
25	Ile	Glu	Thr	Gln	Thr	Asn	Thr	Asp	Arg	Gln	Lys	Thr	Val	Leu	Thr	Phe
				165					170					175		
	Ile	Leu	Leu	Met	Thr	Phe	Phe	Asn	Cys	Cys	Arg	Asn	Asn	Asp	Leu	Met
				180					185					190		
	Asn	Val	Asp	Pro	Ser	Thr	Phe	Lys	Ile	Val	Lys	Asn	Lys	Phe	Val	Gly
			195					200					205			
30	Tyr	Leu	Leu	Gln	Ala	Glu	Val	Lys	Gln	Thr	Lys	Thr	Arg	Lys	Ser	Arg
		210					215					220				
	Asn	Ile	Phe	Phe	Phe	Pro	Ile	Arg	Glu	Asn	Arg	Phe	Asp	Leu	Phe	Leu
	225					230				235					240	
35	Ala	Leu	His	Asp	Phe	Phe	Arg	Thr	Cys	Gln	Pro	Thr	Pro	Lys	Ser	Arg
				245						250				255		
	Leu	Ser	Asp	Gln	Val	Ser	Glu	Gln	Lys	Trp	Gln	Leu	Phe	Arg	Asp	Ser
				260					265					270		
	Met	Val	Ile	Asp	Tyr	Asn	Arg	Phe	Phe	Arg	Lys	Phe	Pro	Ala	Ser	Pro
			275					280					285			
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		290					295					300				
	Met	Asn	Ser	Phe	Leu	His	Lys	Asn	Glu	Leu	Asp	Ser	Trp	Ala	Asn	Ser
	305					310				315					320	
45	Leu	Gly	Asn	Trp	Ser	Ser	Ser	Gln	Asn	Gln	Arg	Glu	Ser	Gly	Ala	Arg
				325					330					335		
	Leu	Gly	Tyr	Thr	His	Gly	Gly	Arg	Asp	Leu	Pro	Gln	Pro	Leu	Phe	Gly
			340					345					350			
	Phe	Leu	Ala	Gly	Tyr	Cys	Val	Arg	Asn	Glu	Glu	Gly	His	Ile	Val	Gly
			355					360					365			

Leu Gly Leu Glu Lys Asp Ile Asn Asp Leu Phe Asp Gly Ile Met Asp
 370 375 380
 Pro Leu Asn Glu Lys Glu Asp Thr Glu Ile Cys Glu Ser Tyr Gly Glu
 385 390 395 400
 5 Trp Ala Lys Ile Val Ser Lys Asp Val Leu Ile Phe Leu Lys Arg Tyr
 405 410 415
 His Ser Lys Asn Ala Cys Arg Arg Tyr Gln Asn Ser Thr Leu Tyr Ala
 420 425 430
 10 Arg Thr Phe Leu Lys Thr Glu Ser Val Thr Leu Ser Gly Ser Lys Gly
 435 440 445
 Ser Glu Glu Pro Ser Ser Pro Val Arg Ile Pro Ile Leu Ser Met Gly
 450 455 460
 Lys Ala Ser Pro Ser Glu Gly Arg Lys Leu Arg Ala Ser Glu His Ala
 465 470 475 480
 15 Asn Asp Asp Asn Glu Ile Glu Lys Ile Asp Ser Asp Ser Ser Gln Ser
 485 490 495
 Glu Glu Ile Pro Ile Glu Met Ser Asp Ser Glu Asp Glu Thr Thr Ala
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 20 Ser Asn Ile Ser Gly Ile Tyr Leu Asp Met Ser Lys Ala Asn Ser Asn
 515 520 525
 Val Val Tyr Ser Pro Pro Ser Gln Thr Gly Arg Ala Ala Gly Ala Gly
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 Arg Lys Arg Gly Val Gly Gly Arg Arg Thr Val Glu Ser Lys Arg Arg
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 25 Arg Val Leu Ala Pro Ile Asn
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 30 <212> PRT
 <213> *Saccharomyces cerevisiae* 2 micron plasmid

 <220>
 <223> F1p recombinase
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 20 25 30
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 35 40 45
 Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile
 50 55 60
 45 Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys
 65 70 75 80
 Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu
 85 90 95
 50 Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Asn Gly Gln Lys His
 100 105 110

Gln Ser Asp Ile Thr Asp Ile Val Ser Ser Leu Gln Leu Gln Phe Glu
 115 120 125
 Ser Ser Glu Glu Ala Asp Lys Gly Asn Ser His Ser Lys Lys Met Leu
 130 135 140
 5 Lys Ala Leu Leu Ser Glu Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys
 145 150 155 160
 Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr
 165 170 175
 10 Leu Tyr Gln Phe Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe
 180 185 190
 Ser Asp Ile Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn
 195 200 205
 Lys Tyr Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr
 210 215 220
 15 Ser Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp
 225 230 235 240
 Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val Leu
 245 250 255
 20 Lys Arg Val Asn Arg Thr Gly Asn Ser Ser Ser Asn Lys Gln Glu Tyr
 260 265 270
 Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys Ala Leu Lys
 275 280 285
 Lys Asn Ala Pro Tyr Pro Ile Phe Ala Ile Lys Asn Gly Pro Lys Ser
 290 295 300
 25 His Ile Gly Arg His Leu Met Thr Ser Phe Leu Ser Met Lys Gly Leu
 305 310 315 320
 Thr Glu Leu Thr Asn Val Val Gly Asn Trp Ser Asp Lys Arg Ala Ser
 325 330 335
 30 Ala Val Ala Arg Thr Thr Tyr Thr His Gln Ile Thr Ala Ile Pro Asp
 340 345 350
 His Tyr Phe Ala Leu Val Ser Arg Tyr Tyr Ala Tyr Asp Pro Ile Ser
 355 360 365
 Lys Glu Met Ile Ala Leu Lys Asp Glu Thr Asn Pro Ile Glu Glu Trp
 370 375 380
 35 Gln His Ile Glu Gln Leu Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr
 385 390 395 400
 Pro Ala Trp Asn Gly Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser
 405 410 415
 40 Ser Tyr Ile Asn Arg Arg Ile
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<211> 594

45 <212> PRT

<213> bacteriophage ϕ BT1

<220>

<223> ϕ BT1 recombinase

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<400> 27

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	Ala	Ser	Arg	Asn	Ala	Gln	Gly	Gly	Ala	Arg	Trp	Val	Val	Ala	Gly	Glu	
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20	Ile	Phe	Ala	Leu	Ile	Ala	Ala	Leu	Ala	Lys	Gln	Asp	Ser	Asp	Leu	Lys	
						150					155					160	
	Ala	Glu	Arg	Leu	Lys	Gly	Ala	Lys	Asp	Glu	Ile	Ala	Ala	Leu	Gly	Gly	
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25	Val	His	Ser	Ser	Ser	Ala	Pro	Phe	Gly	Met	Arg	Ala	Val	Arg	Lys	Lys	
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	Val	Asp	Asn	Leu	Val	Ile	Ser	Val	Leu	Glu	Pro	Asp	Glu	Asp	Asn	Pro	
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	Asp	His	Val	Glu	Leu	Val	Glu	Arg	Met	Ala	Lys	Met	Ser	Phe	Glu	Gly	
			210				215					220					
30	Val	Ser	Asp	Asn	Ala	Ile	Ala	Thr	Thr	Phe	Glu	Lys	Glu	Lys	Ile	Pro	
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	Ser	Pro	Gly	Met	Ala	Glu	Arg	Arg	Ala	Thr	Glu	Lys	Arg	Leu	Ala	Ser	
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	Ala	Gln	Thr	Val	Arg	Trp	Ile	Leu	Asn	His	Pro	Ala	Ile	Gly	Gly	Phe	
			275					280					285				
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			290				295					300					
40	Arg	Asp	Pro	Gly	Gly	Lys	Pro	Leu	Thr	Pro	His	Thr	Gly	Ile	Leu	Ser	
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	Gly	Ser	Lys	Trp	Leu	Glu	Leu	Gln	Glu	Lys	Arg	Ser	Gly	Lys	Asn	Leu	
					325					330					335		
45	Ser	Asp	Arg	Lys	Pro	Gly	Ala	Glu	Val	Glu	Pro	Thr	Leu	Leu	Ser	Gly	
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	Trp	Arg	Phe	Leu	Gly	Cys	Arg	Ile	Cys	Gly	Gly	Ser	Met	Gly	Gln	Ser	
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	Gln	Gly	Gly	Arg	Lys	Arg	Asn	Gly	Asp	Leu	Ala	Glu	Gly	Asn	Tyr	Met	
			370				375					380					

Cys Ala Asn Pro Lys Gly His Gly Gly Leu Ser Val Lys Arg Ser Glu
385 390 395 400

Leu Asp Glu Phe Val Ala Ser Lys Val Trp Ala Arg Leu Arg Thr Ala
405 410 415

5 Asp Met Glu Asp Glu His Asp Gln Ala Trp Ile Ala Ala Ala Glu
420 425 430

Arg Phe Ala Leu Gln His Asp Leu Ala Gly Val Ala Asp Glu Arg Arg
435 440 445

10 Glu Gln Gln Ala His Leu Asp Asn Val Arg Arg Ser Ile Lys Asp Leu
450 455 460

Gln Ala Asp Arg Lys Pro Gly Leu Tyr Val Gly Arg Glu Glu Leu Glu
465 470 475 480

Thr Trp Arg Ser Thr Val Leu Gln Tyr Arg Ser Tyr Glu Ala Glu Cys
485 490 495

15 Thr Thr Arg Leu Ala Glu Leu Asp Glu Lys Met Asn Gly Ser Thr Arg
500 505 510

Val Pro Ser Glu Trp Phe Ser Gly Glu Asp Pro Thr Ala Glu Gly Gly
515 520 525

20 Ile Trp Ala Ser Trp Asp Val Tyr Glu Arg Arg Glu Phe Leu Ser Phe
530 535 540

Phe Leu Asp Ser Val Met Val Asp Arg Gly Arg His Pro Glu Thr Lys
545 550 555 560

Lys Tyr Ile Pro Leu Lys Asp Arg Val Thr Leu Lys Trp Ala Glu Leu
565 570 575

25 Leu Lys Glu Glu Asp Glu Ala Ser Glu Ala Thr Glu Arg Glu Leu Ala
580 585 590

Ala Leu

<210> 28
30 <211> 619
<212> PRT
<213> Streptomyces actinophage TG1

<220>
35 <223> TG1 recombinase

<400> 28

Met Val Ile Leu Ala Gly Gly Tyr Asp Arg Gln Ser Ala Glu Arg Glu
5 10 15

40 Asn Ser Ser Thr Ala Ser Pro Ala Thr Gln Arg Ala Ala Asn Arg Gly
20 25 30

Lys Ala Glu Ala Leu Ala Lys Glu Tyr Ala Arg Asp Gly Val Glu Val
35 40 45

45 Lys Trp Leu Gly His Phe Ser Glu Ala Pro Gly Thr Ser Ala Phe Thr
50 55 60

Gly Val Asp Arg Pro Glu Phe Asn Arg Ile Leu Asp Met Cys Arg Asn
65 70 75 80

Arg Glu Met Asn Met Ile Ile Val His Tyr Ile Ser Arg Leu Ser Arg
85 90 95

50 Glu Glu Pro Leu Asp Ile Ile Pro Val Val Thr Glu Leu Leu Arg Leu

	100	105	110
	Gly Val Thr Ile Val Ser Val Asn Glu Gly Thr Phe Arg Pro Gly Glu		
	115	120	125
5	Met Met Asp Leu Ile His Leu Ile Met Arg Leu Gln Ala Ser His Asp		
	130	135	140
	Glu Ser Lys Asn Lys Ser Val Ala Val Ser Asn Ala Lys Glu Leu Ala		
	145	150	155
	Lys Arg Leu Gly Gly His Thr Gly Ser Thr Pro Tyr Gly Phe Asp Thr		
	165	170	175
10	Val Glu Glu Met Val Pro Asn Pro Glu Asp Gly Gly Lys Leu Val Ala		
	180	185	190
	Ile Arg Arg Leu Val Pro Ser Ala His Thr Trp Glu Gly Ala His Gly		
	195	200	205
15	Ser Glu Gly Ala Val Ile Arg Trp Ala Trp Gln Glu Ile Lys Thr His		
	210	215	220
	Arg Asp Thr Pro Phe Lys Gly Gly Gly Ala Gly Ser Phe His Pro Gly		
	225	230	235
	Ser Leu Asn Gly Leu Cys Glu Arg Leu Tyr Arg Asp Lys Val Pro Thr		
	245	250	255
20	Arg Gly Thr Leu Val Gly Lys Lys Arg Ala Gly Ser Asp Trp Asp Pro		
	260	265	270
	Gly Val Leu Lys Arg Val Leu Ser Asp Pro Arg Ile Ala Gly Tyr Gln		
	275	280	285
25	Ala Asp Ile Ala Tyr Lys Val Arg Ala Asp Gly Ser Arg Gly Gly Phe		
	290	295	300
	Ser His Tyr Lys Ile Arg Arg Asp Pro Val Thr Met Glu Pro Leu Thr		
	305	310	315
	Leu Pro Gly Phe Glu Pro Tyr Ile Pro Pro Ala Glu Trp Trp Glu Leu		
	325	330	335
30	Gln Glu Trp Leu Gln Gly Arg Gly Arg Gly Lys Gly Gln Tyr Arg Gly		
	340	345	350
	Gln Ser Leu Leu Ser Ala Met Asp Val Leu Tyr Cys Tyr Gly Ser Gly		
	355	360	365
35	Gln Leu Asp Pro Glu Thr Gly Tyr Ser Asn Gly Ser Thr Met Ala Gly		
	370	375	380
	Asn Val Arg Glu Gly Asp Gln Ala His Lys Ser Ser Tyr Ala Cys Lys		
	385	390	395
	Cys Pro Arg Arg Val His Asp Gly Ser Ser Cys Ser Ile Thr Met His		
	405	410	415
40	Asn Leu Asp Pro Tyr Ile Val Gly Ala Ile Phe Ala Arg Ile Thr Ala		
	420	425	430
	Phe Asp Pro Ala Asp Pro Asp Asp Leu Glu Gly Asp Thr Ala Ala Leu		
	435	440	445
45	Met Tyr Glu Ala Ala Arg Arg Trp Gly Ala Thr His Glu Arg Pro Glu		
	450	455	460
	Leu Lys Gly Gln Arg Ser Glu Leu Met Ala Gln Arg Ala Asp Ala Val		
	465	470	475
	Lys Ala Leu Glu Glu Leu Tyr Glu Asp Lys Arg Asn Gly Gly Tyr Arg		
	485	490	495

Ser Ala Met Gly Arg Arg Ala Phe Leu Glu Glu Glu Ala Ala Leu Thr
500 505 510

Leu Arg Met Glu Gly Ala Glu Glu Arg Leu Arg Gln Leu Asp Ala Ala
515 520 525

5 Asp Ser Pro Val Leu Pro Ile Gly Glu Trp Leu Gly Asp Arg Gly Ser
530 535 540

Asp Pro Thr Gly Pro Gly Ser Trp Trp Ala Leu Ala Pro Leu Glu Asp
545 550 555 560

10 Arg Arg Ala Phe Val Arg Leu Phe Val Asp Arg Ile Glu Val Ile Lys
565 570 575

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

Arg Val Arg Ile His Trp Ala Lys Pro Lys Val Glu Glu Glu Thr Glu
595 600 605

15 Pro Glu Thr Leu Asn Gly Phe Thr Ala Ala Ala
610 615

<210> 29
20 <211> 509
<212> PRT
<213> *Zygosaccharomyces bailii*

<220>
25 <223> B2 recombinase

<400> 29

Met Ser Glu Phe Ser Glu Leu Val Arg Ile Leu Pro Leu Asp Gln Val
5 10 15

30 Ala Glu Ile Lys Arg Ile Leu Ser Arg Gly Asp Pro Ile Pro Leu Gln
20 25 30

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

35 Lys Lys Arg Lys Ser Ser Pro Ile Lys Leu Ser Thr Phe Thr Lys Tyr
50 55 60

Arg Arg Asn Val Ala Lys Ser Leu Tyr Tyr Asp Met Ser Ser Lys Thr
65 70 75 80

Val Phe Phe Glu Tyr His Leu Lys Asn Thr Gln Asp Leu Gln Glu Gly
85 90 95

40 Leu Glu Gln Ala Ile Ala Pro Tyr Asn Phe Val Val Lys Val His Lys
100 105 110

Lys Pro Ile Asp Trp Gln Lys Gln Leu Ser Ser Val His Glu Arg Lys
115 120 125

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

Lys Leu Ala Glu Thr Lys Asp Ser Thr Trp Ser Phe Ile Glu Arg Thr
145 150 155 160

Met Asp Leu Ile Glu Ala Arg Thr Arg Gln Pro Thr Thr Arg Val Ala
165 170 175

50 Tyr Arg Phe Leu Leu Gln Leu Thr Phe Met Asn Cys Cys Arg Ala Asn

		180		185		190	
		Asp Leu Lys Asn Ala Asp Pro Ser Thr Phe Gln Ile Ile Ala Asp Pro					
		195		200		205	
5		His Leu Gly Arg Ile Leu Arg Ala Phe Val Pro Glu Thr Lys Thr Ser					
		210		215		220	
		Ile Glu Arg Phe Ile Tyr Phe Phe Pro Cys Lys Gly Arg Cys Asp Pro					
		225		230		235	240
		Leu Leu Ala Leu Asp Ser Tyr Leu Leu Trp Val Gly Pro Val Pro Lys					
			245		250		255
10		Thr Gln Thr Thr Asp Glu Glu Thr Gln Tyr Asp Tyr Gln Leu Leu Gln					
			260		265		270
		Asp Thr Leu Leu Ile Ser Tyr Asp Arg Phe Ile Ala Lys Glu Ser Lys					
			275		280		285
15		Glu Asn Ile Phe Lys Ile Pro Asn Gly Pro Lys Ala His Leu Gly Arg					
			290		295		300
		His Leu Met Ala Ser Tyr Leu Gly Asn Asn Ser Leu Lys Ser Glu Ala					
			305		310		315
		Thr Leu Tyr Gly Asn Trp Ser Val Glu Arg Gln Glu Gly Val Ser Lys					
			325		330		335
20		Met Ala Asp Ser Arg Tyr Met His Thr Val Lys Lys Ser Pro Pro Ser					
			340		345		350
		Tyr Leu Phe Ala Phe Leu Ser Gly Tyr Tyr Lys Lys Ser Asn Gln Gly					
			355		360		365
25		Glu Tyr Val Leu Ala Glu Thr Leu Tyr Asn Pro Leu Asp Tyr Asp Lys					
			370		375		380
		Thr Leu Pro Ile Thr Thr Asn Glu Lys Leu Ile Cys Arg Arg Tyr Gly					
			385		390		395
		Lys Asn Ala Lys Val Ile Pro Lys Asp Ala Leu Leu Tyr Leu Tyr Thr					
			405		410		415
30		Tyr Ala Gln Gln Lys Arg Lys Gln Leu Ala Asp Pro Asn Glu Gln Asn					
			420		425		430
		Arg Leu Phe Ser Ser Glu Ser Pro Ala His Pro Phe Leu Thr Pro Gln					
			435		440		445
35		Ser Thr Gly Ser Ser Thr Pro Leu Thr Trp Thr Ala Pro Lys Thr Leu					
			450		455		460
		Ser Thr Gly Leu Met Thr Pro Gly Glu Glu Gly Ser His Gly Phe Pro					
			465		470		475
		Pro Glu Val Glu Glu Gln Asp Asp Gly Thr Leu Pro Met Ser Cys Ala					
			485		490		495
40		Gln Glu Ser Gly Met Asp Arg His Pro Ala Ala Cys Ala Ser Ala Arg					
			500		505		510
		Ile Asn Val					
		515					
45		<210> 30					
		<211> 372					
		<212> PRT					
		<213> <i>Zygosaccharomyces fermentati</i>					
50		<220>					

<223> SM1 recombinase

<400> 30

5	Met	Ala	Thr	Phe	Ser	Lys	Leu	Ser	Glu	Arg	Lys	Arg	Ser	Thr	Phe	Ile	5	10	15
	Lys	Tyr	Ser	Arg	Glu	Ile	Arg	Gln	Ser	Val	Gln	Tyr	Asp	Arg	Glu	Ala	20	25	30
	Gln	Ile	Val	Lys	Phe	Asn	Tyr	His	Leu	Lys	Arg	Pro	His	Glu	Leu	Lys	35	40	45
10	Asp	Val	Leu	Asp	Lys	Thr	Phe	Ala	Pro	Ile	Val	Phe	Glu	Val	Ser	Ser	50	55	60
	Thr	Lys	Lys	Val	Glu	Ser	Met	Val	Glu	Leu	Ala	Lys	Met	Asp	Lys		65	70	75
15	Val	Glu	Gly	Lys	Gly	Gly	His	Asn	Ala	Val	Ala	Glu	Glu	Ile	Thr	Lys	85	90	95
	Ile	Val	Arg	Ala	Asp	Asp	Ile	Trp	Thr	Leu	Leu	Ser	Gly	Val	Glu	Val	100	105	110
	Thr	Ile	Gln	Lys	Arg	Ala	Phe	Lys	Arg	Ser	Leu	Arg	Ala	Glu	Leu	Lys	115	120	125
20	Tyr	Val	Leu	Ile	Thr	Ser	Phe	Phe	Asn	Cys	Ser	Arg	His	Ser	Asp	Leu	130	135	140
	Lys	Asn	Ala	Asp	Pro	Thr	Lys	Phe	Glu	Leu	Val	Lys	Asn	Arg	Tyr	Leu	145	150	155
25	Asn	Arg	Val	Leu	Arg	Val	Leu	Val	Cys	Glu	Thr	Lys	Thr	Arg	Lys	Pro	165	170	175
	Arg	Tyr	Ile	Tyr	Phe	Phe	Pro	Val	Asn	Lys	Lys	Thr	Asp	Pro	Leu	Ile	180	185	190
	Ala	Leu	His	Asp	Leu	Phe	Ser	Glu	Ala	Glu	Pro	Val	Pro	Lys	Ser	Arg	195	200	205
30	Ala	Ser	His	Gln	Lys	Thr	Asp	Gln	Glu	Trp	Gln	Met	Leu	Arg	Asp	Ser	210	215	220
	Leu	Leu	Thr	Asn	Tyr	Asp	Arg	Phe	Ile	Ala	Thr	His	Ala	Lys	Gln	Ala	225	230	235
35	Val	Phe	Gly	Ile	Lys	His	Gly	Pro	Lys	Ser	His	Leu	Gly	Arg	His	Leu	245	250	255
	Met	Ser	Ser	Tyr	Leu	Ser	His	Thr	Asn	His	Gly	Gln	Trp	Val	Ser	Pro	260	265	270
	Phe	Gly	Asn	Trp	Ser	Ala	Gly	Lys	Asp	Thr	Val	Glu	Ser	Asn	Val	Ala	275	280	285
40	Arg	Ala	Lys	Tyr	Val	His	Ile	Gln	Ala	Asp	Ile	Pro	Asp	Glu	Leu	Phe	290	295	300
	Ala	Phe	Leu	Ser	Gln	Tyr	Tyr	Ile	Gln	Thr	Pro	Ser	Gly	Asp	Phe	Glu	305	310	315
45	Leu	Ile	Asp	Ser	Ser	Glu	Gln	Pro	Thr	Thr	Phe	Ile	Asn	Asn	Leu	Ser	325	330	335
	Thr	Gln	Glu	Asp	Ile	Ser	Lys	Ser	Tyr	Gly	Thr	Trp	Thr	Gln	Val	Val	340	345	350
	Gly	Gln	Asp	Val	Leu	Glu	Tyr	Val	His	Ser	Tyr	Ala	Met	Gly	Lys	Leu	355	360	365

Gly Ile Arg Lys
370

<210> 31
5 <211> 490
<212> PRT
<213> *Zygosaccharomyces rouxii*

<220>
10 <223> R/RS recombinase

<400> 31
Met Gln Leu Thr Lys Asp Thr Glu Ile Ser Thr Ile Asn Arg Gln Met
5 5 10 15
15 Ser Asp Phe Ser Glu Leu Ser Gln Ile Leu Pro Leu His Gln Ile Ser
20 20 25 30
Lys Ile Lys Asp Ile Leu Glu Asn Glu Asn Pro Leu Pro Lys Glu Lys
35 40 45
20 Leu Ala Ser His Leu Thr Met Ile Ile Leu Met Ala Asn Leu Ala Ser
50 55 60
Gln Lys Arg Lys Asp Val Pro Val Lys Arg Ser Thr Phe Leu Lys Tyr
65 70 75 80
Gln Arg Ser Ile Ser Lys Thr Leu Gln Tyr Asp Ser Ser Thr Lys Thr
85 90 95
25 Val Ser Phe Glu Tyr His Leu Lys Asp Pro Ser Lys Leu Ile Lys Gly
100 105 110
Leu Glu Asp Val Val Ser Pro Tyr Arg Phe Val Val Gly Val His Glu
115 120 125
30 Lys Pro Asp Asp Val Met Ser His Leu Ser Ala Val His Met Arg Lys
130 135 140
Glu Ala Gly Arg Lys Arg Asp Leu Gly Asn Lys Ile Asn Asp Glu Ile
145 150 155 160
Thr Lys Ile Ala Glu Thr Gln Glu Thr Ile Trp Gly Phe Val Gly Lys
165 170 175
35 Thr Met Asp Leu Ile Glu Ala Arg Thr Thr Arg Pro Thr Thr Lys Ala
180 185 190
Ala Tyr Asn Leu Leu Leu Gln Ala Thr Phe Met Asn Cys Cys Arg Ala
195 200 205
40 Asp Asp Leu Lys Asn Thr Asp Ile Lys Thr Phe Glu Val Ile Pro Asp
210 215 220
Lys His Leu Gly Arg Met Leu Arg Ala Phe Val Pro Glu Thr Lys Thr
225 230 235 240
Gly Thr Arg Phe Val Tyr Phe Phe Pro Cys Lys Gly Arg Cys Asp Pro
245 250 255
45 Leu Leu Ala Leu Asp Ser Tyr Leu Gln Trp Thr Asp Pro Ile Pro Lys
260 265 270
Thr Arg Thr Thr Asp Glu Asp Ala Arg Tyr Asp Tyr Gln Leu Leu Arg
275 280 285
50 Asn Ser Leu Leu Gly Ser Tyr Asp Gly Phe Ile Ser Lys Gln Ser Asp
290 295 300

Glu Ser Ile Phe Lys Ile Pro Asn Gly Pro Lys Ala His Leu Gly Arg
 305 310 315 320
 His Val Thr Ala Ser Tyr Leu Ser Asn Asn Glu Met Asp Lys Glu Ala
 325 330 335
 5 Thr Leu Tyr Gly Asn Trp Ser Ala Ala Arg Glu Glu Gly Val Ser Arg
 340 345 350
 Val Ala Lys Ala Arg Tyr Met His Thr Ile Glu Lys Ser Pro Pro Ser
 355 360 365
 10 Tyr Leu Phe Ala Phe Leu Ser Gly Phe Tyr Asn Ile Thr Ala Glu Arg
 370 375 380
 Ala Cys Glu Leu Val Asp Pro Asn Ser Asn Pro Cys Glu Gln Asp Lys
 385 390 395 400
 Asn Ile Pro Met Ile Ser Asp Ile Glu Thr Leu Met Ala Arg Tyr Gly
 405 410 415
 15 Lys Asn Ala Glu Ile Ile Pro Met Asp Val Leu Val Phe Leu Ser Ser
 420 425 430
 Tyr Ala Arg Phe Lys Asn Asn Glu Gly Lys Glu Tyr Lys Leu Gln Ala
 435 440 445
 Arg Ser Ser Arg Gly Val Pro Asp Phe Pro Asp Asn Gly Arg Thr Ala
 450 455 460
 20 Leu Tyr Asn Ala Leu Thr Ala Ala His Val Lys Arg Arg Lys Ile Ser
 465 470 475 480
 Ile Val Val Gly Arg Ser Ile Asp Thr Ser
 485 490
 25
 <210> 32
 <211> 447
 <212> PRT
 <213> *Kluyveromyces lactis*
 30
 <220>
 <223> KD1 recombinase
 <400> 32
 35 Met Ser Thr Phe Ala Glu Ala Ala His Leu Thr Pro His Gln Cys Ala
 5 10 15
 Asn Glu Ile Asn Glu Ile Leu Glu Ser Asp Thr Phe Asn Ile Asn Ala
 20 25 30
 Lys Glu Ile Arg Asn Lys Leu Ala Ser Leu Phe Ser Ile Leu Thr Met
 35 40 45
 40 Gln Ser Leu Ser Ile Arg Arg Glu Met Lys Ile Asn Thr Tyr Arg Ser
 50 55 60
 Tyr Lys Ser Ala Ile Gly Lys Ser Leu Ser Phe Asp Lys Asp Asp Lys
 65 70 75 80
 45 Ile Ile Lys Phe Thr Val Arg Leu Arg Lys Thr Glu Ser Leu Gln Lys
 85 90 95
 Asp Ile Glu Ser Ala Leu Pro Ser Tyr Lys Val Val Val Ser Pro Phe
 100 105 110
 Lys Asn Gln Glu Val Ser Leu Phe Asp Arg Tyr Glu Glu Thr His Lys
 115 120 125

Tyr Asp Ala Ser Met Val Gly Leu Gln Phe Thr Asn Ile Leu Ser Lys
 130 135 140
 Glu Lys Asp Ile Trp Lys Ile Val Ser Arg Ile Ala Cys Phe Phe Asp
 145 150 155 160
 5 Gln Ser Cys Val Thr Thr Thr Lys Arg Ala Glu Tyr Arg Leu Leu Leu
 165 170 175
 Leu Gly Ala Val Gly Asn Cys Cys Arg Tyr Ser Asp Leu Lys Asn Leu
 180 185 190
 10 Asp Pro Arg Thr Phe Glu Ile Tyr Asn Asn Ser Phe Leu Gly Pro Ile
 195 200 205
 Val Arg Ala Thr Val Thr Glu Thr Lys Ser Arg Thr Glu Arg Tyr Val
 210 215 220
 Asn Phe Tyr Pro Val Asn Gly Asp Cys Asp Leu Leu Ile Ser Leu Tyr
 225 230 235 240
 15 Asp Tyr Leu Arg Val Cys Ser Pro Ile Glu Lys Thr Val Ser Ser Asn
 245 250 255
 Arg Pro Thr Asn Gln Thr His Gln Phe Leu Pro Glu Ser Leu Ala Arg
 260 265 270
 20 Thr Phe Ser Arg Phe Leu Thr Gln His Val Asp Glu Pro Val Phe Lys
 275 280 285
 Ile Trp Asn Gly Pro Lys Ser His Phe Gly Arg His Leu Met Ala Thr
 290 295 300
 Phe Leu Ser Arg Ser Glu Lys Gly Lys Tyr Val Ser Ser Leu Gly Asn
 305 310 315 320
 25 Trp Ala Gly Asp Arg Glu Ile Gln Ser Ala Val Ala Arg Ser His Tyr
 325 330 335
 Ser His Gly Ser Val Thr Val Asp Asp Arg Val Phe Ala Phe Ile Ser
 340 345 350
 30 Gly Phe Tyr Lys Glu Ala Pro Leu Gly Ser Glu Ile Tyr Val Leu Lys
 355 360 365
 Asp Pro Ser Asn Lys Pro Leu Ser Arg Glu Glu Leu Leu Glu Glu Glu
 370 375 380
 Gly Asn Ser Leu Gly Ser Pro Pro Leu Ser Pro Pro Ser Ser Pro Arg
 385 390 395 400
 35 Leu Val Ala Gln Ser Phe Ser Ala His Pro Ser Leu Gln Leu Phe Glu
 405 410 415
 Gln Trp His Gly Ile Ile Ser Asp Glu Val Leu Gln Phe Ile Ala Glu
 420 425 430
 40 Tyr Arg Arg Lys His Glu Leu Arg Ser Gln Arg Thr Val Val Ala
 435 440 445

<210> 33

<211> 60

<212> DNA

45 <213> Artificial Sequence

<220>

<223> oligo-dT adaptor primer

50 <220>

<221> variation

<222> (59)..(60)
<223> degenerate sequence

<400> 33
5 gccctaggcg agaacgagat ctàgctctag aattcggacg tttttttttt ttttttttvn 60

<210> 34
<211> 51
<212> DNA
10 <213> Artificial Sequence

<220>
<223> 'SacII' anchor primer

<220>
15 <221> variation
<222> (26)..(47)
<223> degenerate sequence

<400> 34
20 gagatctagc tctagaattc ggacgnnnnn nnnnnnnnnn nnnnnnngcg g 51

<210> 35
<211> 51
<212> DNA
25 <213> Artificial Sequence

<220>
<223> 'EagI' anchor primer

<220>
30 <221> variation
<222> (26)..(47)
<223> degenerate sequence

<400> 35
35 gagatctagc tctagaattc ggacgnnnnn nnnnnnnnnn nnnnnnngcc g 51

<210> 36
<211> 51
<212> DNA
40 <213> Artificial Sequence

<220>
<223> 'SmaI/XmaI' anchor primer

<220>
45 <221> variation
<222> (26)..(47)
<223> degenerate sequence

<400> 36
50 gagatctagc tctagaattc ggacgnnnnn nnnnnnnnnn nnnnnnncgg g 51

<210> 37
<211> 150
<212> PRT

<213> *Scheffersomyces stipites*

<220>

<223> cytosine deaminase (codA)

5

<400> 37

Met Pro Phe Asn Asp Lys Lys Gly Met Gln Ile Ala Leu Glu Glu Ala
5 10 15

10

Lys Lys Gly Tyr Glu Glu Gly Gly Val Pro Ile Gly Gly Ala Leu Ile
20 25 30

Ser Glu Asp Gly Thr Val Leu Gly Arg Gly His Asn Met Arg Phe Gln
35 40 45

Lys Asp Ser Ala Ile Leu His Gly Glu Met Ser Val Leu Glu Asn Ala
50 55 60

15

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

Leu Ser Pro Cys His Met Cys Ser Gly Ala Cys Leu Met Tyr Gly Ile
85 90 95

20

Lys Arg Val Val Leu Gly Glu Asn Val Asn Phe Val Gly Ala Glu Ala
100 105 110

Leu Leu Arg Ser Glu Gly Val Glu Val Val Asn Leu Asn Asp Pro Glu
115 120 125

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

25

Phe Glu Asp Ile Gly Glu
145 150

<210> 38

<211> 153

30

<212> PRT

<213> *Torulaspora delbrueckii*

<220>

<223> cytosine deaminase (codA)

35

<400> 38

Met Ser Asn Gln Trp Asp Lys Ile Gly Met Asp Val Ala Tyr Glu Glu
5 10 15

40

Ala Leu Lys Gly Phe Ala Gln Gly Gly Val Pro Ile Gly Gly Cys Leu
20 25 30

Ile Asn Asn Lys Asp Gly Thr Ile Leu Gly Arg Gly His Asn Met Arg
35 40 45

Phe Gln Lys Gly Ser Ala Thr Leu His Gly Glu Ile Ser Thr Leu Glu
50 55 60

45

Asn Cys Gly Arg Leu Pro Gly Lys Val Tyr Lys Asp Thr Thr Leu Tyr
65 70 75 80

Thr Thr Leu Ser Pro Cys Asp Met Cys Thr Gly Ala Ile Ile Met Tyr
85 90 95

50

Gly Ile Pro Arg Cys Val Ile Gly Glu Asn Val Asn Phe Lys Ser Pro
100 105 110

Gly Glu Gln Tyr Leu Gln Ser Arg Gly His Glu Val Val Val Val Asp
115 120 125

Asp Glu Arg Cys Lys Ala Ile Met Lys Lys Leu Ile Asp Glu Arg Pro
130 135 140

Gln Asp Trp Phe Glu Asp Ile Gly Glu
145 150

5

<210> 39

<211> 330

<212> DNA

<213> *Phaeodactylum tricornutum*

10

<220>

<223> fcpA terminator

<400> 39

15	cagaagcgtg ctatcgaact caaccaggga cgtgcggcac aaatgggcat ccttgctctc	60
	atggtgcacg aacagttggg agtctctatc cttccttaaa aatttaattt tcattagttg	120
	cagtcaactcc gcttttggtt cacagtcagg aataacacta gctcgtcttc accatggatg	180
	ccaatctcgc ctattcatgg tgtataaaaag ttcaacatcc aaagctagaa cttttggaaa	240
	gagaaagaat atccgaatag ggcacggcgt gccgtattgt tggagtggac tagcagaaag	300
20	tgaggaaggc acaggatgag ttttctcgag	330