

SEQUENCE LISTING

<110> NATIONAL UNIVERSITY CORPORATION KOBE UNIVERSITY

<120> Method of modifying genomic sequence comprising specifically converting nucleobase in targeted DNA sequence and molecular complex used therefor

<130> 092301

<150> JP 2014-043348

<151> 2014-03-05

<150> JP 2014-201859

<151> 2014-09-30

<160> 42

<170> PatentIn version 3.5

<210> 1

<211> 624

<212> DNA

<213> Petromyzon marinus

<220>

<221> CDS

<222> (1).. (624)

<400> 1

atg acc gac gct gag tac gtg aga atc cat gag aag ttg gac atc tac	48
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acg ttt aag aaa cag ttt ttc aac aac aaa aaa tcc gtg tcg cat aga	96
Thr Phe Lys Lys Gln Phe Phe Asn Asn Lys Lys Ser Val Ser His Arg	
20 25 30	

tgc tac gtt ctc ttt gaa tta aaa cga cgg ggt gaa cgt aga gcg tgt	144
Cys Tyr Val Leu Phe Glu Leu Lys Arg Arg Gly Glu Arg Arg Ala Cys	
35 40 45	

ttt tgg ggc tat gct gtg aat aaa cca cag agc ggg aca gaa cgt ggc	192
Phe Trp Gly Tyr Ala Val Asn Lys Pro Gln Ser Gly Thr Glu Arg Gly	
50 55 60	

att cac gcc gaa atc ttt agc att aga aaa gtc gaa gaa tac ctg cgc	240
Ile His Ala Glu Ile Phe Ser Ile Arg Lys Val Glu Glu Tyr Leu Arg	
65 70 75 80	

gac aac ccc gga caa ttc acg ata aat tgg tac tca tcc tgg agt cct	288
Asp Asn Pro Gly Gln Phe Thr Ile Asn Trp Tyr Ser Ser Trp Ser Pro	
85 90 95	

tgt gca gat tgc gct gaa aag atc tta gaa tgg tat aac cag gag ctg	336
Cys Ala Asp Cys Ala Glu Lys Ile Leu Glu Trp Tyr Asn Gln Glu Leu	

(1)

100	105	110	
cgg ggg aac ggc cac act ttg aaa atc tgg gct tgc aaa ctc tat tac			384
Arg Gly Asn Gly His Thr Leu Lys Ile Trp Ala Cys Lys Leu Tyr Tyr			
115	120	125	
gag aaa aat gcg agg aat caa att ggg ctg tgg aac ctc aga gat aac			432
Glu Lys Asn Ala Arg Asn Gln Ile Gly Leu Trp Asn Leu Arg Asp Asn			
130	135	140	
ggg gtt ggg ttg aat gta atg gta agt gaa cac tac caa tgt tgc agg			480
Gly Val Gly Leu Asn Val Met Val Ser Glu His Tyr Gln Cys Cys Arg			
145	150	155	160
aaa ata ttc atc caa tgc tgc cac aat caa ttg aat gag aat aga tgg			528
Lys Ile Phe Ile Gln Ser Ser His Asn Gln Leu Asn Glu Asn Arg Trp			
165	170	175	
ctt gag aag act ttg aag cga gct gaa aaa cga cgg agc gag ttg tcc			576
Leu Glu Lys Thr Leu Lys Arg Ala Glu Lys Arg Arg Ser Glu Leu Ser			
180	185	190	
att atg att cag gta aaa ata ctc cac acc act aag agt cct gct gtt			624
Ile Met Ile Gln Val Lys Ile Leu His Thr Thr Lys Ser Pro Ala Val			
195	200	205	

<210> 2
 <211> 208
 <212> PRT
 <213> Petromyzon marinus

<400> 2

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Cys Tyr Val Leu Phe Glu Leu Lys Arg Arg Gly Glu Arg Arg Ala Cys	
35 40 45	
Phe Trp Gly Tyr Ala Val Asn Lys Pro Gln Ser Gly Thr Glu Arg Gly	
50 55 60	
Ile His Ala Glu Ile Phe Ser Ile Arg Lys Val Glu Glu Tyr Leu Arg	
65 70 75 80	
Asp Asn Pro Gly Gln Phe Thr Ile Asn Trp Tyr Ser Ser Trp Ser Pro	
85 90 95	

Cys Ala Asp Cys Ala Glu Lys Ile Leu Glu Trp Tyr Asn Gln Glu Leu
100 105 110

Arg Gly Asn Gly His Thr Leu Lys Ile Trp Ala Cys Lys Leu Tyr Tyr
115 120 125

Glu Lys Asn Ala Arg Asn Gln Ile Gly Leu Trp Asn Leu Arg Asp Asn
130 135 140

Gly Val Gly Leu Asn Val Met Val Ser Glu His Tyr Gln Cys Cys Arg
145 150 155 160

Lys Ile Phe Ile Gln Ser Ser His Asn Gln Leu Asn Glu Asn Arg Trp
165 170 175

Leu Glu Lys Thr Leu Lys Arg Ala Glu Lys Arg Arg Ser Glu Leu Ser
180 185 190

Ile Met Ile Gln Val Lys Ile Leu His Thr Thr Lys Ser Pro Ala Val
195 200 205

<210> 3
<211> 600
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1).. (600)

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aat gtc cgc tgg gct aag ggt cgg cgt gag acc tac ctg tgc tac gta 96
Asn Val Arg Trp Ala Lys Gly Arg Arg Glu Thr Tyr Leu Cys Tyr Val
20 25 30

gtg aag agg cgt gac agt gct aca tcc ttt tca ctg gac ttt ggt tat 144
Val Lys Arg Arg Asp Ser Ala Thr Ser Phe Ser Leu Asp Phe Gly Tyr
35 40 45

ctt cgc aat aag aac ggc tgc cac gtg gaa ttg ctc ttc ctc cgc tac 192
Leu Arg Asn Lys Asn Gly Cys His Val Glu Leu Leu Phe Leu Arg Tyr
50 55 60

atc tcg gac tgg gac cta gac cct ggc cgc tgc tac cgc gtc acc tgg 240
(3)

Ile	Ser	Asp	Trp	Asp	Leu	Asp	Pro	Gly	Arg	Cys	Tyr	Arg	Val	Thr	Trp		
65					70					75					80		
ttc	acc	tcc	tgg	agc	ccc	tgc	tac	gac	tgt	gcc	cga	cat	gtg	gcc	gac		288
Phe	Thr	Ser	Trp	Ser	Pro	Cys	Tyr	Asp	Cys	Ala	Arg	His	Val	Ala	Asp		
				85					90					95			
ttt	ctg	cga	ggg	aac	ccc	tac	ctc	agt	ctg	agg	atc	ttc	acc	gcg	cgc		336
Phe	Leu	Arg	Gly	Asn	Pro	Tyr	Leu	Ser	Leu	Arg	Ile	Phe	Thr	Ala	Arg		
			100					105					110				
ctc	tac	ttc	tgt	gag	gac	cgc	aag	gct	gag	ccc	gag	ggg	ctg	cgg	cgg		384
Leu	Tyr	Phe	Cys	Glu	Asp	Arg	Lys	Ala	Glu	Pro	Glu	Gly	Leu	Arg	Arg		
		115					120					125					
ctg	cac	cgc	gcc	ggg	gtg	caa	ata	gcc	atc	atg	acc	ttc	aaa	gat	tat		432
Leu	His	Arg	Ala	Gly	Val	Gln	Ile	Ala	Ile	Met	Thr	Phe	Lys	Asp	Tyr		
		130				135					140						
ttt	tac	tgc	tgg	aat	act	ttt	gta	gaa	aac	cat	gaa	aga	act	ttc	aaa		480
Phe	Tyr	Cys	Trp	Asn	Thr	Phe	Val	Glu	Asn	His	Glu	Arg	Thr	Phe	Lys		
		145			150					155					160		
gcc	tgg	gaa	ggg	ctg	cat	gaa	aat	tca	gtt	cgt	ctc	tcc	aga	cag	ctt		528
Ala	Trp	Glu	Gly	Leu	His	Glu	Asn	Ser	Val	Arg	Leu	Ser	Arg	Gln	Leu		
			165					170						175			
cgg	cgc	atc	ctt	ttg	ccc	ctg	tat	gag	gtt	gat	gac	tta	cga	gac	gca		576
Arg	Arg	Ile	Leu	Leu	Pro	Leu	Tyr	Glu	Val	Asp	Asp	Leu	Arg	Asp	Ala		
			180					185					190				
ttt	cgt	act	ttg	gga	ctt	ctc	gac										600
Phe	Arg	Thr	Leu	Gly	Leu	Leu	Asp										
		195					200										

<210> 4
 <211> 200
 <212> PRT
 <213> Homo sapiens

<400> 4

Met	Asp	Ser	Leu	Leu	Met	Asn	Arg	Arg	Lys	Phe	Leu	Tyr	Gln	Phe	Lys		
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Asn	Val	Arg	Trp	Ala	Lys	Gly	Arg	Arg	Glu	Thr	Tyr	Leu	Cys	Tyr	Val		
			20					25					30				
Val	Lys	Arg	Arg	Asp	Ser	Ala	Thr	Ser	Phe	Ser	Leu	Asp	Phe	Gly	Tyr		
		35				40						45					
Leu	Arg	Asn	Lys	Asn	Gly	Cys	His	Val	Glu	Leu	Leu	Phe	Leu	Arg	Tyr		
		50			55						60						

Ile Ser Asp Trp Asp Leu Asp Pro Gly Arg Cys Tyr Arg Val Thr Trp
65 70 75 80

Phe Thr Ser Trp Ser Pro Cys Tyr Asp Cys Ala Arg His Val Ala Asp
85 90 95

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

Leu Tyr Phe Cys Glu Asp Arg Lys Ala Glu Pro Glu Gly Leu Arg Arg
115 120 125

Leu His Arg Ala Gly Val Gln Ile Ala Ile Met Thr Phe Lys Asp Tyr
130 135 140

Phe Tyr Cys Trp Asn Thr Phe Val Glu Asn His Glu Arg Thr Phe Lys
145 150 155 160

Ala Trp Glu Gly Leu His Glu Asn Ser Val Arg Leu Ser Arg Gln Leu
165 170 175

Arg Arg Ile Leu Leu Pro Leu Tyr Glu Val Asp Asp Leu Arg Asp Ala
180 185 190

Phe Arg Thr Leu Gly Leu Leu Asp
195 200

<210> 5
<211> 4116
<212> DNA
<213> Artificial Sequence

<220>
<223> Streptococcus pyogenes-derived Cas9 CDS optimized for eucaryotic expression.

<220>
<221> CDS
<222> (1).. (4116)

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48

ggt tgg gcc gtc att acg gac gag tac aag gtg ccg agc aaa aaa ttc Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys Val Pro Ser Lys Lys Phe 20 25 30	96
aaa gtt ctg ggc aat acc gat cgc cac agc ata aag aag aac ctc att Lys Val Leu Gly Asn Thr Asp Arg His Ser Ile Lys Lys Asn Leu Ile 35 40 45	144
ggc gcc ctc ctg ttc gac tcc ggg gag acg gcc gaa gcc acg cgg ctc Gly Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala Glu Ala Thr Arg Leu 50 55 60	192
aaa aga aca gca cgg cgc aga tat acc cgc aga aag aat cgg atc tgc Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Cys 65 70 75 80	240
tac ctg cag gag atc ttt agt aat gag atg gct aag gtg gat gac tct Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp Asp Ser 85 90 95	288
ttc ttc cat agg ctg gag gag tcc ttt ttg gtg gag gag gat aaa aag Phe Phe His Arg Leu Glu Glu Ser Phe Leu Val Glu Glu Asp Lys Lys 100 105 110	336
cac gag cgc cac cca atc ttt ggc aat atc gtg gac gag gtg gcg tac His Glu Arg His Pro Ile Phe Gly Asn Ile Val Asp Glu Val Ala Tyr 115 120 125	384
cat gaa aag tac cca acc ata tat cat ctg agg aag aag ctt gta gac His Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu Val Asp 130 135 140	432
agt act gat aag gct gac ttg cgg ttg atc tat ctc gcg ctg gcg cat Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu Ala His 145 150 155 160	480
atg atc aaa ttt cgg gga cac ttc ctc atc gag ggg gac ctg aac cca Met Ile Lys Phe Arg Gly His Phe Leu Ile Glu Gly Asp Leu Asn Pro 165 170 175	528
gac aac agc gat gtc gac aaa ctc ttt atc caa ctg gtt cag act tac Asp Asn Ser Asp Val Asp Lys Leu Phe Ile Gln Leu Val Gln Thr Tyr 180 185 190	576
aat cag ctt ttc gaa gag aac ccg atc aac gca tcc gga gtt gac gcc Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn Ala Ser Gly Val Asp Ala 195 200 205	624
aaa gca atc ctg agc gct agg ctg tcc aaa tcc cgg cgg ctc gaa aac Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn 210 215 220	672
ctc atc gca cag ctc cct ggg gag aag aag aac ggc ctg ttt ggt aat Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn 225 230 235 240	720
ctt atc gcc ctg tca ctc ggg ctg acc ccc aac ttt aaa tct aac ttc	768

Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn Phe Lys Ser Asn Phe	
245 250 255	
gac ctg gcc gaa gat gcc aag ctt caa ctg agc aaa gac acc tac gat	816
Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp	
260 265 270	
gat gat ctc gac aat ctg ctg gcc cag atc ggc gac cag tac gca gac	864
Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr Ala Asp	
275 280 285	
ctt ttt ttg gcg gca aag aac ctg tca gac gcc att ctg ctg agt gat	912
Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp	
290 295 300	
att ctg cga gtg aac acg gag atc acc aaa gct ccg ctg agc gct agt	960
Ile Leu Arg Val Asn Thr Glu Ile Thr Lys Ala Pro Leu Ser Ala Ser	
305 310 315 320	
atg atc aag cgc tat gat gag cac cac caa gac ttg act ttg ctg aag	1008
Met Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys	
325 330 335	
gcc ctt gtc aga cag caa ctg cct gag aag tac aag gaa att ttc ttc	1056
Ala Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe	
340 345 350	
gat cag tct aaa aat ggc tac gcc gga tac att gac ggc gga gca agc	1104
Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser	
355 360 365	
cag gag gaa ttt tac aaa ttt att aag ccc atc ttg gaa aaa atg gac	1152
Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp	
370 375 380	
ggc acc gag gag ctg ctg gta aag ctt aac aga gaa gat ctg ttg cgc	1200
Gly Thr Glu Glu Leu Leu Val Lys Leu Asn Arg Glu Asp Leu Leu Arg	
385 390 395 400	
aaa cag cgc act ttc gac aat gga agc atc ccc cac cag att cac ctg	1248
Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu	
405 410 415	
ggc gaa ctg cac gct atc ctc agg cgg caa gag gat ttc tac ccc ttt	1296
Gly Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp Phe Tyr Pro Phe	
420 425 430	
ttg aaa gat aac agg gaa aag att gag aaa atc ctc aca ttt cgg ata	1344
Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys Ile Leu Thr Phe Arg Ile	
435 440 445	
ccc tac tat gta ggc ccc ctc gcc cgg gga aat tcc aga ttc gcg tgg	1392
Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp	
450 455 460	
atg act cgc aaa tca gaa gag acc atc act ccc tgg aac ttc gag gaa	1440
Met Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu	

465	470	475	480	
gtc gtc gat aag ggg gcc tct gcc cag tcc ttc atc gaa agg atg act				1488
Val Val Asp Lys Gly Ala Ser Ala Gln Ser Phe Ile Glu Arg Met Thr	485	490	495	
aac ttt gat aaa aat ctg cct aac gaa aag gtg ctt cct aaa cac tct				1536
Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu Pro Lys His Ser	500	505	510	
ctg ctg tac gag tac ttc aca gtt tat aac gag ctc acc aag gtc aaa				1584
Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys	515	520	525	
tac gtc aca gaa ggg atg aga aag cca gca ttc ctg tct gga gag cag				1632
Tyr Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln	530	535	540	
aag aaa gct atc gtg gac ctc ctc ttc aag acg aac cgg aaa gtt acc				1680
Lys Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr	545	550	555	560
gtg aaa cag ctc aaa gaa gac tat ttc aaa aag att gaa tgt ttc gac				1728
Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp	565	570	575	
tct gtt gaa atc agc gga gtg gag gat cgc ttc aac gca tcc ctg gga				1776
Ser Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly	580	585	590	
acg tat cac gat ctc ctg aaa atc att aaa gac aag gac ttc ctg gac				1824
Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp	595	600	605	
aat gag gag aac gag gac att ctt gag gac att gtc ctc acc ctt acg				1872
Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr	610	615	620	
ttg ttt gaa gat agg gag atg att gaa gaa cgc ttg aaa act tac gct				1920
Leu Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala	625	630	635	640
cat ctc ttc gac gac aaa gtc atg aaa cag ctc aag agg cgc cga tat				1968
His Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr	645	650	655	
aca gga tgg ggg cgg ctg tca aga aaa ctg atc aat ggg atc cga gac				2016
Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp	660	665	670	
aag cag agt gga aag aca atc ctg gat ttt ctt aag tcc gat gga ttt				2064
Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe	675	680	685	
gcc aac cgg aac ttc atg cag ttg atc cat gat gac tct ctc acc ttt				2112
Ala Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe	690	695	700	

aag gag gac atc cag aaa gca caa gtt tct ggc cag ggg gac agt ctt Lys Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln Gly Asp Ser Leu 705 710 715 720	2160
cac gag cac atc gct aat ctt gca ggt agc cca gct atc aaa aag gga His Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala Ile Lys Lys Gly 725 730 735	2208
ata ctg cag acc gtt aag gtc gtg gat gaa ctc gtc aaa gta atg gga Ile Leu Gln Thr Val Lys Val Val Asp Glu Leu Val Lys Val Met Gly 740 745 750	2256
agg cat aag ccc gag aat atc gtt atc gag atg gcc cga gag aac caa Arg His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln 755 760 765	2304
act acc cag aag gga cag aag aac agt agg gaa agg atg aag agg att Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile 770 775 780	2352
gaa gag ggt ata aaa gaa ctg ggg tcc caa atc ctt aag gaa cac cca Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His Pro 785 790 795 800	2400
gtt gaa aac acc cag ctt cag aat gag aag ctc tac ctg tac tac ctg Val Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu 805 810 815	2448
cag aac ggc agg gac atg tac gtg gat cag gaa ctg gac atc aat cgg Gln Asn Gly Arg Asp Met Tyr Val Asp Gln Glu Leu Asp Ile Asn Arg 820 825 830	2496
ctc tcc gac tac gac gtg gat cat atc gtg ccc cag tct ttt ctc aaa Leu Ser Asp Tyr Asp Val Asp His Ile Val Pro Gln Ser Phe Leu Lys 835 840 845	2544
gat gat tct att gat aat aaa gtg ttg aca aga tcc gat aaa aat aga Asp Asp Ser Ile Asp Asn Lys Val Leu Thr Arg Ser Asp Lys Asn Arg 850 855 860	2592
ggg aag agt gat aac gtc ccc tca gaa gaa gtt gtc aag aaa atg aaa Gly Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys 865 870 875 880	2640
aat tat tgg cgg cag ctg ctg aac gcc aaa ctg atc aca caa cgg aag Asn Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys 885 890 895	2688
ttc gat aat ctg act aag gct gaa cga ggt ggc ctg tct gag ttg gat Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp 900 905 910	2736
aaa gcc ggc ttc atc aaa agg cag ctt gtt gag aca cgc cag atc acc Lys Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr 915 920 925	2784

aag cac gtg gcc caa att ctc gat tca cgc atg aac acc aag tac gat Lys His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp 930 935 940	2832
gaa aat gac aaa ctg att cga gag gtg aaa gtt att act ctg aag tct Glu Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu Lys Ser 945 950 955 960	2880
aag ctg gtc tca gat ttc aga aag gac ttt cag ttt tat aag gtg aga Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg 965 970 975	2928
gag atc aac aat tac cac cat gcg cat gat gcc tac ctg aat gca gtg Glu Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val 980 985 990	2976
gta ggc act gca ctt atc aaa aaa tat ccc aag ctt gaa tct gaa ttt Val Gly Thr Ala Leu Ile Lys Lys Tyr Pro Lys Leu Glu Ser Glu Phe 995 1000 1005	3024
gtt tac gga gac tat aaa gtg tac gat gtt agg aaa atg atc gca Val Tyr Gly Asp Tyr Lys Val Tyr Asp Val Arg Lys Met Ile Ala 1010 1015 1020	3069
aag tct gag cag gaa ata ggc aag gcc acc gct aag tac ttc ttt Lys Ser Glu Gln Glu Ile Gly Lys Ala Thr Ala Lys Tyr Phe Phe 1025 1030 1035	3114
tac agc aat att atg aat ttt ttc aag acc gag att aca ctg gcc Tyr Ser Asn Ile Met Asn Phe Phe Lys Thr Glu Ile Thr Leu Ala 1040 1045 1050	3159
aat gga gag att cgg aag cga cca ctt atc gaa aca aac gga gaa Asn Gly Glu Ile Arg Lys Arg Pro Leu Ile Glu Thr Asn Gly Glu 1055 1060 1065	3204
aca gga gaa atc gtg tgg gac aag ggt agg gat ttc gcg aca gtc Thr Gly Glu Ile Val Trp Asp Lys Gly Arg Asp Phe Ala Thr Val 1070 1075 1080	3249
cgg aag gtc ctg tcc atg ccg cag gtg aac atc gtt aaa aag acc Arg Lys Val Leu Ser Met Pro Gln Val Asn Ile Val Lys Lys Thr 1085 1090 1095	3294
gaa gta cag acc gga ggc ttc tcc aag gaa agt atc ctc ccg aaa Glu Val Gln Thr Gly Gly Phe Ser Lys Glu Ser Ile Leu Pro Lys 1100 1105 1110	3339
agg aac agc gac aag ctg atc gca cgc aaa aaa gat tgg gac ccc Arg Asn Ser Asp Lys Leu Ile Ala Arg Lys Lys Asp Trp Asp Pro 1115 1120 1125	3384
aag aaa tac ggc gga ttc gat tct cct aca gtc gct tac agt gta Lys Lys Tyr Gly Gly Phe Asp Ser Pro Thr Val Ala Tyr Ser Val 1130 1135 1140	3429
ctg gtt gtg gcc aaa gtg gag aaa ggg aag tct aaa aaa ctc aaa	3474

Leu Val Val Ala Lys Val Glu Lys Gly Lys Ser Lys Lys Leu Lys	
1145 1150 1155	
agc gtc aag gaa ctg ctg ggc atc aca atc atg gag cga tca agc	3519
Ser Val Lys Glu Leu Leu Gly Ile Thr Ile Met Glu Arg Ser Ser	
1160 1165 1170	
ttc gaa aaa aac ccc atc gac ttt ctc gag gcg aaa gga tat aaa	3564
Phe Glu Lys Asn Pro Ile Asp Phe Leu Glu Ala Lys Gly Tyr Lys	
1175 1180 1185	
gag gtc aaa aaa gac ctc atc att aag ctt ccc aag tac tct ctc	3609
Glu Val Lys Lys Asp Leu Ile Ile Lys Leu Pro Lys Tyr Ser Leu	
1190 1195 1200	
ttt gag ctt gaa aac ggc cgg aaa cga atg ctc gct agt gcg ggc	3654
Phe Glu Leu Glu Asn Gly Arg Lys Arg Met Leu Ala Ser Ala Gly	
1205 1210 1215	
gag ctg cag aaa ggt aac gag ctg gca ctg ccc tct aaa tac gtt	3699
Glu Leu Gln Lys Gly Asn Glu Leu Ala Leu Pro Ser Lys Tyr Val	
1220 1225 1230	
aat ttc ttg tat ctg gcc agc cac tat gaa aag ctc aaa ggg tct	3744
Asn Phe Leu Tyr Leu Ala Ser His Tyr Glu Lys Leu Lys Gly Ser	
1235 1240 1245	
ccc gaa gat aat gag cag aag cag ctg ttc gtg gaa caa cac aaa	3789
Pro Glu Asp Asn Glu Gln Lys Gln Leu Phe Val Glu Gln His Lys	
1250 1255 1260	
cac tac ctt gat gag atc atc gag caa ata agc gaa ttc tcc aaa	3834
His Tyr Leu Asp Glu Ile Ile Glu Gln Ile Ser Glu Phe Ser Lys	
1265 1270 1275	
aga gtg atc ctc gcc gac gct aac ctc gat aag gtg ctt tct gct	3879
Arg Val Ile Leu Ala Asp Ala Asn Leu Asp Lys Val Leu Ser Ala	
1280 1285 1290	
tac aat aag cac agg gat aag ccc atc agg gag cag gca gaa aac	3924
Tyr Asn Lys His Arg Asp Lys Pro Ile Arg Glu Gln Ala Glu Asn	
1295 1300 1305	
att atc cac ttg ttt act ctg acc aac ttg ggc gcg cct gca gcc	3969
Ile Ile His Leu Phe Thr Leu Thr Asn Leu Gly Ala Pro Ala Ala	
1310 1315 1320	
ttc aag tac ttc gac acc acc ata gac aga aag cgg tac acc tct	4014
Phe Lys Tyr Phe Asp Thr Thr Ile Asp Arg Lys Arg Tyr Thr Ser	
1325 1330 1335	
aca aag gag gtc ctg gac gcc aca ctg att cat cag tca att acg	4059
Thr Lys Glu Val Leu Asp Ala Thr Leu Ile His Gln Ser Ile Thr	
1340 1345 1350	
ggg ctc tat gaa aca aga atc gac ctc tct cag ctc ggt gga gac	4104
Gly Leu Tyr Glu Thr Arg Ile Asp Leu Ser Gln Leu Gly Gly Asp	

1355

1360

1365

agc agg gct gac
 Ser Arg Ala Asp
 1370

4116

<210> 6
 <211> 1372
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 6

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

Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys Val Pro Ser Lys Lys Phe
 20 25 30

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

Gly Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala Glu Ala Thr Arg Leu
 50 55 60

Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Cys
 65 70 75 80

Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp Asp Ser
 85 90 95

Phe Phe His Arg Leu Glu Glu Ser Phe Leu Val Glu Glu Asp Lys Lys
 100 105 110

His Glu Arg His Pro Ile Phe Gly Asn Ile Val Asp Glu Val Ala Tyr
 115 120 125

His Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu Val Asp
 130 135 140

Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu Ala His
 145 150 155 160

Met Ile Lys Phe Arg Gly His Phe Leu Ile Glu Gly Asp Leu Asn Pro
165 170 175

Asp Asn Ser Asp Val Asp Lys Leu Phe Ile Gln Leu Val Gln Thr Tyr
180 185 190

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

Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn
210 215 220

Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn
225 230 235 240

Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn Phe Lys Ser Asn Phe
245 250 255

Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp
260 265 270

Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr Ala Asp
275 280 285

Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp
290 295 300

Ile Leu Arg Val Asn Thr Glu Ile Thr Lys Ala Pro Leu Ser Ala Ser
305 310 315 320

Met Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys
325 330 335

Ala Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe
340 345 350

Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser
355 360 365

Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp
370 375 380

Gly Thr Glu Glu Leu Leu Val Lys Leu Asn Arg Glu Asp Leu Leu Arg
(13)

385		390		395		400
Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu						
		405		410		415
Gly Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp Phe Tyr Pro Phe						
		420		425		430
Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys Ile Leu Thr Phe Arg Ile						
		435		440		445
Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp						
		450		455		460
Met Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu						
		465		470		480
Val Val Asp Lys Gly Ala Ser Ala Gln Ser Phe Ile Glu Arg Met Thr						
		485		490		495
Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu Pro Lys His Ser						
		500		505		510
Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys						
		515		520		525
Tyr Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln						
		530		535		540
Lys Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr						
		545		550		560
Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp						
		565		570		575
Ser Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly						
		580		585		590
Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp						
		595		600		605
Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr						
		610		615		620

Leu Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala
625 630 635 640

His Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr
645 650 655

Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp
660 665 670

Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe
675 680 685

Ala Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe
690 695 700

Lys Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln Gly Asp Ser Leu
705 710 715 720

His Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala Ile Lys Lys Gly
725 730 735

Ile Leu Gln Thr Val Lys Val Val Asp Glu Leu Val Lys Val Met Gly
740 745 750

Arg His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln
755 760 765

Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile
770 775 780

Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His Pro
785 790 795 800

Val Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu
805 810 815

Gln Asn Gly Arg Asp Met Tyr Val Asp Gln Glu Leu Asp Ile Asn Arg
820 825 830

Leu Ser Asp Tyr Asp Val Asp His Ile Val Pro Gln Ser Phe Leu Lys
835 840 845

Asp Asp Ser Ile Asp Asn Lys Val Leu Thr Arg Ser Asp Lys Asn Arg
850 855 860

Gly Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys
865 870 875 880

Asn Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys
885 890 895

Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp
900 905 910

Lys Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr
915 920 925

Lys His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp
930 935 940

Glu Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu Lys Ser
945 950 955 960

Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg
965 970 975

Glu Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val
980 985 990

Val Gly Thr Ala Leu Ile Lys Lys Tyr Pro Lys Leu Glu Ser Glu Phe
995 1000 1005

Val Tyr Gly Asp Tyr Lys Val Tyr Asp Val Arg Lys Met Ile Ala
1010 1015 1020

Lys Ser Glu Gln Glu Ile Gly Lys Ala Thr Ala Lys Tyr Phe Phe
1025 1030 1035

Tyr Ser Asn Ile Met Asn Phe Phe Lys Thr Glu Ile Thr Leu Ala
1040 1045 1050

Asn Gly Glu Ile Arg Lys Arg Pro Leu Ile Glu Thr Asn Gly Glu
1055 1060 1065

Thr Gly Glu Ile Val Trp Asp Lys Gly Arg Asp Phe Ala Thr Val
1070 1075 1080

Arg Lys Val Leu Ser Met Pro Gln Val Asn Ile Val Lys Lys Thr
1085 1090 1095

Glu Val Gln Thr Gly Gly Phe Ser Lys Glu Ser Ile Leu Pro Lys
1100 1105 1110

Arg Asn Ser Asp Lys Leu Ile Ala Arg Lys Lys Asp Trp Asp Pro
1115 1120 1125

Lys Lys Tyr Gly Gly Phe Asp Ser Pro Thr Val Ala Tyr Ser Val
1130 1135 1140

Leu Val Val Ala Lys Val Glu Lys Gly Lys Ser Lys Lys Leu Lys
1145 1150 1155

Ser Val Lys Glu Leu Leu Gly Ile Thr Ile Met Glu Arg Ser Ser
1160 1165 1170

Phe Glu Lys Asn Pro Ile Asp Phe Leu Glu Ala Lys Gly Tyr Lys
1175 1180 1185

Glu Val Lys Lys Asp Leu Ile Ile Lys Leu Pro Lys Tyr Ser Leu
1190 1195 1200

Phe Glu Leu Glu Asn Gly Arg Lys Arg Met Leu Ala Ser Ala Gly
1205 1210 1215

Glu Leu Gln Lys Gly Asn Glu Leu Ala Leu Pro Ser Lys Tyr Val
1220 1225 1230

Asn Phe Leu Tyr Leu Ala Ser His Tyr Glu Lys Leu Lys Gly Ser
1235 1240 1245

Pro Glu Asp Asn Glu Gln Lys Gln Leu Phe Val Glu Gln His Lys
1250 1255 1260

His Tyr Leu Asp Glu Ile Ile Glu Gln Ile Ser Glu Phe Ser Lys
1265 1270 1275

Arg Val Ile Leu Ala Asp Ala Asn Leu Asp Lys Val Leu Ser Ala
(17)

1280		1285		1290
Tyr Asn Lys His Arg Asp Lys Pro Ile Arg Glu Gln Ala Glu Asn				
1295		1300		1305
Ile Ile His Leu Phe Thr Leu Thr Asn Leu Gly Ala Pro Ala Ala				
1310		1315		1320
Phe Lys Tyr Phe Asp Thr Thr Ile Asp Arg Lys Arg Tyr Thr Ser				
1325		1330		1335
Thr Lys Glu Val Leu Asp Ala Thr Leu Ile His Gln Ser Ile Thr				
1340		1345		1350
Gly Leu Tyr Glu Thr Arg Ile Asp Leu Ser Gln Leu Gly Gly Asp				
1355		1360		1365
Ser Arg Ala Asp				
1370				

<210> 7
 <211> 83
 <212> DNA
 <213> Streptococcus pyogenes

<400> 7	
gttttagagc tagaaatagc aagttaaaat aaggctagtc cgttatcaac ttgaaaaagt	60
ggcaccgagt cgggtggtgct ttt	83

<210> 8
 <211> 665
 <212> DNA
 <213> Saccharomyces cerevisiae

<400> 8	
tttcaaaaat tcttactttt tttttggatg gacgcaaaga agtttaataa tcatattaca	60
tggcattacc accatataca tatccatata catatccata tctaatttta cttatatgtt	120
gtggaaatgt aaagagcccc attatcttag cctaaaaaaa ctttctcttt ggaactttca	180
gtaatacgct taactgctca ttgctatatt gaagtacgga ttagaagccg ccgagcgggt	240
gacagccctc cgaaggaaga ctctcctccg tgcgtcctcg tcttcaccgg tcgcgttcct	300
gaaacgcaga tgtgcctcgc gccgcactgc tccgaacaat aaagattcta caatactagc	360
ttttatgggt atgaagagga aaaattggca gtaacctggc ccacaaacc ttcaaataa	420

cgaatcaa	at	taacaacc	at	aggatgataa	tgcgattagt	tttttagcct	tatttctggg	480
gtaattaatc	agcgaagcga	tgatttttga	tctattaaca	gatataataa	tgcaaaaact			540
gcataaccac	ttaaactaat	actttcaaca	ttttcggttt	gtattacttc	ttattcaa	at		600
gtaataaaaag	tatcaacaaa	aaattgttaa	tatacctcta	tactttaacg	tcaaggagaa			660
aaaac								665

<210> 9
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Nuclear transition signal.

<220>
 <221> CDS
 <222> (1)..(21)

<400>	9	
ccc aag aag aag agg aag gtg		21
Pro Lys Lys Lys Arg Lys Val		
1	5	

<210> 10
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400>	10
Pro Lys Lys Lys Arg Lys Val	
1	5

<210> 11
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> GS linker

<220>
 <221> CDS
 <222> (1)..(15)

<400> 11
 ggt gga gga ggt tct
 Gly Gly Gly Gly Ser
 1 5 15

<210> 12
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 12
 Gly Gly Gly Gly Ser
 1 5

<210> 13
 <211> 66
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Flag tag

<220>
 <221> CDS
 <222> (1).. (66)

<400> 13
 gac tat aag gac cac gac gga gac tac aag gat cat gat att gat tac
 Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp Tyr
 1 5 10 15 48

aaa gac gat gac gat aag
 Lys Asp Asp Asp Asp Lys
 20 66

<210> 14
 <211> 22
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 14
 Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp Tyr
 1 5 10 15

Lys Asp Asp Asp Asp Lys
20

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Strep-tag

<220>
<221> CDS
<222> (1).. (24)

<400> 15
tgg agc cac ccg cag ttc gaa aaa
Trp Ser His Pro Gln Phe Glu Lys
1 5

24

<210> 16
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 16

Trp Ser His Pro Gln Phe Glu Lys
1 5

<210> 17
<211> 171
<212> DNA
<213> Artificial Sequence

<220>
<223> SH3 domain

<220>
<221> CDS
<222> (1).. (171)

<400> 17
gca gag tat gtg cgg gcc ctc ttt gac ttt aat ggg aat gat gaa gaa
Ala Glu Tyr Val Arg Ala Leu Phe Asp Phe Asn Gly Asn Asp Glu Glu
1 5 10 15

48

gat ctt ccc ttt aag aaa gga gac atc ctg aga atc cgg gat aag cct
(21)

96

Asp Leu Pro Phe Lys Lys Gly Asp Ile Leu Arg Ile Arg Asp Lys Pro
 20 25 30

gaa gag cag tgg tgg aat gca gag gac agc gaa gga aag agg ggg atg 144
 Glu Glu Gln Trp Trp Asn Ala Glu Asp Ser Glu Gly Lys Arg Gly Met
 35 40 45

att cct gtc cct tac gtg gag aag tat 171
 Ile Pro Val Pro Tyr Val Glu Lys Tyr
 50 55

<210> 18
 <211> 57
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 18

Ala Glu Tyr Val Arg Ala Leu Phe Asp Phe Asn Gly Asn Asp Glu Glu
 1 5 10 15

Asp Leu Pro Phe Lys Lys Gly Asp Ile Leu Arg Ile Arg Asp Lys Pro
 20 25 30

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

Ile Pro Val Pro Tyr Val Glu Lys Tyr
 50 55

<210> 19
 <211> 188
 <212> DNA
 <213> Saccharomyces cerevisiae

<400> 19
 gcgaatttct tatgatttat gatTTTTatt attaaataag ttataaaaaa aataagtgtgta 60
 tacaaatttt aaagtgactc ttaggtttta aaacgaaaat tcttattctt gagtaactct 120
 ttctgttagg tcaggttgct ttctcaggta tagcatgagg tcgctcttat tgaccacacc 180
 tctaccgg 188

<210> 20
 <211> 417
 <212> DNA
 <213> Saccharomyces cerevisiae

<400> 20
 ataccaggca tggagcttat ctggtccgtt cgagttttcg acgagtttgg agacattctt 60
 tatagatgtc cttttttttt aatgatattc gttaaagaac aaaaagtcaa agcagtttaa 120
 cctaacacct gttgttgatg ctacttgaaa caaggcttct aggccaatac ttaaaaaggt 180
 aatttcaata gcggtttata tatctgtttg cttttcaaga tattatgtaa acgcacgatg 240
 tttttcgccc aggctttatt tttttgttg ttgttgtctt ctccaagaat tttctcgggc 300
 agatctttgt cggaatgtaa aaaagcgcgt aattaaactt tctattatgc tgactaaaat 360
 ggaagtgatc accaaaggct atttctgatt atataatcta gtcattactc gctcgag 417

<210> 21
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> SH3-binding ligand

<220>
 <221> CDS
 <222> (1).. (33)

<400> 21
 cct cca cct gct ctg cca cct aag aga agg aga 33
 Pro Pro Pro Ala Leu Pro Pro Lys Arg Arg Arg
 1 5 10

<210> 22
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 22
 Pro Pro Pro Ala Leu Pro Pro Lys Arg Arg Arg
 1 5 10

<210> 23
 <211> 269
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 23
 tctttgaaaa gataatgtat gattatgctt tcactcatat ttatacagaa acttgatgtt 60
 (23)

ttctttcgag tatatacaag gtgattacat gtacgtttga agtacaactc tagattttgt	120
agtgccctct tgggctagcg gtaaagggtgc gcattttttc acaccctaca atgttctgtt	180
caaaagattt tgggtcaaacg ctgtagaagt gaaagttggt gcgcatgttt cggcgttcga	240
aacttctccg cagtgaaaga taaatgatc	269

<210> 24
 <211> 14
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 24	
tgttttttat gtct	14

<210> 25
 <211> 20
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 25	
gatacgttct ctatggagga	20

<210> 26
 <211> 20
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 26	
ttggagaaac ccaggtgcct	20

<210> 27
 <211> 20
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 27	
aaccacagtg cctggggtcc	20

<210> 28
 <211> 20
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 28	
ttggccaagt cattcaattt	20

<210> 29
 <211> 20

<212> DNA
 <213> *Saccharomyces cerevisiae*

 <400> 29
 ataacggaat ccaactgggc 20

 <210> 30
 <211> 20
 <212> DNA
 <213> *Saccharomyces cerevisiae*

 <400> 30
 gtcaattacg aagactgaac 20

 <210> 31
 <211> 19
 <212> DNA
 <213> *Saccharomyces cerevisiae*

 <400> 31
 gtcaatagga tcccctttt 19

 <210> 32
 <211> 10126
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Plasmid carrying dCas9-PmCDA1 fusion protein and chimeric RNA
 targeting galk gene of *E. coli*

 <220>
 <221> misc_feature
 <222> (5561).. (5580)
 <223> n is a, c, g, or t

 <400> 32
 atcgccattc gccattcagg ctgcgcaact gttgggaagg gcgatcggtg cgggcctctt 60
 cgctattacg ccagctggcg aaagggggat gtgctgcaag gcgattaagt tgggtaacgc 120
 cagggttttc ccagtcacga cgttgtaaaa cgacggccag tgaattcgag ctcggtaccc 180
 ggccgcaaac aacagataaa acgaaaggcc cagtctttcg actgagcctt tcgttttatt 240
 tgatgcctgt caagtaacag caggactctt agtgggtgtg agtatatttta cctgaatcat 300
 aatggacaac tcgctccgtc gtttttcagc tcgcttcaaa gtctttctcaa gccatctatt 360
 ctcatccaat tgattgtgcg acgattggat gaatatatttc ctgcaacatt ggtagtgttc 420
 acttaccatt acattcaacc caaccccggtt atctctgagg ttccacagcc caatttgatt 480

cctcgcattt ttctcgtaat agagtttgca agcccagatt ttcaaagtgt ggccgttccc	540
ccgcagctcc tggttatacc attctaagat cttttcagcg caatctgcac aaggactcca	600
ggatgagtac caatttatcg tgaattgtcc ggggttgtcg cgcaggtatt cttcgacttt	660
tctaattgcta aagatttcgg cgtgaatgcc acgttctgtc ccgctctgtg gtttattcac	720
agcatagccc caaaaacacg ctctacgttc accccgtcgt tttaattcaa agagaacgta	780
gcatctatgc gacacggatt ttttgttggt gaaaaactgt ttcttaaacg tgtagatgtc	840
caactttctca tggatttctca cgtactcagc gtcggtcato ctagacttat cgtcatcgtc	900
tttgtaatca atatcatgat ccttgtagtc tccgtcgtgg tccttatagt ctccggactc	960
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ataatgacta gctaaatata aaaaattcac atatttgctt ggagagcca gctcatttcc	1680
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taaaaagtca atcggatttt ttcaaagga acttctttcc ataattgtga tocctagtaa	1860
ctctttaacg gattttaact tcttcgattt ccccttttcc accttagcaa ccactaggac	1920
tgaataagct accgttggac tatcaaaacc accatatttt tttagatccc agtctttttt	1980
acgagcaata agcttgtccg aatttctttt tggtaaaatt gactccttgg agaatccgcc	2040
tgtctgtact tctgttttct tgacaatatt gacttggggc atggacaata ctttgcgcac	2100
tgtggcaaaa tctcgccctt tatcccagac aatttctcca gtttcccat tagtttcgat	2160
tagagggcgt ttgcgaatct ctccatttgc aagtgttaatt tctgttttga agaagttcat	2220

gatattagag taaaagaaat attttgcggt tgctttgcct atttcttgct cagacttagc	2280
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tttatcagaa cgcgttaaga ccttattgtc tattgaatcg tctttaagga aactttgtgg	2820
aacaatggca tcgacatcat aatcacttaa acgattaata tctaattctt ggtccacata	2880
catgtctctt ccattttgga gataatagag atagagcttt tcattttgca attgagtatt	2940
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