

<110> CJ CheilJedang Corporation

<120> GERANYLGERANYL PYROPHOSPHATE SYNTHASE VARIANT AND METHOD OF PRODUCING TETRATERPENE, PRECURSOR THEREOF, AND MATERIAL HAVING TETRATERPENE AS PRECURSOR USING THE SAME

<130> OPA22028

<150> KR 10-2021-0074819

<151> 2021-06-09

<160> 91

<170> KoPatentIn 3.0

<210> 1

<211> 327

<212> PRT

<213> Artificial Sequence

<220>

<223> GGS1_WT

<400> 1

Met Asp Tyr Asn Ser Ala Asp Phe Lys Glu Ile Trp Gly Lys Ala Ala
1 5 10 15

Asp Thr Ala Leu Leu Gly Pro Tyr Asn Tyr Leu Ala Asn Asn Arg Gly
20 25 30

His Asn Ile Arg Glu His Leu Ile Ala Ala Phe Gly Ala Val Ile Lys
35 40 45

Val Asp Lys Ser Asp Leu Glu Thr Ile Ser His Ile Thr Lys Ile Leu
50 55 60

His Asn Ser Ser Leu Leu Val Asp Asp Val Glu Asp Asn Ser Met Leu
65 70 75 80

Arg Arg Gly Leu Pro Ala Ala His Cys Leu Phe Gly Val Pro Gln Thr
85 90 95

Ile Asn Ser Ala Asn Tyr Met Tyr Phe Val Ala Leu Gln Glu Val Leu
100 105 110

Lys Leu Lys Ser Tyr Asp Ala Val Ser Ile Phe Thr Glu Glu Met Ile
115 120 125

Asn Leu His Arg Gly Gln Gly Met Asp Leu Tyr Trp Arg Glu Thr Leu

130		135		140	
Thr Cys Pro Ser Glu Asp Glu Tyr Leu Glu Met Val Val His Lys Thr					
145		150		155	160
Gly Gly Leu Phe Arg Leu Ala Leu Arg Leu Met Leu Ser Val Ala Ser					
		165		170	175
Lys Gln Glu Asp His Glu Lys Ile Asn Phe Asp Leu Thr His Leu Thr					
		180		185	190
Asp Thr Leu Gly Val Ile Tyr Gln Ile Leu Asp Asp Tyr Leu Asn Leu					
		195		200	205
Gln Ser Thr Glu Leu Thr Glu Asn Lys Gly Phe Cys Glu Asp Ile Ser					
		210		215	220
Glu Gly Lys Phe Ser Phe Pro Leu Ile His Ser Ile Arg Thr Asn Pro					
		225		230	235
Asp Asn His Glu Ile Leu Asn Ile Leu Lys Gln Arg Thr Ser Asp Ala					
		245		250	255
Ser Leu Lys Lys Tyr Ala Val Asp Tyr Met Arg Thr Glu Thr Lys Ser					
		260		265	270
Phe Asp Tyr Cys Leu Lys Arg Ile Gln Ala Met Ser Leu Lys Ala Ser					
		275		280	285
Ser Tyr Ile Asp Asp Leu Ala Ala Ala Gly His Asp Val Ser Lys Leu					
		290		295	300
Arg Ala Ile Leu His Tyr Phe Val Ser Thr Ser Asp Cys Glu Glu Arg					
		305		310	315
Lys Tyr Phe Glu Asp Ala Gln					
		325			

<210> 2
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 <213> Artificial Sequence

<220>
 <223> ggs1_WT

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gcagcgttcg gagcggttat caaggtggac aagagcgatc tcgagaccat ttcgcacatc	180
accaagattt tgcataactc gtcgctgctt gttgatgacg tggaagacaa ctcgatgctc	240
cgacgaggcc tgccggcagc ccattgtctg tttggagtcc cccaaaccat caactccgcc	300
aactacatgt actttgtggc tctgcaggag gtgctcaagc tcaagtctta tgatgccgtc	360
tccattttca ccgaggaaat gatcaacttg catagaggtc agggatatgga tctctactgg	420
agagaaacac tcacttgccc ctcggaagac gagtatctgg agatggtggt gcacaagacc	480
ggtggactgt ttcggctggc tctgagactt atgctgtcgg tggcatcgaa acaggaggac	540
catgaaaaga tcaactttga tctcacacac cttaccgaca cactgggagt catttaccag	600
attctggatg attacctcaa cctgcagtcc acggaattga ccgagaacaa gggattctgc	660
gaagatatca gcgaaggaaa gttttcgttt ccgctgattc acagcatacg caccaaccg	720
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tacgccgtgg actacatgag aacagaaacc aagagtttcg actactgcct caagaggata	840
caggccatgt cactcaaggc aagttcgtac attgatgatc tagcagcagc tggccacgat	900
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aagtactttg aggatgcgca gtga	984

<210> 3
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 <213> Artificial Sequence

<220>
 <223> GGS1_M103I

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 Asp Thr Ala Leu Leu Gly Pro Tyr Asn Tyr Leu Ala Asn Asn Arg Gly
 20 25 30

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

Arg Ala Ile Leu His Tyr Phe Val Ser Thr Ser Asp Cys Glu Glu Arg
 305 310 315 320

Lys Tyr Phe Glu Asp Ala Gln
 325

<210> 4
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 <212> DNA
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 <223> ggs1_G309A

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 gcagcgttcg gagcggttat caaggtggac aagagcgatc tcgagaccat ttcgcacatc 180
 accaagattt tgcataactc gtcgctgctt gttgatgacg tggaagacaa ctcgatgctc 240
 cgacgaggcc tgccggcagc ccattgtctg tttggagtcc cccaaccat caactccgcc 300
 aactacatat actttgtggc tctgcaggag gtgctcaagc tcaagtctta tgatgccgtc 360
 tccattttca ccgaggaaat gatcaacttg catagaggtc agggatatgga tctctactgg 420
 agagaaacac tcacttgccc ctcggaagac gagtatctgg agatggtggt gcacaagacc 480
 ggtggactgt ttcggctggc tctgagactt atgctgtcgg tggcatcgaa acaggaggac 540
 catgaaaaga tcaactttga tctcacacac cttaccgaca cactgggagt catttaccag 600
 attctggatg attacctcaa cctgcagtcc acggaattga ccgagaacaa gggattctgc 660
 gaagatatca gcgaaggaaa gttttcgttt ccgctgattc acagcatag caccaaccgc 720
 gataaccacg agattctcaa cattctcaaa cagcgaacaa gcgacgcttc actcaaaaag 780
 tacgccgtgg actacatgag aacagaaacc aagagtttcg actactgcct caagaggata 840
 caggccatgt cactcaaggc aagttcgtac attgatgac tagcagcagc tggccacgat 900
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aagtactttg aggatgcgca gtga

984

<210> 5
<211> 327
<212> PRT
<213> Artificial Sequence

<220>
<223> GGS1_F43I

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Asp Thr Ala Leu Leu Gly Pro Tyr Asn Tyr Leu Ala Asn Asn Arg Gly
20 25 30
His Asn Ile Arg Glu His Leu Ile Ala Ala Ile Gly Ala Val Ile Lys
35 40 45
Val Asp Lys Ser Asp Leu Glu Thr Ile Ser His Ile Thr Lys Ile Leu
50 55 60
His Asn Ser Ser Leu Leu Val Asp Asp Val Glu Asp Asn Ser Met Leu
65 70 75 80
Arg Arg Gly Leu Pro Ala Ala His Cys Leu Phe Gly Val Pro Gln Thr
85 90 95
Ile Asn Ser Ala Asn Tyr Met Tyr Phe Val Ala Leu Gln Glu Val Leu
100 105 110
Lys Leu Lys Ser Tyr Asp Ala Val Ser Ile Phe Thr Glu Glu Met Ile
115 120 125
Asn Leu His Arg Gly Gln Gly Met Asp Leu Tyr Trp Arg Glu Thr Leu
130 135 140
Thr Cys Pro Ser Glu Asp Glu Tyr Leu Glu Met Val Val His Lys Thr
145 150 155 160
Gly Gly Leu Phe Arg Leu Ala Leu Arg Leu Met Leu Ser Val Ala Ser
165 170 175
Lys Gln Glu Asp His Glu Lys Ile Asn Phe Asp Leu Thr His Leu Thr
180 185 190
Asp Thr Leu Gly Val Ile Tyr Gln Ile Leu Asp Asp Tyr Leu Asn Leu

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

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 <213> Artificial Sequence

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 <223> ggs1_T127A

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gcagcgatcg gagcggttat caaggtggac aagagcgatc tcgagaccat ttcgcacatc	180
accaagattt tgcataactc gtcgctgctt gttgatgacg tggaagacaa ctcgatgctc	240
cgacgaggcc tgccggcagc ccattgtctg tttggagtcc cccaaccat caactccgcc	300
aactacatgt actttgtggc tctgcaggag gtgctcaagc tcaagtctta tgatgccgtc	360
tccattttca ccgaggaaat gatcaacttg catagaggtc agggatatga tctctactgg	420

agagaaacac tcacttgccc ctcggaagac gagtatctgg agatggtggt gcacaagacc 480
 ggtggactgt ttcggctggc tctgagactt atgctgtcgg tggcatcgaa acaggaggac 540
 catgaaaaga tcaactttga tctcacacac cttaccgaca cactgggagt catttaccag 600
 attctggatg attacctcaa cctgcagtcc acggaattga ccgagaacaa gggattctgc 660
 gaagatatca gcgaaggaaa gttttcgttt ccgctgattc acagcatacg caccaacccg 720
 gataaccacg agatttctcaa catttctcaaa cagcgaacaa gcgacgcttc actcaaaaag 780
 tacgccgtgg actacatgag aacagaaacc aagagtttcg actactgcct caagaggata 840
 caggccatgt cactcaaggc aagttcgtac attgatgatc tagcagcagc tggccacgat 900
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 aagtactttg aggatgcgca gtga 984

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

 <220>
 <223> GGS1_N29T/L90R

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

Ile Asn Ser Ala Asn Tyr Met Tyr Phe Val Ala Leu Gln Glu Val Leu
 100 105 110
 Lys Leu Lys Ser Tyr Asp Ala Val Ser Ile Phe Thr Glu Glu Met Ile
 115 120 125
 Asn Leu His Arg Gly Gln Gly Met Asp Leu Tyr Trp Arg Glu Thr Leu
 130 135 140
 Thr Cys Pro Ser Glu Asp Glu Tyr Leu Glu Met Val Val His Lys Thr
 145 150 155 160
 Gly Gly Leu Phe Arg Leu Ala Leu Arg Leu Met Leu Ser Val Ala Ser
 165 170 175
 Lys Gln Glu Asp His Glu Lys Ile Asn Phe Asp Leu Thr His Leu Thr
 180 185 190
 Asp Thr Leu Gly Val Ile Tyr Gln Ile Leu Asp Asp Tyr Leu Asn Leu
 195 200 205
 Gln Ser Thr Glu Leu Thr Glu Asn Lys Gly Phe Cys Glu Asp Ile Ser
 210 215 220
 Glu Gly Lys Phe Ser Phe Pro Leu Ile His Ser Ile Arg Thr Asn Pro
 225 230 235 240
 Asp Asn His Glu Ile Leu Asn Ile Leu Lys Gln Arg Thr Ser Asp Ala
 245 250 255
 Ser Leu Lys Lys Tyr Ala Val Asp Tyr Met Arg Thr Glu Thr Lys Ser
 260 265 270
 Phe Asp Tyr Cys Leu Lys Arg Ile Gln Ala Met Ser Leu Lys Ala Ser
 275 280 285
 Ser Tyr Ile Asp Asp Leu Ala Ala Ala Gly His Asp Val Ser Lys Leu
 290 295 300
 Arg Ala Ile Leu His Tyr Phe Val Ser Thr Ser Asp Cys Glu Glu Arg
 305 310 315 320
 Lys Tyr Phe Glu Asp Ala Gln
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<210> 8
 <211> 984
 <212> DNA
 <213> Artificial Sequence

<220>

<223> ggs1_A86C_T269G

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gcagcgttcg gagcggttat caaggtggac aagagcgatc tcgagaccat ttcgcacatc	180
accaagattt tgcataactc gtcgctgctt gttgatgacg tggaagacaa ctcgatgctc	240
cgacgaggcc tgccggcagc ccattgtcgg tttggagtcc cccaaaccat caactccgcc	300
aactacatgt actttgtggc tctgcaggag gtgctcaagc tcaagtctta tgatgccgtc	360
tccattttca ccgaggaaat gatcaacttg catagaggtc agggatatgga tctctactgg	420
agagaaacac tcacttgccc ctcggaagac gagtatctgg agatggtggt gcacaagacc	480
ggtggactgt ttcggctggc tctgagactt atgctgtcgg tggcatcgaa acaggaggac	540
catgaaaaga tcaactttga tctcacacac cttaccgaca cactgggagt catttaccag	600
attctggatg attacctcaa cctgcagtcc acggaattga ccgagaacaa gggattctgc	660
gaagatatca gcgaaggaaa gttttcgttt ccgctgattc acagcatagc caccaaccgc	720
gataaccacg agattctcaa cattctcaaa cagcgaacaa gcgacgcttc actcaaaaag	780
tacgccgtgg actacatgag aacagaaacc aagagtttcg actactgcct caagaggata	840
caggccatgt cactcaaggc aagttcgtac attgatgatc tagcagcagc tggccacgat	900
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aagtactttg aggatgcgca gtga	984

<210> 9

<211> 327

<212> PRT

<213> Artificial Sequence

<220>

<223> GGS1_N29T

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

	260		265		270										
Phe	Asp	Tyr	Cys	Leu	Lys	Arg	Ile	Gln	Ala	Met	Ser	Leu	Lys	Ala	Ser
	275						280					285			
Ser	Tyr	Ile	Asp	Asp	Leu	Ala	Ala	Ala	Gly	His	Asp	Val	Ser	Lys	Leu
	290					295					300				
Arg	Ala	Ile	Leu	His	Tyr	Phe	Val	Ser	Thr	Ser	Asp	Cys	Glu	Glu	Arg
305					310					315					320
Lys	Tyr	Phe	Glu	Asp	Ala	Gln									
				325											

<210> 10
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 <212> DNA
 <213> Artificial Sequence

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 <223> ggs1_A86C

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gcagcgttcg gagcggttat caaggtggac aagagcgatc tcgagaccat ttcgcacatc	180
accaagattt tgcataactc gtcgctgctt gttgatgacg tggaagacaa ctcatgctc	240
cgacgaggcc tgccggcagc ccattgtctg tttggagtcc cccaaccat caactccgcc	300
aactacatgt actttgtggc tctgcaggag gtgctcaagc tcaagtctta tgatgccgtc	360
tccattttca ccgaggaaat gatcaacttg catagaggtc agggatatgga tctctactgg	420
agagaaacac tcacttgccc ctcggaagac gagtatctgg agatggtggt gcacaagacc	480
ggtggactgt ttcggctggc tctgagactt atgctgtcgg tggcatcgaa acaggaggac	540
catgaaaaga tcaactttga tctcacacac cttaccgaca cactgggagt catttaccag	600
attctggatg attacctcaa cctgcagtcc acggaattga ccgagaacaa gggattctgc	660
gaagatatca gcgaaggaaa gttttcgttt ccgctgattc acagcatacg caccaaccgc	720
gataaccacg agatttctaa catttctaaa cagcgaacaa gcgacgcttc actcaaaaag	780

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 aagtactttg aggatgca gtga 984

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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> GGS1_L90R

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

Gly Gly Leu Phe Arg Leu Ala Leu Arg Leu Met Leu Ser Val Ala Ser
 165 170 175
 Lys Gln Glu Asp His Glu Lys Ile Asn Phe Asp Leu Thr His Leu Thr
 180 185 190
 Asp Thr Leu Gly Val Ile Tyr Gln Ile Leu Asp Asp Tyr Leu Asn Leu
 195 200 205
 Gln Ser Thr Glu Leu Thr Glu Asn Lys Gly Phe Cys Glu Asp Ile Ser
 210 215 220
 Glu Gly Lys Phe Ser Phe Pro Leu Ile His Ser Ile Arg Thr Asn Pro
 225 230 235 240
 Asp Asn His Glu Ile Leu Asn Ile Leu Lys Gln Arg Thr Ser Asp Ala
 245 250 255
 Ser Leu Lys Lys Tyr Ala Val Asp Tyr Met Arg Thr Glu Thr Lys Ser
 260 265 270
 Phe Asp Tyr Cys Leu Lys Arg Ile Gln Ala Met Ser Leu Lys Ala Ser
 275 280 285
 Ser Tyr Ile Asp Asp Leu Ala Ala Ala Gly His Asp Val Ser Lys Leu
 290 295 300
 Arg Ala Ile Leu His Tyr Phe Val Ser Thr Ser Asp Cys Glu Glu Arg
 305 310 315 320
 Lys Tyr Phe Glu Asp Ala Gln
 325

<210> 12
 <211> 984
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ggs1_T269G

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 gcagcgttcg gagcggttat caaggtggac aagagcgatc tcgagaccat ttcgcacatc 180

accaagattt tgcataactc gtcgctgctt gttgatgacg tggaagacaa ctcgatgctc 240
 cgacgaggcc tgccggcagc ccattgtcgg tttggagtcc cccaaaccat caactccgcc 300
 aactacatgt actttgtggc tctgcaggag gtgctcaagc tcaagtctta tgatgccgtc 360
 tccattttca ccgaggaaat gatcaacttg catagaggtc agggatatgga tctctactgg 420
 agagaaacac tcacttgccc ctcggaagac gagtatctgg agatgggtgg gcacaagacc 480
 ggtggactgt ttcggctggc tctgagactt atgctgtcgg tggcatcgaa acaggaggac 540
 catgaaaaga tcaactttga tctcacacac cttaccgaca cactgggagt catttaccag 600
 attctggatg attacctcaa cctgcagtcc acggaattga ccgagaacaa gggattctgc 660
 gaagatatca gcgaaggaaa gttttcgttt ccgctgattc acagcatacg caccaacccg 720
 gataaccacg agatttctcaa catttctaaa cagcgaacaa gcgacgcttc actcaaaaag 780
 tacgccgtgg actacatgag aacagaaacc aagagtttcg actactgcct caagaggata 840
 caggccatgt cactcaaggc aagttcgtac attgatgac tagcagcagc tggccacgat 900
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 aagtactttg aggatgcgca gtga 984

<210> 13
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<220>
 <223> GGS1_I122V/R141K

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 20 25 30
 His Asn Ile Arg Glu His Leu Ile Ala Ala Phe Gly Ala Val Ile Lys
 35 40 45
 Val Asp Lys Ser Asp Leu Glu Thr Ile Ser His Ile Thr Lys Ile Leu
 50 55 60

His Asn Ser Ser Leu Leu Val Asp Asp Val Glu Asp Asn Ser Met Leu
 65 70 75 80
 Arg Arg Gly Leu Pro Ala Ala His Cys Leu Phe Gly Val Pro Gln Thr
 85 90 95
 Ile Asn Ser Ala Asn Tyr Met Tyr Phe Val Ala Leu Gln Glu Val Leu
 100 105 110
 Lys Leu Lys Ser Tyr Asp Ala Val Ser Val Phe Thr Glu Glu Met Ile
 115 120 125
 Asn Leu His Arg Gly Gln Gly Met Asp Leu Tyr Trp Lys Glu Thr Leu
 130 135 140
 Thr Cys Pro Ser Glu Asp Glu Tyr Leu Glu Met Val Val His Lys Thr
 145 150 155 160
 Gly Gly Leu Phe Arg Leu Ala Leu Arg Leu Met Leu Ser Val Ala Ser
 165 170 175
 Lys Gln Glu Asp His Glu Lys Ile Asn Phe Asp Leu Thr His Leu Thr
 180 185 190
 Asp Thr Leu Gly Val Ile Tyr Gln Ile Leu Asp Asp Tyr Leu Asn Leu
 195 200 205
 Gln Ser Thr Glu Leu Thr Glu Asn Lys Gly Phe Cys Glu Asp Ile Ser
 210 215 220
 Glu Gly Lys Phe Ser Phe Pro Leu Ile His Ser Ile Arg Thr Asn Pro
 225 230 235 240
 Asp Asn His Glu Ile Leu Asn Ile Leu Lys Gln Arg Thr Ser Asp Ala
 245 250 255
 Ser Leu Lys Lys Tyr Ala Val Asp Tyr Met Arg Thr Glu Thr Lys Ser
 260 265 270
 Phe Asp Tyr Cys Leu Lys Arg Ile Gln Ala Met Ser Leu Lys Ala Ser
 275 280 285
 Ser Tyr Ile Asp Asp Leu Ala Ala Ala Gly His Asp Val Ser Lys Leu
 290 295 300
 Arg Ala Ile Leu His Tyr Phe Val Ser Thr Ser Asp Cys Glu Glu Arg
 305 310 315 320
 Lys Tyr Phe Glu Asp Ala Gln

<210> 14
 <211> 984
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ggs1_A364G_G422A

<400> 14
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 gcagcgttcg gagcggttat caaggtggac aagagcgatc tcgagaccat ttcgcacatc 180
 accaagattt tgcataactc gtcgctgctt gttgatgacg tggaagacaa ctcgatgctc 240
 cgacgaggcc tgccggcagc ccattgtctg tttggagtcc cccaaaccat caactccgcc 300
 aactacatgt actttgtggc tctgcaggag gtgctcaagc tcaagtctta tgatgccgtc 360
 tccgttttca ccgaggaaat gatcaacttg catagaggtc agggatatgga tctctactgg 420
 aaagaaacac tcacttgccc ctcggaagac gagtatctgg agatggtggt gcacaagacc 480
 ggtggactgt ttcggctggc tctgagactt atgctgtcgg tggcatcgaa acaggaggac 540
 catgaaaaga tcaactttga tctcacacac cttaccgaca cactgggagt catttaccag 600
 attctggatg attacctcaa cctgcagtcc acggaattga ccgagaacaa gggattctgc 660
 gaagatatca gcgaaggaaa gttttcgttt ccgctgattc acagcatacg caccaaccg 720
 gataaccacg agatttctaa catttctaaa cagcgaacaa gcgacgcttc actcaaaaag 780
 tacgccgtgg actacatgag aacagaaacc aagagtttcg actactgcct caagaggata 840
 caggccatgt cactcaaggc aagttcgtac attgatgatc tagcagcagc tggccacgat 900
 gtctccaagc tacgagccat tttgcattat tttgtgtcca cctctgactg tgaggagaga 960
 aagtactttg aggatgcgca gtga 984

<210> 15
 <211> 327

<212> PRT
<213> Artificial Sequence

<220>
<223> GGS1_I122V

<400> 15
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1 5 10 15
Asp Thr Ala Leu Leu Gly Pro Tyr Asn Tyr Leu Ala Asn Asn Arg Gly
20 25 30
His Asn Ile Arg Glu His Leu Ile Ala Ala Phe Gly Ala Val Ile Lys
35 40 45
Val Asp Lys Ser Asp Leu Glu Thr Ile Ser His Ile Thr Lys Ile Leu
50 55 60
His Asn Ser Ser Leu Leu Val Asp Asp Val Glu Asp Asn Ser Met Leu
65 70 75 80
Arg Arg Gly Leu Pro Ala Ala His Cys Leu Phe Gly Val Pro Gln Thr
85 90 95
Ile Asn Ser Ala Asn Tyr Met Tyr Phe Val Ala Leu Gln Glu Val Leu
100 105 110
Lys Leu Lys Ser Tyr Asp Ala Val Ser Val Phe Thr Glu Glu Met Ile
115 120 125
Asn Leu His Arg Gly Gln Gly Met Asp Leu Tyr Trp Arg Glu Thr Leu
130 135 140
Thr Cys Pro Ser Glu Asp Glu Tyr Leu Glu Met Val Val His Lys Thr
145 150 155 160
Gly Gly Leu Phe Arg Leu Ala Leu Arg Leu Met Leu Ser Val Ala Ser
165 170 175
Lys Gln Glu Asp His Glu Lys Ile Asn Phe Asp Leu Thr His Leu Thr
180 185 190
Asp Thr Leu Gly Val Ile Tyr Gln Ile Leu Asp Asp Tyr Leu Asn Leu
195 200 205
Gln Ser Thr Glu Leu Thr Glu Asn Lys Gly Phe Cys Glu Asp Ile Ser
210 215 220

Glu Gly Lys Phe Ser Phe Pro Leu Ile His Ser Ile Arg Thr Asn Pro
 225 230 235 240
 Asp Asn His Glu Ile Leu Asn Ile Leu Lys Gln Arg Thr Ser Asp Ala
 245 250 255
 Ser Leu Lys Lys Tyr Ala Val Asp Tyr Met Arg Thr Glu Thr Lys Ser
 260 265 270
 Phe Asp Tyr Cys Leu Lys Arg Ile Gln Ala Met Ser Leu Lys Ala Ser
 275 280 285
 Ser Tyr Ile Asp Asp Leu Ala Ala Ala Gly His Asp Val Ser Lys Leu
 290 295 300
 Arg Ala Ile Leu His Tyr Phe Val Ser Thr Ser Asp Cys Glu Glu Arg
 305 310 315 320
 Lys Tyr Phe Glu Asp Ala Gln
 325

<210> 16
 <211> 984
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> ggs1_A364G

<400> 16
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 gcagcgttcg gagcggttat caaggtggac aagagcgatc tcgagaccat ttcgcacatc 180
 accaagattt tgcataactc gtcgctgctt gttgatgacg tggaagacaa ctcgatgctc 240
 cgacgaggcc tgccggcagc ccattgtctg tttggagtcc cccaaccat caactccgcc 300
 aactacatgt actttgtggc tctgcaggag gtgctcaagc tcaagtctta tgatgccgtc 360
 tccgttttca ccgaggaaat gatcaacttg catagaggtc agggatatgga tctctactgg 420
 agagaaacac tcacttgccc ctcggaagac gagtatctgg agatggtggt gcacaagacc 480
 ggtggactgt ttcggctggc tctgagactt atgctgtcgg tggcatcgaa acaggaggac 540

catgaaaaga tcaactttga tctcacacac cttaccgaca cactgggagt catttaccag 600
attctggatg attacctcaa cctgcagtcc acggaattga ccgagaacaa gggattctgc 660
gaagatatca gcgaaggaaa gttttcgttt ccgctgattc acagcatacg caccaaccgc 720
gataaccacg agatttctcaa catttctcaaa cagcgaacaa gcgacgcttc actcaaaaag 780
tacgccgtgg actacatgag aacagaaacc aagagtttcg actactgcct caagaggata 840
caggccatgt cactcaaggc aagttcgtac attgatgadc tagcagcagc tggccacgat 900
gtctccaagc tacgagccat tttgcattat tttgtgtcca cctctgactg tgaggagaga 960
aagtactttg aggatgacga gtga 984

<210> 17
<211> 327
<212> PRT
<213> Artificial Sequence

<220>
<223> GGS1_R141K

<400> 17
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Asp Thr Ala Leu Leu Gly Pro Tyr Asn Tyr Leu Ala Asn Asn Arg Gly
20 25 30
His Asn Ile Arg Glu His Leu Ile Ala Ala Phe Gly Ala Val Ile Lys
35 40 45
Val Asp Lys Ser Asp Leu Glu Thr Ile Ser His Ile Thr Lys Ile Leu
50 55 60
His Asn Ser Ser Leu Leu Val Asp Asp Val Glu Asp Asn Ser Met Leu
65 70 75 80
Arg Arg Gly Leu Pro Ala Ala His Cys Leu Phe Gly Val Pro Gln Thr
85 90 95
Ile Asn Ser Ala Asn Tyr Met Tyr Phe Val Ala Leu Gln Glu Val Leu
100 105 110
Lys Leu Lys Ser Tyr Asp Ala Val Ser Ile Phe Thr Glu Glu Met Ile
115 120 125

Asn Leu His Arg Gly Gln Gly Met Asp Leu Tyr Trp Lys Glu Thr Leu
 130 135 140
 Thr Cys Pro Ser Glu Asp Glu Tyr Leu Glu Met Val Val His Lys Thr
 145 150 155 160
 Gly Gly Leu Phe Arg Leu Ala Leu Arg Leu Met Leu Ser Val Ala Ser
 165 170 175
 Lys Gln Glu Asp His Glu Lys Ile Asn Phe Asp Leu Thr His Leu Thr
 180 185 190
 Asp Thr Leu Gly Val Ile Tyr Gln Ile Leu Asp Asp Tyr Leu Asn Leu
 195 200 205
 Gln Ser Thr Glu Leu Thr Glu Asn Lys Gly Phe Cys Glu Asp Ile Ser
 210 215 220
 Glu Gly Lys Phe Ser Phe Pro Leu Ile His Ser Ile Arg Thr Asn Pro
 225 230 235 240
 Asp Asn His Glu Ile Leu Asn Ile Leu Lys Gln Arg Thr Ser Asp Ala
 245 250 255
 Ser Leu Lys Lys Tyr Ala Val Asp Tyr Met Arg Thr Glu Thr Lys Ser
 260 265 270
 Phe Asp Tyr Cys Leu Lys Arg Ile Gln Ala Met Ser Leu Lys Ala Ser
 275 280 285
 Ser Tyr Ile Asp Asp Leu Ala Ala Ala Gly His Asp Val Ser Lys Leu
 290 295 300
 Arg Ala Ile Leu His Tyr Phe Val Ser Thr Ser Asp Cys Glu Glu Arg
 305 310 315 320
 Lys Tyr Phe Glu Asp Ala Gln
 325

<210> 18
 <211> 984
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ggs1_G422A

<400> 18
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gcagcgttcg gagcggttat caaggtggac aagagcgatc tcgagaccat ttcgcacatc 180
accaagattt tgcataactc gtcgctgctt gttgatgacg tggaagacaa ctcgatgctc 240
cgacgaggcc tgccggcagc ccattgtctg tttggagtcc cccaaaccat caactccgcc 300
aactacatgt actttgtggc tctgcaggag gtgctcaagc tcaagtctta tgatgccgtc 360
tccattttca ccgaggaaat gatcaacttg catagaggtc agggatatgga tctctactgg 420
aaagaaacac tcacttgccc ctcggaagac gagtatctgg agatgggtgg gcacaagacc 480
gggtggactgt ttcggctggc tctgagactt atgctgtcgg tggcatcgaa acaggaggac 540
catgaaaaga tcaactttga tctcacacac cttaccgaca cactgggagt catttaccag 600
attctggatg attacctcaa cctgcagtcc acggaattga ccgagaacaa gggattctgc 660
gaagatatca gcgaaggaaa gttttcgttt ccgctgattc acagcatagc caccaacccg 720
gataaccacg agatttctaa catttctaaa cagcgaacaa gcgacgcttc actcaaaaag 780
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caggccatgt cactcaaggc aagttcgtac attgatgatc tagcagcagc tggccacgat 900
gtctccaagc tacgagccat tttgcattat tttgtgtcca cctctgactg tgaggagaga 960
aagtactttg aggatgcgca gtga 984

<210> 19
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 19
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<210> 20

<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 20
gaatgtaagc gtgacataac taattacatg aggtaccta ctgcgcatcc tcaaagtac 59

<210> 21
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 21
gaggcccttt cgtcttcaag aattcgagtt tggcgcccg 40

<210> 22
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 22
tgacataact aattacatga ggtaccgat ctttttgat ctgcttaatt aatgctgtag 60

60

<210> 23
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 23

ctacagcatt aattaagcag atccaaaagg atccggtacc tcatgtaatt agttatgtca 60

60

<210> 24
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 24
agtcagacag atactcgtcg cggccgcggc gcgccgcaaa ttaaagcctt cgagc 55

<210> 25
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 25
gctcgaaggc tttaatttgc ggcgcgccgc ggccgcgacg agtatctgtc tgact 55

<210> 26
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 26
acgggcgcca aactcgaatt cttgaagacg aaagggcctc 40

<210> 27
<211> 2019
<212> DNA
<213> Artificial Sequence

<220>

<223> X. dendrorhous crtYB

<400> 27

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ctcggcctgc tcacttcccc gattttgaca aaatttgaca tctacaaaat atcgatcctc	120
gtattttattg cgtttagtgc aaccacacca tgggactcat ggatcatcag aaatggcgca	180
tggacatatc catcagcgga gagtggccaa ggcgtgtttg gaacgtttct agatgttcca	240
tatgaagagt acgctttctt tgtcattcaa accgtaatca ccggcttggt ctacgtcttg	300
gcaactaggc accttctccc atctctcgcg cttcccaaga ctagatcgtc cgccctttct	360
ctcgcgctca aggcgctcat ccctctgccc attatctacc tatttaccgc tcaccccagc	420
ccatcgcccg acccgctcgt gacagatcac tacttctaca tgcgggcact ctccttactc	480
atcacccac ctacatgct cttggcagca ttatcaggcg aatatgcttt cgattggaaa	540
agtggccgag caaagtcaac tattgcagca atcatgatcc cgacggtgta tctgatttgg	600
gtagattatg ttgctgtcgg tcaagactct tggtcgatca acgatgagaa gattgtaggg	660
tggaggcttg gaggtgtact acccattgag gaagctatgt tcttcttact gacgaatcta	720
atgattgttc tgggtctgtc tgcctgcgat catactcagg ccctatacct gctacacggt	780
cgaactatth atggcaacaa aaagatgcca tcttcatttc ccctcattac accgcctgtg	840
ctctccctgt tttttagcag ccgaccatac tcttctcagc caaaacgtga cttggaactg	900
gcagtcaagt tgttgaggga aaagagccgg agcttttttg ttgcctcggc tggatttcct	960
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atcgactctc ctgaagtatc ttccaacccg catgccacaa ttgacatggt ctccgatttt	1080
cttaccctac tatttgggcc cccgctacac ctttcgcaac ctgacaagat cttttcttcg	1140
cctttacttc ctccttcgca cccttcccga cccacgggaa tgtatcccct cccgcctcct	1200
ccttcgctct cgcctgccga gctcgttcaa ttccttaccg aaagggttcc cgttcaatac	1260
catttcgcct tcaggttgct cgctaagttg caagggtga tccctcgata cccactcgac	1320
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gctcgggaaga cgcctatcga gaccacagct gacttgctgg actatggtct atgtgtagca	1440
ggctcagtcg ccgagctatt ggtctatgtc tcttgggcaa gtgcaccaag tcaggtccct	1500
gccaccatag aagaaagaga agctgtgtta gtggcaagcc gagagatggg aactgccctt	1560
cagttggtga acattgctag ggacattaaa ggggacgcaa cagaaggag attttaccta	1620
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gcctacgcag aggatcttgc caaacattct tataaggga ttgaccgact tcctaccgag	1860
gttcaagcgg gaatgcgagc ggcttgcgcg agctacctac tgatcggccg agagatcaaa	1920
gtcgtttgga aaggagacgt cggagagaga aggacagttg ccggatggag gagagtacgg	1980
aaagtcttga gtgtggtcat gagcggatgg gaagggcag	2019

<210> 28
 <211> 1966
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> X. dendrorhous crtI

<400> 28	
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aacgactact ccggaggctc atgctcttta atcgagcgag atggttatcg attcgatcag	180
gggcccagtt tgctgctctt gccagatctc ttcaagcaga cattcgaaga tttgggagag	240
aagatggaag attgggtcga tctcatcaag tgtgaacca actatgtttg ccacttcac	300
gatgaagaga ctttcactct ttcaaccgac atggcggttg tcaagcggga agtcgagcgt	360
tttgaaggca aagatggatt tgatcggttc ttgtcgttta tccaagaagc ccacagacat	420
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cggctacagt tcattggcca aatcctggct cttcaccctc tcgagtctat ctggacaaga	540

gtttgtcgat atttcaagac cgacagatta cgaagagtct tctcgtttgc agtgatgtac	600
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accgagggca tctggtatcc gagaggaggc ttttggcagg ttcctaatac tcttcttcag	720
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cacgccgatg ttgtgattgt caatgctgac ctcgtttacg cctccgagca cttgattcct	900
gacgatgcca gaaacaagat tggccaactg ggtgaagtca agagaagttg gtgggctgac	960
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gttccctcgc gaatcgatcc ttctgccgct cccgaaggca aagatgctat cgtcattctt	1200
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gaccgatccc cagctccaga tcccaatatg tcaactctcg taccatatgg aaaacctctc	1620
aaatcaaatg gaacgggtat cgattctcag gtccagctga agttcatgga tttggagaga	1680
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tcagagtcac acccggtctc tcaacgtccg tttgagggtc agacaattgt tagtctcgaa	1920
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<210> 29
 <211> 2830
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TEFINtp-crtYB-CYC1t

<400> 29
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 aacctcccc ggttcccaca cttgccgtta agggcgtagg gtactgcagt ctggaatcta 180
 cgcttggtca gactttgtac tagtttcttt gtctggccat cgggtaacc catgccggac 240
 gcaaaataga ctactgaaaa tttttttgct ttgtggttgg gactttagcc aagggtataa 300
 aagaccaccg tccccgaatt acctttctc ttcttttctc tctctccttg tcaactcaca 360
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 acacaagacg ccacgtcatc cgaccagcac tttttgcagt actaaccgca gacggctctc 540
 gcatattacc agatccatct gatctatact ctcccaattc ttggtcttct cggctctgctc 600
 acttccccga ttttgacaaa atttgacatc taaaaaatat cgatcctcgt atttattgagc 660
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gggtgtactac ccattgagga agctatgttc ttcttactga cgaatctaata gattgttctg	1260
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ccttcgcacc cttcccgacc cacgggaatg tatcccctcc cgcctcctcc ttcgctctcg	1740
cctgccgagc tcgttcaatt ccttaccgaa agggttcccg ttcaatacca tttcgcttc	1800
agggtgctcg ctaagttgca agggctgac cctcgatacc cactcgacga actccttaga	1860
ggatacacca ctgatcttat ctttccttta tcgacagagg cagtccaggc tcggaagacg	1920
cctatcgaga ccacagctga cttgctggac tatggcttat gtgtagcagg ctcagtcgcc	1980
gagctattgg tctatgtctc ttgggcaagt gcaccaagtc aggtccctgc caccatagaa	2040
gaaagagaag ctgtgttagt ggcaagccga gagatgggaa ctgcccttca gttggtgaac	2100
attgctaggg acattaaagg ggacgcaaca gaaggagat tttacctacc actctcattc	2160
tttggctctc gggatgaatc aaagcttgcg atcccactg attggacgga acctcggcct	2220
caagatttcg acaaaactcct cagtctatct ccttcgtcca cattaccatc ttcaaagccc	2280
tcagaaagct tccggttcga atggaagacg tactcgcttc cattagtcgc ctacgcagag	2340
gatcttgcca aacattctta taagggaatt gaccgacttc ctaccgaggt tcaagcggga	2400
atgcgagcgg cttgcgcgag ctacctactg atcggccgag agatcaaagt cgtttgga	2460
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ttcaaat	ttttttt	ctgtacagac	gcgtgtacgc	atgtaacatt	atactgaaaa	2760
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<220>
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cggcgagagc	ccccttctcc	ccacatatca
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agggcgtagg	gtactgcagt	ctggaatcta
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gtctggccat	cgggtaacc	catgccggac
		240
gcaaaataga	ctactgaaaa	tttttttgct
ttgtggttgg	gacttttagcc	aagggtataa
		300
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ttcttttctc	tctctccttg	tcaactcaca
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cccgaatcg	ttaagcattt	ccttctgagt
ataagaatca	ttcaaatgg	tgagtttcag
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<220>
 <223> Primer

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<210> 33
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<400> 33	
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<210> 34
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<400> 35
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<210> 36
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<400> 36
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<400> 37
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<220>
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<400> 38
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<210> 39
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<220>
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<400> 39
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<210> 40
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<220>
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<400> 40
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<210> 41
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<220>
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<400> 41
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<210> 42
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<223> Primer

<400> 42

agtctcctct tcaccaccaa aagcggacta cgagaaggac gccg

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<210> 43

<211> 30

<212> DNA

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<220>

<223> Primer

<400> 43

ccactcgtca ccaacagtgc cgtgtgttgc

30

<210> 44

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 44

tcgtacgtct ataccaacag atgg

24

<210> 45

<211> 24

<212> DNA

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<220>

<223> Primer

<400> 45

cgcatacaca cacactgccg gggg

24

<210> 46

<211> 550
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 aataacatca actgtgggtc ttcaacaggc ctaaggaacg aaacaagccg gaccaagatc 240
 aggttcaagg tgagtactga gaaggaatag aaggcctaaa ggcgcaaacc gacaggtggc 300
 aacagctcca caccgaccac gaaggccacg aaatcaaggg gtcctaaagt tagtctttgt 360
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 actaacacag 550

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<220>
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<400> 47
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<210> 48
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<220>
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<400> 48
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<400> 49
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<210> 50
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<220>
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<400> 50
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<210> 51
<211> 42
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<220>
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<400> 51
ctttttgcag tactaaccgc agtgcctcct gtctgactcg tc 42

<210> 52
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<210> 53
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<220>
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<400> 53
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<400> 56

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<210> 57

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<220>

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<400> 57

gctgtctctg cgagagcacg tcga

24

<210> 58

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<400> 58

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<211> 19

<212> DNA

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<220>

<223> Primer

<400> 59

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19

<210> 60

<211> 20
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<220>
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<400> 60
aaagccagca atgacgttgc 20

<210> 61
<211> 40
<212> DNA
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<220>
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<400> 61
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<211> 40
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<220>
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<220>
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<210> 64
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<210> 66
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<400> 67

gggtatggat ctctactgga aagaaacact cacttgcccc 40

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<220>
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 aggcagcagc aattgccacg ggctttgagc acacggccgg gtgtggtccc attcccatcg 480
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<220>
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<400> 70
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<210> 71
 <211> 41
 <212> DNA
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<220>
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<400> 71
 gcgccgcaaa cccgggtctct gagatttgcc acccaacgtc g 41

<210> 72
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<220>
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<400> 72
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<210> 73
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<220>
 <223> Primer

<400> 73
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<210> 74
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<213> Artificial Sequence

<220>

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<400> 74

ctttttgcag tactaaccgc agtgcctcct gtctgactcg tc

42

<210> 75

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<211> 21

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<400> 77

taacctggtc aaataccaat g

21

<210> 78

<211> 43
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<400> 78
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<210> 79
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<400> 79
gaaatccgcg ctgttataat cctgcggtta gtactgcaaa a 41

<210> 80
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<220>
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<400> 80
atctcttcta gatagatgcc t 21

<210> 81
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<400> 82
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<400> 83
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<210> 84
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<400> 84
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<210> 85
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<400> 85

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<210> 86
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<400> 86
cccagtcaca ataccaccag attataacag cgcggatttc 40

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<210> 88
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<220>
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<400> 88
cattgggtatt tgaccagggtt atgcctcctg tctgactcgt c 41

<210> 89
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<400> 89
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<210> 90
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<212> DNA
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<220>
<223> Primer

<400> 90
attggtatatt gaccaggta caagttgta caattgttga 40

<210> 91
<211> 21
<212> DNA
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<220>
<223> Primer

<400> 91
tgaaagtcct ggaagcagta c 21