

F1_001_Sequence_listing
SEQUENCE LISTING

<110> F1 Oncology, Inc.
F1 Oncology, SEZC

<120> METHODS AND COMPOSITIONS FOR TRANSDUCING LYMPHOCYTES AND
REGULATED EXPANSION THEREOF

<130> F1.001.W0.01

<140> Not yet assigned

<141> 2017-03-18

<150> 62/467,039

<151> 2017-03-03

<150> 62/390,093

<151> 2016-03-19

<150> 62/360,041

<151> 2016-07-08

<160> 255

<170> PatentIn version 3.5

<210> 1

<211> 42

<212> PRT

<213> Homo sapiens

<400> 1

Lys	Arg	Gly	Arg	Lys	Lys	Leu	Leu	Tyr	Ile	Phe	Lys	Gln	Pro	Phe	Met
1				5					10					15	

Arg	Pro	Val	Gln	Thr	Thr	Gln	Glu	Glu	Asp	Gly	Cys	Ser	Cys	Arg	Phe
			20				25						30		

Pro	Glu	Glu	Glu	Glu	Gly	Gly	Cys	Glu	Leu
		35					40		

<210> 2

<211> 41

<212> PRT

F1_001_Sequence_listing

<213> Homo sapiens

<400> 2

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
1 5 10 15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
20 25 30

Pro Arg Asp Phe Ala Ala Tyr Arg Ser
35 40

<210> 3

<211> 41

<212> PRT

<213> Homo sapiens

<400> 3

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
1 5 10 15

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Ala Tyr Ala Ala
20 25 30

Ala Arg Asp Phe Ala Ala Tyr Arg Ser
35 40

<210> 4

<211> 35

<212> PRT

<213> Homo sapiens

<400> 4

Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro Asn Gly Glu Tyr
1 5 10 15

Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser Arg Leu Thr Asp
20 25 30

F1_001_Sequence_listing

Val Thr Leu
35

<210> 5
<211> 37
<212> PRT
<213> Homo sapiens

<400> 5

Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
1 5 10 15

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
20 25 30

Thr Leu Ala Lys Ile
35

<210> 6
<211> 49
<212> PRT
<213> Homo sapiens

<400> 6

His Gln Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser Pro Val Glu
1 5 10 15

Pro Ala Glu Pro Cys Arg Tyr Ser Cys Pro Arg Glu Glu Glu Gly Ser
20 25 30

Thr Ile Pro Ile Gln Glu Asp Tyr Arg Lys Pro Glu Pro Ala Cys Ser
35 40 45

Pro

F1_001_Sequence_listing

<210> 7
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 7

Cys Cys Leu Arg Arg His Gln Gly Lys Gln Asn Glu Leu Ser Asp Thr
 1 5 10 15

Ala Gly Arg Glu Ile Asn Leu Val Asp Ala His Leu Lys Ser Glu Gln
 20 25 30

Thr Glu Ala Ser Thr Arg Gln Asn Ser Gln Val Leu Leu Ser Glu Thr
 35 40 45

Gly Ile Tyr Asp Asn Asp Pro Asp Leu Cys Phe Arg Met Gln Glu Gly
 50 55 60

Ser Glu Val Tyr Ser Asn Pro Cys Leu Glu Glu Asn Lys Pro Gly Ile
 65 70 75 80

Val Tyr Ala Ser Leu Asn His Ser Val Ile Gly Pro Asn Ser Arg Leu
 85 90 95

Ala Arg Asn Val Lys Glu Ala Pro Thr Glu Tyr Ala Ser Ile Cys Val
 100 105 110

Arg Ser

<210> 8
 <211> 187
 <212> PRT
 <213> Homo sapiens

<400> 8

Arg Arg Ala Cys Arg Lys Arg Ile Arg Gln Lys Leu His Leu Cys Tyr
 1 5 10 15

F1_001_Sequence_listing

Pro Val Gln Thr Ser Gln Pro Lys Leu Glu Leu Val Asp Ser Arg Pro
20 25 30

Arg Arg Ser Ser Thr Gln Leu Arg Ser Gly Ala Ser Val Thr Glu Pro
35 40 45

Val Ala Glu Glu Arg Gly Leu Met Ser Gln Pro Leu Met Glu Thr Cys
50 55 60

His Ser Val Gly Ala Ala Tyr Leu Glu Ser Leu Pro Leu Gln Asp Ala
65 70 75 80

Ser Pro Ala Gly Gly Pro Ser Ser Pro Arg Asp Leu Pro Glu Pro Arg
85 90 95

Val Ser Thr Glu His Thr Asn Asn Lys Ile Glu Lys Ile Tyr Ile Met
100 105 110

Lys Ala Asp Thr Val Ile Val Gly Thr Val Lys Ala Glu Leu Pro Glu
115 120 125

Gly Arg Gly Leu Ala Gly Pro Ala Glu Pro Glu Leu Glu Glu Glu Leu
130 135 140

Glu Ala Asp His Thr Pro His Tyr Pro Glu Gln Glu Thr Glu Pro Pro
145 150 155 160

Leu Gly Ser Cys Ser Asp Val Met Leu Ser Val Glu Glu Glu Gly Lys
165 170 175

Glu Asp Pro Leu Pro Thr Ala Ala Ser Gly Lys
180 185

<210> 9

<211> 54

F1_001_Sequence_listing

<212> PRT

<213> Homo sapiens

<400> 9

His Ile Trp Gln Leu Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln
1 5 10 15

Leu Leu Leu Glu Val Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln
20 25 30

Phe Pro Glu Glu Glu Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg
35 40 45

Leu Gly Asp Leu Trp Val
50

<210> 10

<211> 60

<212> PRT

<213> Homo sapiens

<400> 10

Cys Val Lys Arg Arg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val
1 5 10 15

Ser Val Gln Arg Lys Arg Gln Glu Ala Glu Gly Glu Ala Thr Val Ile
20 25 30

Glu Ala Leu Gln Ala Pro Pro Asp Val Thr Thr Val Ala Val Glu Glu
35 40 45

Thr Ile Pro Ser Phe Thr Gly Arg Ser Pro Asn His
50 55 60

<210> 11

<211> 163

<212> PRT

<213> Homo sapiens

F1_001_Sequence_listing

<400> 11

Met Lys Trp Lys Ala Leu Phe Thr Ala Ala Ile Leu Gln Ala Gln Leu
1 5 10 15

Pro Ile Thr Glu Ala Gln Ser Phe Gly Leu Leu Asp Pro Lys Leu Cys
20 25 30

Tyr Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val Ile Leu Thr Ala
35 40 45

Leu Phe Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
50 55 60

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
65 70 75 80

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
85 90 95

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
100 105 110

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
115 120 125

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
130 135 140

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
145 150 155 160

Pro Pro Arg

<210> 12

F1_001_Sequence_listing

<211> 164

<212> PRT

<213> Homo sapiens

<400> 12

Met Lys Trp Lys Ala Leu Phe Thr Ala Ala Ile Leu Gln Ala Gln Leu
1 5 10 15

Pro Ile Thr Glu Ala Gln Ser Phe Gly Leu Leu Asp Pro Lys Leu Cys
20 25 30

Tyr Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val Ile Leu Thr Ala
35 40 45

Leu Phe Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
50 55 60

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
65 70 75 80

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
85 90 95

Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
100 105 110

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
115 120 125

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
130 135 140

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
145 150 155 160

Leu Pro Pro Arg

F1_001_Sequence_listing

<210> 13
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 13

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
 1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
 20 25 30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
 35 40 45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
 50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
 65 70 75 80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
 85 90 95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 100 105 110

<210> 14
 <211> 21
 <212> PRT
 <213> Homo sapiens

<400> 14

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
 1 5 10 15

F1_001_Sequence_listing

Val Leu Asp Lys Arg
20

<210> 15
<211> 22
<212> PRT
<213> Homo sapiens

<400> 15

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
1 5 10 15

Ser Glu Ile Gly Met Lys
20

<210> 16
<211> 21
<212> PRT
<213> Homo sapiens

<400> 16

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
1 5 10 15

Ala Leu His Met Gln
20

<210> 17
<211> 171
<212> PRT
<213> Homo sapiens

<400> 17

Met Glu His Ser Thr Phe Leu Ser Gly Leu Val Leu Ala Thr Leu Leu
1 5 10 15

Ser Gln Val Ser Pro Phe Lys Ile Pro Ile Glu Glu Leu Glu Asp Arg
20 25 30

F1_001_Sequence_listing

Val Phe Val Asn Cys Asn Thr Ser Ile Thr Trp Val Glu Gly Thr Val
35 40 45

Gly Thr Leu Leu Ser Asp Ile Thr Arg Leu Asp Leu Gly Lys Arg Ile
50 55 60

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

Asp Lys Glu Ser Thr Val Gln Val His Tyr Arg Met Cys Gln Ser Cys
85 90 95

Val Glu Leu Asp Pro Ala Thr Val Ala Gly Ile Ile Val Thr Asp Val
100 105 110

Ile Ala Thr Leu Leu Leu Ala Leu Gly Val Phe Cys Phe Ala Gly His
115 120 125

Glu Thr Gly Arg Leu Ser Gly Ala Ala Asp Thr Gln Ala Leu Leu Arg
130 135 140

Asn Asp Gln Val Tyr Gln Pro Leu Arg Asp Arg Asp Asp Ala Gln Tyr
145 150 155 160

Ser His Leu Gly Gly Asn Trp Ala Arg Asn Lys
165 170

<210> 18
<211> 127
<212> PRT
<213> Homo sapiens

<400> 18

Met Glu His Ser Thr Phe Leu Ser Gly Leu Val Leu Ala Thr Leu Leu
1 5 10 15

F1_001_Sequence_listing

Ser Gln Val Ser Pro Phe Lys Ile Pro Ile Glu Glu Leu Glu Asp Arg
20 25 30

Val Phe Val Asn Cys Asn Thr Ser Ile Thr Trp Val Glu Gly Thr Val
35 40 45

Gly Thr Leu Leu Ser Asp Ile Thr Arg Leu Asp Leu Gly Lys Arg Ile
50 55 60

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

Asp Lys Glu Ser Thr Val Gln Val His Tyr Arg Thr Ala Asp Thr Gln
85 90 95

Ala Leu Leu Arg Asn Asp Gln Val Tyr Gln Pro Leu Arg Asp Arg Asp
100 105 110

Asp Ala Gln Tyr Ser His Leu Gly Gly Asn Trp Ala Arg Asn Lys
115 120 125

<210> 19
<211> 21
<212> PRT
<213> Homo sapiens

<400> 19

Asp Gln Val Tyr Gln Pro Leu Arg Asp Arg Asp Asp Ala Gln Tyr Ser
1 5 10 15

His Leu Gly Gly Asn
20

<210> 20
<211> 206
<212> PRT
<213> Homo sapiens

F1_001_Sequence_listing

<400> 20

Met Gln Ser Gly Thr His Trp Arg Val Leu Gly Leu Cys Leu Leu Ser
1 5 10 15

Val Gly Val Trp Gly Gln Asp Gly Asn Glu Glu Met Gly Gly Ile Thr
20 25 30

Gln Thr Pro Tyr Lys Val Ser Ile Ser Gly Thr Thr Val Ile Leu Thr
35 40 45

Cys Pro Gln Tyr Pro Gly Ser Glu Ile Leu Trp Gln His Asn Asp Lys
50 55 60

Asn Ile Gly Gly Asp Glu Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp
65 70 75 80

His Leu Ser Leu Lys Glu Phe Ser Glu Leu Glu Gln Ser Gly Tyr Tyr
85 90 95

Val Cys Tyr Pro Arg Gly Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu
100 105 110

Tyr Leu Arg Ala Arg Val Cys Glu Asn Cys Met Glu Met Asp Met Ser
115 120 125

Val Ala Thr Ile Val Ile Val Asp Ile Cys Ile Thr Gly Gly Leu Leu
130 135 140

Leu Leu Val Tyr Tyr Trp Ser Lys Asn Arg Lys Ala Lys Ala Lys Pro
145 150 155 160

Val Thr Arg Gly Ala Gly Ala Gly Gly Arg Gln Arg Gly Gln Asn Lys
165 170 175

Glu Arg Pro Pro Pro Val Pro Asn Pro Asp Tyr Glu Pro Ile Arg Lys
180 185 190

F1_001_Sequence_listing

Gly Gln Arg Asp Leu Tyr Ser Gly Leu Asn Gln Arg Arg Ile
 195 200 205

<210> 21
 <211> 21
 <212> PRT
 <213> Homo sapiens

<400> 21

Asn Pro Asp Tyr Glu Pro Ile Arg Lys Gly Gln Arg Asp Leu Tyr Ser
 1 5 10 15

Gly Leu Asn Gln Arg
 20

<210> 22
 <211> 182
 <212> PRT
 <213> Homo sapiens

<400> 22

Met Glu Gln Gly Lys Gly Leu Ala Val Leu Ile Leu Ala Ile Ile Leu
 1 5 10 15

Leu Gln Gly Thr Leu Ala Gln Ser Ile Lys Gly Asn His Leu Val Lys
 20 25 30

Val Tyr Asp Tyr Gln Glu Asp Gly Ser Val Leu Leu Thr Cys Asp Ala
 35 40 45

Glu Ala Lys Asn Ile Thr Trp Phe Lys Asp Gly Lys Met Ile Gly Phe
 50 55 60

Leu Thr Glu Asp Lys Lys Lys Trp Asn Leu Gly Ser Asn Ala Lys Asp
 65 70 75 80

F1_001_Sequence_listing

Pro Arg Gly Met Tyr Gln Cys Lys Gly Ser Gln Asn Lys Ser Lys Pro
85 90 95

Leu Gln Val Tyr Tyr Arg Met Cys Gln Asn Cys Ile Glu Leu Asn Ala
100 105 110

Ala Thr Ile Ser Gly Phe Leu Phe Ala Glu Ile Val Ser Ile Phe Val
115 120 125

Leu Ala Val Gly Val Tyr Phe Ile Ala Gly Gln Asp Gly Val Arg Gln
130 135 140

Ser Arg Ala Ser Asp Lys Gln Thr Leu Leu Pro Asn Asp Gln Leu Tyr
145 150 155 160

Gln Pro Leu Lys Asp Arg Glu Asp Asp Gln Tyr Ser His Leu Gln Gly
165 170 175

Asn Gln Leu Arg Arg Asn
180

<210> 23
<211> 21
<212> PRT
<213> Homo sapiens

<400> 23

Asp Gln Leu Tyr Gln Pro Leu Lys Asp Arg Glu Asp Asp Gln Tyr Ser
1 5 10 15

His Leu Gln Gly Asn
20

<210> 24
<211> 226
<212> PRT
<213> Homo sapiens

F1_001_Sequence_listing

<400> 24

Met Pro Gly Gly Pro Gly Val Leu Gln Ala Leu Pro Ala Thr Ile Phe
1 5 10 15

Leu Leu Phe Leu Leu Ser Ala Val Tyr Leu Gly Pro Gly Cys Gln Ala
20 25 30

Leu Trp Met His Lys Val Pro Ala Ser Leu Met Val Ser Leu Gly Glu
35 40 45

Asp Ala His Phe Gln Cys Pro His Asn Ser Ser Asn Asn Ala Asn Val
50 55 60

Thr Trp Trp Arg Val Leu His Gly Asn Tyr Thr Trp Pro Pro Glu Phe
65 70 75 80

Leu Gly Pro Gly Glu Asp Pro Asn Gly Thr Leu Ile Ile Gln Asn Val
85 90 95

Asn Lys Ser His Gly Gly Ile Tyr Val Cys Arg Val Gln Glu Gly Asn
100 105 110

Glu Ser Tyr Gln Gln Ser Cys Gly Thr Tyr Leu Arg Val Arg Gln Pro
115 120 125

Pro Pro Arg Pro Phe Leu Asp Met Gly Glu Gly Thr Lys Asn Arg Ile
130 135 140

Ile Thr Ala Glu Gly Ile Ile Leu Leu Phe Cys Ala Val Val Pro Gly
145 150 155 160

Thr Leu Leu Leu Phe Arg Lys Arg Trp Gln Asn Glu Lys Leu Gly Leu
165 170 175

Asp Ala Gly Asp Glu Tyr Glu Asp Glu Asn Leu Tyr Glu Gly Leu Asn
180 185 190

F1_001_Sequence_listing

Leu Asp Asp Cys Ser Met Tyr Glu Asp Ile Ser Arg Gly Leu Gln Gly
195 200 205

Thr Tyr Gln Asp Val Gly Ser Leu Asn Ile Gly Asp Val Gln Leu Glu
210 215 220

Lys Pro
225

<210> 25
<211> 188
<212> PRT
<213> Homo sapiens

<400> 25

Met Pro Gly Gly Pro Gly Val Leu Gln Ala Leu Pro Ala Thr Ile Phe
1 5 10 15

Leu Leu Phe Leu Leu Ser Ala Val Tyr Leu Gly Pro Gly Cys Gln Ala
20 25 30

Leu Trp Met His Lys Val Pro Ala Ser Leu Met Val Ser Leu Gly Glu
35 40 45

Asp Ala His Phe Gln Cys Pro His Asn Ser Ser Asn Asn Ala Asn Val
50 55 60

Thr Trp Trp Arg Val Leu His Gly Asn Tyr Thr Trp Pro Pro Glu Phe
65 70 75 80

Leu Gly Pro Gly Glu Asp Pro Asn Glu Pro Pro Pro Arg Pro Phe Leu
85 90 95

Asp Met Gly Glu Gly Thr Lys Asn Arg Ile Ile Thr Ala Glu Gly Ile
100 105 110

F1_001_Sequence_listing

Ile Leu Leu Phe Cys Ala Val Val Pro Gly Thr Leu Leu Leu Phe Arg
 115 120 125

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

Glu Asp Glu Asn Leu Tyr Glu Gly Leu Asn Leu Asp Asp Cys Ser Met
 145 150 155 160

Tyr Glu Asp Ile Ser Arg Gly Leu Gln Gly Thr Tyr Gln Asp Val Gly
 165 170 175

Ser Leu Asn Ile Gly Asp Val Gln Leu Glu Lys Pro
 180 185

<210> 26
 <211> 21
 <212> PRT
 <213> Homo sapiens

<400> 26

Glu Asn Leu Tyr Glu Gly Leu Asn Leu Asp Asp Cys Ser Met Tyr Glu
 1 5 10 15

Asp Ile Ser Arg Gly
 20

<210> 27
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 27

Met Gly Gly Leu Glu Pro Cys Ser Arg Leu Leu Leu Leu Pro Leu Leu
 1 5 10 15

Leu Ala Val Ser Gly Leu Arg Pro Val Gln Ala Gln Ala Gln Ser Asp

F1_001_Sequence_listing

20 25 30

Cys Ser Cys Ser Thr Val Ser Pro Gly Val Leu Ala Gly Ile Val Met
35 40 45

Gly Asp Leu Val Leu Thr Val Leu Ile Ala Leu Ala Val Tyr Phe Leu
50 55 60

Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu Ala Ala Thr Arg
65 70 75 80

Lys Gln Arg Ile Thr Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly
85 90 95

Gln Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln Arg Pro Tyr Tyr
100 105 110

Lys

<210> 28
<211> 107
<212> PRT
<213> Homo sapiens

<400> 28

Met Gly Gly Leu Glu Pro Cys Ser Arg Leu Leu Leu Leu Pro Leu Leu
1 5 10 15

Leu Ala Val Ser Gly Leu Arg Pro Val Gln Ala Gln Ala Gln Ser Asp
20 25 30

Cys Ser Cys Ser Thr Val Ser Pro Gly Val Leu Ala Gly Ile Val Met
35 40 45

Gly Asp Leu Val Leu Thr Val Leu Ile Ala Leu Ala Val Tyr Phe Leu
50 55 60

F1_001_Sequence_listing

Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu Ala Thr Arg Lys
65 70 75 80

Gln Arg Ile Thr Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln
85 90 95

Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln
100 105

<210> 29
<211> 102
<212> PRT
<213> Homo sapiens

<400> 29

Met Gly Gly Leu Glu Pro Cys Ser Arg Leu Leu Leu Leu Pro Leu Leu
1 5 10 15

Leu Ala Val Ser Asp Cys Ser Cys Ser Thr Val Ser Pro Gly Val Leu
20 25 30

Ala Gly Ile Val Met Gly Asp Leu Val Leu Thr Val Leu Ile Ala Leu
35 40 45

Ala Val Tyr Phe Leu Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala
50 55 60

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

Gln Glu Leu Gln Gly Gln Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr
85 90 95

Gln Arg Pro Tyr Tyr Lys
100

F1_001_Sequence_listing

<210> 30
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 30

Met Gly Gly Leu Glu Pro Cys Ser Arg Leu Leu Leu Leu Pro Leu Leu
 1 5 10 15

Leu Ala Val Ser Asp Cys Ser Cys Ser Thr Val Ser Pro Gly Val Leu
 20 25 30

Ala Gly Ile Val Met Gly Asp Leu Val Leu Thr Val Leu Ile Ala Leu
 35 40 45

Ala Val Tyr Phe Leu Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala
 50 55 60

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

Glu Leu Gln Gly Gln Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln
 85 90 95

Arg Pro Tyr Tyr Lys
 100

<210> 31
 <211> 21
 <212> PRT
 <213> Homo sapiens

<400> 31

Glu Ser Pro Tyr Gln Glu Leu Gln Gly Gln Arg Ser Asp Val Tyr Ser
 1 5 10 15

Asp Leu Asn Thr Gln

F1_001_Sequence_listing

20

<210> 32
 <211> 86
 <212> PRT
 <213> Homo sapiens
 <400> 32

Met Ile Pro Ala Val Val Leu Leu Leu Leu Leu Leu Val Glu Gln Ala
 1 5 10 15

Ala Ala Leu Gly Glu Pro Gln Leu Cys Tyr Ile Leu Asp Ala Ile Leu
 20 25 30

Phe Leu Tyr Gly Ile Val Leu Thr Leu Leu Tyr Cys Arg Leu Lys Ile
 35 40 45

Gln Val Arg Lys Ala Ala Ile Thr Ser Tyr Glu Lys Ser Asp Gly Val
 50 55 60

Tyr Thr Gly Leu Ser Thr Arg Asn Gln Glu Thr Tyr Glu Thr Leu Lys
 65 70 75 80

His Glu Lys Pro Pro Gln
 85

<210> 33
 <211> 21
 <212> PRT
 <213> Homo sapiens
 <400> 33

Asp Gly Val Tyr Thr Gly Leu Ser Thr Arg Asn Gln Glu Thr Tyr Glu
 1 5 10 15

Thr Leu Lys His Glu
 20

F1_001_Sequence_listing

<210> 34
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 34

Arg Pro Arg Arg Ser Pro Ala Gln Asp Gly Lys Val Tyr Ile Asn Met
 1 5 10 15

Pro Gly Arg Gly
 20

<210> 35
 <211> 68
 <212> PRT
 <213> Homo sapiens

<400> 35

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
 1 5 10 15

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
 20 25 30

Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly
 35 40 45

Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala
 50 55 60

Ala Tyr Arg Ser
 65

<210> 36
 <211> 619
 <212> PRT
 <213> Homo sapiens

F1_001_Sequence_listing

<400> 36

Met Pro Asp Pro Ala Ala His Leu Pro Phe Phe Tyr Gly Ser Ile Ser
1 5 10 15

Arg Ala Glu Ala Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly
20 25 30

Leu Phe Leu Leu Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu
35 40 45

Ser Leu Val His Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln
50 55 60

Leu Asn Gly Thr Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro
65 70 75 80

Ala Glu Leu Cys Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys
85 90 95

Asn Leu Arg Lys Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro
100 105 110

Gly Val Phe Asp Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg
115 120 125

Gln Thr Trp Lys Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser
130 135 140

Gln Ala Pro Gln Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg
145 150 155 160

Met Pro Trp Tyr His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys
165 170 175

Leu Tyr Ser Gly Ala Gln Thr Asp Gly Lys Phe Leu Leu Arg Pro Arg
180 185 190

F1_001_Sequence_listing

Lys Glu Gln Gly Thr Tyr Ala Leu Ser Leu Ile Tyr Gly Lys Thr Val
195 200 205

Tyr His Tyr Leu Ile Ser Gln Asp Lys Ala Gly Lys Tyr Cys Ile Pro
210 215 220

Glu Gly Thr Lys Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys
225 230 235 240

Leu Lys Ala Asp Gly Leu Ile Tyr Cys Leu Lys Glu Ala Cys Pro Asn
245 250 255

Ser Ser Ala Ser Asn Ala Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala
260 265 270

His Pro Ser Thr Leu Thr His Pro Gln Arg Arg Ile Asp Thr Leu Asn
275 280 285

Ser Asp Gly Tyr Thr Pro Glu Pro Ala Arg Ile Thr Ser Pro Asp Lys
290 295 300

Pro Arg Pro Met Pro Met Asp Thr Ser Val Tyr Glu Ser Pro Tyr Ser
305 310 315 320

Asp Pro Glu Glu Leu Lys Asp Lys Lys Leu Phe Leu Lys Arg Asp Asn
325 330 335

Leu Leu Ile Ala Asp Ile Glu Leu Gly Cys Gly Asn Phe Gly Ser Val
340 345 350

Arg Gln Gly Val Tyr Arg Met Arg Lys Lys Gln Ile Asp Val Ala Ile
355 360 365

Lys Val Leu Lys Gln Gly Thr Glu Lys Ala Asp Thr Glu Glu Met Met
370 375 380

F1_001_Sequence_listing

Arg Glu Ala Gln Ile Met His Gln Leu Asp Asn Pro Tyr Ile Val Arg
385 390 395 400

Leu Ile Gly Val Cys Gln Ala Glu Ala Leu Met Leu Val Met Glu Met
405 410 415

Ala Gly Gly Gly Pro Leu His Lys Phe Leu Val Gly Lys Arg Glu Glu
420 425 430

Ile Pro Val Ser Asn Val Ala Glu Leu Leu His Gln Val Ser Met Gly
435 440 445

Met Lys Tyr Leu Glu Glu Lys Asn Phe Val His Arg Asp Leu Ala Ala
450 455 460

Arg Asn Val Leu Leu Val Asn Arg His Tyr Ala Lys Ile Ser Asp Phe
465 470 475 480

Gly Leu Ser Lys Ala Leu Gly Ala Asp Asp Ser Tyr Tyr Thr Ala Arg
485 490 495

Ser Ala Gly Lys Trp Pro Leu Lys Trp Tyr Ala Pro Glu Cys Ile Asn
500 505 510

Phe Arg Lys Phe Ser Ser Arg Ser Asp Val Trp Ser Tyr Gly Val Thr
515 520 525

Met Trp Glu Ala Leu Ser Tyr Gly Gln Lys Pro Tyr Lys Lys Met Lys
530 535 540

Gly Pro Glu Val Met Ala Phe Ile Glu Gln Gly Lys Arg Met Glu Cys
545 550 555 560

Pro Pro Glu Cys Pro Pro Glu Leu Tyr Ala Leu Met Ser Asp Cys Trp
565 570 575

F1_001_Sequence_listing

Ile Tyr Lys Trp Glu Asp Arg Pro Asp Phe Leu Thr Val Glu Gln Arg
580 585 590

Met Arg Ala Cys Tyr Tyr Ser Leu Ala Ser Lys Val Glu Gly Pro Pro
595 600 605

Gly Ser Thr Gln Lys Ala Glu Ala Ala Cys Ala
610 615

<210> 37
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic HA Epitope

<400> 37

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1 5

<210> 38
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic FLAG Epitope

<400> 38

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 39
<211> 10
<212> PRT
<213> Artificial sequence

<220>

F1_001_Sequence_listing

<223> synthetic c-myc Epitope

<400> 39

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 40

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic His5 Affinity

<400> 40

His His His His His
1 5

<210> 41

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic HisX6 Affinity

<400> 41

His His His His His His
1 5

<210> 42

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic Strep Tag Affinity

<400> 42

Trp Ser His Pro Gln Phe Glu Lys
1 5

F1_001_Sequence_listing

<210> 43
 <211> 5
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic HisX6 Affinity

<400> 43

Arg Tyr Ile Arg Ser
 1 5

<210> 44
 <211> 4
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic Affinity

<400> 44

Phe His His Thr
 1

<210> 45
 <211> 17
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic Affinity

<400> 45

Trp Glu Ala Ala Ala Arg Glu Ala Cys Cys Arg Glu Cys Cys Ala Arg
 1 5 10 15

Ala

F1_001_Sequence_listing

<210> 46

<211> 24

<212> PRT

<213> Homo sapiens

<400> 46

Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu
1				5				10					15		

Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys
			20				

<210> 47

<211> 23

<212> PRT

<213> Homo sapiens

<400> 47

Leu	Gly	Leu	Leu	Val	Ala	Gly	Val	Leu	Val	Leu	Leu	Val	Ser	Leu	Gly
1				5				10					15		

Val	Ala	Ile	His	Leu	Cys	Cys
			20			

<210> 48

<211> 25

<212> PRT

<213> Homo sapiens

<400> 48

Ala	Leu	Ile	Val	Leu	Gly	Gly	Val	Ala	Gly	Leu	Leu	Leu	Phe	Ile	Gly
1				5				10					15		

Leu	Gly	Ile	Phe	Phe	Cys	Val	Arg	Cys
			20				25	

<210> 49

<211> 23

<212> PRT

F1_001_Sequence_listing

<213> Homo sapiens

<400> 49

Leu	Cys	Tyr	Leu	Leu	Asp	Gly	Ile	Leu	Phe	Ile	Tyr	Gly	Val	Ile	Leu
1				5					10					15	

Thr	Ala	Leu	Phe	Leu	Arg	Val
				20		

<210> 50

<211> 27

<212> PRT

<213> Homo sapiens

<400> 50

Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu
1				5					10					15	

Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val
				20				25		

<210> 51

<211> 26

<212> PRT

<213> Homo sapiens

<400> 51

Val	Ala	Ala	Ile	Leu	Gly	Leu	Gly	Leu	Val	Leu	Gly	Leu	Leu	Gly	Pro
1				5					10					15	

Leu	Ala	Ile	Leu	Leu	Ala	Leu	Tyr	Leu	Leu
				20				25	

<210> 52

<211> 24

<212> PRT

<213> Homo sapiens

<400> 52

F1_001_Sequence_listing

Ala Leu Pro Ala Ala Leu Ala Val Ile Ser Phe Leu Leu Gly Leu Gly
1 5 10 15

Leu Gly Val Ala Cys Val Leu Ala
20

<210> 53
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic Linker 1

<400> 53

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 54
<211> 30
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic Linker 2

<400> 54

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25 30

<210> 55
<211> 14
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic Linker 3

F1_001_Sequence_listing

<400> 55

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 56

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic Linker 4

<400> 56

Gly Gly Ser Gly
1

<210> 57

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic Linker 5

<400> 57

Gly Gly Ser Gly Gly
1 5

<210> 58

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic Linker 6

<400> 58

Gly Ser Gly Ser Gly
1 5

F1_001_Sequence_listing

<210> 59
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic Linker 7

<400> 59

Gly Ser Gly Gly Gly
1 5

<210> 60
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic Linker 8

<400> 60

Gly Gly Gly Ser Gly
1 5

<210> 61
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic Linker 9

<400> 61

Gly Ser Ser Ser Gly
1 5

<210> 62
<211> 4
<212> PRT
<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic Hinge 1

<400> 62

Cys Pro Pro Cys

1

<210> 63

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic Hinge 2

<400> 63

Asp Lys Thr His Thr

1

5

<210> 64

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic Hinge 3

<400> 64

Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg

1

5

10

15

<210> 65

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic Hinge 4

<400> 65

Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr

F1_001_Sequence_listing

1 5

10

<210> 66
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic Hinge 5

<400> 66

Lys Ser Cys Asp Lys Thr His Thr Cys Pro
1 5 10

<210> 67
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic Hinge 6

<400> 67

Lys Cys Cys Val Asp Cys Pro
1 5

<210> 68
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic Hinge 7

<400> 68

Lys Tyr Gly Pro Pro Cys Pro
1 5

<210> 69
<211> 15
<212> PRT

F1_001_Sequence_listing

<213> Artificial sequence

<220>

<223> synthetic Hinge 8

<400> 69

Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro
1				5					10					15

<210> 70

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic Hinge 9

<400> 70

Glu	Arg	Lys	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro
1				5					10		

<210> 71

<211> 17

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic Hinge 10

<400> 71

Glu	Leu	Lys	Thr	Pro	Leu	Gly	Asp	Thr	Thr	His	Thr	Cys	Pro	Arg	Cys
1				5					10					15	

Pro

<210> 72

<211> 12

<212> PRT

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic Hinge 11

<400> 72

Ser	Pro	Asn	Met	Val	Pro	His	Ala	His	His	Ala	Gln
1				5				10			

<210> 73

<211> 45

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic Hinge 12

<400> 73

Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala
1				5				10						15	

Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly
			20					25					30		

Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp
		35					40					45

<210> 74

<211> 21

<212> PRT

<213> Homo sapiens

<400> 74

Met	Ala	Leu	Pro	Val	Thr	Ala	Leu	Leu	Leu	Pro	Leu	Ala	Leu	Leu	Leu
1				5				10					15		

His	Ala	Ala	Arg	Pro
			20	

<210> 75

<211> 24

F1_001_Sequence_listing

<212> PRT

<213> Homo sapiens

<400> 75

Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr	Cys	Gly	Val	Leu	Leu	Leu
1				5					10				15		

Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys
			20				

<210> 76

<211> 27

<212> PRT

<213> Homo sapiens

<400> 76

Phe	Trp	Val	Leu	Val	Val	Val	Gly	Gly	Val	Leu	Ala	Cys	Tyr	Ser	Leu
1				5					10					15	

Leu	Val	Thr	Val	Ala	Phe	Ile	Ile	Phe	Trp	Val
			20					25		

<210> 77

<211> 21

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic 2A-1 Cleavage signal

<400> 77

Gly	Ser	Gly	Glu	Gly	Arg	Gly	Ser	Leu	Leu	Thr	Cys	Gly	Asp	Val	Glu
1				5					10					15	

Glu	Asn	Pro	Gly	Pro
			20	

<210> 78

<211> 357

F1_001_Sequence_listing

<212> PRT

<213> Homo sapiens

<400> 78

Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

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

Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe
35 40 45

Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala
50 55 60

Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu
65 70 75 80

Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile
85 90 95

Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu
100 105 110

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

Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu
130 135 140

Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr
145 150 155 160

Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys
165 170 175

F1_001_Sequence_listing

Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly
180 185 190

Gln Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu
195 200 205

Pro Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys
210 215 220

Val Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu
225 230 235 240

Asn Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu Pro Gln Ala Met
245 250 255

Asn Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala
260 265 270

His Tyr Ile Asp Gly Pro His Cys Val Lys Thr Cys Pro Ala Gly Val
275 280 285

Met Gly Glu Asn Asn Thr Leu Val Trp Lys Tyr Ala Asp Ala Gly His
290 295 300

Val Cys His Leu Cys His Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro
305 310 315 320

Gly Leu Glu Gly Cys Pro Thr Asn Gly Pro Lys Ile Pro Ser Ile Ala
325 330 335

Thr Gly Met Val Gly Ala Leu Leu Leu Leu Val Val Ala Leu Gly
340 345 350

Ile Gly Leu Phe Met
355

F1_001_Sequence_listing

<210> 79
 <211> 45
 <212> PRT
 <213> Homo sapiens

<400> 79

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
 1 5 10 15

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
 20 25 30

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
 35 40 45

<210> 80
 <211> 39
 <212> PRT
 <213> Homo sapiens

<400> 80

Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn
 1 5 10 15

Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu
 20 25 30

Phe Pro Gly Pro Ser Lys Pro
 35

<210> 81
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 81

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
 1 5 10 15

F1_001_Sequence_listing

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
50 55 60

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
65 70 75 80

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
85 90 95

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
100 105 110

Arg

<210> 82
<211> 463
<212> PRT
<213> Homo sapiens

<400> 82

Met Thr Ile Leu Gly Thr Thr Phe Gly Met Val Phe Ser Leu Leu Gln
1 5 10 15

Val Val Ser Gly Glu Ser Gly Tyr Ala Gln Asn Gly Asp Leu Glu Asp
20 25 30

Ala Glu Leu Asp Asp Tyr Ser Phe Ser Cys Tyr Ser Gln Leu Glu Val
35 40 45

F1_001_Sequence_listing

Asn Gly Ser Gln His Ser Leu Thr Cys Ala Phe Glu Asp Pro Asp Val
50 55 60

Asn Thr Thr Asn Leu Glu Phe Glu Ile Cys Gly Ala Leu Val Glu Val
65 70 75 80

Lys Cys Leu Asn Phe Arg Lys Leu Gln Glu Ile Tyr Phe Ile Glu Thr
85 90 95

Lys Lys Phe Leu Leu Ile Gly Lys Ser Asn Ile Cys Val Lys Val Gly
100 105 110

Glu Lys Ser Leu Thr Cys Lys Lys Ile Asp Leu Thr Thr Ile Val Lys
115 120 125

Pro Glu Ala Pro Phe Asp Leu Ser Val Ile Tyr Arg Glu Gly Ala Asn
130 135 140

Asp Phe Val Val Thr Phe Asn Thr Ser His Leu Gln Lys Lys Tyr Val
145 150 155 160

Lys Val Leu Met His Asp Val Ala Tyr Arg Gln Glu Lys Asp Glu Asn
165 170 175

Lys Trp Thr His Val Asn Leu Ser Ser Thr Lys Leu Thr Leu Leu Gln
180 185 190

Arg Lys Leu Gln Pro Ala Ala Met Tyr Glu Ile Lys Val Arg Ser Ile
195 200 205

Pro Asp His Tyr Phe Lys Gly Phe Trp Ser Glu Trp Ser Pro Ser Tyr
210 215 220

Tyr Phe Arg Thr Pro Glu Ile Asn Asn Ser Ser Gly Glu Met Asp Pro
225 230 235 240

F1_001_Sequence_listing

Ile	Leu	Leu	Pro	Pro	Cys	Leu	Thr	Ile	Ser	Ile	Leu	Ser	Phe	Phe	Ser	245	250	255
Val	Ala	Leu	Leu	Val	Ile	Leu	Ala	Cys	Val	Leu	Trp	Lys	Lys	Arg	Ile	260	265	270
Lys	Pro	Ile	Val	Trp	Pro	Ser	Leu	Pro	Asp	His	Lys	Lys	Thr	Leu	Glu	275	280	285
His	Leu	Cys	Lys	Lys	Pro	Arg	Lys	Asn	Leu	Asn	Val	Ser	Phe	Asn	Pro	290	295	300
Glu	Ser	Phe	Leu	Asp	Cys	Gln	Ile	His	Arg	Val	Asp	Asp	Ile	Gln	Ala	305	310	315
Arg	Asp	Glu	Val	Glu	Gly	Phe	Leu	Gln	Asp	Thr	Phe	Pro	Gln	Gln	Leu	325	330	335
Glu	Glu	Ser	Glu	Lys	Gln	Arg	Leu	Gly	Gly	Asp	Val	Gln	Ser	Pro	Asn	340	345	350
Cys	Pro	Ser	Glu	Asp	Val	Val	Val	Thr	Pro	Glu	Ser	Phe	Gly	Arg	Asp	355	360	365
Ser	Ser	Leu	Thr	Cys	Leu	Ala	Gly	Asn	Val	Ser	Ala	Cys	Asp	Ala	Pro	370	375	380
Ile	Leu	Ser	Ser	Ser	Arg	Ser	Leu	Asp	Cys	Arg	Glu	Ser	Gly	Lys	Asn	385	390	395
Gly	Pro	His	Val	Tyr	Gln	Asp	Leu	Leu	Leu	Ser	Leu	Gly	Thr	Thr	Asn	405	410	415
Ser	Thr	Leu	Pro	Pro	Pro	Phe	Ser	Leu	Gln	Ser	Gly	Ile	Leu	Thr	Leu	420	425	430

F1_001_Sequence_listing

Asn Pro Val Ala Gln Gly Gln Pro Ile Leu Thr Ser Leu Gly Ser Asn
 435 440 445

Gln Glu Glu Ala Tyr Val Thr Met Ser Ser Phe Tyr Gln Asn Gln
 450 455 460

<210> 83
 <211> 13673
 <212> DNA
 <213> Artificial sequence

<220>
 <223> synthetic Dox-rapamycin inducible lentiviral genome with
 riboswitch

<400> 83
 gatatctata acaagaaaat atatatataa taagttatca cgtaagtaga acatgaaata 60
 acaatataat tatcgtatga gttaaactctt aaaagtcacg taaaagataa tcatgcgtca 120
 ttttgactca cgcggtcgtt atagttcaaa atcagtgaca cttaccgcat tgacaagcac 180
 gcctcacggg agctccaagc ggcgactgag atgtcctaaa tgcacagcga cggattcgcg 240
 ctatttagaa agagagagca atatttcaag aatgcatgcg tcaattttac gcagactatc 300
 tttctagggt taagacggat cgggagatct cccgatcccc tatggtgcac tctcagtaca 360
 atctgctctg atgccgcata gttaagccag tatctgctcc ctgcttgtgt gttggaggtc 420
 gctgagtagt gcgcgagcaa aatttaagct acaacaaggc aaggcttgac cgacaattgc 480
 atgaagaatc tgcttagggg taggcgtttt gcgctgcttc gcgatgtacg ggccagatat 540
 acgcgttgac attgattatt gactagttat taatagtaat caattacggg gtcattagtt 600
 catagcccat atatggagtt ccgcgttaca taacttacgg taaatggccc gcctggctga 660
 ccgccaacg acccccgcc attgacgtca ataatgacgt atgttcccat agtaacgcca 720
 atagggactt tccattgacg tcaatgggtg gagtatttac ggtaaactgc ccacttgga 780
 gtacatcaag tgtatcatat gccaaagtacg cccctattg acgtcaatga cggtaaattg 840
 cccgcctggc attatgcca gtacatgacc ttatgggact ttcctacttg gcagtacatc 900

F1_001_Sequence_listing

tacgtattag tcatcgctat taccatgggtg atgcgggtttt ggcagtacat caatgggcgt	960
ggatagcgggt ttgactcacg gggattttcca agtctccacc ccattgacgt caatggggagt	1020
ttgtttttgga accaaaaatca acggggacttt ccaaaatgtc gtaacaactc cgccccattg	1080
acgcaaatgg gcggtaggcg tgtacgggtg gaggtctata taagcagagc tctccctatc	1140
agtgatagag atctccctat cagtgataga gatcgtcgac gagctcgttt agtgaaccgt	1200
cagatcgcct ggagacgccc tcgaagccgc ggtgcgggtg ccagggcgtg ccctgggtct	1260
ctctggttag accagatctg agcctgggag ctctctggct aactagggaa cccactgctt	1320
aagcctcaat aaagcttgcc ttgagtgctt caagtagtgt gtgcccgtct gttgtgtgac	1380
tctggtaact agagatccct cagacccttt tagtcagtgt ggaaaatctc tagcagtggc	1440
gcccgaacag ggacttgaaa gcgaaaggga aaccagagga gctctctcga cgcaggactc	1500
ggcttgctga agcgcgcacg gcaagaggcg aggggcggcg actggtgagt acgcaaaaaa	1560
ttttgactag cggaggctag aaggagagag atgggtgcga gagcgtcagt attaagcggg	1620
ggagaattag atcgcgatgg gaaaaaattc ggtaaggcc aggggggaaag aaaaaatata	1680
aattaaaca tatagtatgg gcaagcaggg agctagaacg attcgcagtt aatcctggcc	1740
tgttagaac atcagaaggc tgtagacaaa tactgggaca gctacaacca tcccttcaga	1800
caggatcaga agaacttaga tcattatata atacagtagc aacctctat tgtgtgcatc	1860
aaaggataga gataaaagac accaaggaag ctttagacaa gatagaggaa gagcaaaaca	1920
aaagtaagac caccgcacag caagcggccg ctgatcttca gacctggagg aggagatatg	1980
agggacaatt ggagaagtga attatataaa tataaagtag taaaaattga accattagga	2040
gtagcaccca ccaaggcaaa gagaagagtg gtgcagagag aaaaaagagc agtgggaata	2100
ggagctttgt tccttgggtt cttgggagca gcaggaagca ctatgggcgc agcgtcaatg	2160
acgctgacgg tacaggccag acaattattg tctggtatag tgcagcagca gaacaatttg	2220
ctgagggcta ttgaggcgca acagcatctg ttgcaactca cagtctgggg catcaagcag	2280
ctccaggcaa gaatcctggc tgtggaaaga tacctaaagg atcaacagct cctggggatt	2340

F1_001_Sequence_listing

tggggttgct ctggaaaact catttgcacc actgctgtgc cttggaatgc tagttggagt	2400
aataaatctc tggaacagat ttggaatcac acgacctgga tggagtggga cagagaaatt	2460
aacaattaca caagcttaat acactcctta attgaagaat cgcaaaacca gcaagaaaag	2520
aatgaacaag aattattgga attagataaa tgggcaagtt tgtggaattg gtttaacata	2580
acaaattggc tgtggtatat aaaattattc ataatgatag taggaggctt ggtaggttta	2640
agaatagttt ttgctgtact ttctatagtg aatagagtta ggcagggata ttcaccatta	2700
tcgtttcaga cccacctccc aaccccgagg ggacccgaca ggcccgaagg aatagaagaa	2760
gaaggtggag agagagacag agacagatcc attcgattag tgaacggatc tcgacggtat	2820
cgattagact gtagcccagg aatatggcag ctagattgta cacatttaga aggaaaagtt	2880
atcttggtag cagttcatgt agccagtgga tatatagaag cagaagtaat tccagcagag	2940
acagggcaag aaacagcata cttcctctta aaattagcag gaagatggcc agtaaaaaca	3000
gtacatacag acaatggcag caatttcacc agtactacag ttaaggccgc ctgttggtgg	3060
gcggggatca agcaggaatt tggcattccc tacaatcccc aaagtcaagg agtaatagaa	3120
tctatgaata aagaattaaa gaaaattata ggacaggtaa gagatcaggc tgaacatctt	3180
aagacagcag tacaaatggc agtattcatc cacaatttta aaagaaaagg ggggattggg	3240
gggtacagtg caggggaaag aatagtagac ataatagcaa cagacataca aactaaagaa	3300
ttacaaaaac aaattacaaa aattcaaaat tttcgggttt attacaggga cagcagagat	3360
ccagtttggc tgcattgatc acgtgagggg ctctagactc tagacacaca aaaaaccaac	3420
acacagatct aatgaaaata aagatctttt attgagaaac ttatacaggg tagcataatg	3480
ggctactgac cccgccttca aacctatttg gagactataa gtgaaaatta tcactggttt	3540
tggtagaagc tggacatggt gacatatgct tcttcttgat ttgatcccag ggaagtaaga	3600
atgggctgac cctgagcaac tgggttcaat gtcaggattc cagattggag agaaaatgga	3660
gggggcagcg tgctgtttgt agtcccaagg ctaagcagga ggtcctggta cacatgaggc	3720
ccattcttgc cactctccct gcagtctagg gacctggaag aggagagaat aggggcgtca	3780

F1_001_Sequence_listing

catgcactga cattcccagc caggcatgtg agggatgaat ctcttccaaa gctttctgga	3840
gtgacgacta catcctcaga tgggcagttg gggctctgca catccccctcc aagcctctgc	3900
ttctcagatt cttctagttg ctgaggaaac gtatcttgca gaaaaccttc cacttcatct	3960
ctagcttgaa tgtcatccac cctatgaatc tggcagtcca ggaaactttc aggattgaaa	4020
ctcacattta aatTTTTTct tggtttctta caaagatgtt ccagagtctt cttatgatcg	4080
gggagactgg gccatacgat aggcttaatc ctttttttcc ataacacaca ggccaagatg	4140
accaacagag cgacagagaa aaaactcaaa atgctgatgg tcaggcatgg tggtagtaag	4200
ataggatcca tctccccctga gctattattg atctctggag ttctgaagta ataacttgga	4260
ctccattcac tccagaagcc tttaaaatag tgatcaggga tggatcgaac tttaatctca	4320
tacattgctg ccggttggag ctttctctgc aggagtgtca gctttgtgct ggataaattc	4380
acatgctcc atttgttttc atccttttcc tggcggtaag ctacatcatg cattaaaact	4440
tttacatact tcttttgcaa gtgtgatgta ttaaagtca ccacaaagtc attggctcct	4500
tcccgataga tgacactcag gtcaaaagga gcctcagggt taactatagt ggtaggtct	4560
atTTTTTgc aggttagact cttttctcca accttcacac atatattgct ctttccaatc	4620
agtaagaatt tctttgtctc gatgaaatat atctcttgta gtttcctgaa attcaggcac	4680
tttacctcca cgagggcccc acatatattca aattccagat tggtggtggt gacatctggg	4740
tcctcaaaag cacatgtcag tgaatgctgc gatccattca cttccaactg gctatagcat	4800
gagaatgagt agtcatccag ttctgcatct tccaagtctc catTTTgagc atagccactt	4860
tctccagaaa cgacttgaag taaagaaaaa accatgccaa aagttgtacc tagaattgtc	4920
attgggccgg gatTTTctc cacgtccccg catgttagta gacttccccct gccctcgccg	4980
gagcgagggg gcagggcctg catgtgaagg gcgtcgtagg tgtccttggt ggctgtactg	5040
agaccctggt aaaggccatc gtgccccctg cccctccggc gctcgcttt catcccaatc	5100
tcactgtagg cctccgcat cttatctttc tgcagttcat tgtacaggcc ttcctgaggg	5160
ttcttccttc tcggctttcc ccccatctca ggggtccggc cacgtctctt gtccaaaaca	5220

F1_001_Sequence_listing

tcgtactcct ctcttcgtcc tagattgagc tcgttataga gctggttctg gccctgcttg	5280
tacgcggggg cgtctgcgct cctgctgaac ttcactctca gttcacatcc tccttcttct	5340
tcttctggaa atcggcagct acagccatct tcctcttgag tagtttgtag tggtctcata	5400
aatggttgtt tgaatatata caggagtttc tttctgcccc gtttgtagta aagggtgata	5460
accagtgcga ggagaaggac cccacaagtc ccggccaagg gcgcccagat gtagatatca	5520
caggcgaagt ccagccccct cgtgtgcact gcgccccccg ccgctggccg gcacgcctct	5580
gggcgcaggg acaggggctg cgacgcgatg gtgggcgccc gtgttggtgg tcgcggcgct	5640
ggcgtcgtgg ttgaggagac ggtgactgag gttccttggc cccagtagtc catagcatag	5700
ctaccaccgt agtaataatg tttggcacag tagtaaattg ctgtgtcatc agtttgcaga	5760
ctgttcattt ttaagaaaac ttggctcttg gagttgtcct tgatgatggg cagtctggat	5820
ttgagagctg aattatagta tgtggtttca ctaccccata ttactcccag ccactccaga	5880
ccctttcgtg gaggctggcg aatccagctt acaccatagt cgggtaatga gaccctgag	5940
acagtgcattg tgacggacag gctctgtgag ggcgccacca ggccagggtcc tgactcctgc	6000
agtttcacct cagatccgcc gccacccgac ccaccaccgc ccgagccacc gccacctgtg	6060
atctccagct tgggtcccc cccgaacgtg tacggaagcg tattaccctg ttggcgaagt	6120
agggtggcaat atcttcttgc tccagggtgc taattgtcag agaataatct gttccagacc	6180
cactgccact gaaccttgat gggactcctg agtgtaatct tgatgtatgg tagatcagga	6240
gtttaacagt tccatctggt ttctgctgat accaatttaa atatttacta atgtcctgac	6300
ttgccctgca actgatgggtg actctgtctc ccagagaggc agacagggag gatgtagtct	6360
gtgtcatctg gatgtccggc ctggcggcgt ggagcagcaa ggccagcggc aggagcaagg	6420
cggtcactgg taaggccatg gatcctctag atcacgacac ctgaaatgga agaaaaaac	6480
tttgaaccac tgtctgaggc ttgagaatga accaagatcc aaactcaaaa agggcaaatt	6540
ccaaggagaa ttacatcaag tgccaagctg gcctaacttc agtctccacc cactcagtgt	6600
ggggaaactc catcgcataa aaccctccc cccaacctaa agacgacgta ctccaaaagc	6660

F1_001_Sequence_listing

tcgagaacta atcgagggtgc ctggacggcg cccgggtactc agtggagtca catgaagcga	6720
cggctgagga cggaaaggcc cttttccttt gtgtgggaga aacttataca gggtagcata	6780
atgggctact gaccccgctt tcaaacctat ttggagacta taagtgaata tgactcacc	6840
gcccgtctc ccggcacctt catcttgtcc tttccctcag aaagaggctg ggaggcagag	6900
gctgaggcag cgggtggccgg gacggtagg agaaaaggag tctctgctgg ttttattctg	6960
cagctacctc cccaggaagt ggaggactgt ggggcctttg agaagcacct gccgacaggg	7020
ccaagaaatt cgcactcccc ctttcggttc acaggcagga agccctggag gtttgagggt	7080
ttggggtgtg tgtatgtatc tgtctgtctg aattttgctt tttctctcat ttgaccattg	7140
ttttaatgct ctttttttta aaaaaataa ttcttatcta attcctatct tgattggtaa	7200
agtccatctc taggcaaata caagttctcg atggaaaaca ataagtaatg taaaatacag	7260
catagcaaaa ctttaacctc caaatcaagc ctctacttga atccttttct gagggatgaa	7320
taaggcatag gcatcagggg ctgttgccaa tgtgcattag ctgtttgcag cctcaccttc	7380
tttcatggag tttaagatat agtgtatttt cccaagggtt gaactagctc ttcatttctt	7440
tatgttttaa atgcactgac ctccacatt ccttttttag taaaatattc agaaataatt	7500
taaatacatc attgcaatga aaataaatgt tttttattag gcagaatcca gatgctcaag	7560
gcccttcata atatcccca gtttagtagt tggacttagg gaacaaagga acctttaata	7620
gaaattggac agcaagaaag cgagcttagt gatacttgtg atcctctaga tcacgacacc	7680
tgaaatggaa gaaaaaaaact gcaccttcat cttgtcctt ccctcagaaa gaggctggga	7740
ggcagaggct gaggcagcgg tggccgggac ggtaggaga aaaggagtct ctgctgggtt	7800
tattctgcag ctacctcccc aggaagtgga ggactgtggg gcctttgaga agcacctgcc	7860
gacaggcca agaaattcgc actccccctt tcggttcaca ggcaggaagc cctggagggt	7920
tgagggtttg ggggtgtgtg atgtatctgt ctgtctgaat ttgcttttt ctctcatttg	7980
accattgttt taatgtcct ttttttaaaa aaaataattc ttatctaatt cctatcttga	8040
ttggtaaagt ccatctctag gcaaatacaa gttctcgatg gaaaacaata agtaatgtaa	8100

F1_001_Sequence_listing

aatacagcat agcaaaactt taacctccaa atcaagcctc tacttgaatc cttttctgag	8160
ggatgaataa ggcataggca tcaggggctg ttgccaatgt gcattagctg tttgcagcct	8220
caccttcttt catggagttt aagatatagt gtattttccc aaggtttgaa ctagctcttc	8280
atttctttat gttttaaatg cactgacctc ccacattccc tttttagtaa aatattcaga	8340
aataatttaa atacatcatt gcaatgaaaa taaatgtttt ttattaggca gaatccagat	8400
gctcaaggcc cttcataata tccccagtt tagtagttgg acttagggaa caaaggaacc	8460
tttaatagaa attggacagc aagaaagcga gcttagtgat acttgtaaaa agagacgcgt	8520
ctctaaaagt cctttccatg gctgctcgcc tgtgttgcca cctggattct gcgcgggacg	8580
tccttctgct acgtcccttc ggccctcaat ccagcggacc ttccttcccg cggcctgctg	8640
ccggctctgc ggccctcttc gcgtcttcgc cttcgccctc agacgagtcg gatctccctt	8700
tgggccgcct ccccgcttgg aattcgagct cgggtacctt aagaccaatg acttacaagg	8760
cagctgtaga tcttagccac tttttaaaaag aaaagggggg actggaaggg ctaattcact	8820
cccaacgaag acaagatctg ctttttgctt gtactgggtc tctctggtta gaccagatct	8880
gagcctggga gctctctggc taactaggga acccactgct taagcctcaa taaagcttgc	8940
cttgagtgtc tcaagtagtg tgtgcccgtc tgttgtgtga ctctggtaac tagagatccc	9000
tcagaccctt ttagtcagtg tggaaaatct ctagcagtag tagttcatgt catcttatta	9060
ttcagtattt ataacttgca aagaaatgaa tatcagagag tgagaggaac ttgtttattg	9120
cagcttataa tggttacaaa taaagcaata gcatcacaaa tttcacaaat aaagcatttt	9180
tttcactgca ttctagttgt ggtttgtcca aactcatcaa tgtatcttat catgtctggc	9240
tctagctatc ccgcccctaa ctccgcccac ccgccccta actccgccc a gttccgccc	9300
ttctccgccc catggctgac taattttttt tatttatgca gaggccgagg ccgcctcggc	9360
ctctgagcta ttccagaagt agtgaggagg cttttttgga ggcctaggga cgtatggcca	9420
caacctgggc tccccgggcg cgtactccac ctcacccatc atccacgctg ttttatgagt	9480
aaaggagaag aacttttcac tggagtgtgc ccaattcttg ttgaattaga tggatgatgtt	9540

F1_001_Sequence_listing

aatgggcaca aattttctgt cagtggagag ggtgaagggtg atgcaacata cggaaaactt	9600
acccttaaat ttatttgcac tactggaaaa ctacctgttc catggccaac acttgtcact	9660
actttctctt atggtgttca atgcttttca agatacccag atcatatgaa acggcatgac	9720
tttttcaaga gtgccatgcc cgaaggttat gtacaggaaa gaactatatt tttcaaagat	9780
gacgggaact acaagacacg tgctgaagtc aagtttgaag gtgataccct tgттаataga	9840
atcgagttaa aaggatttga ttttaaagaa gatggaaaca ttcttggaca caaattggaa	9900
tacaactata actcacacaa tgtatacatc atggcagaca aacaaaagaa tggaatcaaa	9960
gttaacttca aaattagaca caacattgaa gatggaagcg ttcaactagc agaccattat	10020
caacaaaata ctccaattgg cgatggccct gtccttttac cagacaacca ttacctgtcc	10080
acacaatctg ccttttcgaa agatcccaac gaaaagagag accacatggt ctttcttgag	10140
tttgtaacag ctgctgggat tacacatggc atggatgaac tatacaaata ggacctccat	10200
agaagacacc gggaccgatc caataacttc gtatagcata cattatacga agttatgcct	10260
ccggactcta gcgtttaaac ttaagcttgg gaagttccta ttccgaagtt cctattctct	10320
agaaagtata ggaacttcta ccgagctcgg atccactagt ccagtgtggt ggaattctgc	10380
agatatccag cacagtggcg gccgctcgag tctagagggc ccgtttaaac ccgctgatca	10440
gcctcgactg tgcccttctag ttgccagcca tctgttgttt gcccctcccc cgtgccttcc	10500
ttgaccctgg aagggtgccac tcccactgtc ctttcctaata aaaatgagga aattgcatcg	10560
cattgtctga gtaggtgtca ttctattctg ggggggtgggg tggggcagga cagcaagggg	10620
gaggattggg aagacaatag caggcatgct ggggatgcgg tgggctctat ggcttctgag	10680
gcggaaagtt aaccctagaa agataatcat attgtgacgt acgttaaaga taatcatgcg	10740
taaaattgac gcatgtgttt tatcggctctg tatatcgagg tttatttatt aatttgaata	10800
gatattaagt tttattatat ttacacttac atactaataa taaattcaac aaacaattta	10860
tttatgttta tttatttatt aaaaaaaaaac aaaaactcaa aatttcttct ataaagtaac	10920
aaaaaccagc tgggggctcga agttcctata ctttctagag aataggaact tctatagtga	10980

F1_001_Sequence_listing

gtcgaataag ggcgacacaa aatttattct aaatgcataa taaatactga taacatctta	11040
tagtttgtat tataattttgt attatcgttg acatgtataa ttttgatatac aaaaactgat	11100
tttcccttta ttatttttcga gatttattttt cttaattctc ttttaacaaac tagaaatatt	11160
gtatatacaa aaaatcataa ataatagatg aatagtttaa ttataggtgt tcatcaatcg	11220
aaaaagcaac gtatcttatt taaagtgcgt tgcttttttc tcatttataa ggttaaataa	11280
ttctcatata tcaagcaaag tgacaggcgc ccttaaatat tctgacaaat gctctttccc	11340
taaactcccc ccataaaaaa acccgccgaa gcgggttttt acgttatttg cggattaacg	11400
attactcgtt atcagaaccg cccagggggc ccgagcttaa gactggccgt cgttttacaa	11460
cacagaaaga gtttgtagaa acgcaaaaag gccatccgtc aggggccttc tgcttagttt	11520
gatgcctggc agttccctac tctcgcttc cgcttcctcg ctcactgact cgctgcgctc	11580
ggtcgttcgg ctgcggcgag cggtatcagc tcaactcaaag gcggtataac ggttatccac	11640
agaatcaggg gataacgcag gaaagaacat gtgagcaaaa ggccagcaaa aggccaggaa	11700
ccgtaaaaag gccgcgttgc tggcgttttt ccataggctc cgccccctg acgagcatca	11760
caaaaatcga cgctcaagtc agagggtggcg aaacccgaca ggactataaa gataccaggc	11820
gtttccccct ggaagctccc tcgtgcgctc tcctgttccg accctgccgc ttaccggata	11880
cctgtccgcc tttctccctt cgggaagcgt ggcgctttct catagctcac gctgtaggta	11940
tctcagttcg gtgtaggtcg ttcgctccaa gctgggctgt gtgcacgaac cccccgttca	12000
gcccgaccgc tgcgccttat ccggtacta tcgtcttgag tccaaccgg taagacacga	12060
cttatcgcca ctggcagcag ccaactggtaa caggattagc agagcgaggt atgtaggcgg	12120
tgctacagag ttcttgaagt ggtgggctaa ctacggctac actagaagaa cagtatttgg	12180
tatctgcgct ctgctgaagc cagttacctt cggaaaaaga gttggtagct cttgatccgg	12240
caaacaaacc accgctggta gcggtggtt ttttgtttgc aagcagcaga ttacgcgcag	12300
aaaaaaagga tctcaagaag atcctttgat cttttctacg gggcttgacg ctcagtggaa	12360
cgacgcgcgc gtaactcacg ttaagggatt ttggatcatga gcttgcgccg tcccgtcaag	12420

F1_001_Sequence_listing

tcagcgtaat gctctgcttt tagaaaaact catcgagcat caaatgaaac tgcaatttat	12480
tcatatcagg attatcaata ccatatTTTT gaaaaagccg tttctgtaat gaaggagaaa	12540
actcaccgag gcagttccat aggatggcaa gatcctggta tcgggtctgcg attccgactc	12600
gtccaacatc aatacaacct attaatTTTcc cctcgtcaaa aataaggTTa tcaagtgaga	12660
aatcaccatg agtgacgact gaatccggTg agaatggcaa aagTTtatgc atttctTTTcc	12720
agacttgTtc aacaggccag ccattacgct cgTcatcaaa atcactcgca tcaaccaaac	12780
cgttattcat tcgtgattgc gcctgagcga ggcgaaatac gcgatcgctg ttaaaaggac	12840
aattacaaac aggaatcgag tgcaaccggc gcaggaacac tgccagcgca tcaacaatat	12900
tttcacctga atcaggatat tcttctaata cctggaacgc tgTTTTTccg gggatcgcag	12960
tggtgagtaa ccatgcatca tcaggagtac ggataaaatg cttgatggTc ggaagtggca	13020
taaattccgt cagccagTTt agtctgacca tctcatctgt aacatcattg gcaacgctac	13080
ctttgccatg tttcagaaac aactctggcg catcgggctt cccatacaag cgatagattg	13140
tcgcacctga ttgcccgaca ttatcgcgag cccatttata cccatataaa tcagcatcca	13200
tgTTTggaatt taatcgcggc ctcgacgTTt cccgttgaat atggctcata ttcttccttt	13260
ttcaatatta ttgaagcatt tatcagggtt attgtctcat gagcggatac atatttgaat	13320
gtatttagaa aaataaacia ataggggtca gtgttacaac caattaacca attctgaaca	13380
ttatcgcgag cccatttata cctgaatatg gTcataaca ccccttgTtt gcctggcggc	13440
agtagcgcg tggtcccacc tgaccccatg ccgaactcag aagtgaacg ccgtagcgcc	13500
gatggtagtg tggggactcc ccatcggaga gtagggaaact gccaggcatc aaataaaacg	13560
aaaggctcag tcgaaagact gggcctttcg cccgggctaa ttagggggTg tcgcccttat	13620
tcgactctat agtgaagTtc ctattctcta gaaagtatag gaacttctga agt	13673

<210> 84

<211> 15025

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic Dox-rapamycin inducible GAG POL ENV

<400> 84

gatatctata acaagaaaat atatatataa taagttatca cgtaagtaga acatgaaata	60
acaatataat tatcgtatga gttaaactctt aaaagtcacg taaaagataa tcatgcgtca	120
ttttgactca cgcggtcgtt atagttcaaa atcagtgaca cttaccgcat tgacaagcac	180
gcctcacggg agctccaagc ggcgactgag atgtcctaaa tgcacagcga cggattcgcg	240
ctatttagaa agagagagca atatttcaag aatgcatgcg tcaattttac gcagactatc	300
tttctagggt taagacggat cgggagatct cccgatcccc tatggtgcac tctcagtaca	360
atctgctctg atgccgcata gttaagccag tatctgctcc ctgcttggtg gttggagggtc	420
gctgagtagt gcgcgagcaa aatttaagct acaacaaggc aaggcttgac cgacaattgc	480
atgaagaatc tgcttagggt taggcgtttt gaagttccta tactttctag agaataggaa	540
cttcggaata ggaacttcgg atgcaatttc ctcattttat taggaaagga cagtgggagt	600
ggcaccttcc aggggtcaagg aaggcacggg ggagggggcaa acaacagatg gctggcaact	660
agaaggcaca gcgttagtga tacttggtggg ccagggcatt agccacacca gccaccactt	720
tctgataggc agcctgcact ggtgggggtga attccgcgga agcttggtga attgttaatt	780
tctctgtccc actccatcca ggtcgtgtga ttccaaatct gttccagaga tttattactc	840
caactagcat tccaaggcac agcagtgggtg caaatgagtt ttccagagca accccaaatc	900
cccaggagct gttgatcctt taggtatcct tccacagcca ggattcctgc ctggagctgc	960
ttgatgcccc agactgtgag ttgcaacaga tgctgttgcg cctcaatagc cctcagcaaa	1020
ttgttctgct gctgcactat accagacaat aattgtctgg cctgtaccgt cagcgtcatt	1080
gacgctgcgc ccatagtgtc tcctgctgct cccaagaacc caaggaacaa agctcctgcg	1140
gccgctccgg aattccatgt gttaatcctc atcctgtcta cttgccacac aatcatcacc	1200
tgccatctgt tttccataat ccctgatgat ctttgctttt cttcttggca ctacttttat	1260
gtcactatta tcttgtatta ctactgcccc ttcacctttc cagaggagct ttgctgggtcc	1320

F1_001_Sequence_listing

tttccaaact ggatctctgc tgtccctgta ataaacccga aaatTTtgaa tttttgtaat	1380
ttgtttttgt aattcttttag tttgtatgtc tgttgctatt atgtctacta ttctttcccc	1440
tgcactgtac cccccaatcc ccccttttct tttaaaattg tggatgaata ctgccatttg	1500
tactgctgtc ttaagatgtt cagcctgatc tcttacctgt cctataattt tctttaattc	1560
tttattcata gattctatta ctcttgact ttggggattg tagggaatgc caaattcctg	1620
cttgatcccc gccaccaac aggcggcctt aactgtagta ctggtgaaat tgctgccatt	1680
gtctgtatgt actgttttta ctggccatct tcctgctaatt ttttaagagga agtatgctgt	1740
ttcttgccct gtctctgctg gaattacttc tgcttctata tatccactgg ctacatgaac	1800
tgctaccaag ataacttttc ctcttaaagt tgtacaatct agctgccata ttcttgggct	1860
acagtctact tgtccatgca tggcttcccc ttttagctga ctttatcac agctggctac	1920
tatttctttt gctactacag gtggtagggt aaaatcacta gccattgctc tccaattact	1980
gtgatatttc tcatgttctt ctgggcctt atctattcca tctaaaaata gtactttcct	2040
gattccagca ctgaccaatt tatctacttg ttcatctcct ccaattcctt tgtgtgctgg	2100
tacccatgcc aggtagactt tttccttttt tattaactgc tctattattt gactgactaa	2160
ctctgattca ctcttatctg gttgtgcttg aatgattccc aatgcatatt gtgagtctgt	2220
cactatgttt acttctaata ccgaatcctg caaagctaga tgaattgctt gtaactcagt	2280
cttctgattt gttgtgtccg ttagggggac aactttttgt cttcctctgt cagttacata	2340
tcctgctttt cctaatttag tttccctatt ggctgcccc tctacataga aagtttctgc	2400
tcctattatg gggtctttct ctaactggta ccataacttc actaaggag gggatttgac	2460
aaactccac tcaggaatcc aggtggcttg ccaatactct gtccaccatg cttcccatgt	2520
ttccttttgt atgggtaatt taaatttagg agtctttccc catattacta tgctttctgt	2580
ggctattttt tgactgcct ctgttaattg tttcacatca ttagtgtggg cacccttcat	2640
tcttgcatatc tttcctgttt tcagattttt aaatggctct tgataaattt gatatgtcca	2700
ttggccttgc ccctgcttct gtatttctgc tattaagtct tttgatgggt cataatacac	2760

F1_001_Sequence_listing

tccatgtacc ggttctttta gaatctccct gttttctgcc agttctagct ctgcttcttc	2820
tgtagtggt actacttctg ttagtgcttt ggttccccta agaagtttac ataattgcct	2880
tactttaatc cctgcataaa tctgacttgc ccaattcaat tttcccacta atttctgtat	2940
gtcattgaca gtccagctgt ctttttctgg cagcactata ggctgtactg tccatttatc	3000
aggatggagt tcataaccca tccaaaggaa tggaggttct ttctgatgtt ttttgtctgg	3060
tgtggtaa at cccacactca acagatgttg tctcagttcc tctatttttg ttctatgctg	3120
ccctatttct aagtcagatc ctacatacaa atcatccatg tattgataga tgactatgtc	3180
tggattttgt tttctaaaag gctctaagat ttttgtcatg ctacactgga atattgctgg	3240
tgatcctttc catccctgtg gaagcacatt gtactgatat ctaatccctg gtgtctcatt	3300
gtttatacta ggtatggtaa atgcagtata cttcctgaag tctttatcta agggaaactga	3360
aaaatatgca tcgcccacat ccagtactgt tactgatttt ttctgtttta accctgcagg	3420
atgtgggtatt cctaattgaa cttcccagaa atcttgagtt ctcttattaa gttctctgaa	3480
atctactaat tttctccatt tagtactgtc ttttttcttt atggcaaata ctggagtatt	3540
gtatggattt tcaggcccaa tttttgaaat ttttccttcc ttttccattt ctgtacaaat	3600
ttctactaat gcttttattt tttcttctgt caatggccat tgtttaactt ttgggccatc	3660
cattcctggc ttttaatttta ctggtacagt ctcaatagga ctaatgggaa aatttaaagt	3720
gcagccaatc tgagtcaaca gatttcttcc aattatgttg acaggtgtag gtcctactaa	3780
tactgtacct atagctttat gtccgcagat ttctatgagt atctgatcat actgtcttac	3840
tttgataaaa cctccaattc cccctatcat ttttggtttc catcttcctg gcaaattcat	3900
ttcttcta at actgtatcat ctgctcctgt atctaataga gcttccttta attgcccccc	3960
tatctttatt gtgacgaggg gtcgctgcca aagagtgatc tgagggaagc taaaggatac	4020
agttccttgt ctatcggtc ctgcttctga gagggagttg ttgtctcttc cccaaacctg	4080
aagctctctt ctggtggggc tgttggctct ggtctgctct gaagaaaatt ccctggcctt	4140
cccttgtggg aaggccagat cttccctaaa aaattagcct gtctctcagt acaatctttc	4200

F1_001_Sequence_listing

atttgggtgtc cttcctttcc acattttcaa cagccctttt tcctaggggc cctgcaattt	4260
ttggctatgt gcccttcttt gccacaattg aaacacttaa cagtctttct ttggttccta	4320
aaattgcctt tctgtatcat tatggtagct ggatttgtta cttggctcat tgcttcagcc	4380
aaaactcttg ctttatggcc ggggtcccccc actccctgac atgctgtcat catttcttct	4440
agtgtcgctc ctgggtcccaa tgcttttaaa atagtcttac aatctgggtt cgcatttttg	4500
accaacaagg tttctgtcat ccaatttttt acctcttgtg aagcttgctc ggctcttaga	4560
gttttataga atcgggtctac atagtctcta aagggttcct ttggtccttg tcttatgtcc	4620
agaatgctgg tagggctata cattcttact attttattta atcccaggat tatccatctt	4680
ttatagattt ctctacttg gataggtgga ttatgtgtca tccatcctat ttgttcctga	4740
agggtactag tagttcctgc tatgtcactt ccccttgggt ctctcatctg gcctggtgca	4800
ataggccctg catgcactgg atgcactcta tcccattctg cagcttcctc attgatggtc	4860
tcttttaaca tttgcatggc tgcttgatgt cccccactg tgtttagcat ggtgtttaaa	4920
tcttgtgggg tggctccttc tgataatgct gaaaacatgg gtatcacttc tgggctgaaa	4980
gccttctctt ctactacttt taccatgca tttaaagttc taggtgatat ggctgatgt	5040
accatttgcc cctggatgtt ctgcactata gggtaatttt ggctgacctg attgctgtgt	5100
cctgtgtcag ctgctgcttg ctgtgctttt ttcttacttt tgttttgctc ttcctctatc	5160
ttgtctaaag cttccttgggt gtcttttatc tctatccttt gatgcacaca atagagggtt	5220
gctactgtat tatataatga tctaagttct tctgatcctg tctgaaggga tggttgtagc	5280
tgtcccagta tttgtctaca gccttctgat gtttctaaca ggccaggatt aactgcgaat	5340
cgttctagct ccctgcttgc ccatactata tgttttaatt tatatttttt ctttccccct	5400
ggccttaacc gaattttttc ccatcgatct aattctcccc cgcttaatac tgacgctctc	5460
gcacccatgg cggcggcaga tctcgaattc agatctcacg tgctttgcca aagtgatggg	5520
ccagcacaca gaccagcacg ttgcccagga gctgtgggag gaagataaga ggtatgaaca	5580
tgattagcaa aagggcctag cttggactca gaataatcca gccttatccc aaccataaaa	5640

F1_001_Sequence_listing

taaaagcaga atggtagctg gattgtagct gctattagca atatgaaacc tcttacatca	5700
gttacaattht atatgcagaa atattttatat gcagaaatat tgctattgcc ttaacccaga	5760
aattatcact gttattctttt agaatgggtgc aaagaggcat gatacattgt atcattattg	5820
ccctgaaaga aagagattag ggaaagtatt agaaataaga taaacaaaaa agtatattaa	5880
aagaagaaaag catttttttaa aattacaaat gcaaaattac cctgatttgg tcaatatgtg	5940
taccctgtta cttctcccct tcctatgaca tgaacttaac catagaaaag aaggggaaag	6000
aaaacatcaa ggggtcccata gactcacctt gaagttctca ggatccgagc tcggtaccac	6060
atgtaagctt cgaggggagg ctggatcggt cccgggtgtct tctatggagg tcaaaacagc	6120
gtggatggcg tctccaggcg atctgacggt tcactaaacg ctgcttcgcg atgtacgggc	6180
cagatatacg cgttgcgatc tgacggttca ctaaacgagc tctgcttata taggcctccc	6240
accgtacacg ccacctcgac atactcgagt ttactcccta tcagtgatag agaacgtatg	6300
aagagtttac tccctatcag tgatagagaa cgtatgcaga ctttactccc tatcagtgat	6360
agagaacgta taaggagttt actccctatc agtgatagag aacgtatgac cagtttactc	6420
cctatcagtg atagagaacg tatctacagt ttactcccta tcagtgatag agaacgtata	6480
tccagtttac tccctatcag tgatagagaa cgtataagct ttaggcgtgt acggtgggcg	6540
cctataaaaag cagagctcgt ttagtgaacc gtcagatcgc ctggagcaat tccacaacac	6600
ttttgtctta taccaacttt ccgtaccact tcctaccctc gtaaatacgtc gacgagctcg	6660
tttagtgaac cgtcagatcg cctggagacg ccctcgaagc cgcgggtgcgg gtgccagggc	6720
gtgcccttgg gctccatgtc catcatgggt ctcaagggtga acgtctctgc catattcatg	6780
gcagtactgt taactctcca aacacccacc ggtcaaattcc attggggcaa tctctctaag	6840
ataggggtgg taggaatagg aagtgcagc taaaaagtta tgactcgttc cagccatcaa	6900
tcattagtca taaaattaat gcccaatata actctcctca ataactgcac gagggtagag	6960
attgcagaat acaggagact actgagaaca gttttggaac caattagaga tgcacttaat	7020
gcaatgaccc agaataataag accggttcag agtgtagctt caagtaggag acacaagaga	7080

F1_001_Sequence_listing

tttgcgggag tagtcctggc aggtgcggcc ctaggcgttg ccacagctgc tcagataaca	7140
gccggcattg cacttcacca gtccatgctg aactctcaag ccatcgacaa tctgagagcg	7200
agcctggaaa ctactaatca ggcaattgag gcaatcagac aagcagggca ggagatgata	7260
ttggctgttc aggggtgtcca agactacatc aataatgagc tgataccgtc tatgaaccaa	7320
ctatcttgtg atttaatcgg ccagaagctc gggctcaaat tgctcagata ctatacagaa	7380
atcctgtcat tattttggccc cagcttacgg gaccccatat ctgcggagat atctatccag	7440
gctttgagct atgcgcttgg aggagacatc aataagggtgt tagaaaagct cggatacagt	7500
ggaggtgatt tactgggcat cttagagagc agaggaataa agggccggat aactcacgtc	7560
gacacagagt cctacttcat tgtcctcagt atagcctatc cgacgctgtc cgagattaag	7620
ggggtgattg tccaccggct agaggggggtc tcgtacaaca taggctctca agagtgggtat	7680
accactgtgc ccaagtatgt tgcaacccaa gggtagctta tctcgaattt tgatgagtca	7740
tcgtgtactt tcatgccaga ggggactgtg tgcagccaaa atgccttgta cccgatgagt	7800
cctctgctcc aagaatgcct ccgggggtcc accaagtcct gtgctcgtac actcgtatcc	7860
gggtcttttg ggaaccggtt cattttatca caagggaacc taatagccaa ttgtgcatca	7920
atcctttgca agtgttacac aacaggaacg atcattaatc aagaccctga caagatccta	7980
acatacattg ctgccgatca ctgcccggta gtcgaggtga acggcgtgac catccaagtc	8040
gggagcagga ggtatccaga cgctgtgtac ttgcacagaa ttgacctcggt tcctcccata	8100
tcattggaga ggttggacgt agggacaaat ctgggggaatg caattgctaa gttggaggat	8160
gccaaggaat tgttggagtc atcggaccag atattgagga gtatgaaagg tttatcgagc	8220
actagcatag tctacatcct gattgcagtg tgtcttggag ggttgatagg gatccccgct	8280
ttaatatgtt gctgcagggg gcgttgaccc ctctccctcc ccccccccta acgttactgg	8340
ccgaagccgc ttggaataag gccggtgtgc gtttgtctat atgttatctt ccaccatatt	8400
gccgtctttt ggcaatgtga gggcccgga acctggccct gtcttcttga cgagcattcc	8460
taggggtctt tcccctctcg ccaaaggaat gcaaggtctg ttgaatgtcg tgaaggaagc	8520

F1_001_Sequence_listing

agttcctctg gaagcttctt gaagacaaac aacgtctgta gcgacccttt gcaggcagcg	8580
gaacccccca cctggcgaca ggtgcctctg cggccaaaag ccacgtgtat aagatacacc	8640
tgcaaaggcg gcacaacccc agtgccacgt tgtgagttgg atagttgtgg aaagagtcaa	8700
atggctctcc tcaagcgtat tcaacaaggg gctgaaggat gcccagaagg taccctattg	8760
tatgggatct gatctggggc ctcggtacac atgctttaca tgtgtttagt cgaggttaaa	8820
aaaacgtcta ggccccccga accacgggga cgtggttttc ctttgaaaaa cacgatgata	8880
atatggccac aaccatggga agtaggatag tcattaacag agaacatctt atgattgata	8940
gaccttatgt tttgctggct gttctgtttg tcatgtttct gagcttgatc gggttgctag	9000
ccattgcagg cattagactt catcgggcag ccatctacac cgcagagatc cataaaaagcc	9060
tcagcaccaa tctagatgta actaactcaa tcgagcatca ggtcaaggac gtgctgacac	9120
cactcttcaa aatcatcggg gatgaagtgg gcctgaggac acctcagaga ttcactgacc	9180
tagtgaaaatt catctctgac aagattaaat tccttaatcc ggatagggag tacgacttca	9240
gagatctcac ttggtgtatc aacccgccag agagaatcaa attggattat gatcaatact	9300
gtgcagatgt ggctgctgaa gagctcatga atgcattggg gaactcaact ctactggaga	9360
ccagaacaac caatcagttc ctagctgtct caaagggaac ctgctcaggg cccactacaa	9420
tcagagggtca atttcaaac atgtcgctgt ccctgttaga cttgtattta ggctcagggtt	9480
acaatgtgtc atctatagtc actatgacat cccagggaat gtatggggga acttacctag	9540
tggaaaagcc taatctgagc agcaaaaggc cagagttgtc acaactgagc atgtaccgag	9600
tgtttgaagt aggtgttatc agaaatccgg gtttgggggc tccggtgttc catatgacaa	9660
actatcttga gcaaccagtc agtaatgac tcagcaactg tatggtggct ttgggggagc	9720
tcaaactcgc agccctttgt cacggggaag attctatcac aattccctat cagggatcag	9780
ggaaaagggt cagcttccag ctcgtcaagc taggtgtctg gaaatcccca accgacatgc	9840
aatcctgggt ccccttatca acggatgac cagtgataga caggctttac ctctcatctc	9900
acagagggtg tatcgctgac aaycaagcaa aatgggctgt cccgacaaca cgaacagatg	9960

F1_001_Sequence_listing

acaagttgcg aatggagaca tgcttccaac aggcgtgtaa gggtaaaatc caagcactct	10020
gcgagaatcc cgagtgggca ccattgaagg ataacaggat tccttcatac ggggtcttgt	10080
ctgttgatct gagtctgaca gttgagctta aaatcaaaat tgcttcggga ttcgggccat	10140
tgatcacaca cggttcaggg atggacctat acaaatccaa ccacaacaat gtgtattggc	10200
tgactatccc rccaatgaag aacctagcct taggtgtaat caacacattg gagtggatac	10260
cgagattcaa ggtagtccc tacctcttca mtgtcccaat taaggaagca ggcgaagact	10320
gcatgcccc aacataccta cctgcggagg tggatgggtga tgtcaaactc agttccaatc	10380
tggtgattct acctggtcaa gatctccaat atgttttggc aacctacgat acttccaggg	10440
ttgaacatgc tgtggtttat tacgtttaca gcccagccg ctcattttct tacttttatc	10500
cttttaggtt gcctataaag ggggtcccca tcgaattaca agtggaatgc ttcacatggg	10560
acaaaaaact ctggtgccgt cacttctgtg tgcttcgga ctcagaatct ggtggacata	10620
tcactcactc tgggatgggtg ggcattgggag tcagctgcac agtcacccgg gaagatggaa	10680
ccaatcgag atagggctgc tagtgaacya atcwcattgat gtcacccaga catcaggcat	10740
accactagt gtgaaataga catcagaatt aagaaaaatg ggctccccgg gcgcgtactc	10800
cacctacccc atcatccacg ctcggcaata aaaagacaga ataaaacgca cgggtgttgg	10860
gtcgtttgtt cgccgggagc gtactccacc tcacccatca tccacgtgt tttatggata	10920
gcactgagaa cgatcatcaag cccttcatgc gcttcaaggt gcacatggag ggctccgtga	10980
acggccacga gttcgagatc gagggcgagg gcgagggcaa gccctacgag ggcacccaga	11040
ccgccaagct gcaggtgacc aaggcgggcc ccctgccctt cgcctgggac atcctgtccc	11100
cccagttcca gtacggctcc aaggtgtacg tgaagcacc cgccgacatc cccgactaca	11160
agaagctgtc cttccccgag ggcttcaagt gggagcgcgt gatgaacttc gaggacggcg	11220
gcgtgggtgac cgtgaccag gactcctccc tgcaggacgg caccttcac taccacgtga	11280
agttcatcgg cgtgaacttc ccctccgacg gccccgtaat gcagaagaag actctgggct	11340
gggagccctc caccgagcgc ctgtaccccc gcgacggcgt gctgaagggc gagatccaca	11400

F1_001_Sequence_listing

aggcgctgaa gctgaagggc ggcggccact acctggtgga gttcaagtca atctacatgg	11460
ccaagaagcc cgtgaagctg cccggctact actacgtgga ctccaagctg gacatcacct	11520
cccacaacga ggactacacc gtggtggagc agtacgagcg cgccgaggcc cgccaccacc	11580
tgttccagta ggacctccat agaagacacc gggaccgatc caataacttc gtatagcata	11640
cattatacga agttatgcct ccggactcta gcgtttaaac ttaagcttgg taccgagctc	11700
ggatccacta gtccagtgtg gtggaattct gcagatatcc agcacagtgg cggccgctcg	11760
agtctagagg gcccgtttaa acccgctgat cagcctcgac tgtgccttct agttgccagc	11820
catctgttgt ttgcccctcc cccgtgcctt ccttgaccct ggaagggtgcc actcccactg	11880
tcctttccta ataaaatgag gaaattgcat cgcatgtgt gagtaggtgt cattctattc	11940
tgggggggtgg ggtggggcag gacagcaagg gggaggattg ggaagacaat agcaggcatg	12000
ctgggggatgc ggtgggctct atggcttctg aggcggaaag ttaaccctag aaagataatc	12060
atattgtgac gtacgttaaa gataatcatg cgtaaaattg acgcatgtgt tttatcggtc	12120
tgtatatcga ggtttattta ttaatttgaa tagatattaa gttttattat atttacactt	12180
acatactaata aataaattca acaacaatt tatttatgtt tatttattta ttaaaaaaaaa	12240
acaaaaactc aaaatttctt ctataaagta acaaaaacca gctggggctc gaagttccta	12300
tactttctag agaataggaa cttctatagt gagtcgaata agggcgacac aaaatttatt	12360
ctaaatgcat aataaatact gataacatct tatagtttgt attatatttt gtattatcgt	12420
tgacatgtat aattttgata tcaaaaactg attttccctt tattattttc gagatttatt	12480
ttcttaattc tctttaacaa actagaaata ttgtatatac aaaaaatcat aaataataga	12540
tgaatagttt aattataggt gttcatcaat cgaaaaagca acgtatctta tttaaagtgc	12600
gttgcttttt tctcatthtat aaggttaaat aattctcata tatcaagcaa agtgacaggc	12660
gcccttaaat attctgacaa atgctctttc cctaaactcc ccccataaaa aaacccgccg	12720
aagcggggtt ttacgttatt tgcggattaa cgattactcg ttatcagaac cgcccagggg	12780
gcccagagctt aagactggcc gtcgttttac aacacagaaa gagtttgtag aaacgcaaaa	12840

F1_001_Sequence_listing

aggccatccg tcaggggcct tctgcttagt ttgatgcctg gcagttccct actctcgcct	12900
tccgcttcct cgctcactga ctcgctgcgc tcggtcgttc ggctgcggcg agcgggtatca	12960
gctcactcaa aggcggtaat acggttatcc acagaatcag gggataacgc aggaaagaac	13020
atgtgagcaa aaggccagca aaaggccagg aaccgtaaaa aggccgcgtt gctggcggtt	13080
ttccataggc tccgcccccc tgacgagcat cacaaaaatc gacgctcaag tcagagggtg	13140
cgaaacccga caggactata aagataccag gcgtttcccc ctggaagctc cctcgtgcgc	13200
tctcctgttc cgaccctgcc gcttaccgga tacctgtccg cttttctccc ttcgggaagc	13260
gtggcgcttt ctcatagctc acgctgtagg tatctcagtt cggtgtaggt cgttcgctcc	13320
aagctgggct gtgtgcacga accccccgtt cagcccgacc gctgcgcctt atccggtaac	13380
tatcgtcttg agtccaaccc ggtaagacac gacttatcgc cactggcagc agccactggt	13440
aacaggatta gcagagcgag gtatgtaggc ggtgctacag agttcttgaa gtggtgggct	13500
aactacggct acactagaag aacagtattt ggtatctgcg ctctgctgaa gccagttacc	13560
ttcggaaaaa gagttggtag ctcttgatcc ggcaaacaaa ccaccgctgg tagcggtggt	13620
ttttttgttt gcaagcagca gattacgcgc agaaaaaaag gatctcaaga agatcctttg	13680
atcttttcta cggggtctga cgctcagtgg aacgacgcgc gcgtaactca cgtaaggga	13740
ttttggtcat gagcttgcgc cgtcccgta agtcagcgta atgctctgct tttagaaaaa	13800
ctcatcgagc atcaaatgaa actgcaatth attcatatca ggattatcaa taccatattt	13860
ttgaaaaagc cgtttctgta atgaaggaga aaactcaccg aggcagttcc ataggatggc	13920
aagatcctgg tatcgggtctg cgattccgac tcgtccaaca tcaatacaac ctattaattt	13980
cccctcgtca aaaataaggt tatcaagtga gaaatcacca tgagtacga ctgaatccgg	14040
tgagaatggc aaaagtttat gcatttcttt ccagacttgt tcaacaggcc agccattacg	14100
ctcgtcatca aaatcactcg catcaaccaa accgttattc attcgtgatt gcgcctgagc	14160
gaggcgaaat acgcgatcgc tggtaaaaagg acaattacaa acaggaatcg agtgcaaccg	14220
gcgcaggaac actgccagcg catcaacaat attttcacct gaatcaggat attcttctaa	14280

F1_001_Sequence_listing

tacctggaac gctgtttttc cggggatcgc agtggtagt aaccatgcat catcaggagt	14340
acggataaaa tgcttgatgg tcggaagtgg cataaattcc gtcagccagt ttagtctgac	14400
catctcatct gtaacatcat tggcaacgct acctttgcca tgtttcagaa acaactctgg	14460
cgcacgggc ttcccataca agcgatagat tgtcgcacct gattgcccga cattatcgcg	14520
agcccattta taccatata aatcagcatc catgttggaa tttaatcgcg gcctcgacgt	14580
ttcccgttga atatggctca tattcttcct ttttcaatat tattgaagca tttatcaggg	14640
ttattgtctc atgagcggat acatatttga atgtatttag aaaaataaac aaataggggt	14700
cagtgttaca accaattaac caattctgaa cattatcgcg agcccattta tacctgaata	14760
tggctcataa cacccttgt ttgcctggcg gcagtagcgc ggtgggtccca cctgacccca	14820
tgccgaactc agaagtgaac cgccgtagcg ccgatggtag tgtggggact ccccatgcga	14880
gagtagggaa ctgccaggca tcaaataaaa cgaaaggctc agtcgaaaga ctgggccttt	14940
cgccggggct aattaggggg tgctgcccctt attcgactct atagtgaagt tcctattctc	15000
tagaaagtat aggaacttct gaagt	15025

<210> 85

<211> 6584

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic Rapamycin-inducible TET activator

<400> 85

gatattctata acaagaaaat atatataata taagttatca cgtaagtaga acatgaaata	60
acaatataat tatcgtatga gttaaattctt aaaagtcacg taaaagataa tcatgcgtca	120
ttttgactca cgcggtcgtt atagttcaaa atcagtgaca cttaccgcat tgacaagcac	180
gcctcacggg agctccaagc ggcgactgag atgtcctaaa tgcacagcga cggattcgcg	240
ctatttagaa agagagagca atatttcaag aatgcatgcg tcaattttac gcagactatc	300
tttctagggt taagacggat cgggagatct cccgatcccc tatggtgcac tctcagtaca	360

F1_001_Sequence_listing

atctgctctg atgccgcata gttaagccag tatctgctcc ctgcttgtgt gttggaggtc	420
gctgagtagt gcgcgagcaa aatttaagct acaacaaggc aaggcttgac cgacaattgc	480
atgaagaatc tgcttagggg taggcgtttt gcgctgcttc gcgatgtacg ggccagatat	540
acgcgttctc catagaagac accgaataaa atatctttat tttcattaca tctgtgtgtt	600
ggttttttgt gtgaatcgat agtactaaca tacgctctcc atcaaaacaa aacgaaacaa	660
aacaaactag caaaataggc tgtccccagt gcaagtgcag gtgccagaac atttctctgg	720
accgatccaa taacttcgta tagcatacat tatacgaagt tatgcctccg gactctagcg	780
ttttagttat tactagcgct accggactca gatctcgagc tcaagcttcg aattctgcag	840
tcgacggtag cgcggttac gcgtgctagc taatgatggg cgctcgagta atgatgggcg	900
gtcgactaat gatgggcgct cgagtaatga tgggcgctta gctaataatg ggcgctcgag	960
taatgatggg cggtcgacta atgatgggcg ctcgagtaat gatgggcgtc tagctaata	1020
tgggcgctcg agtaataatg ggcggtcgac taatgatggg cgctcgagta atgatgggcg	1080
tctagaacgc gaattaattc aacattttga ccccccata atatttttcc agaattaaca	1140
gtataaattg catctcttgt tcaagagttc cctatcactc tctttaatca ctactcacag	1200
taacctcaac tcctgccaca agcttgccct gcagcgggaa ttccaaactt aagcttggtg	1260
ccgagctcgg atccactagt ccagtgtggt ggaattctgc agatatccag cacagtggcg	1320
gccgctcgag tctagagggc ccgttttaaac ccgctgatca atgtctagac tggacaagag	1380
caaagtcata aactctgctc tggaattact caatggagtc ggtatcgaag gcctgacgac	1440
aaggaaaactc gctcaaaaagc tgggagttga gcagcctacc ctgtactggc acgtgaagaa	1500
caagcgggcc ctgctcgatg ccctgccaat cgagatgctg gacaggcatc ataccactc	1560
ctgccccctg gaaggcgagt catggcaaga ctttctgcgg aacaacgcca agtcataaccg	1620
ctgtgctctc ctctcacatc gcgacggggc taaagtgcac ctcggcaccg gcccaacaga	1680
gaaacagtac gaaaccctgg aaaatcagct cgcgttcctg tgtcagcaag gcttctccct	1740
ggagaacgca ctgtacgctc tgtccgccgt gggccacttt aactgggct gcgtattgga	1800

F1_001_Sequence_listing

ggaacaggag catcaagtag caaaagagga aagagagaca cctaccaccg attctatgcc	1860
cccacttctg aaacaagcaa ttgagctgtt cgaccggcag ggagccgaac ctgccttcct	1920
tttcggcctg gaactaatca tatgtggcct ggagaaacag ctaaagtgcg aaagcggcgg	1980
gccgaccgac gcccttgacg attttgactt agacatgctc ccagccgatg cccttgacga	2040
ctttgacctt gatatgctgc ctgctgacgc tcttgacgat ttgaccttg acatgctccc	2100
cgggtaagtc cctccccccc ccctaacgtt actggccgaa gccgcttgga ataaggccgg	2160
tgtgcgtttg tctatatgtt attttccacc atattgccgt cttttggcaa tgtgagggcc	2220
cggaaacctg gccctgtctt cttgacgagc attcctaggg gtctttcccc tctcgccaaa	2280
ggaatgcaag gtctgttgaa tgtcgtgaag gaagcagttc ctctggaagc ttcttgaaga	2340
caaacaacgt ctgtagcgac cttttgcagg cagcgggaacc cccacctgg cgacagggtgc	2400
ctctgcggcc aaaagccacg tgtataagat acacctgcaa aggcggcaca accccagtgc	2460
cacgttgtga gttggatagt tgtggaaaaga gtcaaatggc tctcctcaag cgtattcaac	2520
aaggggctga aggatgcccc gaaggtagcc cattgtatgg gatctgatct ggggcctcgg	2580
tgcacatgct ttacatgtgt ttagtcgagg ttaaaaaacg tctaggcccc ccgaaccacg	2640
gggacgtggt tttcctttga aaaacacgat gataaatgga tagcactgag aacgtcatca	2700
agcccttcat gcgcttcaag gtgcacatgg agggctccgt gaacggccac gagttcgaga	2760
tcgagggcga gggcgagggc aagccctacg agggcaccca gaccgccaag ctgcagggtga	2820
ccaagggcgg cccctgccc ttcgcctggg acatcctgtc ccccagttc cagtacggct	2880
ccaaggtgta cgtgaagcac cccgccgaca tccccgacta caagaagctg tccttccccg	2940
agggcttcaa gtgggagcgc gtgatgaact tcgaggacgg cggcgtggtg accgtgaccc	3000
aggactcctc cctgcaggac ggcaccttca tctaccacgt gaagttcatc ggcgtgaact	3060
tcccctccga cggccccgta atgcagaaga agactctggg ctgggagccc tccaccgagc	3120
gcctgtaccc ccgcgacggc gtgctgaagg gcgagatcca caaggcgctg aagctgaagg	3180
gcggcggcca ctacctggtg gagttcaagt caatctacat ggccaagaag cccgtgaagc	3240

F1_001_Sequence_listing

tgcccggtcta ctactacgtg gactccaagc tggacatcac ctcccacaac gaggactaca	3300
ccgtggtgga gcagtacgag cgcgccgagg cccgccacca cctgttccag tagctcgact	3360
gtgccttcta gttgccagcc atctgttggt tgccccctccc ccgtgccttc cttgaccctg	3420
gaaggtgcca ctcccactgt cttttcctaa taaaatgagg aaattgcatc gcattgtctg	3480
agtaggtgtc attctattct ggggggtggg gtggggcagg acagcaaggg ggaggattgg	3540
gaagacaata gcaggcatgc tggggatgcg gtgggctcta tggcttctga ggcggaagt	3600
taaccctaga aagataatca tattgtgacg tacgttaaag ataatcatgc gtaaaattga	3660
cgcattgtgtt ttatcgggtct gtatatcgag gtttatttat taatttgaat agatattaag	3720
ttttattata tttaactta catactaata ataaattcaa caaacaattt atttatgttt	3780
atttatttat taaaaaaaa caaaaactca aaatttcttc tataaagtaa caaaaaccag	3840
ctggggctcg aagttcctat actttctaga gaataggaac ttctatagtg agtcgaataa	3900
gggcgacaca aaatttattc taaatgcata ataaatactg ataacatctt atagtttgta	3960
ttatattttg tattatcggt gacatgtata attttgatat caaaaactga ttttcccttt	4020
attattttcg agatttat ttcttaattct ctttaacaaa ctagaaatat tgtatataca	4080
aaaaatcata aataatagat gaatagttta attataggtg ttcattcaatc gaaaaagcaa	4140
cgtatcttat ttaaagtgcg ttgctttttt ctcatattata aggttaaata attctcatat	4200
atcaagcaaa gtgacaggcg cccttaaata ttctgacaaa tgctctttcc ctaaactccc	4260
cccataaaaa aaccgcccga agcgggtttt tacgttat ttgcggattaac gattactcgt	4320
tatcagaacc gcccaggggg cccgagctta agactggccg tcgtttttaca acacagaaag	4380
agtttgtaga aacgcaaaaa ggccatccgt caggggcctt ctgcttagtt tgatgcctgg	4440
cagttcccta ctctgcctt ccgcttcctc gctcactgac tcgctgcgct cggtcgttcg	4500
gctgcggcga gcggtatcag ctactcaaaa ggccgtaata cggttatcca cagaatcagg	4560
ggataacgca ggaaagaaca tgtgagcaaa aggccagcaa aaggccagga accgtaaaaa	4620
ggccgcgttg ctggcgtttt tccataggct ccgccccctt gacgagcatc aaaaaaatcg	4680

F1_001_Sequence_listing

acgctcaagt cagagggtggc gaaacccgac aggactataa agataccagg cgtttcccc	4740
tggaagctcc ctcgtgcgct ctctgtttcc gaccctgccg cttaccggat acctgtccgc	4800
ctttctccct tcgggaagcg tggcgctttc tcatagctca cgctgtaggt atctcagttc	4860
ggtgtaggtc gttcgctcca agctgggctg tgtgcacgaa cccccgttc agcccgaccg	4920
ctgcgctta tccggtaact atcgtcttga gtccaacccg gtaagacacg acttatcgcc	4980
actggcagca gccactggta acaggattag cagagcgagg tatgtaggcg gtgctacaga	5040
gttcttgaag tgggtgggcta actacggcta cactagaaga acagtatttg gtatctgcgc	5100
tctgctgaag ccagttacct tcggaaaaag agttggtagc tcttgatccg gcaaacaac	5160
caccgctggg agcgggtggt tttttgtttg caagcagcag attacgcgca gaaaaaaagg	5220
atctcaagaa gatcctttga tcttttctac ggggtctgac gctcagtgga acgacgcgcg	5280
cgtaactcac gttaagggat tttggcatg agcttgcgcc gtcccgtcaa gtcagcgtaa	5340
tgctctgctt ttagaaaaac tcatcgagca tcaaatgaaa ctgcaattta ttcatatcag	5400
gattatcaat accatatttt tgaaaaagcc gtttctgtaa tgaaggagaa aactcaccga	5460
ggcagttcca taggatggca agatcctggg atcgggtctgc gattccgact cgtccaacat	5520
caatacaacc tattaatttc cctcgtcaa aaataagggt atcaagtgag aaatcaccat	5580
gagtgcgcac tgaatccggg gagaatggca aaagtttatg catttctttc cagacttggt	5640
caacaggcca gccattacgc tcgtcatcaa aatcactcgc atcaaccaa ccgttattca	5700
ttcgtgattg cgcctgagcg aggcgaaata cgcgatcgt gttaaaagga caattacaaa	5760
caggaatcga gtgcaaccgg cgcaggaaca ctgccagcgc atcaacaata ttttcacctg	5820
aatcaggata ttcttcta atctggaacg ctgtttttcc ggggatcgca gtggtgagta	5880
accatgcac atcaggagta cggataaaat gcttgatggg cggaagtggc ataaattccg	5940
tcagccagtt tagtctgacc atctcatctg taacatcatt ggcaacgcta cctttgccat	6000
gtttcagaaa caactctggc gcatcgggct tcccatacaa gcgatagatt gtcgcacctg	6060
attgcccgc attatcgca gcccatatat acccatataa atcagcatcc atgttggaat	6120

F1_001_Sequence_listing

ttaatcgcgg cctcgacgtt tcccgttgaa tatggctcat attcttcctt tttcaatatt	6180
attgaagcat ttatcagggt tattgtctca tgagcggata catatttgaa tgtatttaga	6240
aaaataaaca aataggggtc agtgttacaa ccaattaacc aattctgaac attatcgcga	6300
gcccatttat acctgaatat ggctcataac accccttggt tgcctggcgg cagtagcgcg	6360
gtggtcccac ctgaccccat gccgaactca gaagtgaac gccgtagcgc cgatggtagt	6420
gtggggactc cccatgcgag agtagggaac tgccaggcat caaataaaac gaaaggctca	6480
gtcgaaagac tgggcctttc gcccgggcta attaggggggt gtcgccctta ttcgactcta	6540
tagtgaagtt cctattctct agaaagtata ggaacttctg aagt	6584

<210> 86

<211> 11528

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic Rapamycin inducer inducible REV srcVpx

<400> 86

gatatctata acaagaaaat atatatataa taagttatca cgtaagtaga acatgaaata	60
acaatataat tatcgtatga gttaaactct aaaagtcacg taaaagataa tcatgcgtca	120
ttttgactca cgcggtcggt atagttcaaa atcagtgaca cttaccgcat tgacaagcac	180
gcctcacggg agctccaagc ggcgactgag atgtcctaaa tgcacagcga cggattcgcg	240
ctatttagaa agagagagca atatttcaag aatgcatgcg tcaattttac gcagactatc	300
tttctagggt taagacggat cgggagatct cccgatcccc tatgggtgcac tctcagtaca	360
atctgctctg atgccgcata gttaagccag tatctgctcc ctgcttgtgt gttggaggctc	420
gctgagtagt gcgcgagcaa aatttaagct acaacaaggc aaggcttgac cgacaattgc	480
atgaagaatc tgcttagggt taggcgtttt gcgctgcttc gcgatgtacg ggccagatat	540
acgcgttgac attgattatt gactagttat taatagtaat caattacggg gtcattagtt	600
catagcccat atatggagtt ccgcgttaca taacttacgg taaatggccc gcctggctga	660

F1_001_Sequence_listing

ccgccaacg acccccgccc attgacgtca ataatgacgt atgttcccat agtaacgcca	720
atagggactt tccattgacg tcaatgggtg gagtattttac ggtaaactgc ccacttggca	780
gtacatcaag tgtatcatat gccaaagtacg cccctattg acgtcaatga cggtaaattg	840
cccgctggc attatgcca gtacatgacc ttatgggact ttcctacttg gcagtacatc	900
tacgtattag tcatcgctat taccatgggtg atgcgggtttt ggtagtacat caatgggcgt	960
ggatagcggg ttgactcacg gggattttcca agtctccacc ccattgacgt caatggggagt	1020
ttgttttga accaaaatca acgggacttt ccaaaatgtc gtaacaactc cgccccattg	1080
acgcaaatgg gcggtaggcg tgtacgggtg gaggtctata taagcagagc tcggcattga	1140
ttattgacta gttattaata gtaatcaatt acgggggtcat tagttcatag cccatatatg	1200
gagttccgcg ttacataact tacggtaaatt ggcccgctg gctgaccgcc caacgacccc	1260
cgccattga cgtcaataat gacgtatgtt cccatagtaa cgccaatagg gactttccat	1320
tgacgtcaat ggggtggagta ttacggtaa actgcccact tggcagtaca tcaagtgtat	1380
catatgcca gtccgcccc tattgacgtc aatgacggta aatggcccgct ctggcattat	1440
gcccagtaca tgaccttacg ggacttttctt acttggcagt acatctacgt attagtcac	1500
gctattacca tgggtgatgcg gttttggcag tacaccaatg ggcgtggata gcggtttgac	1560
tcacggggat ttccaagtct ccacccatt gacgtcaatg ggagtttggt ttggcaccaa	1620
aatcaacggg actttccaaa atgtcgtaac aactgcatc gccgccccg ttgacgcaaa	1680
tgggcggtag gcgtgtacgg tgggaggtct atataagcag agctcgttta gtgaaccgtc	1740
agatcactag aagctttatt gcggtagttt atcacagtta aattgctaac gcagtcagt	1800
cttctgacac aacagtctcg aacttaagct gcagtgactc tcttaaggta gccttgaga	1860
agttggctgt gaggcactgg gcaggtaagt atcaaggtta caagacagg ttaaggagac	1920
caatagaaac tgggcttgtc gagacagaga agactcttgc gtttctgata ggcacctatt	1980
ggtcttactg acatccactt tgcctttctc tccacagggt tccactccca gttcaattac	2040
agctcttaag gctagagtac ttaatacgac tcactatagg ctagcctcga gaattcatgg	2100

F1_001_Sequence_listing

cttctagaat cctctggcat gagatgtggc atgaaggcct ggaagaggca tctcgtttgt	2160
actttgggga aaggaacgtg aaaggcatgt ttgagggtgct ggagcccttg catgctatga	2220
tggaacgggg cccccagact ctgaaggaaa catcctttta tcaggcctat ggtcgagatt	2280
taatggaggc ccaagagtgg tgcaggaagt acatgaaatc agggaatgtc aaggacctcc	2340
tccaagcctg ggacctctat tatcatgtgt tccgacgaat ctcaaagact agagatgagt	2400
ttcccaccat ggtgtttcct tctgggcaga tcagccaggc ctgggccttg gccccggccc	2460
ctccccaagt cctgccccag gctccagccc ctgcccctgc tccagccatg gtatcagctc	2520
tggcccaggc cccagcccct gtcccagtcc tagccccagg ccctcctcag gctgtggccc	2580
cacctgcccc caagcccacc caggctgggg aaggaacgct gtcagaggcc ctgctgcagc	2640
tgcagtttga tgatgaagac ctgggggcct tgcttggaac cagcacagac ccagctgtgt	2700
tcacagacct ggcatccgtc gacaactccg agtttcagca gctgctgaac cagggcatac	2760
ctgtggcccc ccacacaact gagcccatgc tgatggagta ccctgaggct ataactcgcc	2820
tagtgacagg ggcccagagg cccccgacc cagctcctgc tccactgggg gccccggggc	2880
tccccaatgg cctcctttca ggagatgaag acttctcctc cattgcggac atggacttct	2940
cagccctgct gagtcatatc agctccacta gttattaaga attcacgct cgagcatgca	3000
tctagggcgg ccaattccgc ccctctcccc cccccccctc tccctcccc ccccctaacg	3060
ttactggccg aagccgcttg gaataaggcc ggtgtgcgtt tgtctatatg ttattttcca	3120
ccatattgcc gtcttttggc aatgtgaggg ccgggaaacc tggccctgtc ttcttgacga	3180
gcattcctag gggctctttcc cctctcgcca aaggaatgca aggtctgttg aatgtcgtga	3240
aggaagcagt tcctctggaa gcttcttgaa gacaaacaac gtctgtagcg accctttgca	3300
ggcagcggaa cccccacct ggcgacagg gcctctgcgg ccaaaagcca cgtgtataag	3360
atacacctgc aaaggcggca caaccccagt gccacgttgt gagttggata gttgtggaaa	3420
gagtcaaattg gctctcctca agcgtattca acaaggggct gaaggatgcc cagaaggtag	3480
cccattgtat gggatctgat ctggggcctc ggtgcacatg ctttacatgt gtttagtcga	3540

F1_001_Sequence_listing

ggttaaaaaa acgtctaggc cccccgaacc acggggacgt ggttttcctt tgaaaaacac	3600
gatgataagc ttgccacaac ccgggatcct ctagagtcga catggactat cctgctgcca	3660
agaggggtcaa gttggactct agagaacgcc catatgcttg ccctgtcgag tcctgcgatc	3720
gccgcttttc tcgctcggat gagcttacct gccatatccg catccacaca ggccagaagc	3780
ccttccagtg tcgaatctgc atgcgtaact tcagtcgtag tgaccacctt accacccaca	3840
tccgcaccca cacaggcggc ggccgcagga ggaagaaacg caccagcata gagaccaaca	3900
tccgtgtggc cttagagaag agtttcttgg agaatacaaaa gcctacctcg gaagagatca	3960
ctatgattgc tgatcagctc aatatggaaa aagaggatgat tcgtgtttgg ttctgtaacc	4020
gccgccagaa agaaaaaaga atcaacacta gaggagtgca ggtggaaacc atctccccgg	4080
gagacggggcg caccttcccc aagcgcggcc agacctgcgt ggtgcactac accgggatgc	4140
ttgaagatgg aaagaaatth gattcctccc gggacagaaa caagcccttt aagtttatgc	4200
taggcaagca ggaggtgatc cgaggctggg aagaaggggt tgcccagatg agtgtgggtc	4260
agagagccaa actgactata tctccagatt atgcctatgg tgccactggg caccaggca	4320
tcatcccacc acatgccact ctgctcttcg atgtggagct tctaaaactg gaagtcgagg	4380
gcgtgcaggt ggaaaccatc tccccaggag acgggcgcac cttccccaag cgcggccaga	4440
cctgcgtggg gcactacacc gggatgcttg aagatggaaa gaaatttgat tcctcccggg	4500
acagaaacaa gccctttaag tttatgctag gcaagcagga ggtgatccga ggctgggaag	4560
aaggggttgc ccagatgagt gtgggtcaga gagccaaact gactatatct ccagattatg	4620
cctatgggtg cactgggcac ccaggcatca tcccaccaca tgccactctc gtcttcgatg	4680
tggagcttct aaaactggaa actagaggag tgcaggtgga aaccatctcc ccaggagacg	4740
ggcgcacctt cccaagcgc ggccagacct gcgtggtgca ctacaccggg atgcttgaag	4800
atggaaaagaa atttgattcc tcccgggaca gaaacaagcc ctttaagttt atgctaggca	4860
agcaggaggt gatccgaggc tgggaagaag gggttgccca gatgagtgtg ggtcagagag	4920
ccaaactgac tataatctcca gattatgcct atggtgccac tgggcaccca ggcatcatcc	4980

F1_001_Sequence_listing

caccacatgc cactctcgtc ttcgatgtgg agcttctaaa actggaaact agttattaag	5040
tcgacccggg cggccgcttc ccttttagtga gggttaatgc ttcgagcaga catgataaga	5100
tacattgatg agtttggaca aaccacaact agaatgcagt gaaaaaaatg ctttatttgt	5160
gaaatttgtg atgctattgc tttatttgtg accattataa gctgcaataa acaagttaac	5220
ctccatagaa gacaccggga ccgatccaat aacttcgtat agcatacatt atacgaagtt	5280
atggctgcta gtgaacyaat cwcgatgatgt caccagaca tcaggcatac ccactagtgt	5340
gaaatagaca tcagaattaa gaaaaatggg ctccccgggc gcgtactcca cctcacccat	5400
catccacgct cggcaataaa aagacagaat aaaacgcacg ggtgttgggt cgtttgttcg	5460
ttttatggat agcactgaga acgtcatcaa gcccttcatg cgcttcaagg tgcacatgga	5520
gggctccgtg aacggccacg agttcgagat cgagggcgag ggcgaggga agccctacga	5580
gggcacccag accgccaagc tgcagggtgac caagggcggc cccctgccct tcgcctggga	5640
catcctgtcc cccagttcc agtacggctc caaggtgtac gtgaagcacc ccgccgacat	5700
ccccgactac aagaagctgt ctttccccga gggcttcaag tgggagcgcg tgatgaactt	5760
cgaggacggc ggcgtgggtga ccgtgaccca ggactcctcc ctgcaggacg gcaccttcat	5820
ctaccacgtg aagttcatcg gcgtgaactt cccctccgac ggccccgtaa tgcagaagaa	5880
gactctgggc tgggagccct ccaccgagcg cctgtacccc cgcgacggcg tgctgaaggg	5940
cgagatccac aaggcgctga agctgaaggg cggcggccac tacctgggtg agttcaagtc	6000
aatctacatg gccaaagaagc ccgtgaagct gcccggctac tactacgtgg actccaagct	6060
ggacatcacc tcccacaacg aggactacac cgtgggtggag cagtacgagc gcgccgaggc	6120
ccgccaccac ctgttccagt aggacctcca tagaagacac cgaataaaat atctttat	6180
tcattacatc tgtgtgttgg ttttttgtgt gaatcgatag tactaacata cgctctccat	6240
caaaacaaaa cgaaacaaaa caaactagca aaataggctg tccccagtgc aagtcaggt	6300
gccagaacat ttctctggac cgatccaata acttcgtata gcatacatta tacgaagtta	6360
tgctccgga ctctagcgtt ttagttatta ctagcgctac cggactcaga tctcgagctc	6420

F1_001_Sequence_listing

aagcttcgaa ttctgcagtc gacggtagcg cggcttacgc gtgctagcta atgatgggcg	6480
ctcgagtaat gatgggcggt cgactaatga tgggcgctcg agtaatgatg ggcgtctagc	6540
taatgatggg cgctcgagta atgatgggcg gtcgactaat gatgggcgct cgagtaatga	6600
tgggcgtcta gctaatgatg ggcgctcgag taatgatggg cggtcgacta atgatgggcg	6660
ctcgagtaat gatgggcgct tagaacgcga attaatcaaa cattttgaca ccccccataat	6720
atttttccag aattaacagt ataaattgca tctcttggtc aagagttccc tatcactctc	6780
tttaatcact actcacagta acctcaactc ctgccacaag cttgccctgc agcgggaatt	6840
ccaaacttaa gcttggtagc gagctcggtt ccactagttc agtgtggtgg aattctgcag	6900
atatccagca cagtggcggc cgctcgagtc tagaggggccc gtttaaaccg gctgatcaga	6960
tggcaggaag aagcgggagc agcgacgaag acctcctcaa ggcagtcaga ctcatcaagt	7020
ttctctatca aagcaaccca cctcccaacc ccgaggggac ccgacaggcc cgaaggaata	7080
gaagaagaag gtggagagag agacagagac agatccattc gattagtga cggatcctta	7140
gcacttattt gggacgatct gcggacgctg tgcctcttca gctaccaccg cttgagagac	7200
ttactcttga ttgtgacgag gattgtggaa cttctgggac gcaggggggtg ggaagccctc	7260
aaatattggt ggaatctcct acaatattgg agtcaggagc taaagaatag tccctcccc	7320
ccccctaacg ttactggccg aagccgcttg gaataaggcc ggtgtgctgt tgtctatatg	7380
ttattttcca ccatattgcc gtcttttggc aatgtgaggg ccggaacc tggccctgtc	7440
ttcttgacga gcattcctag gggcttttcc cctctcgcca aaggaatgca aggtctgttg	7500
aatgtcgtga aggaagcagt tcctctggaa gcttcttgaa gacaaacaac gtctgtagcg	7560
accctttgca ggcagcggaa cccccacct ggcgacaggc gcctctgcgg ccaaaagcca	7620
cgtgtataag atacacctgc aaaggcggca caacccagc gccacgttgt gagttggata	7680
gttggtgaaa gaggcaaatg gctctcctca agcgtattca acaaggggct gaaggatgcc	7740
cagaaggtag cccattgtat gggatctgat ctggggcctc ggtgcacatg ctttacatgt	7800
gtttagtcga ggttaaaaaa cgtctaggcc ccccgaaacca cggggacgtg gttttccttt	7860

F1_001_Sequence_listing

gaaaaacacg atgataatgg ggaggaggaa gaggaagccg aaggatccga aggcgagggt	7920
gttggcggag gcggtattaca aggacgacga tgacaagatg tcagatccca gggagagaat	7980
cccacctgga aacagtggag aagagacaat aggagaggcc ttcgaatggc taaacagaac	8040
agtagaggag ataaacagag aggcagtaaa ccacctacca agggagctga ttttccaggt	8100
ttggcaaagg tcttgggaat actggcatga tgaacaaggg atgtcacaaa gctatgtaaa	8160
atacagatac ttgtgtttta tgcaaaaggc tttattttatg cattgcaaga aaggctgtag	8220
atgtctaggg gaaggacacg gggcaggagg atggagacca ggacctcctc ctcctcccc	8280
tccaggacta gcataacctc gactgtgcct tctagttgcc agccatctgt tgtttgcccc	8340
tccccgtgc cttccttgac cctggaaggt gccactccca ctgtcctttc ctaataaaat	8400
gaggaaattg catcgcattg tctgagtagg tgtcattcta ttctgggggg tggggtgggg	8460
caggacagca agggggagga ttgggaagac aatagcaggc atgctgggga tgcggtgggc	8520
tctatggctt ctgaggcgga aagttaaccc tagaaagata atcatattgt gacgtacgtt	8580
aaagataatc atgcgtaaaa ttgacgcatg tgttttatcg gtctgtatat cgaggtttat	8640
ttattaatth gaatagatat taagttttat tataatttaca cttacatact aataataaat	8700
tcaacaaaca atttatttat gtttatttat ttattaaaaa aaaacaaaaa ctcaaaattt	8760
cttctataaa gtaacaaaaa ccagctgggg ctcgaagtgc ctatactttc tagagaatag	8820
gaacttctat agtgagtcga ataagggcga cacaaaattt attctaaatg cataataaat	8880
actgataaca tcttatagtt tgtattatat tttgtattat cgttgacatg tataattttg	8940
atatcaaaaa ctgattttcc ctttattatt ttcgagattt attttcttaa ttctctttaa	9000
caaactagaa atattgtata tacaaaaaat cataaataat agatgaatag tttaattata	9060
ggtgttcac aatcgaaaaa gcaacgtatc ttatttaaag tgcgttgctt ttttctcatt	9120
tataaggtta aataattctc atatatcaag caaagtgaca ggcgccctta aatattctga	9180
caaatgctct ttcctaaac tccccccata aaaaaacccg ccgaagcggg tttttacgtt	9240
atttgcggat taacgattac tcgttatcag aaccgcccag ggggcccag ctttaagactg	9300

F1_001_Sequence_listing

gccgtcgttt tacaacacag aaagagtttg tagaaacgca aaaaggccat ccgtcagggg	9360
ccttctgctt agtttgatgc ctggcagttc cctactctcg ctttccgctt cctcgtcac	9420
tgactcgctg cgctcggtcg ttcggctgcg gcgagcggta tcagctcact caaaggcgg	9480
aatacggtta tccacagaat caggggataa cgcaggaaag aacatgtgag caaaaggcca	9540
gcaaaaggcc aggaaccgta aaaaggccgc gttgctggcg tttttccata ggctccgccc	9600
ccctgacgag catcacaaaa atcgacgctc aagtcagagg tggcgaaacc cgacaggact	9660
ataaagatac caggcgtttc cccctggaag ctccctcgtg cgctctcctg ttccgaccct	9720
gccgcttacc ggatacctgt ccgcctttct cccttcggga agcgtggcgc ttttcatag	9780
ctcacgctgt aggtatctca gttcgggtgta ggtcgttcgc tccaagctgg gctgtgtgca	9840
cgaaccccc gttcagcccg accgctgcgc cttatccggg aactatcgtc ttgagtccaa	9900
cccggtaaga cacgacttat cgccactggc agcagccact ggtaacagga ttagcagagc	9960
gaggtatgta ggcggtgcta cagagttctt gaagtgggtg gctaactacg gctacactag	10020
aagaacagta tttggtatct gcgctctgct gaagccagtt accttcggaa aaagagttgg	10080
tagctcttga tccggcaaac aaaccaccgc tggtagcggg ggtttttttg tttgcaagca	10140
gcagattacg cgcaaaaaa aaggatctca agaagatcct ttgatctttt ctacggggtc	10200
tgacgctcag tggaacgacg cgcgcgtaac tcacgttaag ggatttttgt catgagcttg	10260
cgccgtcccc tcaagtcagc gtaatgctct gcttttagaa aaactcatcg agcatcaaat	10320
gaaactgcaa tttattcata tcaggattat caataccata tttttgaaaa agccgtttct	10380
gtaatgaagg agaaaaactca ccgaggcagt tccataggat ggcaagatcc tggatatcgg	10440
ctgcgattcc gactcgtcca acatcaatac aacctattaa tttcccctcg tcaaaaataa	10500
ggttatcaag tgagaaatca ccatgagtga cgactgaatc cggtgagaat ggcaaaagtt	10560
tatgcatttc tttccagact tgttcaacag gccagccatt acgctcgtca tcaaaatcac	10620
tcgcatcaac caaaccgtta ttcattcgtg attgcgcctg agcgaggcga aatacgcgat	10680
cgctgttaaa aggacaatta caaacaggaa tcgagtgcaa ccggcgcagg aacactgcca	10740

F1_001_Sequence_listing

```
gcgcatacaac aatatatttca cctgaatcag gatattcttc taataacctgg aacgctgttt 10800
ttccgggggat cgcagtggtg agtaaccatg catcatcagg agtacggata aaatgcttga 10860
tggtcggaag tggcataaat tccgtcagcc agtttagtct gaccatctca tctgtaacat 10920
cattggcaac gctacctttg ccatgtttca gaaacaactc tggcgcacg ggcttcccat 10980
acaagcgata gattgtcgca cctgattgcc cgacattatc gcgagcccat ttatacccat 11040
ataaatcagc atccatgttg gaatttaatc gcggcctcga cgtttcccgt tgaatatggc 11100
tcatattctt cttttttcaa tattattgaa gcatttatca gggttattgt ctcagagcg 11160
gatacatatt tgaatgtatt tagaaaaata aacaaatagg ggtcagtggt acaaccaatt 11220
aaccaattct gaacattatc gcgagcccat ttatacctga atatggctca taacaccct 11280
tgtttgcctg gcggcagtag cgcggtgggtc ccacctgacc ccatgccgaa ctcagaagt 11340
aaacgccgta gcgccgatgg tagtgtgggg actccccatg cgagagtagg gaactgccag 11400
gcatcaaata aaacgaaagg ctcagtcgaa agactgggcc ttctgcccgg gctaattagg 11460
gggtgtcgcc cttattcgac tctatagtga agttcctatt ctctagaaag tataggaact 11520
tctgaagt 11528
```

```
<210> 87
<211> 76
<212> RNA
<213> Artificial sequence
```

```
<220>
<223> synthetic Evolved aptamer
```

```
<400> 87
gggcggcacu uauacagcga agcauaaugg cuacugacgc ccucaaacc uauuugcaga 60
cuauaagugu cgcgcg 76
```

```
<210> 88
<211> 73
<212> RNA
<213> Artificial sequence
```

F1_001_Sequence_listing

<220>

<223> synthetic Evolved aptamer

<400> 88

gggcggcacu uauacaggggu agcauaaugg cuuaggacgc cuucaaaccu aucaagacua 60

uaagugucgc gcg 73

<210> 89

<211> 75

<212> RNA

<213> Artificial sequence

<220>

<223> synthetic Evolved aptamer

<400> 89

gggcggcacu uauacaggggu agcauaaugg gcuacuugac gccuucaccu auuuguagac 60

uauaaguguc gcgcg 75

<210> 90

<211> 76

<212> RNA

<213> Artificial sequence

<220>

<223> synthetic Evolved aptamer

<400> 90

gggcggcacu uauacagcgu agcauaaugg gcugcagacg ccgucaaacc uauuugcaga 60

cuauaagugu cgcgcg 76

<210> 91

<211> 74

<212> RNA

<213> Artificial sequence

<220>

<223> synthetic Evolved aptamer

<400> 91

gggcggcacu uauacaccgu agcauaaugg gcuacugccg ccgucgaccu uuuggagacu 60

F1_001_Sequence_listing

auaagugucg cgcg 74

<210> 92
<211> 75
<212> RNA
<213> Artificial sequence

<220>
<223> synthetic Evolved aptamer

<400> 92
gggcggcacu uauacagguc agcauaaugu gcuagugcgc cuucaaaccu auuuagagac 60

uauaaguguc gcgcg 75

<210> 93
<211> 76
<212> RNA
<213> Artificial sequence

<220>
<223> synthetic Evolved aptamer

<400> 93
gggcggcacu uauacagcuu agcguaaugg cuacugacgc cguccaaacc uauuuacaga 60

cuauaagugu cgcgcg 76

<210> 94
<211> 76
<212> RNA
<213> Artificial sequence

<220>
<223> synthetic Evolved aptamer

<400> 94
gggcggcacu uauacagggg agcauaaugg gcuacugacg ccuuuaaacc uauuugagga 60

cuauaagugu cgcgcg 76

<210> 95
<211> 74

F1_001_Sequence_listing

```

<212> RNA
<213> Artificial sequence

<220>
<223> synthetic Evolved aptamer

<400> 95
gggcggcacu uauacaugga agcauaaugg gcugccgacg gcccuuaacc uuuggagacu      60
auaagugucg cgcg                                                             74

<210> 96
<211> 79
<212> RNA
<213> Artificial sequence

<220>
<223> synthetic Evolved aptamer

<400> 96
gggcggcacu uauacagauu agcauaaugg gcuacugacc ccgccggcaa accuauuuuga      60
agacuauaag ugucgcgcg                                                         79

<210> 97
<211> 75
<212> RNA
<213> Artificial sequence

<220>
<223> synthetic Evolved aptamer

<400> 97
gggcggcacu uauacagugu agcauaaugg gcuacugucg caucaaaccu auuuggagac      60
uauaaguguc gcgcg                                                             75

<210> 98
<211> 76
<212> RNA
<213> Artificial sequence

<220>
<223> synthetic Evolved aptamer

```

F1_001_Sequence_listing

<400> 98
 gggcggcacu uauacaguga agcauaaugg gcuacugaca cccuuaaacc uauuugcaga 60
 cuauaagugu cgcgcg 76

<210> 99
 <211> 76
 <212> RNA
 <213> Artificial sequence

<220>
 <223> synthetic Evolved aptamer

<400> 99
 gggcggcacu uauacagagu agcauaaugg gcuacagacg ccgucaaacc uauuuaccga 60
 cuauaagugu cgcgcg 76

<210> 100
 <211> 75
 <212> RNA
 <213> Artificial sequence

<220>
 <223> synthetic Evolved aptamer

<400> 100
 gggcggcacu uauacagggg gcauaauggg cuagugacgc cuucaaaccu auuuguagac 60
 uauaaguguc ggcgcg 75

<210> 101
 <211> 461
 <212> PRT
 <213> Homo sapiens

<400> 101

Met Thr Ile Leu Gly Thr Thr Phe Gly Met Val Phe Ser Leu Leu Gln
 1 5 10 15

Val Val Ser Gly Glu Ser Gly Tyr Ala Gln Asn Gly Asp Leu Glu Asp
 20 25 30

F1_001_Sequence_listing

Ala Glu Leu Asp Asp Tyr Ser Phe Ser Cys Tyr Ser Gln Leu Glu Val
35 40 45

Asn Gly Ser Gln His Ser Leu Thr Cys Ala Phe Glu Asp Pro Asp Val
50 55 60

Asn Thr Thr Asn Leu Glu Phe Glu Ile Cys Gly Ala Leu Val Glu Val
65 70 75 80

Lys Cys Leu Asn Phe Arg Lys Leu Gln Glu Ile Tyr Phe Ile Glu Thr
85 90 95

Lys Lys Phe Leu Leu Ile Gly Lys Ser Asn Ile Cys Val Lys Val Gly
100 105 110

Glu Lys Ser Leu Thr Cys Lys Lys Ile Asp Leu Thr Thr Ile Val Lys
115 120 125

Pro Glu Ala Pro Phe Asp Leu Ser Val Ile Tyr Arg Glu Gly Ala Asn
130 135 140

Asp Phe Val Val Thr Phe Asn Thr Ser His Leu Gln Lys Lys Tyr Val
145 150 155 160

Lys Val Leu Met His Asp Val Ala Tyr Arg Gln Glu Lys Asp Glu Asn
165 170 175

Lys Trp Thr His Val Asn Leu Ser Ser Thr Lys Leu Thr Leu Leu Gln
180 185 190

Arg Lys Leu Gln Pro Ala Ala Met Tyr Glu Ile Lys Val Arg Ser Ile
195 200 205

Pro Asp His Tyr Phe Lys Gly Phe Trp Ser Glu Trp Ser Pro Ser Tyr
210 215 220

F1_001_Sequence_listing

Tyr Phe Arg Thr Pro Glu Ile Asn Asn Ser Ser Gly Glu Met Asp Pro
225 230 235 240

Ile Leu Leu Thr Ile Ser Lys Cys His Leu Ser Phe Phe Ser Val Ala
245 250 255

Leu Leu Val Ile Leu Ala Cys Val Leu Trp Lys Lys Arg Ile Lys Pro
260 265 270

Ile Val Trp Pro Ser Leu Pro Asp His Lys Lys Thr Leu Glu His Leu
275 280 285

Cys Lys Lys Pro Arg Lys Asn Leu Asn Val Ser Phe Asn Pro Glu Ser
290 295 300

Phe Leu Asp Cys Gln Ile His Arg Val Asp Asp Ile Gln Ala Arg Asp
305 310 315 320

Glu Val Glu Gly Phe Leu Gln Asp Thr Phe Pro Gln Gln Leu Glu Glu
325 330 335

Ser Glu Lys Gln Arg Leu Gly Gly Asp Val Gln Ser Pro Asn Cys Pro
340 345 350

Ser Glu Asp Val Val Val Thr Pro Glu Ser Phe Gly Arg Asp Ser Ser
355 360 365

Leu Thr Cys Leu Ala Gly Asn Val Ser Ala Cys Asp Ala Pro Ile Leu
370 375 380

Ser Ser Ser Arg Ser Leu Asp Cys Arg Glu Ser Gly Lys Asn Gly Pro
385 390 395 400

His Val Tyr Gln Asp Leu Leu Leu Ser Leu Gly Thr Thr Asn Ser Thr
405 410 415

F1_001_Sequence_listing

Leu Pro Pro Pro Phe Ser Leu Gln Ser Gly Ile Leu Thr Leu Asn Pro
 420 425 430

Val Ala Gln Gly Gln Pro Ile Leu Thr Ser Leu Gly Ser Asn Gln Glu
 435 440 445

Glu Ala Tyr Val Thr Met Ser Ser Phe Tyr Gln Asn Gln
 450 455 460

<210> 102
 <211> 463
 <212> PRT
 <213> Homo sapiens

<400> 102

Met Thr Ile Leu Gly Thr Thr Phe Gly Met Val Phe Ser Leu Leu Gln
 1 5 10 15

Val Val Ser Gly Glu Ser Gly Tyr Ala Gln Asn Gly Asp Leu Glu Asp
 20 25 30

Ala Glu Leu Asp Asp Tyr Ser Phe Ser Cys Tyr Ser Gln Leu Glu Val
 35 40 45

Asn Gly Ser Gln His Ser Leu Thr Cys Ala Phe Glu Asp Pro Asp Val
 50 55 60

Asn Thr Thr Asn Leu Glu Phe Glu Ile Cys Gly Ala Leu Val Glu Val
 65 70 75 80

Lys Cys Leu Asn Phe Arg Lys Leu Gln Glu Ile Tyr Phe Ile Glu Thr
 85 90 95

Lys Lys Phe Leu Leu Ile Gly Lys Ser Asn Ile Cys Val Lys Val Gly
 100 105 110

F1_001_Sequence_listing

Glu Lys Ser Leu Thr Cys Lys Lys Ile Asp Leu Thr Thr Ile Val Lys
 115 120 125

Pro Glu Ala Pro Phe Asp Leu Ser Val Ile Tyr Arg Glu Gly Ala Asn
 130 135 140

Asp Phe Val Val Thr Phe Asn Thr Ser His Leu Gln Lys Lys Tyr Val
 145 150 155 160

Lys Val Leu Met His Asp Val Ala Tyr Arg Gln Glu Lys Asp Glu Asn
 165 170 175

Lys Trp Thr His Val Asn Leu Ser Ser Thr Lys Leu Thr Leu Leu Gln
 180 185 190

Arg Lys Leu Gln Pro Ala Ala Met Tyr Glu Ile Lys Val Arg Ser Ile
 195 200 205

Pro Asp His Tyr Phe Lys Gly Phe Trp Ser Glu Trp Ser Pro Ser Tyr
 210 215 220

Tyr Phe Arg Thr Pro Glu Ile Asn Asn Ser Ser Gly Glu Met Asp Pro
 225 230 235 240

Ile Phe Ser Cys Gly Pro Leu Thr Ile Ser Ile Leu Ser Phe Phe Ser
 245 250 255

Val Ala Leu Leu Val Ile Leu Ala Cys Val Leu Trp Lys Lys Arg Ile
 260 265 270

Lys Pro Ile Val Trp Pro Ser Leu Pro Asp His Lys Lys Thr Leu Glu
 275 280 285

His Leu Cys Lys Lys Pro Arg Lys Asn Leu Asn Val Ser Phe Asn Pro
 290 295 300

F1_001_Sequence_listing

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

Arg Asp Glu Val Glu Gly Phe Leu Gln Asp Thr Phe Pro Gln Gln Leu
325 330 335

Glu Glu Ser Glu Lys Gln Arg Leu Gly Gly Asp Val Gln Ser Pro Asn
340 345 350

Cys Pro Ser Glu Asp Val Val Val Thr Pro Glu Ser Phe Gly Arg Asp
355 360 365

Ser Ser Leu Thr Cys Leu Ala Gly Asn Val Ser Ala Cys Asp Ala Pro
370 375 380

Ile Leu Ser Ser Ser Arg Ser Leu Asp Cys Arg Glu Ser Gly Lys Asn
385 390 395 400

Gly Pro His Val Tyr Gln Asp Leu Leu Leu Ser Leu Gly Thr Thr Asn
405 410 415

Ser Thr Leu Pro Pro Pro Phe Ser Leu Gln Ser Gly Ile Leu Thr Leu
420 425 430

Asn Pro Val Ala Gln Gly Gln Pro Ile Leu Thr Ser Leu Gly Ser Asn
435 440 445

Gln Glu Glu Ala Tyr Val Thr Met Ser Ser Phe Tyr Gln Asn Gln
450 455 460

<210> 103
<211> 462
<212> PRT
<213> Homo sapiens

<400> 103

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

F1_001_Sequence_listing

```

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

```

F1_001_Sequence_listing

195

200

205

Pro Asp His Tyr Phe Lys Gly Phe Trp Ser Glu Trp Ser Pro Ser Tyr
210 215 220

Tyr Phe Arg Thr Pro Glu Ile Asn Asn Ser Ser Gly Glu Met Asp Pro
225 230 235 240

Ile Leu Leu Thr Cys His Leu Ile Ser Ile Leu Ser Phe Phe Ser Val
245 250 255

Ala Leu Leu Val Ile Leu Ala Cys Val Leu Trp Lys Lys Arg Ile Lys
260 265 270

Pro Ile Val Trp Pro Ser Leu Pro Asp His Lys Lys Thr Leu Glu His
275 280 285

Leu Cys Lys Lys Pro Arg Lys Asn Leu Asn Val Ser Phe Asn Pro Glu
290 295 300

Ser Phe Leu Asp Cys Gln Ile His Arg Val Asp Asp Ile Gln Ala Arg
305 310 315 320

Asp Glu Val Glu Gly Phe Leu Gln Asp Thr Phe Pro Gln Gln Leu Glu
325 330 335

Glu Ser Glu Lys Gln Arg Leu Gly Gly Asp Val Gln Ser Pro Asn Cys
340 345 350

Pro Ser Glu Asp Val Val Val Thr Pro Glu Ser Phe Gly Arg Asp Ser
355 360 365

Ser Leu Thr Cys Leu Ala Gly Asn Val Ser Ala Cys Asp Ala Pro Ile
370 375 380

Leu Ser Ser Ser Arg Ser Leu Asp Cys Arg Glu Ser Gly Lys Asn Gly

F1_001_Sequence_listing

385 390 395 400

Pro His Val Tyr Gln Asp Leu Leu Leu Ser Leu Gly Thr Thr Asn Ser
405 410 415

Thr Leu Pro Pro Pro Phe Ser Leu Gln Ser Gly Ile Leu Thr Leu Asn
420 425 430

Pro Val Ala Gln Gly Gln Pro Ile Leu Thr Ser Leu Gly Ser Asn Gln
435 440 445

Glu Glu Ala Tyr Val Thr Met Ser Ser Phe Tyr Gln Asn Gln
450 455 460

<210> 104
<211> 466
<212> PRT
<213> Homo sapiens

<400> 104

Met Thr Ile Leu Gly Thr Thr Phe Gly Met Val Phe Ser Leu Leu Gln
1 5 10 15

Val Val Ser Gly Glu Ser Gly Tyr Ala Gln Asn Gly Asp Leu Glu Asp
20 25 30

Ala Glu Leu Asp Asp Tyr Ser Phe Ser Cys Tyr Ser Gln Leu Glu Val
35 40 45

Asn Gly Ser Gln His Ser Leu Thr Cys Ala Phe Glu Asp Pro Asp Val
50 55 60

Asn Thr Thr Asn Leu Glu Phe Glu Ile Cys Gly Ala Leu Val Glu Val
65 70 75 80

Lys Cys Leu Asn Phe Arg Lys Leu Gln Glu Ile Tyr Phe Ile Glu Thr
85 90 95

F1_001_Sequence_listing

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

F1_001_Sequence_listing

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

Phe Asn Pro Glu Ser Phe Leu Asp Cys Gln Ile His Arg Val Asp Asp
305 310 315 320

Ile Gln Ala Arg Asp Glu Val Glu Gly Phe Leu Gln Asp Thr Phe Pro
325 330 335

Gln Gln Leu Glu Glu Ser Glu Lys Gln Arg Leu Gly Gly Asp Val Gln
340 345 350

Ser Pro Asn Cys Pro Ser Glu Asp Val Val Val Thr Pro Glu Ser Phe
355 360 365

Gly Arg Asp Ser Ser Leu Thr Cys Leu Ala Gly Asn Val Ser Ala Cys
370 375 380

Asp Ala Pro Ile Leu Ser Ser Ser Arg Ser Leu Asp Cys Arg Glu Ser
385 390 395 400

Gly Lys Asn Gly Pro His Val Tyr Gln Asp Leu Leu Leu Ser Leu Gly
405 410 415

Thr Thr Asn Ser Thr Leu Pro Pro Pro Phe Ser Leu Gln Ser Gly Ile
420 425 430

Leu Thr Leu Asn Pro Val Ala Gln Gly Gln Pro Ile Leu Thr Ser Leu
435 440 445

Gly Ser Asn Gln Glu Glu Ala Tyr Val Thr Met Ser Ser Phe Tyr Gln
450 455 460

Asn Gln
465

F1_001_Sequence_listing

<210> 105
 <211> 523
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic Fc-delta-30

<400> 105

Met Ser Ile Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala
 1 5 10 15

Val Leu Leu Thr Leu Gln Thr Pro Thr Gly Gln Ile His Trp Gly Asn
 20 25 30

Leu Ser Lys Ile Gly Val Val Gly Ile Gly Ser Ala Ser Tyr Lys Val
 35 40 45

Met Thr Arg Ser Ser His Gln Ser Leu Val Ile Lys Leu Met Pro Asn
 50 55 60

Ile Thr Leu Leu Asn Asn Cys Thr Arg Val Glu Ile Ala Glu Tyr Arg
 65 70 75 80

Arg Leu Leu Arg Thr Val Leu Glu Pro Ile Arg Asp Ala Leu Asn Ala
 85 90 95

Met Thr Gln Asn Ile Arg Pro Val Gln Ser Val Ala Ser Ser Arg Arg
 100 105 110

His Lys Arg Phe Ala Gly Val Val Leu Ala Gly Ala Ala Leu Gly Val
 115 120 125

Ala Thr Ala Ala Gln Ile Thr Ala Gly Ile Ala Leu His Gln Ser Met
 130 135 140

F1_001_Sequence_listing

Leu Asn Ser Gln Ala Ile Asp Asn Leu Arg Ala Ser Leu Glu Thr Thr
145 150 155 160

Asn Gln Ala Ile Glu Ala Ile Arg Gln Ala Gly Gln Glu Met Ile Leu
165 170 175

Ala Val Gln Gly Val Gln Asp Tyr Ile Asn Asn Glu Leu Ile Pro Ser
180 185 190

Met Asn Gln Leu Ser Cys Asp Leu Ile Gly Gln Lys Leu Gly Leu Lys
195 200 205

Leu Leu Arg Tyr Tyr Thr Glu Ile Leu Ser Leu Phe Gly Pro Ser Leu
210 215 220

Arg Asp Pro Ile Ser Ala Glu Ile Ser Ile Gln Ala Leu Ser Tyr Ala
225 230 235 240

Leu Gly Gly Asp Ile Asn Lys Val Leu Glu Lys Leu Gly Tyr Ser Gly
245 250 255

Gly Asp Leu Leu Gly Ile Leu Glu Ser Arg Gly Ile Lys Ala Arg Ile
260 265 270

Thr His Val Asp Thr Glu Ser Tyr Phe Ile Val Leu Ser Ile Ala Tyr
275 280 285

Pro Thr Leu Ser Glu Ile Lys Gly Val Ile Val His Arg Leu Glu Gly
290 295 300

Val Ser Tyr Asn Ile Gly Ser Gln Glu Trp Tyr Thr Thr Val Pro Lys
305 310 315 320

Tyr Val Ala Thr Gln Gly Tyr Leu Ile Ser Asn Phe Asp Glu Ser Ser
325 330 335

F1_001_Sequence_listing

Cys Thr Phe Met Pro Glu Gly Thr Val Cys Ser Gln Asn Ala Leu Tyr
 340 345 350

Pro Met Ser Pro Leu Leu Gln Glu Cys Leu Arg Gly Ser Thr Lys Ser
 355 360 365

Cys Ala Arg Thr Leu Val Ser Gly Ser Phe Gly Asn Arg Phe Ile Leu
 370 375 380

Ser Gln Gly Asn Leu Ile Ala Asn Cys Ala Ser Ile Leu Cys Lys Cys
 385 390 395 400

Tyr Thr Thr Gly Thr Ile Ile Asn Gln Asp Pro Asp Lys Ile Leu Thr
 405 410 415

Tyr Ile Ala Ala Asp His Cys Pro Val Val Glu Val Asn Gly Val Thr
 420 425 430

Ile Gln Val Gly Ser Arg Arg Tyr Pro Asp Ala Val Tyr Leu His Arg
 435 440 445

Ile Asp Leu Gly Pro Pro Ile Ser Leu Glu Arg Leu Asp Val Gly Thr
 450 455 460

Asn Leu Gly Asn Ala Ile Ala Lys Leu Glu Asp Ala Lys Glu Leu Leu
 465 470 475 480

Glu Ser Ser Asp Gln Ile Leu Arg Ser Met Lys Gly Leu Ser Ser Thr
 485 490 495

Ser Ile Val Tyr Ile Leu Ile Ala Val Cys Leu Gly Gly Leu Ile Gly
 500 505 510

Ile Pro Ala Leu Ile Cys Cys Cys Arg Gly Arg
 515 520

F1_001_Sequence_listing

<210> 106
 <211> 599
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic Hc-delta-18

<400> 106

Met Gly Ser Arg Ile Val Ile Asn Arg Glu His Leu Met Ile Asp Arg
 1 5 10 15

Pro Tyr Val Leu Leu Ala Val Leu Phe Val Met Ser Leu Ser Leu Ile
 20 25 30

Gly Leu Leu Ala Ile Ala Gly Ile Arg Leu His Arg Ala Ala Ile Tyr
 35 40 45

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

Ser Ile Glu His Gln Val Lys Asp Val Leu Thr Pro Leu Phe Lys Ile
 65 70 75 80

Ile Gly Asp Glu Val Gly Leu Arg Thr Pro Gln Arg Phe Thr Asp Leu
 85 90 95

Val Lys Phe Ile Ser Asp Lys Ile Lys Phe Leu Asn Pro Asp Arg Glu
 100 105 110

Tyr Asp Phe Arg Asp Leu Thr Trp Cys Ile Asn Pro Pro Glu Arg Ile
 115 120 125

Lys Leu Asp Tyr Asp Gln Tyr Cys Ala Asp Val Ala Ala Glu Glu Leu
 130 135 140

Met Asn Ala Leu Val Asn Ser Thr Leu Leu Glu Thr Arg Thr Thr Asn
 145 150 155 160

F1_001_Sequence_listing

Gln Phe Leu Ala Val Ser Lys Gly Asn Cys Ser Gly Pro Thr Thr Ile
165 170 175

Arg Gly Gln Phe Ser Asn Met Ser Leu Ser Leu Leu Asp Leu Tyr Leu
180 185 190

Ser Arg Gly Tyr Asn Val Ser Ser Ile Val Thr Met Thr Ser Gln Gly
195 200 205

Met Tyr Gly Gly Thr Tyr Leu Val Glu Lys Pro Asn Leu Ser Ser Lys
210 215 220

Arg Ser Glu Leu Ser Gln Leu Ser Met Tyr Arg Val Phe Glu Val Gly
225 230 235 240

Val Ile Arg Asn Pro Gly Leu Gly Ala Pro Val Phe His Met Thr Asn
245 250 255

Tyr Leu Glu Gln Pro Val Ser Asn Asp Leu Ser Asn Cys Met Val Ala
260 265 270

Leu Gly Glu Leu Lys Leu Ala Ala Leu Cys His Gly Glu Asp Ser Ile
275 280 285

Thr Ile Pro Tyr Gln Gly Ser Gly Lys Gly Val Ser Phe Gln Leu Val
290 295 300

Lys Leu Gly Val Trp Lys Ser Pro Thr Asp Met Gln Ser Trp Val Pro
305 310 315 320

Leu Ser Thr Asp Asp Pro Val Ile Asp Arg Leu Tyr Leu Ser Ser His
325 330 335

Arg Gly Val Ile Ala Asp Asn Gln Ala Lys Trp Ala Val Pro Thr Thr
340 345 350

F1_001_Sequence_listing

Arg Thr Asp Asp Lys Leu Arg Met Glu Thr Cys Phe Gln Gln Ala Cys
355 360 365

Lys Gly Lys Ile Gln Ala Leu Cys Glu Asn Pro Glu Trp Ala Pro Leu
370 375 380

Lys Asp Asn Arg Ile Pro Ser Tyr Gly Val Leu Ser Val Asp Leu Ser
385 390 395 400

Leu Thr Val Glu Leu Lys Ile Lys Ile Ala Ser Gly Phe Gly Pro Leu
405 410 415

Ile Thr His Gly Ser Gly Met Asp Leu Tyr Lys Ser Asn His Asn Asn
420 425 430

Val Tyr Trp Leu Thr Ile Pro Pro Met Lys Asn Leu Ala Leu Gly Val
435 440 445

Ile Asn Thr Leu Glu Trp Ile Pro Arg Phe Lys Val Ser Pro Asn Leu
450 455 460

Phe Thr Val Pro Ile Lys Glu Ala Gly Glu Asp Cys His Ala Pro Thr
465 470 475 480

Tyr Leu Pro Ala Glu Val Asp Gly Asp Val Lys Leu Ser Ser Asn Leu
485 490 495

Val Ile Leu Pro Gly Gln Asp Leu Gln Tyr Val Leu Ala Thr Tyr Asp
500 505 510

Thr Ser Arg Val Glu His Ala Val Val Tyr Tyr Val Tyr Ser Pro Gly
515 520 525

Arg Ser Phe Ser Tyr Phe Tyr Pro Phe Arg Leu Pro Ile Lys Gly Val
530 535 540

F1_001_Sequence_listing

Pro Ile Glu Leu Gln Val Glu Cys Phe Thr Trp Asp Gln Lys Leu Trp
545 550 555 560

Cys Arg His Phe Cys Val Leu Ala Asp Ser Glu Ser Gly Gly His Ile
565 570 575

Thr His Ser Gly Met Val Gly Met Gly Val Ser Cys Thr Val Thr Arg
580 585 590

Glu Asp Gly Thr Asn Arg Arg
595

<210> 107
<211> 529
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic DAFss-IL7-DAF fusion

<400> 107

Met Thr Val Ala Arg Pro Ser Val Pro Ala Ala Leu Pro Leu Leu Gly
1 5 10 15

Glu Leu Pro Arg Leu Leu Leu Leu Val Leu Leu Cys Leu Pro Ala Asp
20 25 30

Cys Asp Ile Glu Gly Lys Asp Gly Lys Gln Tyr Glu Ser Val Leu Met
35 40 45

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

Cys Leu Asn Asn Glu Phe Asn Phe Phe Lys Arg His Ile Cys Asp Ala
65 70 75 80

F1_001_Sequence_listing

Asn Lys Glu Gly Met Phe Leu Phe Arg Ala Ala Arg Lys Leu Arg Gln
85 90 95

Phe Leu Lys Met Asn Ser Thr Gly Asp Phe Asp Leu His Leu Leu Lys
100 105 110

Val Ser Glu Gly Thr Thr Ile Leu Leu Asn Cys Thr Gly Gln Val Lys
115 120 125

Gly Arg Lys Pro Ala Ala Leu Gly Glu Ala Gln Pro Thr Lys Ser Leu
130 135 140

Glu Glu Asn Lys Ser Leu Lys Glu Gln Lys Lys Leu Asn Asp Leu Cys
145 150 155 160

Phe Leu Lys Arg Leu Leu Gln Glu Ile Lys Thr Cys Trp Asn Lys Ile
165 170 175

Leu Met Gly Thr Lys Glu His Cys Gly Leu Pro Pro Asp Val Pro Asn
180 185 190

Ala Gln Pro Ala Leu Glu Gly Arg Thr Ser Phe Pro Glu Asp Thr Val
195 200 205

Ile Thr Tyr Lys Cys Glu Glu Ser Phe Val Lys Ile Pro Gly Glu Lys
210 215 220

Asp Ser Val Ile Cys Leu Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu
225 230 235 240

Phe Cys Asn Arg Ser Cys Glu Val Pro Thr Arg Leu Asn Ser Ala Ser
245 250 255

Leu Lys Gln Pro Tyr Ile Thr Gln Asn Tyr Phe Pro Val Gly Thr Val
260 265 270

F1_001_Sequence_listing

Val Glu Tyr Glu Cys Arg Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser
275 280 285

Pro Lys Leu Thr Cys Leu Gln Asn Leu Lys Trp Ser Thr Ala Val Glu
290 295 300

Phe Cys Lys Lys Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly
305 310 315 320

Gln Ile Asp Val Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe
325 330 335

Ser Cys Asn Thr Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys
340 345 350

Leu Ile Ser Gly Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys
355 360 365

Arg Glu Ile Tyr Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile
370 375 380

Gln Gly Glu Arg Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala
385 390 395 400

Cys Asn Lys Gly Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr
405 410 415

Val Asn Asn Asp Glu Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg
420 425 430

Gly Lys Ser Leu Thr Ser Lys Val Pro Pro Thr Val Gln Lys Pro Thr
435 440 445

Thr Val Asn Val Pro Thr Thr Glu Val Ser Pro Thr Ser Gln Lys Thr
450 455 460

F1_001_Sequence_listing

Thr Thr Lys Thr Thr Thr Pro Asn Ala Gln Ala Thr Arg Ser Thr Pro
465 470 475 480

Val Ser Arg Thr Thr Lys His Phe His Glu Thr Thr Pro Asn Lys Gly
485 490 495

Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser Gly His Thr Cys
500 505 510

Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr Met Gly Leu Leu
515 520 525

Thr

<210> 108
<211> 49
<212> DNA
<213> Artificial sequence

<220>
<223> synthetic 582-1

<400> 108
acagcttagc gtaatggcta ctgacgccgt ccaaacctat ttacagact 49

<210> 109
<211> 49
<212> DNA
<213> Artificial sequence

<220>
<223> synthetic 582-2

<400> 109
acagcttagg ataatggcta ctgacgccgt ccaaacctat ttacagact 49

<210> 110
<211> 49
<212> DNA
<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 582-3

<400> 110

acagcttagc ataatggcta ctgacgccgt ccaaacctat tcacagact 49

<210> 111

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-4

<400> 111

acagcttagc ataatggcta ctgacgccgt ccaaacctat tgacagact 49

<210> 112

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-5

<400> 112

acagcatagc ataatggcta ctgacgccgt ccaaacctat ttacagact 49

<210> 113

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-6

<400> 113

acagcttagc ataatggcta ctgacgccgt ccaaacctat gtacagact 49

<210> 114

<211> 48

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 582-7

<400> 114

acagctagcg taatggctac tgacgccgtc caaacctatt tacagact 48

<210> 115

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-8

<400> 115

acagcttagc attatggcta ctgacgccgt ccaaacctat ttacagact 49

<210> 116

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-9

<400> 116

acagttagca taatggctac tgacgccgtc caaacctatt tacagact 48

<210> 117

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-10

<400> 117

acagcttagc ataatggcta ctgacgcggt ccaaacctat ttacagact 49

<210> 118

<211> 49

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 582-11

<400> 118

acagcttagc ttaatggcta ctgacgccgt ccaaacctat ttacagact

49

<210> 119

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-12

<400> 119

acagcttagc ataatggcta ctgacgccgt ccaaaccat ttacagact

49

<210> 120

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-13

<400> 120

acagcttagc ataatggcta ctgacgccgt ccaaaccaat ttacagact

49

<210> 121

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-14

<400> 121

acagcttagc ataatggata ctgacgccgt ccaaacctat ttacagact

49

<210> 122

<211> 49

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 582-15

<400> 122

acagcttagc attgtggcta ctgacgccgt ccaaacctat ttacagact 49

<210> 123

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-16

<400> 123

acaggttagc ataatggcta ccgacgccgt ccaaacctat ttacagact 49

<210> 124

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-17

<400> 124

acagcttagc gtaatggcta ctgacgccgc ccaaacctat ttacagact 49

<210> 125

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-18

<400> 125

acagcttagc ataatggcta ctgacgccgt ccaaaactat ttccagact 49

<210> 126

<211> 49

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 582-19

<400> 126

acagcctagc ataagggcta ctgacgccgt ccaaacctat ttacagact

49

<210> 127

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-20

<400> 127

acagcttagc ataatggcta ctgaggccgt ccaaacctat ttacagact

49

<210> 128

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-21

<400> 128

acagcttacc ttaatggcta ctgacgccgt ccaaacctat ttacagact

49

<210> 129

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-22

<400> 129

acagcttagc ataatggcta ccgacgctgt ccaaacctat ttacagact

49

<210> 130

<211> 49

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 582-23

<400> 130

acagcttagc gtaatggcta ctggcgccgt ccaaacctat ttacagact

49

<210> 131

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-24

<400> 131

acagcttagc atactggcta ctgacgccgc ccaaacctat ttacagact

49

<210> 132

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-25

<400> 132

acagcttagc ataatggcta ctgacgccgt cctaacctat ttacagact

49

<210> 133

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-26

<400> 133

acaggttagc ataatgccta ctgacgccgt ccaaacctat ttacagact

49

<210> 134

<211> 49

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 582-27

<400> 134

acagcttagc ataattgcta ctgacgccgt tcaaacctat ttacagact

49

<210> 135

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-28

<400> 135

acagcttagc ataaaggcta ctgacgccgt ccaaacctat ttacagact

49

<210> 136

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-29

<400> 136

acagcttagc gtaatggcta ctgacgccgt ctaaacctat ttccagact

49

<210> 137

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-30

<400> 137

acaggttagc ataattggcta ctgacgccgt ccaaacctat ttagagact

49

<210> 138

<211> 49

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 582-31

<400> 138

acagggtagc gtaatggcta ctgacgccgt ccaaacctat ttacagact

49

<210> 139

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-32

<400> 139

acagcgtagc ataatggcta ctgacgccgt tcaaacctat ttacagact

49

<210> 140

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-33

<400> 140

acagcttagc ataatggcta ctgacgccgt ccaaactcat ttacagact

49

<210> 141

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-34

<400> 141

acagcgtagc atagtggcta ctgacgccgt ccaaacctat ttacagact

49

<210> 142

<211> 49

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 582-35

<400> 142

acagcttagt gtaatggcta ctgacgctgt ccaaacctat ttacagact 49

<210> 143

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-36

<400> 143

acagcttagc ataatggcta ctgacggcgt tcaaacctat ttacagact 49

<210> 144

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-37

<400> 144

acaggtagc ataatggcta ctgacgccgt ccaaacctat ttatagact 49

<210> 145

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 582-38

<400> 145

acagcttagc ataatggcta ctgacgccgt ccaaacctat tgtcgact 48

<210> 146

<211> 48

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 582-39

<400> 146

acagcttagc ataatggcta ctgacgccgt ccaaacctat ttacgact 48

<210> 147

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 769-1

<400> 147

acaggtcagc ataatgtgct agtgcgcctt caaacctatt tagagact 48

<210> 148

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 769-2

<400> 148

acaggtcagc ataatgtgct agtgcgcctt caaacctatt tagagact 48

<210> 149

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 769-3

<400> 149

acaggttagc ataatgtgct attgcgcctt caaacctatt tagagact 48

<210> 150

<211> 48

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 769-4

<400> 150

acaggtcagc ataatgtgct agtgcgcatt caaacctatt tagagact 48

<210> 151

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 769-5

<400> 151

acaggttagc ataatgtgct agtgcgcctt caaacctatt ttgagact 48

<210> 152

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 769-6

<400> 152

acaggttatc ataatgtgct agtgcgcctt caaacctatt tagagact 48

<210> 153

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 769-7

<400> 153

acaggttagc atgatgtgct agtgcgcctt caaacctatt tagagact 48

<210> 154

<211> 48

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 769-8

<400> 154

acaggttagc ataatgggct agtgcgcctt caaacctatt tagagact 48

<210> 155

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 769-9

<400> 155

acaggtcagc aaaatgtgca agtgcgcctt caaacctatt tagagact 48

<210> 156

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 769-10

<400> 156

acaggtcagc ataatgtgct agtgcgcctt caaacctatc tggagact 48

<210> 157

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 769-11

<400> 157

acagcttagc ataatgtgct agtgcgcctt caaacctatt tagagact 48

<210> 158

<211> 48

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 769-12

<400> 158

acaggtcagc ataatgtgct agtgcgcctt caaacctatt tacagact 48

<210> 159

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 769-13

<400> 159

acaggtcagc ataatgtgct agtgcgcctt caaacatatt tagagact 48

<210> 160

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 769-14

<400> 160

acaggtagc ataatgtgct agtgcgcctt caaacctatt tagagact 48

<210> 161

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 769-15

<400> 161

acaggttagc ataatgtgct agtgcgcctt caaacctatt tagagact 48

<210> 162

<211> 48

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 769-16

<400> 162

acaggtagc ataatgtgcc agtgcgcctt caaacctatt tagagact 48

<210> 163

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 769-17

<400> 163

acaggtcagc ataatgggct agtgcgcctt caaacctatt tagagact 48

<210> 164

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 795-1

<400> 164

acagcgaagc ataatggcta ctgacgccct caaacctat ttgcagact 49

<210> 165

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 795-2

<400> 165

acagcgaagc ataatggcta ctgacgccct caaacctat ttacagact 49

<210> 166

<211> 49

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 795-3

<400> 166

acagcgaagc ataatggctt ctgacgccct caaacctat ttgcagact

49

<210> 167

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 795-4

<400> 167

acagccaagc atactggcta ctgacgccct caaacctat ttgcagact

49

<210> 168

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 795-5

<400> 168

acagcgaagc ataatggcta ctgacgcccg caaacctat ttgcagact

49

<210> 169

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 795-6

<400> 169

acagcgaagc ataatggcta ctgacggcct caaacctat ttgcagact

49

<210> 170

<211> 49

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 795-7

<400> 170

acagcgaggc ataatggcta ctgacgccct caaacctat ttgcagact 49

<210> 171

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 795-8

<400> 171

acagcgaagc ataatggcta ctgacgcctt caaacctat ttgcagact 49

<210> 172

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 795-9

<400> 172

acagcgaagc ataatggcta cagacgccct caaacctat ttgcagact 49

<210> 173

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 795-10

<400> 173

acagcgaagc ataatggcta ctgacgccct caaacctat ttgagact 48

<210> 174

<211> 48

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 795-11

<400> 174

acagcgaagc ataatggcta ctgacgccct caaacctat tgtcgact 48

<210> 175

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 795-12

<400> 175

acagccaagc ataatggcta ctgacgccct caaacctat ttgcagact 49

<210> 176

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 795-13

<400> 176

acagcgaagc ataatggcta ctgacgccct caaacctat ttggcgact 49

<210> 177

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 795-14

<400> 177

acagcgaagc ataatgtcta ctgacgccct caaacctat ttgcagact 49

<210> 178

<211> 49

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 795-15

<400> 178

acagcgaagc ataatggcta ctgacgccgt caaacctat ttgtagact

49

<210> 179

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 795-16

<400> 179

acagcgaagc ataatggcta ctgacgccct caaaccttat ttgcagact

49

<210> 180

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 795-17

<400> 180

acaggtagca taatggctac tgacgccctc aaaccttatt tgcagact

48

<210> 181

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 795-18

<400> 181

acagcgaagc ataatggcta ctgacgccct caaacctat ttctagact

49

<210> 182

<211> 49

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 795-19

<400> 182

acagcgaagc ataatggcta ctgacgccct caaacctat ttgtagact

49

<210> 183

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 935-1

<400> 183

acaggtagc ataatgggct acttgacgcc ttcacctatt tgtagact

48

<210> 184

<211> 47

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 935-2

<400> 184

acaggtagc ataatgggct acttgacgcc ttcacctatt tgagact

47

<210> 185

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 935-3

<400> 185

acaggtagc ataatgggct actttacgcc ttcacctatt tgtagact

48

<210> 186

<211> 48

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 935-4

<400> 186

acagggtagc ataatgggct acttgacgcc ttcacctatt tctagact 48

<210> 187

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 935-5

<400> 187

acagggtagc ataatgggct acttgacgcc ttcacctatt tggagact 48

<210> 188

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 935-6

<400> 188

acagggtagc atagtgggct acttgacgcc ttcacctatt tgtagact 48

<210> 189

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 935-7

<400> 189

acagggtagc atgatgggct acttgacgcc ttcacctatt tgtagact 48

<210> 190

<211> 48

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 935-8

<400> 190

acagggtagc ataatgggct acttgacgcc ttcacctatt agtagact 48

<210> 191

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 935-9

<400> 191

acagggtagc ataatgggct atttgacgcc ttcacctatt tgtagact 48

<210> 192

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 935-10

<400> 192

acagggtagc ataatgggct acttgccgcc ttcacctatt tgtagact 48

<210> 193

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 935-11

<400> 193

acagtgtagc ataattggct acttgacgcc ttcacctatt tgtagact 48

<210> 194

<211> 48

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 935-12

<400> 194

acagggtagc ataatgggct acttgacgct ttcacctttt tgtagact 48

<210> 195

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 935-13

<400> 195

acagggtagc ataaggggct acttgacgcc ttcacctatt tgtagact 48

<210> 196

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 935-14

<400> 196

acagggtagc ataatgggact acttgacgcc ttcacctatt tgtagact 48

<210> 197

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 935-15

<400> 197

acagggtagc ataatgggct acttgatgcc ttcacctatt tgtagact 48

<210> 198

<211> 49

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 946-1

<400> 198

acagcgtagc ataatgggct gcagacgccg tcaaacctat ttgcagact 49

<210> 199

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 946-2

<400> 199

acagcgtagc ataatgggct gcagacgcag tcaaacctat ttgcagact 49

<210> 200

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 946-3

<400> 200

acatgtagca taatgggcta ctgacgccgt caaacctatt tgcagact 48

<210> 201

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 946-4

<400> 201

acagcgtagc atagtgggct gcagacgccg tcaaacctat ttgcagact 49

<210> 202

<211> 49

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 946-5

<400> 202

acagtgtagc ataatgggct gcagacgcct tcaaacctat ttggagact 49

<210> 203

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 946-6

<400> 203

acagtgtagc ataatgggct gctgacgccg tcaaacctat ttgaagact 49

<210> 204

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 946-7

<400> 204

acagcgtagc ataatgggct acaggcgccg tcaaacctat ttgcagact 49

<210> 205

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 946-8

<400> 205

acagcgtagc ataatgggct actggcgccg tcaaacctat ttgcagact 49

<210> 206

<211> 48

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 946-9

<400> 206

acagcgtagc ataatgggct gcagacgccg tcaaacctat ttgagact 48

<210> 207

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 946-10

<400> 207

acaggtagca taatgggctg cagacgccgt caaacctatt tgcagact 48

<210> 208

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 946-11

<400> 208

acaggtagca taatgggctg ctgacgccgt caaacctatt tacagact 48

<210> 209

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 946-12

<400> 209

acagcgtagc atattgggct gcagacgccg tcaaacctat ttgcagact 49

<210> 210

<211> 49

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 946-13

<400> 210

acagcgtagc ataatgggct gcagacgcct tcaaacctat ttggagact 49

<210> 211

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 946-14

<400> 211

acagtgttagc ataatgggct gcagacgccg tcaaacctat ttgagact 48

<210> 212

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 946-15

<400> 212

acagcgtagc ataatgggct gctgacgccg tcaaacctat ttggagact 49

<210> 213

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 946-16

<400> 213

acagcgtagc ataatgggct gcagacgccg tcaaacctat ttacagact 49

<210> 214

<211> 49

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic 946-17

<400> 214

acagcgtagc ataatgggct gctgacgccg tcaaacctat ttgcagact 49

<210> 215

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 946-18

<400> 215

acagggtagc ataatgggct gcagacgccg tcaaacctat ttggagact 49

<210> 216

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 946-19

<400> 216

acagcgtagc ataatgggct acagacgccg tcaaacctat ttgcagact 49

<210> 217

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic 946-20

<400> 217

acagcgtcgc ataatgggct gcagacgccg tcaaacttat ttgcagact 49

<210> 218

<211> 49

<212> DNA

<213> Artificial sequence

F1_001_Sequence_listing

<220>
 <223> synthetic 946-21

 <400> 218
 acagcgtagc ataatgggct tcagacgccg tcaaacctat ttgcagact 49

 <210> 219
 <211> 48
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> synthetic 946-22

 <400> 219
 acatgtagca taatgggctg cagacgccgt caaacctatt tggagact 48

 <210> 220
 <211> 47
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> synthetic 961-1

 <400> 220
 acaccgtagc ataatgggct actgccgccg tcgacctttt ggagact 47

 <210> 221
 <211> 46
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> synthetic 996-1

 <400> 221
 acaggtagc ataatggcctt aggacgcctt caaacctatc aagact 46

 <210> 222
 <211> 49
 <212> DNA
 <213> Artificial sequence

F1_001_Sequence_listing

<220>

<223> synthetic Family 582 Consensus

<220>

<221> misc_feature

<222> (5)..(5)

<223> n at position 5 can be C, G, or no nucleotide

<220>

<221> misc_feature

<222> (6)..(6)

<223> n at position 6 can be A, C, G, T, or no nucleotide

<220>

<221> misc_feature

<222> (45)..(45)

<223> n at position 45 can be A or no nucleotide

<400> 222

acagnntasb dtwvdksmta cygrsgsbg yyywaamyhat kbhbngact

49

<210> 223

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic Family 769 Consensus

<400> 223

acagskyakc awratgkgch aktgcgcm ytaaacmtaty tdsagact

48

<210> 224

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic Family 795 Consensus

<220>

<221> misc_feature

<222> (5)..(5)

F1_001_Sequence_listing

<223> n at position 5 can be C or no nucleotide

<220>

<221> misc_feature

<222> (40)..(40)

<223> n at position 40 can be T or no nucleotide

<220>

<221> misc_feature

<222> (44)..(44)

<223> n at position 44 can be C, G, T, or no nucleotide

<400> 224

acagnswrgc atamtgkctw cwgacgscbk caaamcytan ttvnmgact

49

<210> 225

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic Family 935 Consensus

<220>

<221> misc_feature

<222> (43)..(43)

<223> n at position 43 can be G, T, or no nucleotide

<400> 225

acagkgctgc atrrkkggrct ayttkhcgcy tycacctwtt wsnagact

48

<210> 226

<211> 49

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic Family 946 Consensus

<220>

<221> misc_feature

<222> (4)..(4)

<223> n at position 4 can be G or no nucleotide

F1_001_Sequence_listing

<220>
 <221> misc_feature
 <222> (5)..(5)
 <223> n at position 5 can be C, G, T, or no nucleotide

<220>
 <221> misc_feature
 <222> (44)..(44)
 <223> n at position 44 can be A, C, G, or no nucleotide

<400> 226
 acanngtmgc atadtgggct dcwgrcgcmk tcaaayctat ttrnagact

49

<210> 227
 <211> 11
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic Membrane-targeting domain of Src-Flag-Vpx

<400> 227

Met	Gly	Ser	Ser	Lys	Ser	Lys	Pro	Lys	Asp	Pro
1				5					10	

<210> 228
 <211> 8
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic Viral protease cleavage domain

<400> 228

Lys	Ala	Arg	Val	Leu	Ala	Glu	Ala
1				5			

<210> 229
 <211> 458
 <212> PRT
 <213> Homo sapiens

<400> 229

F1_001_Sequence_listing

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

F1_001_Sequence_listing

Arg	Lys	Leu	Gln	Pro	Ala	Ala	Met	Tyr	Glu	Ile	Lys	Val	Arg	Ser	Ile	195	200	205	
Pro	Asp	His	Tyr	Phe	Lys	Gly	Phe	Trp	Ser	Glu	Trp	Ser	Pro	Ser	Tyr	210	215	220	
Tyr	Phe	Arg	Thr	Pro	Glu	Ile	Asn	Asn	Ser	Ser	Gly	Glu	Met	Asp	Pro	225	230	235	240
Ile	Leu	Leu	Thr	Ile	Ser	Ile	Leu	Ser	Phe	Phe	Ser	Val	Ala	Leu	Leu	245	250	255	
Val	Ile	Leu	Ala	Cys	Val	Leu	Trp	Lys	Lys	Arg	Ile	Lys	Pro	Ile	Val	260	265	270	
Trp	Pro	Ser	Leu	Pro	Asp	His	Lys	Lys	Thr	Leu	Glu	His	Leu	Cys	Lys	275	280	285	
Lys	Pro	Arg	Lys	Asn	Leu	Asn	Val	Ser	Phe	Asn	Pro	Glu	Ser	Phe	Leu	290	295	300	
Asp	Cys	Gln	Ile	His	Arg	Val	Asp	Asp	Ile	Gln	Ala	Arg	Asp	Glu	Val	305	310	315	320
Glu	Gly	Phe	Leu	Gln	Asp	Thr	Phe	Pro	Gln	Gln	Leu	Glu	Glu	Ser	Glu	325	330	335	
Lys	Gln	Arg	Leu	Gly	Gly	Asp	Val	Gln	Ser	Pro	Asn	Cys	Pro	Ser	Glu	340	345	350	
Asp	Val	Val	Ile	Thr	Pro	Glu	Ser	Phe	Gly	Arg	Asp	Ser	Ser	Leu	Thr	355	360	365	
Cys	Leu	Ala	Gly	Asn	Val	Ser	Ala	Cys	Asp	Ala	Pro	Ile	Leu	Ser	Ser	370	375	380	

F1_001_Sequence_listing

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

Tyr Gln Asp Leu Leu Leu Ser Leu Gly Thr Thr Asn Ser Thr Leu Pro
405 410 415

Pro Pro Phe Ser Leu Gln Ser Gly Ile Leu Thr Leu Asn Pro Val Ala
420 425 430

Gln Gly Gln Pro Ile Leu Thr Ser Leu Gly Ser Asn Gln Glu Glu Ala
435 440 445

Tyr Val Thr Met Ser Ser Phe Tyr Gln Asn
450 455

<210> 230
<211> 723
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic GFP - linker - P2A -IL7Ra IncPPCL codon(exceptP2A) and
splice optimized

<400> 230

Met Ser Gly Gly Glu Glu Leu Phe Ala Gly Ile Val Pro Val Leu Ile
1 5 10 15

Glu Leu Asp Gly Asp Val His Gly His Lys Phe Ser Val Arg Gly Glu
20 25 30

Gly Glu Gly Asp Ala Asp Tyr Gly Lys Leu Glu Ile Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

F1_001_Sequence_listing

Cys Tyr Gly Ile Gln Cys Phe Ala Arg Tyr Pro Glu His Met Lys Met
65 70 75 80

Asn Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Ile Gln Glu Arg
85 90 95

Thr Ile Gln Phe Gln Asp Asp Gly Lys Tyr Lys Thr Arg Gly Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Lys
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Ser
130 135 140

Phe Asn Ser His Asn Val Tyr Ile Arg Pro Asp Lys Ala Asn Asn Gly
145 150 155 160

Leu Glu Ala Asn Phe Lys Thr Arg His Asn Ile Glu Gly Gly Gly Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Thr Asn Val Pro Leu Gly Asp Gly Pro
180 185 190

Val Leu Ile Pro Ile Asn His Tyr Leu Ser Thr Gln Thr Lys Ile Ser
195 200 205

Lys Asp Arg Asn Glu Ala Arg Asp His Met Val Leu Leu Glu Ser Phe
210 215 220

Ser Ala Cys Cys His Thr His Gly Met Asp Glu Leu Tyr Arg Gly Ser
225 230 235 240

Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu
245 250 255

F1_001_Sequence_listing

Asn Pro Gly Pro Met Thr Ile Leu Gly Thr Thr Phe Gly Met Val Phe
260 265 270

Ser Leu Leu Gln Val Val Ser Gly Glu Ser Gly Tyr Ala Gln Asn Gly
275 280 285

Asp Leu Glu Asp Ala Glu Leu Asp Asp Tyr Ser Phe Ser Cys Tyr Ser
290 295 300

Gln Leu Glu Val Asn Gly Ser Gln His Ser Leu Thr Cys Ala Phe Glu
305 310 315 320

Asp Pro Asp Val Asn Ile Thr Asn Leu Glu Phe Glu Ile Cys Gly Ala
325 330 335

Leu Val Glu Val Lys Cys Leu Asn Phe Arg Lys Leu Gln Glu Ile Tyr
340 345 350

Phe Ile Glu Thr Lys Lys Phe Leu Leu Ile Gly Lys Ser Asn Ile Cys
355 360 365

Val Lys Val Gly Glu Lys Ser Leu Thr Cys Lys Lys Ile Asp Leu Thr
370 375 380

Thr Ile Val Lys Pro Glu Ala Pro Phe Asp Leu Ser Val Val Tyr Arg
385 390 395 400

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

Lys Lys Tyr Val Lys Val Leu Met His Asp Val Ala Tyr Arg Gln Glu
420 425 430

Lys Asp Glu Asn Lys Trp Thr His Val Asn Leu Ser Ser Thr Lys Leu
435 440 445

F1_001_Sequence_listing

Thr Leu Leu Gln Arg Lys Leu Gln Pro Ala Ala Met Tyr Glu Ile Lys
450 455 460

Val Arg Ser Ile Pro Asp His Tyr Phe Lys Gly Phe Trp Ser Glu Trp
465 470 475 480

Ser Pro Ser Tyr Tyr Phe Arg Thr Pro Glu Ile Asn Asn Ser Ser Gly
485 490 495

Glu Met Asp Pro Ile Leu Leu Pro Pro Cys Leu Thr Ile Ser Ile Leu
500 505 510

Ser Phe Phe Ser Val Ala Leu Leu Val Ile Leu Ala Cys Val Leu Trp
515 520 525

Lys Lys Arg Ile Lys Pro Ile Val Trp Pro Ser Leu Pro Asp His Lys
530 535 540

Lys Thr Leu Glu His Leu Cys Lys Lys Pro Arg Lys Asn Leu Asn Val
545 550 555 560

Ser Phe Asn Pro Glu Ser Phe Leu Asp Cys Gln Ile His Arg Val Asp
565 570 575

Asp Ile Gln Ala Arg Asp Glu Val Glu Gly Phe Leu Gln Asp Thr Phe
580 585 590

Pro Gln Gln Leu Glu Glu Ser Glu Lys Gln Arg Leu Gly Gly Asp Val
595 600 605

Gln Ser Pro Asn Cys Pro Ser Glu Asp Val Val Ile Thr Pro Glu Ser
610 615 620

Phe Gly Arg Asp Ser Ser Leu Thr Cys Leu Ala Gly Asn Val Ser Ala
625 630 635 640

F1_001_Sequence_listing

Cys Asp Ala Pro Ile Leu Ser Ser Ser Arg Ser Leu Asp Cys Arg Glu
645 650 655

Ser Gly Lys Asn Gly Pro His Val Tyr Gln Asp Leu Leu Leu Ser Leu
660 665 670

Gly Thr Thr Asn Ser Thr Leu Pro Pro Pro Phe Ser Leu Gln Ser Gly
675 680 685

Ile Leu Thr Leu Asn Pro Val Ala Gln Gly Gln Pro Ile Leu Thr Ser
690 695 700

Leu Gly Ser Asn Gln Glu Glu Ala Tyr Val Thr Met Ser Ser Phe Tyr
705 710 715 720

Gln Asn Gln

<210> 231
<211> 733
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic GFP - linker - P2A - Myc Tag - IL7Ra IncPPCL
codon(exceptP2A) and splice optimized

<400> 231

Met Ser Gly Gly Glu Glu Leu Phe Ala Gly Ile Val Pro Val Leu Ile
1 5 10 15

Glu Leu Asp Gly Asp Val His Gly His Lys Phe Ser Val Arg Gly Glu
20 25 30

Gly Glu Gly Asp Ala Asp Tyr Gly Lys Leu Glu Ile Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu

F1_001_Sequence_listing

50

55

60

Cys Tyr Gly Ile Gln Cys Phe Ala Arg Tyr Pro Glu His Met Lys Met
65 70 75 80

Asn Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Ile Gln Glu Arg
85 90 95

Thr Ile Gln Phe Gln Asp Asp Gly Lys Tyr Lys Thr Arg Gly Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Lys
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Ser
130 135 140

Phe Asn Ser His Asn Val Tyr Ile Arg Pro Asp Lys Ala Asn Asn Gly
145 150 155 160

Leu Glu Ala Asn Phe Lys Thr Arg His Asn Ile Glu Gly Gly Gly Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Thr Asn Val Pro Leu Gly Asp Gly Pro
180 185 190

Val Leu Ile Pro Ile Asn His Tyr Leu Ser Thr Gln Thr Lys Ile Ser
195 200 205

Lys Asp Arg Asn Glu Ala Arg Asp His Met Val Leu Leu Glu Ser Phe
210 215 220

Ser Ala Cys Cys His Thr His Gly Met Asp Glu Leu Tyr Arg Gly Ser
225 230 235 240

Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu

F1_001_Sequence_listing

245

250

255

Asn Pro Gly Pro Met Thr Ile Leu Gly Thr Thr Phe Gly Met Val Phe
260 265 270

Ser Leu Leu Gln Val Val Ser Gly Glu Gln Lys Leu Ile Ser Glu Glu
275 280 285

Asp Leu Glu Ser Gly Tyr Ala Gln Asn Gly Asp Leu Glu Asp Ala Glu
290 295 300

Leu Asp Asp Tyr Ser Phe Ser Cys Tyr Ser Gln Leu Glu Val Asn Gly
305 310 315 320

Ser Gln His Ser Leu Thr Cys Ala Phe Glu Asp Pro Asp Val Asn Ile
325 330 335

Thr Asn Leu Glu Phe Glu Ile Cys Gly Ala Leu Val Glu Val Lys Cys
340 345 350

Leu Asn Phe Arg Lys Leu Gln Glu Ile Tyr Phe Ile Glu Thr Lys Lys
355 360 365

Phe Leu Leu Ile Gly Lys Ser Asn Ile Cys Val Lys Val Gly Glu Lys
370 375 380

Ser Leu Thr Cys Lys Lys Ile Asp Leu Thr Thr Ile Val Lys Pro Glu
385 390 395 400

Ala Pro Phe Asp Leu Ser Val Val Tyr Arg Glu Gly Ala Asn Asp Phe
405 410 415

Val Val Thr Phe Asn Thr Ser His Leu Gln Lys Lys Tyr Val Lys Val
420 425 430

Leu Met His Asp Val Ala Tyr Arg Gln Glu Lys Asp Glu Asn Lys Trp

F1_001_Sequence_listing

435

440

445

Thr His Val Asn Leu Ser Ser Thr Lys Leu Thr Leu Leu Gln Arg Lys
450 455 460

Leu Gln Pro Ala Ala Met Tyr Glu Ile Lys Val Arg Ser Ile Pro Asp
465 470 475 480

His Tyr Phe Lys Gly Phe Trp Ser Glu Trp Ser Pro Ser Tyr Tyr Phe
485 490 495

Arg Thr Pro Glu Ile Asn Asn Ser Ser Gly Glu Met Asp Pro Ile Leu
500 505 510

Leu Pro Pro Cys Leu Thr Ile Ser Ile Leu Ser Phe Phe Ser Val Ala
515 520 525

Leu Leu Val Ile Leu Ala Cys Val Leu Trp Lys Lys Arg Ile Lys Pro
530 535 540

Ile Val Trp Pro Ser Leu Pro Asp His Lys Lys Thr Leu Glu His Leu
545 550 555 560

Cys Lys Lys Pro Arg Lys Asn Leu Asn Val Ser Phe Asn Pro Glu Ser
565 570 575

Phe Leu Asp Cys Gln Ile His Arg Val Asp Asp Ile Gln Ala Arg Asp
580 585 590

Glu Val Glu Gly Phe Leu Gln Asp Thr Phe Pro Gln Gln Leu Glu Glu
595 600 605

Ser Glu Lys Gln Arg Leu Gly Gly Asp Val Gln Ser Pro Asn Cys Pro
610 615 620

Ser Glu Asp Val Val Ile Thr Pro Glu Ser Phe Gly Arg Asp Ser Ser

625 630 635 640

F1_001_Sequence_listing

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

F1_001_Sequence_listing

Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu
245 250 255

Asn Pro Gly Pro Met Thr Ile Leu Gly Thr Thr Phe Gly Met Val Phe
260 265 270

Ser Leu Leu Gln Val Val Ser Gly Glu Gln Lys Leu Ile Ser Glu Glu
275 280 285

Asp Leu Glu Ser Gly Tyr Ala Gln Asn Gly Asp Leu Glu Asp Ala Glu
290 295 300

Leu Asp Asp Tyr Ser Phe Ser Cys Tyr Ser Gln Leu Glu Val Asn Gly
305 310 315 320

Ser Gln His Ser Leu Thr Cys Ala Phe Glu Asp Pro Asp Val Asn Ile
325 330 335

Thr Asn Leu Glu Phe Glu Ile Cys Gly Ala Leu Val Glu Val Lys Cys
340 345 350

Leu Asn Phe Arg Lys Leu Gln Glu Ile Tyr Phe Ile Glu Thr Lys Lys
355 360 365

Phe Leu Leu Ile Gly Lys Ser Asn Ile Cys Val Lys Val Gly Glu Lys
370 375 380

Ser Leu Thr Cys Lys Lys Ile Asp Leu Thr Thr Ile Val Lys Pro Glu
385 390 395 400

Ala Pro Phe Asp Leu Ser Val Val Tyr Arg Glu Gly Ala Asn Asp Phe
405 410 415

Val Val Thr Phe Asn Thr Ser His Leu Gln Lys Lys Tyr Val Lys Val
420 425 430

F1_001_Sequence_listing

Leu Met His Asp Val Ala Tyr Arg Gln Glu Lys Asp Glu Asn Lys Trp
 435 440 445

Thr His Val Asn Leu Ser Ser Thr Lys Leu Thr Leu Leu Gln Arg Lys
 450 455 460

Leu Gln Pro Ala Ala Met Tyr Glu Ile Lys Val Arg Ser Ile Pro Asp
 465 470 475 480

His Tyr Phe Lys Gly Phe Trp Ser Glu Trp Ser Pro Ser Tyr Tyr Phe
 485 490 495

Arg Thr Pro Glu Ile Asn Asn Ser Ser Gly Glu Met Asp Pro Ile Leu
 500 505 510

Leu Pro Pro Cys Leu Thr Ile Ser Ile Leu Ser Phe Phe Ser Val Ala
 515 520 525

Leu Leu Val Ile Leu Ala Cys Val Leu Trp Lys Lys Arg Ile Lys Pro
 530 535 540

Ile Val Trp Pro Ser Leu Pro Asp His Lys Lys Thr Leu Glu His Leu
 545 550 555 560

Cys Lys Lys Pro Arg Lys Val Ser Val Phe Gly Ala
 565 570

<210> 233

<211> 562

<212> PRT

<213> Artificial sequence

<220>

<223> synthetic GFP - linker - P2A - IL7RaSP - IL7RaIncPPCL C-terminal
 truncation codon(exceptP2A) and splice optimized

<400> 233

F1_001_Sequence_listing

```

Met Ser Gly Gly Glu Glu Leu Phe Ala Gly Ile Val Pro Val Leu Ile
1          5          10          15

Glu Leu Asp Gly Asp Val His Gly His Lys Phe Ser Val Arg Gly Glu
20          25          30

Gly Glu Gly Asp Ala Asp Tyr Gly Lys Leu Glu Ile Lys Phe Ile Cys
35          40          45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50          55          60

Cys Tyr Gly Ile Gln Cys Phe Ala Arg Tyr Pro Glu His Met Lys Met
65          70          75          80

Asn Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Ile Gln Glu Arg
85          90          95

Thr Ile Gln Phe Gln Asp Asp Gly Lys Tyr Lys Thr Arg Gly Glu Val
100         105         110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Lys
115         120         125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Ser
130         135         140

Phe Asn Ser His Asn Val Tyr Ile Arg Pro Asp Lys Ala Asn Asn Gly
145         150         155         160

Leu Glu Ala Asn Phe Lys Thr Arg His Asn Ile Glu Gly Gly Gly Val
165         170         175

Gln Leu Ala Asp His Tyr Gln Thr Asn Val Pro Leu Gly Asp Gly Pro
180         185         190

```

F1_001_Sequence_listing

Val	Leu	Ile	Pro	Ile	Asn	His	Tyr	Leu	Ser	Thr	Gln	Thr	Lys	Ile	Ser	195	200	205
Lys	Asp	Arg	Asn	Glu	Ala	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Ser	Phe	210	215	220
Ser	Ala	Cys	Cys	His	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Arg	Gly	Ser	225	230	235
Gly	Ala	Thr	Asn	Phe	Ser	Leu	Leu	Lys	Gln	Ala	Gly	Asp	Val	Glu	Glu	245	250	255
Asn	Pro	Gly	Pro	Met	Thr	Ile	Leu	Gly	Thr	Thr	Phe	Gly	Met	Val	Phe	260	265	270
Ser	Leu	Leu	Gln	Val	Val	Ser	Gly	Glu	Ser	Gly	Tyr	Ala	Gln	Asn	Gly	275	280	285
Asp	Leu	Glu	Asp	Ala	Glu	Leu	Asp	Asp	Tyr	Ser	Phe	Ser	Cys	Tyr	Ser	290	295	300
Gln	Leu	Glu	Val	Asn	Gly	Ser	Gln	His	Ser	Leu	Thr	Cys	Ala	Phe	Glu	305	310	315
Asp	Pro	Asp	Val	Asn	Ile	Thr	Asn	Leu	Glu	Phe	Glu	Ile	Cys	Gly	Ala	325	330	335
Leu	Val	Glu	Val	Lys	Cys	Leu	Asn	Phe	Arg	Lys	Leu	Gln	Glu	Ile	Tyr	340	345	350
Phe	Ile	Glu	Thr	Lys	Lys	Phe	Leu	Leu	Ile	Gly	Lys	Ser	Asn	Ile	Cys	355	360	365
Val	Lys	Val	Gly	Glu	Lys	Ser	Leu	Thr	Cys	Lys	Lys	Ile	Asp	Leu	Thr	370	375	380

F1_001_Sequence_listing

Thr Ile Val Lys Pro Glu Ala Pro Phe Asp Leu Ser Val Val Tyr Arg
385 390 395 400

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

Lys Lys Tyr Val Lys Val Leu Met His Asp Val Ala Tyr Arg Gln Glu
420 425 430

Lys Asp Glu Asn Lys Trp Thr His Val Asn Leu Ser Ser Thr Lys Leu
435 440 445

Thr Leu Leu Gln Arg Lys Leu Gln Pro Ala Ala Met Tyr Glu Ile Lys
450 455 460

Val Arg Ser Ile Pro Asp His Tyr Phe Lys Gly Phe Trp Ser Glu Trp
465 470 475 480

Ser Pro Ser Tyr Tyr Phe Arg Thr Pro Glu Ile Asn Asn Ser Ser Gly
485 490 495

Glu Met Asp Pro Ile Leu Leu Pro Pro Cys Leu Thr Ile Ser Ile Leu
500 505 510

Ser Phe Phe Ser Val Ala Leu Leu Val Ile Leu Ala Cys Val Leu Trp
515 520 525

Lys Lys Arg Ile Lys Pro Ile Val Trp Pro Ser Leu Pro Asp His Lys
530 535 540

Lys Thr Leu Glu His Leu Cys Lys Lys Pro Arg Lys Val Ser Val Phe
545 550 555 560

Gly Ala

F1_001_Sequence_listing

<210> 234
 <211> 824
 <212> PRT
 <213> Artificial sequence

 <220>
 <223> synthetic GFP - linker - P2A - eTag - IL7RaIncPPCL N-terminal
 deletion codon(exceptP2A) and splice optimized

 <400> 234

 Met Ser Gly Gly Glu Glu Leu Phe Ala Gly Ile Val Pro Val Leu Ile
 1 5 10 15

 Glu Leu Asp Gly Asp Val His Gly His Lys Phe Ser Val Arg Gly Glu
 20 25 30

 Gly Glu Gly Asp Ala Asp Tyr Gly Lys Leu Glu Ile Lys Phe Ile Cys
 35 40 45

 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

 Cys Tyr Gly Ile Gln Cys Phe Ala Arg Tyr Pro Glu His Met Lys Met
 65 70 75 80

 Asn Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Ile Gln Glu Arg
 85 90 95

 Thr Ile Gln Phe Gln Asp Asp Gly Lys Tyr Lys Thr Arg Gly Glu Val
 100 105 110

 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Lys
 115 120 125

 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Ser
 130 135 140

F1_001_Sequence_listing

Phe Asn Ser His Asn Val Tyr Ile Arg Pro Asp Lys Ala Asn Asn Gly
145 150 155 160

Leu Glu Ala Asn Phe Lys Thr Arg His Asn Ile Glu Gly Gly Gly Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Thr Asn Val Pro Leu Gly Asp Gly Pro
180 185 190

Val Leu Ile Pro Ile Asn His Tyr Leu Ser Thr Gln Thr Lys Ile Ser
195 200 205

Lys Asp Arg Asn Glu Ala Arg Asp His Met Val Leu Leu Glu Ser Phe
210 215 220

Ser Ala Cys Cys His Thr His Gly Met Asp Glu Leu Tyr Arg Gly Ser
225 230 235 240

Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu
245 250 255

Asn Pro Gly Pro Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu
260 265 270

Leu Pro His Pro Ala Phe Leu Leu Ile Pro Arg Lys Val Cys Asn Gly
275 280 285

Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn
290 295 300

Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile
305 310 315 320

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

F1_001_Sequence_listing

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

Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala
355 360 365

Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln
370 375 380

Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg
385 390 395 400

Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys
405 410 415

Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr
420 425 430

Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys
435 440 445

Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys
450 455 460

Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg
465 470 475 480

Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg
485 490 495

Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu
500 505 510

Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys
515 520 525

F1_001_Sequence_listing

Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val Lys Thr Cys
530 535 540

Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp Lys Tyr Ala
545 550 555 560

Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys Thr Tyr Gly
565 570 575

Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly Pro Glu Ile
580 585 590

Asn Asn Ser Ser Gly Glu Met Asp Pro Ile Leu Leu Pro Pro Cys Leu
595 600 605

Thr Ile Ser Ile Leu Ser Phe Phe Ser Val Ala Leu Leu Val Ile Leu
610 615 620

Ala Cys Val Leu Trp Lys Lys Arg Ile Lys Pro Ile Val Trp Pro Ser
625 630 635 640

Leu Pro Asp His Lys Lys Thr Leu Glu His Leu Cys Lys Lys Pro Arg
645 650 655

Lys Asn Leu Asn Val Ser Phe Asn Pro Glu Ser Phe Leu Asp Cys Gln
660 665 670

Ile His Arg Val Asp Asp Ile Gln Ala Arg Asp Glu Val Glu Gly Phe
675 680 685

Leu Gln Asp Thr Phe Pro Gln Gln Leu Glu Glu Ser Glu Lys Gln Arg
690 695 700

Leu Gly Gly Asp Val Gln Ser Pro Asn Cys Pro Ser Glu Asp Val Val
705 710 715 720

F1_001_Sequence_listing

Ile Thr Pro Glu Ser Phe Gly Arg Asp Ser Ser Leu Thr Cys Leu Ala
725 730 735

Gly Asn Val Ser Ala Cys Asp Ala Pro Ile Leu Ser Ser Ser Arg Ser
740 745 750

Leu Asp Cys Arg Glu Ser Gly Lys Asn Gly Pro His Val Tyr Gln Asp
755 760 765

Leu Leu Leu Ser Leu Gly Thr Thr Asn Ser Thr Leu Pro Pro Pro Phe
770 775 780

Ser Leu Gln Ser Gly Ile Leu Thr Leu Asn Pro Val Ala Gln Gly Gln
785 790 795 800

Pro Ile Leu Thr Ser Leu Gly Ser Asn Gln Glu Glu Ala Tyr Val Thr
805 810 815

Met Ser Ser Phe Tyr Gln Asn Gln
820

<210> 235
<211> 593
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic MV(ed)-HD24

<400> 235

Met Asn Arg Glu His Leu Met Ile Asp Arg Pro Tyr Val Leu Leu Ala
1 5 10 15

Val Leu Phe Val Met Ser Leu Ser Leu Ile Gly Leu Leu Ala Ile Ala
20 25 30

Gly Ile Arg Leu His Arg Ala Ala Ile Tyr Thr Ala Glu Ile His Lys
35 40 45

F1_001_Sequence_listing

Ser Leu Ser Thr Asn Leu Asp Val Thr Asn Ser Ile Glu His Gln Val
50 55 60

Lys Asp Val Leu Thr Pro Leu Phe Lys Ile Ile Gly Asp Glu Val Gly
65 70 75 80

Leu Arg Thr Pro Gln Arg Phe Thr Asp Leu Val Lys Phe Ile Ser Asp
85 90 95

Lys Ile Lys Phe Leu Asn Pro Asp Arg Glu Tyr Asp Phe Arg Asp Leu
100 105 110

Thr Trp Cys Ile Asn Pro Pro Glu Arg Ile Lys Leu Asp Tyr Asp Gln
115 120 125

Tyr Cys Ala Asp Val Ala Ala Glu Glu Leu Met Asn Ala Leu Val Asn
130 135 140

Ser Thr Leu Leu Glu Thr Arg Thr Thr Asn Gln Phe Leu Ala Val Ser
145 150 155 160

Lys Gly Asn Cys Ser Gly Pro Thr Thr Ile Arg Gly Gln Phe Ser Asn
165 170 175

Met Ser Leu Ser Leu Leu Asp Leu Tyr Leu Ser Arg Gly Tyr Asn Val
180 185 190

Ser Ser Ile Val Thr Met Thr Ser Gln Gly Met Tyr Gly Gly Thr Tyr
195 200 205

Leu Val Glu Lys Pro Asn Leu Ser Ser Lys Arg Ser Glu Leu Ser Gln
210 215 220

Leu Ser Met Tyr Arg Val Phe Glu Val Gly Val Ile Arg Asn Pro Gly
225 230 235 240

F1_001_Sequence_listing

Leu Gly Ala Pro Val Phe His Met Thr Asn Tyr Leu Glu Gln Pro Val
245 250 255

Ser Asn Asp Leu Ser Asn Cys Met Val Ala Leu Gly Glu Leu Lys Leu
260 265 270

Ala Ala Leu Cys His Gly Glu Asp Ser Ile Thr Ile Pro Tyr Gln Gly
275 280 285

Ser Gly Lys Gly Val Ser Phe Gln Leu Val Lys Leu Gly Val Trp Lys
290 295 300

Ser Pro Thr Asp Met Gln Ser Trp Val Pro Leu Ser Thr Asp Asp Pro
305 310 315 320

Val Ile Asp Arg Leu Tyr Leu Ser Ser His Arg Gly Val Ile Ala Asp
325 330 335

Asn Gln Ala Lys Trp Ala Val Pro Thr Thr Arg Thr Asp Asp Lys Leu
340 345 350

Arg Met Glu Thr Cys Phe Gln Gln Ala Cys Lys Gly Lys Ile Gln Ala
355 360 365

Leu Cys Glu Asn Pro Glu Trp Ala Pro Leu Lys Asp Asn Arg Ile Pro
370 375 380

Ser Tyr Gly Val Leu Ser Val Asp Leu Ser Leu Thr Val Glu Leu Lys
385 390 395 400

Ile Lys Ile Ala Ser Gly Phe Gly Pro Leu Ile Thr His Gly Ser Gly
405 410 415

Met Asp Leu Tyr Lys Ser Asn His Asn Asn Val Tyr Trp Leu Thr Ile
420 425 430

F1_001_Sequence_listing

Pro Pro Met Lys Asn Leu Ala Leu Gly Val Ile Asn Thr Leu Glu Trp
435 440 445

Ile Pro Arg Phe Lys Val Ser Pro Asn Leu Phe Thr Val Pro Ile Lys
450 455 460

Glu Ala Gly Glu Asp Cys His Ala Pro Thr Tyr Leu Pro Ala Glu Val
465 470 475 480

Asp Gly Asp Val Lys Leu Ser Ser Asn Leu Val Ile Leu Pro Gly Gln
485 490 495

Asp Leu Gln Tyr Val Leu Ala Thr Tyr Asp Thr Ser Arg Val Glu His
500 505 510

Ala Val Val Tyr Tyr Val Tyr Ser Pro Gly Arg Ser Phe Ser Tyr Phe
515 520 525

Tyr Pro Phe Arg Leu Pro Ile Lys Gly Val Pro Ile Glu Leu Gln Val
530 535 540

Glu Cys Phe Thr Trp Asp Gln Lys Leu Trp Cys Arg His Phe Cys Val
545 550 555 560

Leu Ala Asp Ser Glu Ser Gly Gly His Ile Thr His Ser Gly Met Val
565 570 575

Gly Met Gly Val Ser Cys Thr Val Thr Arg Glu Asp Gly Thr Asn Arg
580 585 590

Arg

<210> 236

<211> 1275

F1_001_Sequence_listing

<212> DNA

<213> Mesoplasma florum

<400> 236

aaaaaaaata aaatcaatag caaatattaa gattttttaag aaataaaaaa ttaatattaa	60
tttacaactg aatataaaaag aaactttatac agggtagcat aatgggctac tgaccccgcc	120
ttcaaacctt tttggagact ataagtgaag aaccactctt taattattaa agtttctttt	180
tatgtccaaa agacaagaag aaactttttt atttagttga atttataata agagaaaaag	240
aaaggatatt atatggcaaa aataaaaaac caatattaca acgagtctgt ttcgccaatt	300
gaatatgctg aacaaggatt taaaggaaaa atgcgttcag taaactgaaa cgtagttaa	360
gatgaaaaag atttagaggt atgaaataga attacacaaa acttctgatt gcctgaaaaa	420
attccagttt caaatgattt aacttcatga agaactttga caccagaatg acaagaatta	480
attacaagaa cttttacagg attaacattg ttagatacaa ttcaagctac tgttggtgat	540
gtggctcaag ttcctaactc attaaactgac catgaacaag taattttacac aaactttgca	600
tttatgggtg cagttcacgc tagatcatat ggttcaatct tttcaacttt atgttcaagt	660
gaacaaattg aagaggctca tgaatgagtt atcaatacag aaacattaca agaaagagct	720
aaagcattaa ttccttatta tgtgaatgat gaccctttaa agtcaaaagt tgcagctgct	780
ttaatgccag gcttcttatt atatggaggc ttctattttac cattttacct atcagctaga	840
ggtaaattac caaacacttc agatattatt agattaatat taagagataa agttatacat	900
aactactata gtgggttataa atatcaaaaag aaagttgcta aactttctcc agaaaaacaa	960
gctgaaatga aagaatttgt ttttaaatta ttatatgaat taatagattt agaaaaagct	1020
tatttgaaag aattgtatga ggatttttga ttagctgatg atgctattag atttagtggt	1080
tacaacgcag gtaaattttt acaaaattta ggttatgatt caccgtttac agaagaagaa	1140
acaagaattg agccagaaat attcacacaa ttatcagcta gagctgatga aaacatgat	1200
ttcttttcag ggaatggctc atcatatatt atgggagttt cagaagaaac tgaagatgac	1260
gattgggagt tttaa	1275

F1_001_Sequence_listing

```

<210> 237
<211> 64
<212> RNA
<213> Mesoplasma florum

<400> 237
acuuauacag gguagcauaa ugggcuacug accccgccuu caaaccuauu uggagacuau      60

aagu                                                                    64

<210> 238
<211> 69
<212> RNA
<213> Artificial sequence

<220>
<223> synthetic Deoxyguanosine riboswitch aptamer mutations

<220>
<221> misc_feature
<222> (10)..(13)
<223> n at positions 10-13 can be A, C, G, or T

<220>
<221> misc_feature
<222> (27)..(29)
<223> n at positions 27-29 can be A, C, G, or T

<220>
<221> misc_feature
<222> (31)..(32)
<223> n at positions 31-32 can be A, C, G, or T

<220>
<221> misc_feature
<222> (33)..(40)
<223> n at positions 33-40 can be A, C, G, T, or no nucleotide

<220>
<221> misc_feature
<222> (44)..(46)
<223> n at positions 44-46 can be A, C, G, or T

<220>
<221> misc_feature

```

F1_001_Sequence_listing

<222> (57)..(59)
 <223> n at positions 57-59 can be A, C, G, or T

<400> 238
 acuuauacan nnnagcauaa ugggcunng nnnnnnnnnn gccnnnaaac cuauuunng 60
 acuauaagu 69

<210> 239
 <211> 84
 <212> DNA
 <213> Artificial sequence

<220>
 <223> synthetic Oligo library for screen

<220>
 <221> misc_feature
 <222> (19)..(21)
 <223> n at positions 19-21 can be A, C, G, or T

<220>
 <221> misc_feature
 <222> (32)..(34)
 <223> n at positions 32-34 can be A, C, G, or T

<220>
 <221> misc_feature
 <222> (38)..(39)
 <223> n at positions 38-39 can be A, C, G, or T

<220>
 <221> misc_feature
 <222> (40)..(47)
 <223> n at positions 40-47 can be A, C, G, T, or no nucleotide

<220>
 <221> misc_feature
 <222> (49)..(51)
 <223> n at positions 49-51 can be A, C, G, or T

<220>
 <221> misc_feature
 <222> (65)..(68)
 <223> n at positions 65-68 can be A, C, G, or T

F1_001_Sequence_listing

<400> 239
cgcgcgacac ttatagtcnn naaatagggt tnnnggcnnn nnnnnnnncnn nagcccatta 60
tgctnnnntg tataagtgcc gccc 84

<210> 240
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> synthetic T7 promoter amplification primer

<400> 240
taatacgact cactataggg cggcacttat aca 33

<210> 241
<211> 18
<212> DNA
<213> Artificial sequence

<220>
<223> synthetic Reverse amplification primer

<400> 241
cgcgcgacac ttatagtc 18

<210> 242
<211> 915
<212> DNA
<213> Bacillus subtilis

<400> 242
tcaaaagcct ggcggcgcgg tcgtcagact cttttatatc gaatcccctt gaaatacgaa 60
tgatatctaa aaaaacaaaa ttaaagttcg ggaattttta ttttcagcct atgcaagaga 120
ttagaatctt gatataatth attacaatat aataggaaca ctcatataat cgcgtggata 180
tggcacgcaa gtttctaccg ggcaccgtaa atgtccgact atgggtgagc aatggaaccg 240
cacgtgtacg gttttttgtg atatcagcat tgcttgctct ttattttgagc gggcaatgct 300
ttttttattc tcataacgga ggtagacagg atggaagcac tgaaacggaa aatagaggaa 360

F1_001_Sequence_listing

```
gaaggcgtcg tattatctga tcaggtattg aaagtggatt cttttttgaa tcaccaaatt 420
gatccgctgc ttatgcagag aattggtgat gaatttgcgt ctaggtttgc aaaagacggt 480
attacaaaaa ttgtgacaat cgaatcatca ggtatcgctc ccgctgtaat gacgggcttg 540
aagctgggtg tgccagttgt cttcgcgaga aagcataaat cgттаacact caccgacaac 600
ttgctgacag cgtctgttta ttcctttacg aagcaaacag aaagccaaat cgcagtgtct 660
gggacccacc tgtcggatca ggatcatgtg ctgattatcg atgatttttt ggcaaattgga 720
caggcagcgc acgggcttgt gtcgattgtg aagcaagcgg gagcttctat tgcgggaatc 780
ggcattgtta ttgaaaagtc atttcagccg ggaagagatg aacttgtaaa actgggctac 840
cgagtggaat ctttggcaag aattcagtct ttagaagaag gaaaagtgtc cttcgtagag 900
gaggttcatt catga 915
```

```
<210> 243
<211> 69
<212> RNA
<213> Bacillus subtilis
```

```
<400> 243
cacucauaua aucgcgugga uauggcacgc aaguuucuaс cgggcaccgu aaauguccga 60
cuaugggug 69
```

```
<210> 244
<211> 74
<212> RNA
<213> Artificial sequence
```

```
<220>
<223> synthetic Guanosine xpt riboswitch aptamer mutations
```

```
<220>
<221> misc_feature
<222> (11)..(14)
<223> n at positions 11-14 can be A, C, G, or T
```

```
<220>
<221> misc_feature
```

F1_001_Sequence_listing

<222> (30)..(35)

<223> n at positions 30-35 can be A, C, G, or T

<220>

<221> misc_feature

<222> (36)..(43)

<223> n at positions 36-43 can be A, C, G, T, or no nucleotide

<220>

<221> misc_feature

<222> (47)..(49)

<223> n at positions 47-49 can be A, C, G, or T

<220>

<221> misc_feature

<222> (61)..(63)

<223> n at positions 61-63 can be A, C, G, or T

<400> 244

cacucauaua nnnncgugga uauggcacgn nngnnnnnnn nnnaccnnnu accguaaaug 60

nnngacuaug ggug 74

<210> 245

<211> 89

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic Oligo library for screen

<220>

<221> misc_feature

<222> (20)..(22)

<223> n at positions 20-22 can be A, C, G, or T

<220>

<221> misc_feature

<222> (34)..(36)

<223> n at positions 34-36 can be A, C, G, or T

<220>

<221> misc_feature

<222> (40)..(41)

<223> n at positions 40-41 can be A, C, G, or T

F1_001_Sequence_listing

```

<220>
<221> misc_feature
<222> (42)..(49)
<223> n at positions 42-49 can be A, C, G, T, or no nucleotide

<220>
<221> misc_feature
<222> (51)..(53)
<223> n at positions 51-53 can be A, C, G, or T

<220>
<221> misc_feature
<222> (69)..(72)
<223> n at positions 69-72 can be A, C, G, or T

<400> 245
cgcgcgacca cccatagtcn nncatttacg gtgnnnggtn nnnnnnnnnc nnncggtgcca      60

tatccacggn nntatatgag tggccgccc                                           89

<210> 246
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> synthetic T7 promoter amplification primer

<400> 246
taatacgact cactataggg cgccactca tata                                     34

<210> 247
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> synthetic Reverse amplification primer

<400> 247
cgcgcgacca cccatagtc                                                         19

<210> 248
<211> 152
<212> RNA

```

F1_001_Sequence_listing

<213> Artificial sequence

<220>

<223> synthetic Oligo 1 Transcribed RNA

<400> 248

gggcggcacu uauacaggggu agcauaaugg gcuacugacg ccuucuaaacc uauuuggaga 60

cuauaagugu cgcgcggggc ggcacuuaua cagggguagca uaaugggcua cugacgccuu 120

caaaccuauu uggagacuau aagugucgcg cg 152

<210> 249

<211> 76

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic Oligo 1 Synthesized template

<400> 249

cgcgcgacac ttatagtctc caaatagggtt tgaaggcgtc agtagcccat tatgctaccc 60

tgtataagtg ccgccc 76

<210> 250

<211> 79

<212> RNA

<213> Artificial sequence

<220>

<223> synthetic Oligo 2 Transcribed RNA

<400> 250

gggcggcacu uauacaggggu agcauaaugg gcuacugacc ccgccucaa accuauuugg 60

agacuauaag ugucgcgcg 79

<210> 251

<211> 79

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic Oligo 2 Synthesized template

F1_001_Sequence_listing

<400> 251
 cgcgcgacac ttatagtctc caaatagggtt tgaaggcggg gtcagtagcc cattatgcta 60
 ccctgtataa gtgccgccc 79

<210> 252
 <211> 560
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic DAFss-aCD3scFv(UCHT1)IgG1 Fc-CD14GPI

<400> 252

Met Thr Val Ala Arg Pro Ser Val Pro Ala Ala Leu Pro Leu Leu Gly
 1 5 10 15

Glu Leu Pro Arg Leu Leu Leu Leu Val Leu Leu Cys Leu Pro Asp Ile
 20 25 30

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 35 40 45

Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn
 50 55 60

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr
 65 70 75 80

Thr Ser Arg Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 85 90 95

Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
 100 105 110

Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe
 115 120 125

F1_001_Sequence_listing

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

F1_001_Sequence_listing

Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	325	330	335	
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	340	345	350	
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	355	360	365	
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	370	375	380	
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	385	390	395	400
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	405	410	415	
Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	420	425	430	
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	435	440	445	
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	450	455	460	
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	465	470	475	480
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	485	490	495	
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Val	Asp	Asn	Leu	Thr	Leu	Asp	500	505	510	

F1_001_Sequence_listing

Gly Asn Pro Phe Leu Val Pro Gly Thr Ala Leu Pro His Glu Gly Ser
515 520 525

Met Asn Ser Gly Val Val Pro Ala Cys Ala Arg Ser Thr Leu Ser Val
530 535 540

Gly Val Ser Gly Thr Leu Val Leu Leu Gln Gly Ala Arg Gly Phe Ala
545 550 555 560

<210> 253
<211> 276
<212> PRT
<213> Artificial sequence

<220>
<223> synthetic DAFss-CD80ECD-CD16GPI

<400> 253

Met Thr Val Ala Arg Pro Ser Val Pro Ala Ala Leu Pro Leu Leu Gly
1 5 10 15

Glu Leu Pro Arg Leu Leu Leu Leu Val Leu Leu Cys Leu Pro Val Ile
20 25 30

His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu Ser Cys Gly His
35 40 45

Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile Tyr Trp Gln Lys
50 55 60

Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp Met Asn Ile Trp
65 70 75 80

Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr Asn Asn Leu Ser
85 90 95

Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly Thr Tyr Glu Cys

F1_001_Sequence_listing

100

105

110

Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg Glu His Leu Ala
115 120 125

Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr Pro Ser Ile Ser
130 135 140

Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile Ile Cys Ser Thr
145 150 155 160

Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu Glu Asn Gly Glu
165 170 175

Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp Pro Glu Thr Glu
180 185 190

Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met Thr Thr Asn His
195 200 205

Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg Val Asn Gln Thr
210 215 220

Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro Asp Asn Val Ser
225 230 235 240

Thr Ile Ser Ser Phe Ser Pro Pro Gly Tyr Gln Val Ser Phe Cys Leu
245 250 255

Val Met Val Leu Leu Phe Ala Val Asp Thr Gly Leu Tyr Phe Ser Val
260 265 270

Lys Thr Asn Ile
275

<210> 254

F1_001_Sequence_listing

<211> 533
 <212> PRT
 <213> Artificial sequence

<220>
 <223> synthetic DAFss-IL7-DAF

<400> 254

Met Ala Thr Thr Met Thr Val Ala Arg Pro Ser Val Pro Ala Ala Leu
 1 5 10 15

Pro Leu Leu Gly Glu Leu Pro Arg Leu Leu Leu Leu Val Leu Leu Cys
 20 25 30

Leu Pro Ala Asp Cys Asp Ile Glu Gly Lys Asp Gly Lys Gln Tyr Glu
 35 40 45

Ser Val Leu Met Val Ser Ile Asp Gln Leu Leu Asp Ser Met Lys Glu
 50 55 60

Ile Gly Ser Asn Cys Leu Asn Asn Glu Phe Asn Phe Phe Lys Arg His
 65 70 75 80

Ile Cys Asp Ala Asn Lys Glu Gly Met Phe Leu Phe Arg Ala Ala Arg
 85 90 95

Lys Leu Arg Gln Phe Leu Lys Met Asn Ser Thr Gly Asp Phe Asp Leu
 100 105 110

His Leu Leu Lys Val Ser Glu Gly Thr Thr Ile Leu Leu Asn Cys Thr
 115 120 125

Gly Gln Val Lys Gly Arg Lys Pro Ala Ala Leu Gly Glu Ala Gln Pro
 130 135 140

Thr Lys Ser Leu Glu Glu Asn Lys Ser Leu Lys Glu Gln Lys Lys Leu
 145 150 155 160

F1_001_Sequence_listing

Asn Asp Leu Cys Phe Leu Lys Arg Leu Leu Gln Glu Ile Lys Thr Cys
165 170 175

Trp Asn Lys Ile Leu Met Gly Thr Lys Glu His Cys Gly Leu Pro Pro
180 185 190

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

Glu Asp Thr Val Ile Thr Tyr Lys Cys Glu Glu Ser Phe Val Lys Ile
210 215 220

Pro Gly Glu Lys Asp Ser Val Ile Cys Leu Lys Gly Ser Gln Trp Ser
225 230 235 240

Asp Ile Glu Glu Phe Cys Asn Arg Ser Cys Glu Val Pro Thr Arg Leu
245 250 255

Asn Ser Ala Ser Leu Lys Gln Pro Tyr Ile Thr Gln Asn Tyr Phe Pro
260 265 270

Val Gly Thr Val Val Glu Tyr Glu Cys Arg Pro Gly Tyr Arg Arg Glu
275 280 285

Pro Ser Leu Ser Pro Lys Leu Thr Cys Leu Gln Asn Leu Lys Trp Ser
290 295 300

Thr Ala Val Glu Phe Cys Lys Lys Lys Ser Cys Pro Asn Pro Gly Glu
305 310 315 320

Ile Arg Asn Gly Gln Ile Asp Val Pro Gly Gly Ile Leu Phe Gly Ala
325 330 335

Thr Ile Ser Phe Ser Cys Asn Thr Gly Tyr Lys Leu Phe Gly Ser Thr
340 345 350

F1_001_Sequence_listing

Ser Ser Phe Cys Leu Ile Ser Gly Ser Ser Val Gln Trp Ser Asp Pro
 355 360 365

Leu Pro Glu Cys Arg Glu Ile Tyr Cys Pro Ala Pro Pro Gln Ile Asp
 370 375 380

Asn Gly Ile Ile Gln Gly Glu Arg Asp His Tyr Gly Tyr Arg Gln Ser
 385 390 395 400

Val Thr Tyr Ala Cys Asn Lys Gly Phe Thr Met Ile Gly Glu His Ser
 405 410 415

Ile Tyr Cys Thr Val Asn Asn Asp Glu Gly Glu Trp Ser Gly Pro Pro
 420 425 430

Pro Glu Cys Arg Gly Lys Ser Leu Thr Ser Lys Val Pro Pro Thr Val
 435 440 445

Gln Lys Pro Thr Thr Val Asn Val Pro Thr Thr Glu Val Ser Pro Thr
 450 455 460

Ser Gln Lys Thr Thr Thr Lys Thr Thr Thr Pro Asn Ala Gln Ala Thr
 465 470 475 480

Arg Ser Thr Pro Val Ser Arg Thr Thr Lys His Phe His Glu Thr Thr
 485 490 495

Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser
 500 505 510

Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr
 515 520 525

Met Gly Leu Leu Thr
 530

F1_001_Sequence_listing

<210> 255
 <211> 1823
 <212> DNA
 <213> Artificial sequence

<220>
 <223> synthetic EF-1a promoter with miRs

<400> 255
 ggctccggtg cccgtcagtg ggcagagcgc acatcgccca cagtccccga gaagttgggg 60
 ggagggggtcg gcaattgaac cggtagcctag agaagggtggc gcgggggtaaa ctgggaaagt 120
 gatgtcgtgt actggctccg cttttttccc gaggggtgggg gagaaccgta tataagtgca 180
 gtagtcgccg tgaacgttct ttttcgcaac gggtttgccg ccagaacaca ggtaagtgcc 240
 gtgtgtgggtt cccgcgggcc tggcctcttt acgggttatg gcccttgctg gccttgaatt 300
 acttccacct ggctgcagta cgtgattctt gatcccgagc ttcgggttgg aagtgggtgg 360
 gagagttcga ggccttgctg ttaaggagcc ctttcgcctc gtgcttgagt tgaggcctgg 420
 cctgggcgct ggggccgccc cgtgcgaatc tgggtggcacc ttcgcgcctg tctcgtgct 480
 ttcgataagt ctctagccat ttaaaatttt tgatgacctg ctgcgacgct ttttttctgg 540
 caagatagtc ttgtaaatgc gggccaagat ctgcacactg gtatttcggt ttttggggcc 600
 gcgggcgggc acggggcccc tgcgtcccag cgcacatgtt cggcgaggcg gggcctgcga 660
 gcgcggccac cgagaatcgg acgggggtag tctcaagctg gccggcctgc tctggtgcct 720
 ggccctgcgc cgccgtgtat cggccgccc tgggcggcaa ggctggcccc gtcggcacca 780
 gttgcgtgag cggaaaagat gccgcttccc ggccctgctg caggagctc aaaatggagg 840
 acgcggcgct cgggagagcg ggcgggtgag tcacccacac aaaggaaaag ggcctttccg 900
 tcctcagccg tcgcttcatg tgactccact gagtaccggg cgccgtccag gcacctcgat 960
 tagttcctgg aggcttgctg aaggctgtat gctgacatgg tacagttcaa tgggtggttt 1020
 ggccactgac tgaccaccat tgctgtacca tgtcaggaca caaggcctgt tactagcact 1080
 cacatggaac aaatggccca cattgggtgcc ggatgaagct cttatgttgc acggtcactt 1140

F1_001_Sequence_listing		
ggaggcttgc tgaaggctgt atgctgtcag tctgttcac ttctggcggtt ttggccactg	1200	
actgacgcca gaaggaacag actgacagga cacaaggcct gttactagca ctcacatgga	1260	
acaaatggcc gttgccggag tcttggcagc gagagatcac tatcaactaa ctggaggctt	1320	
gctgaaggct gtatgctgaa gcgtgaagtg aatcaacggg ttttggccac tgactgaccc	1380	
gttgatactt cacgcttcag gacacaaggc ctgttactag cactcacatg gaacaaatgg	1440	
ccgtgttaat tgtccatgta gcgaggcatc cttatggcgt ggctggaggc ttgctgaagg	1500	
ctgtatgctg gcagtatcct agtacattga cgttttggcc actgactgac gtcaatgtta	1560	
ggatactgcc aggacacaag gcctgttact agcactcaca tggaacaaat ggccgctttt	1620	
ggagtacgtc gtcttttaggt tggggggagg ggttttatgc gatggagttt cccacactg	1680	
agtgggtgga gactgaagtt aggccagctt ggcacttgat gtaattctcc ttggaatttg	1740	
ccctttttga gtttggatct tggttcattc tcaagcctca gacagtgggtt caaagttttt	1800	
ttcttccatt tcagggtgtcg tga	1823	