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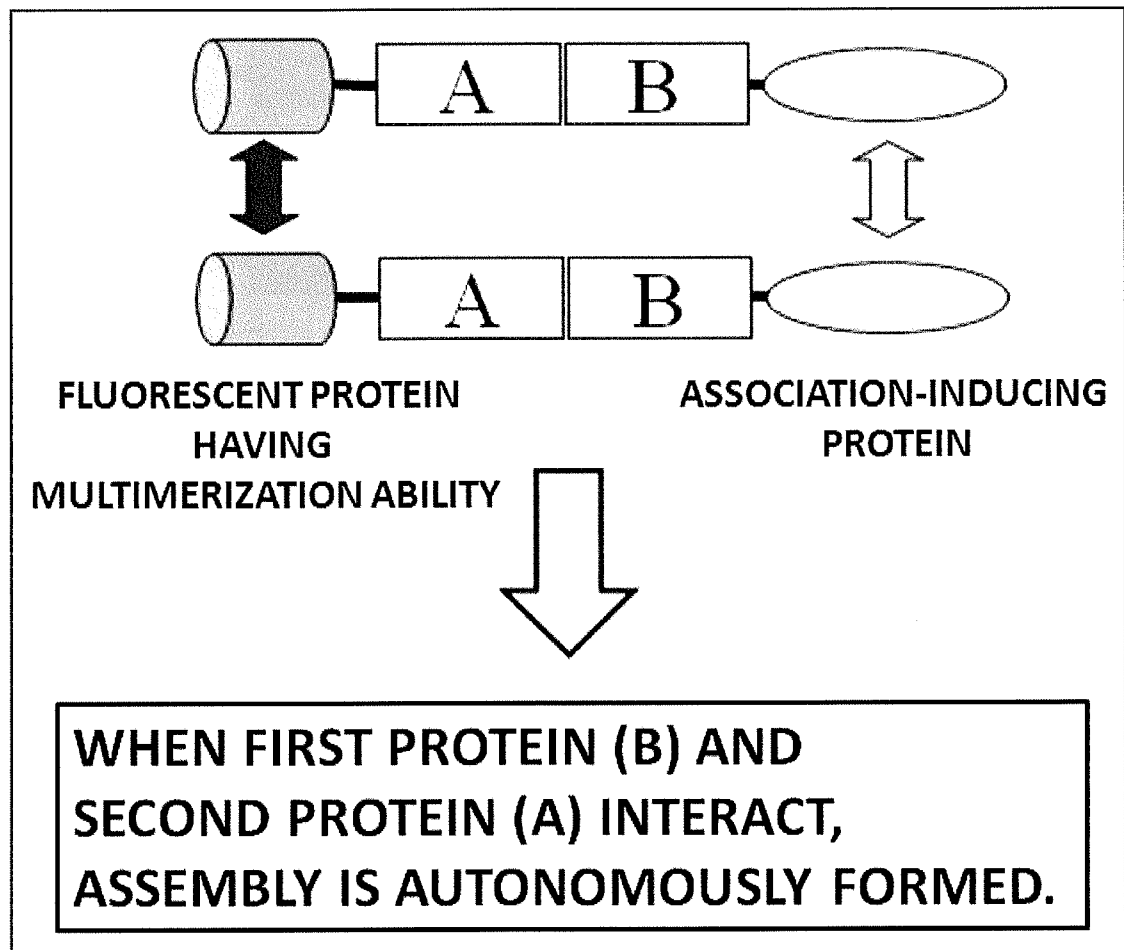


Fig. 2

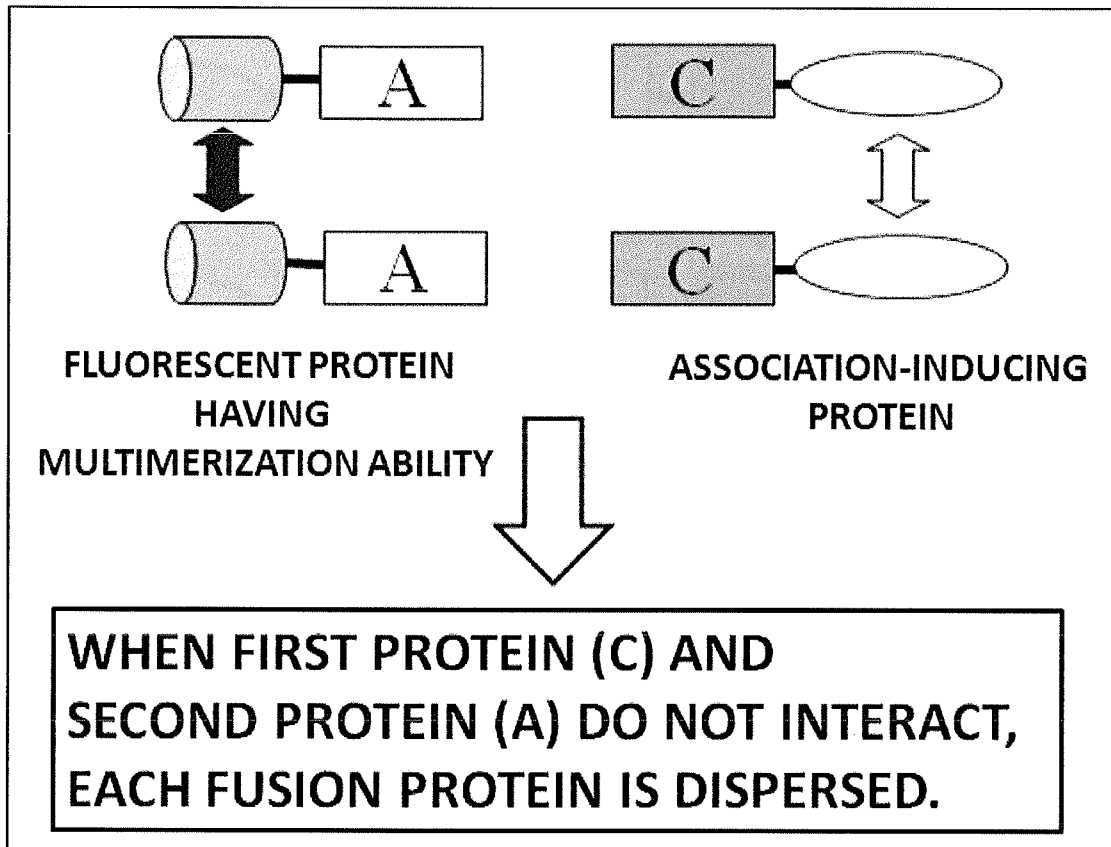


Fig. 3

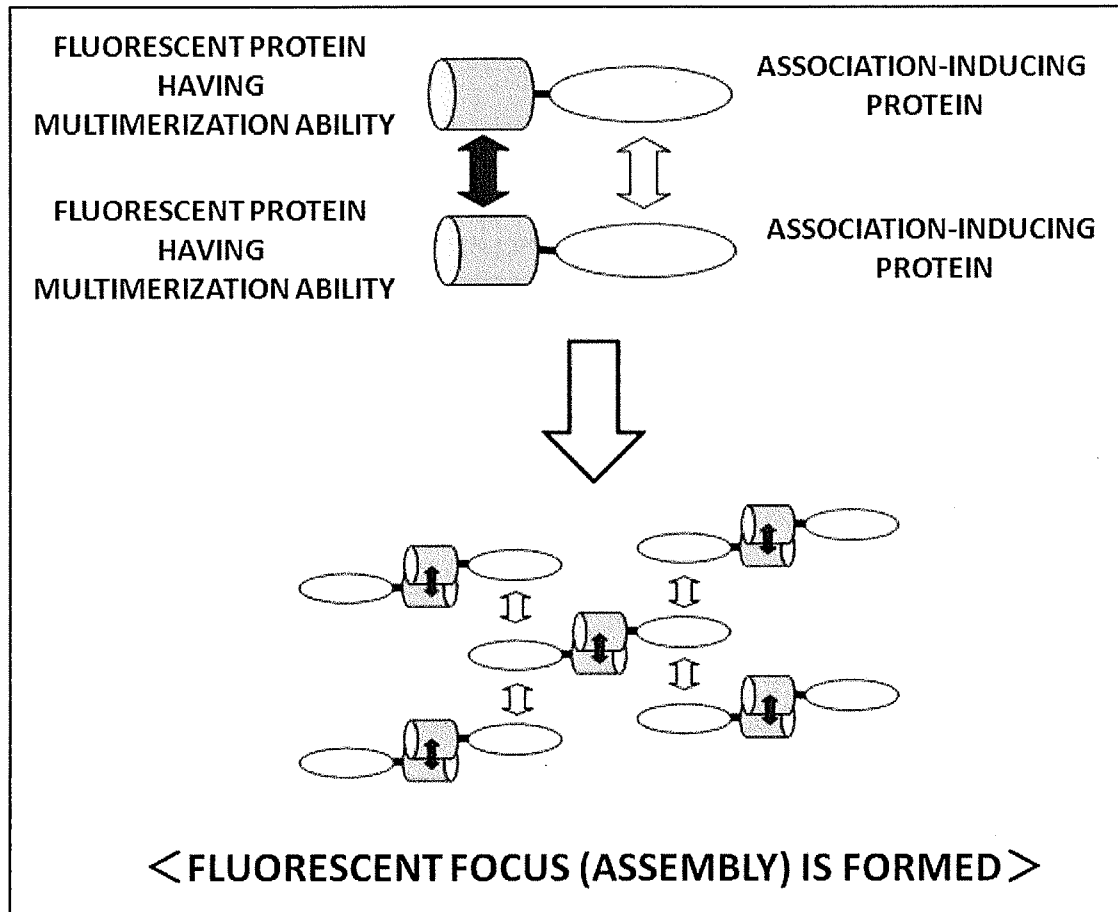


Fig. 4

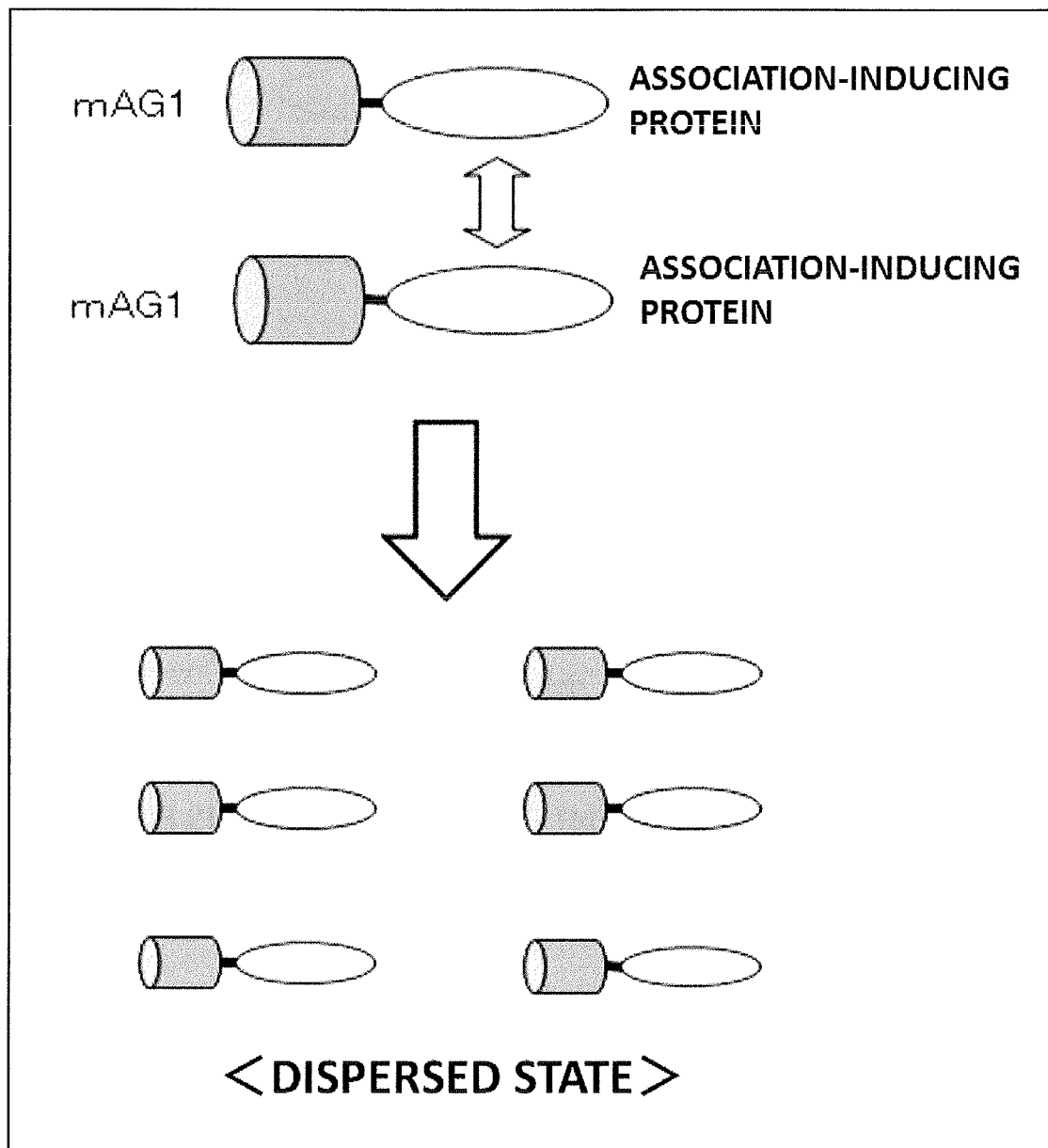


Fig. 5

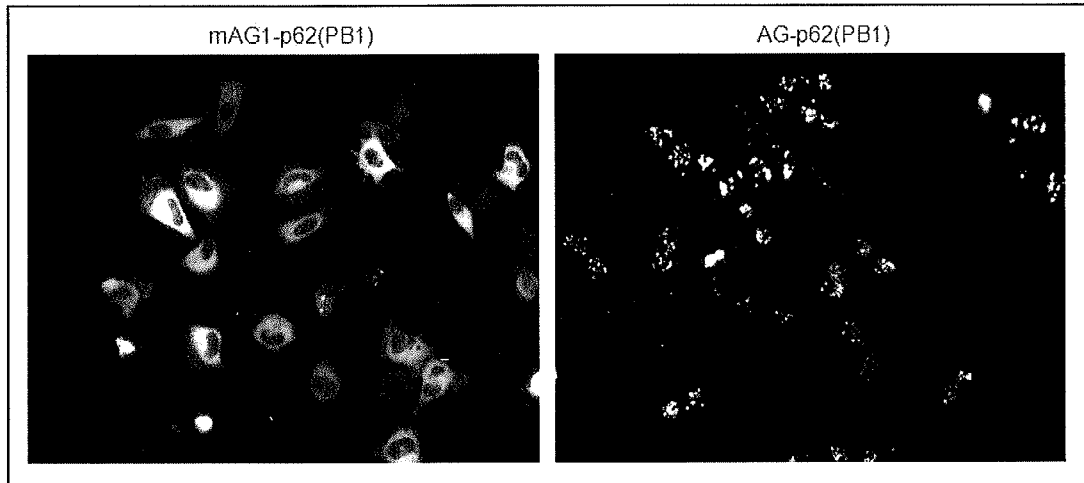


Fig. 6

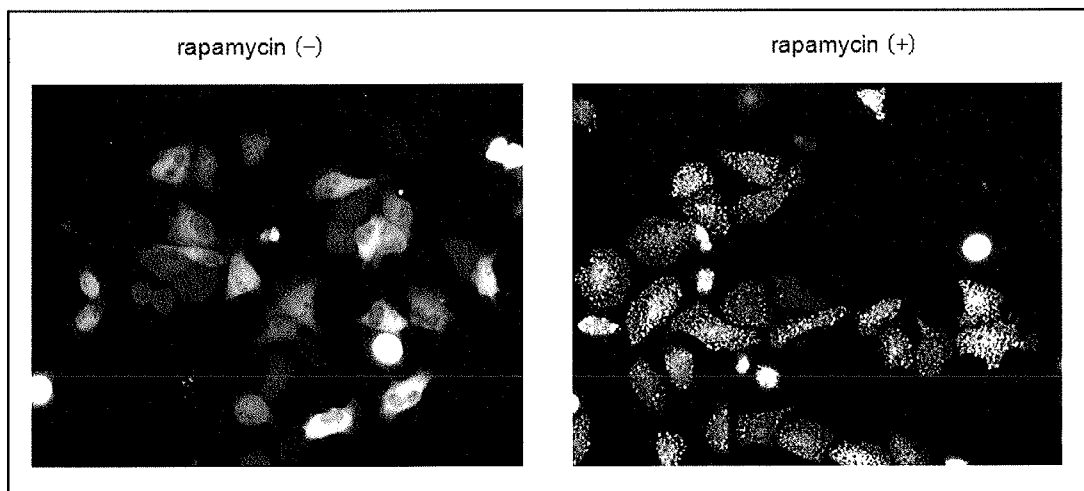


Fig. 7

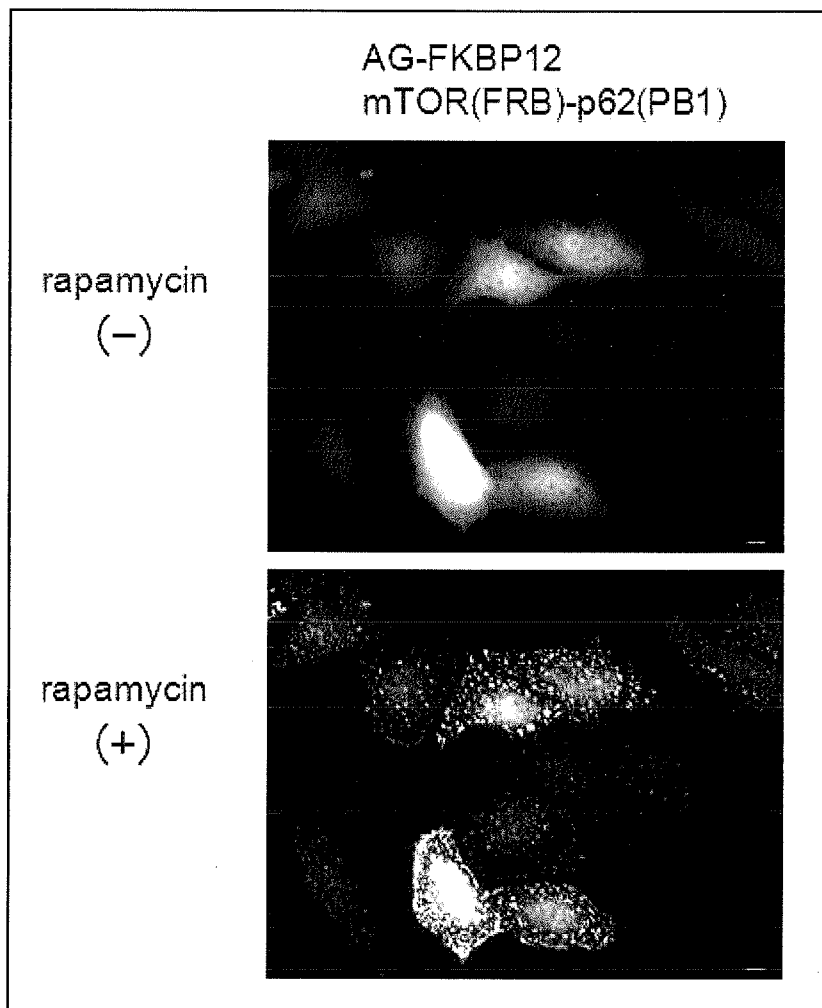


Fig. 8

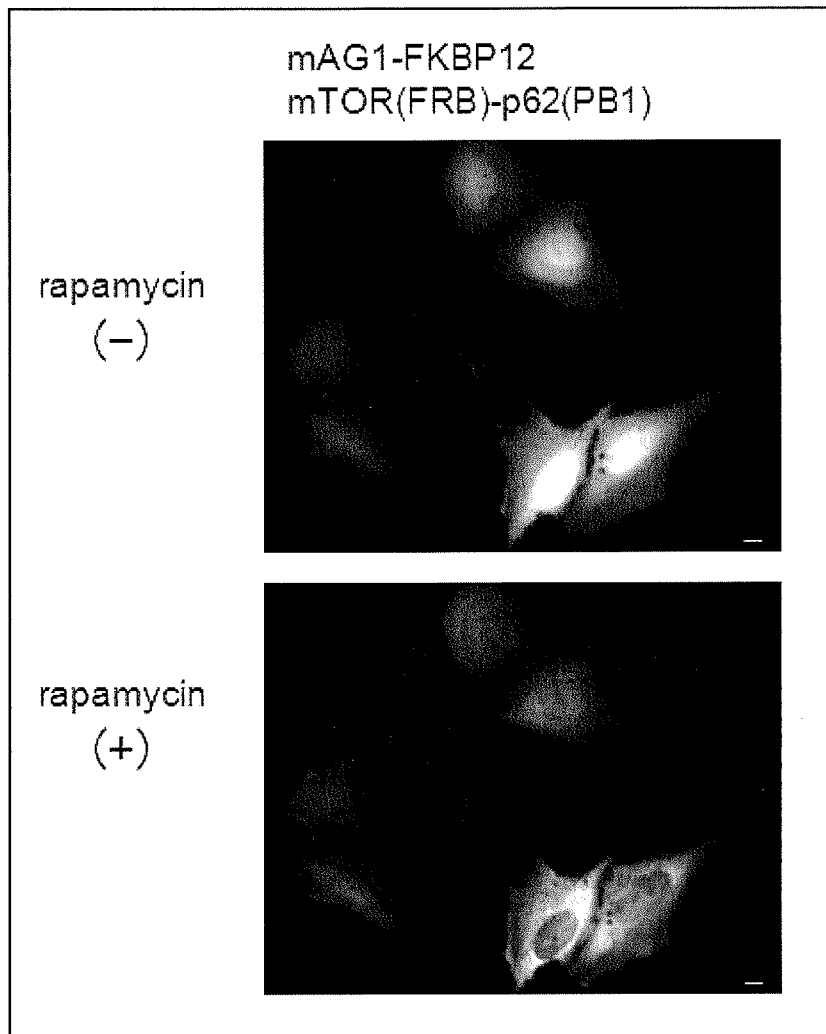


Fig. 9

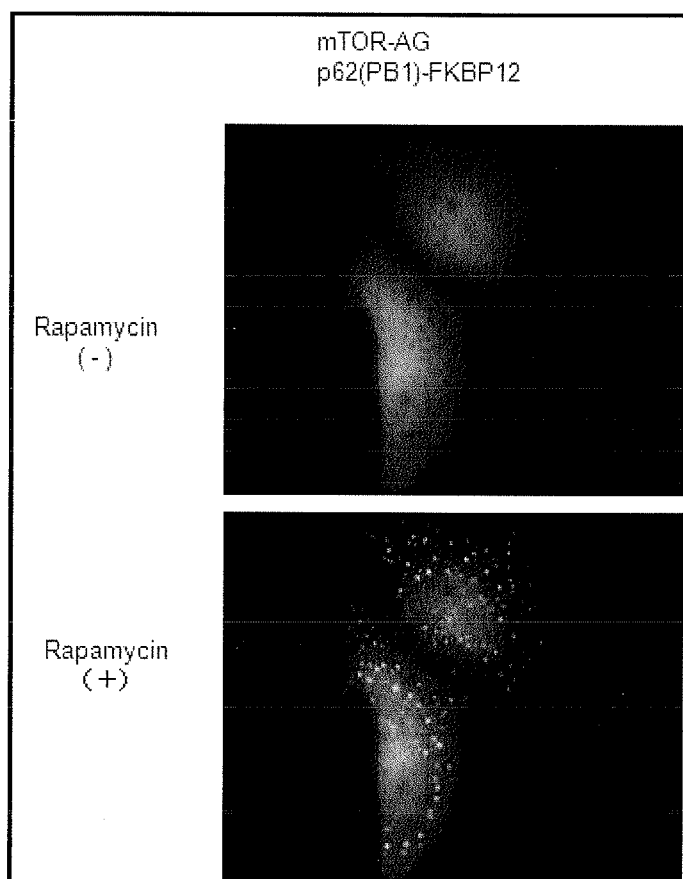


Fig. 10

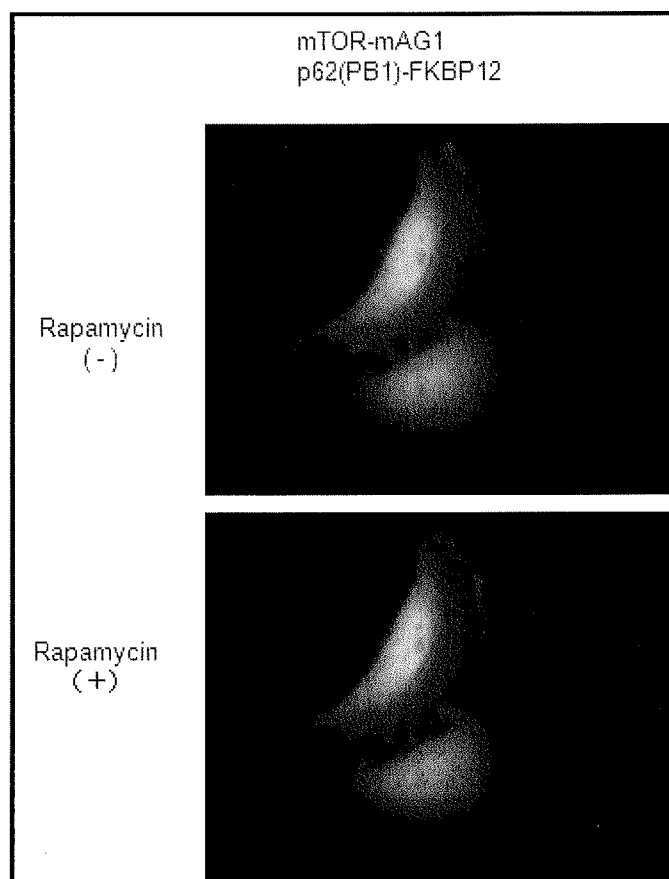


Fig. 11

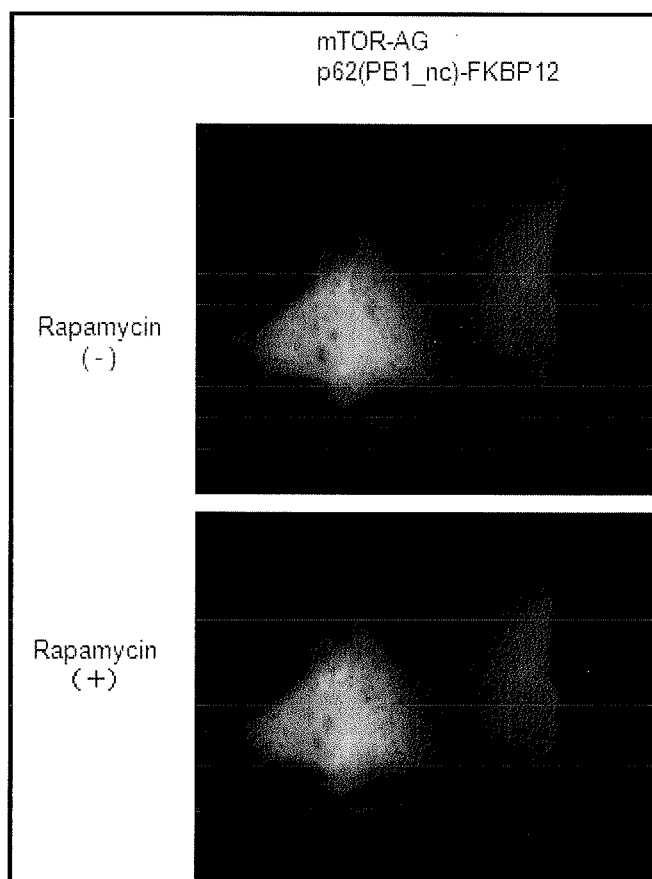


Fig. 12

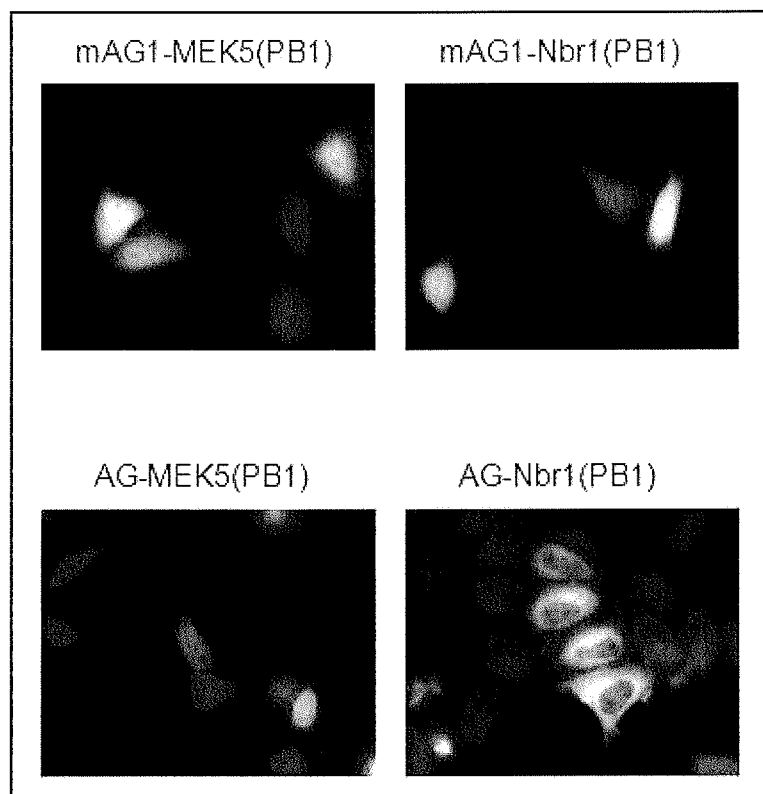


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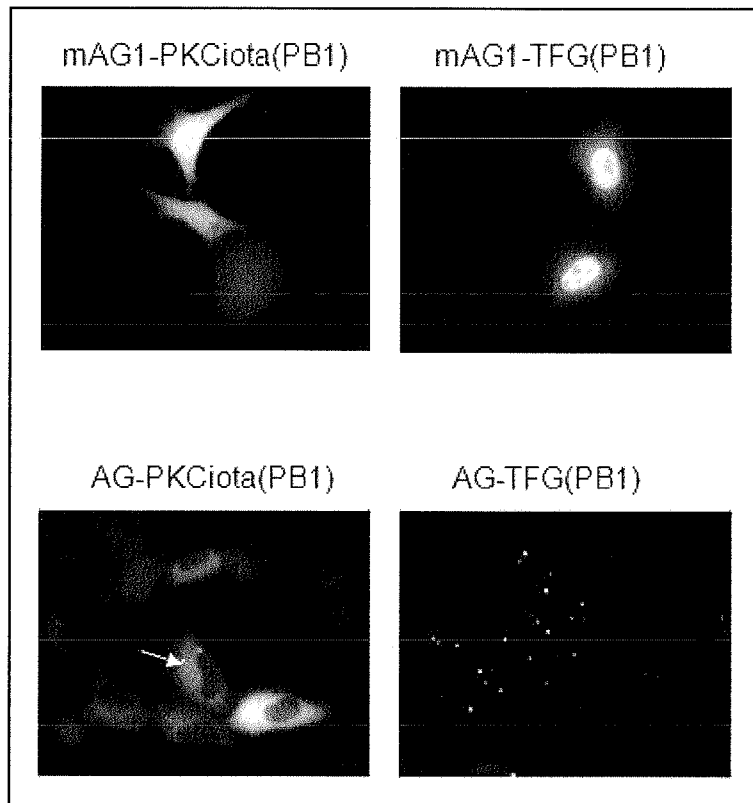


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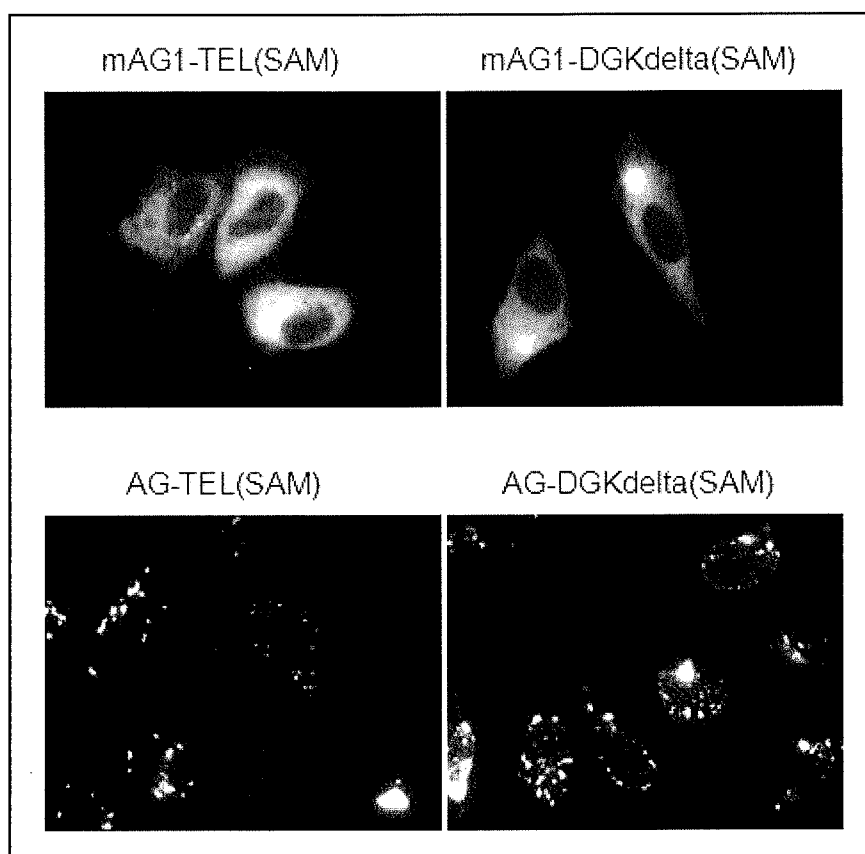


Fig. 15

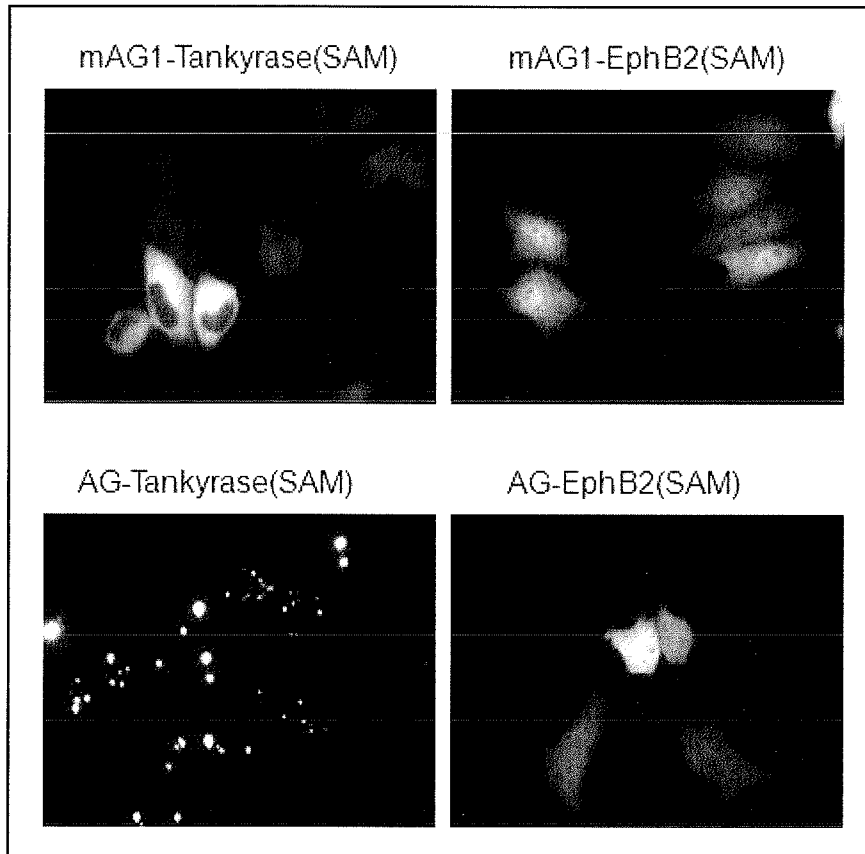


Fig. 16

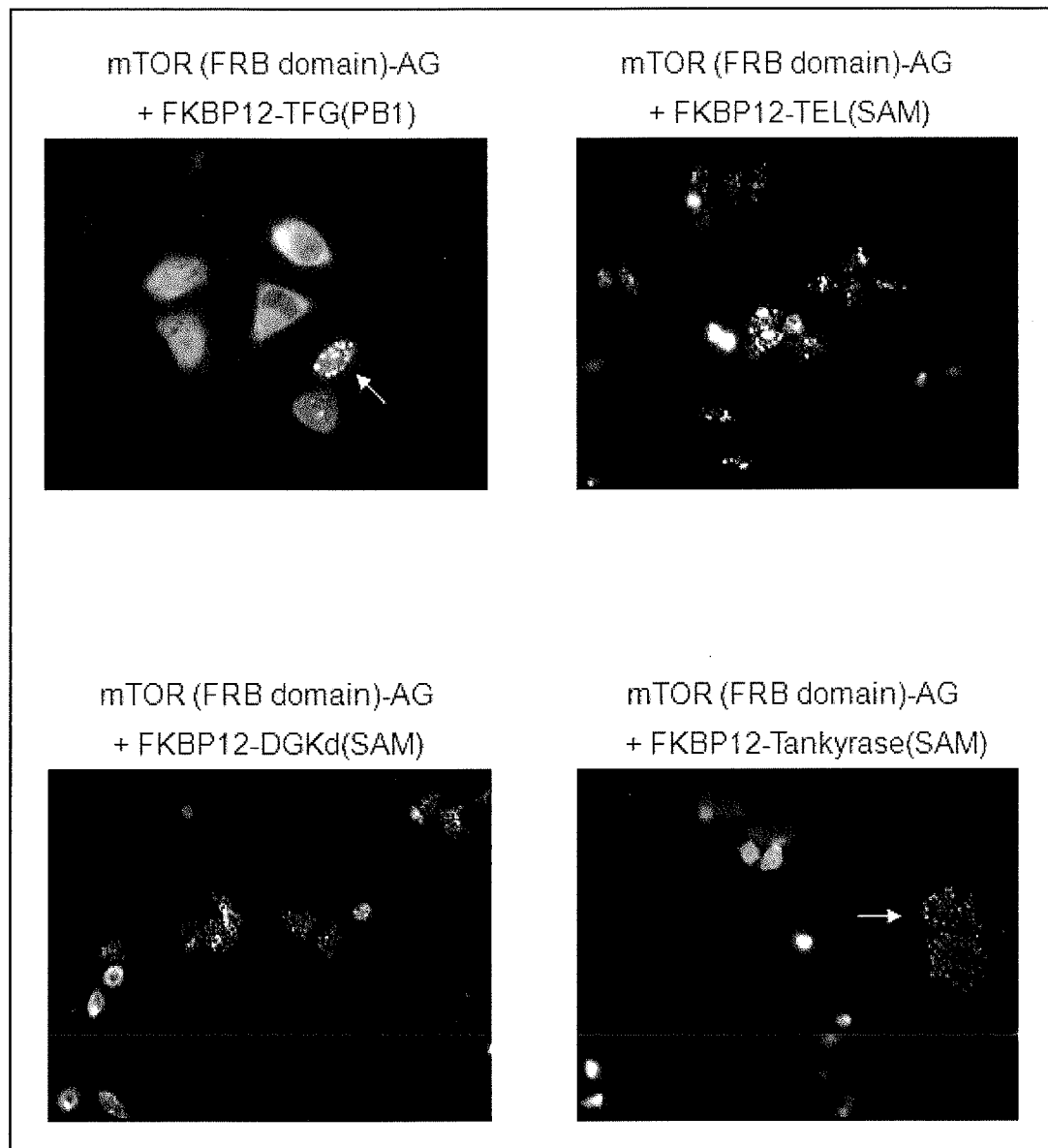


Fig. 17

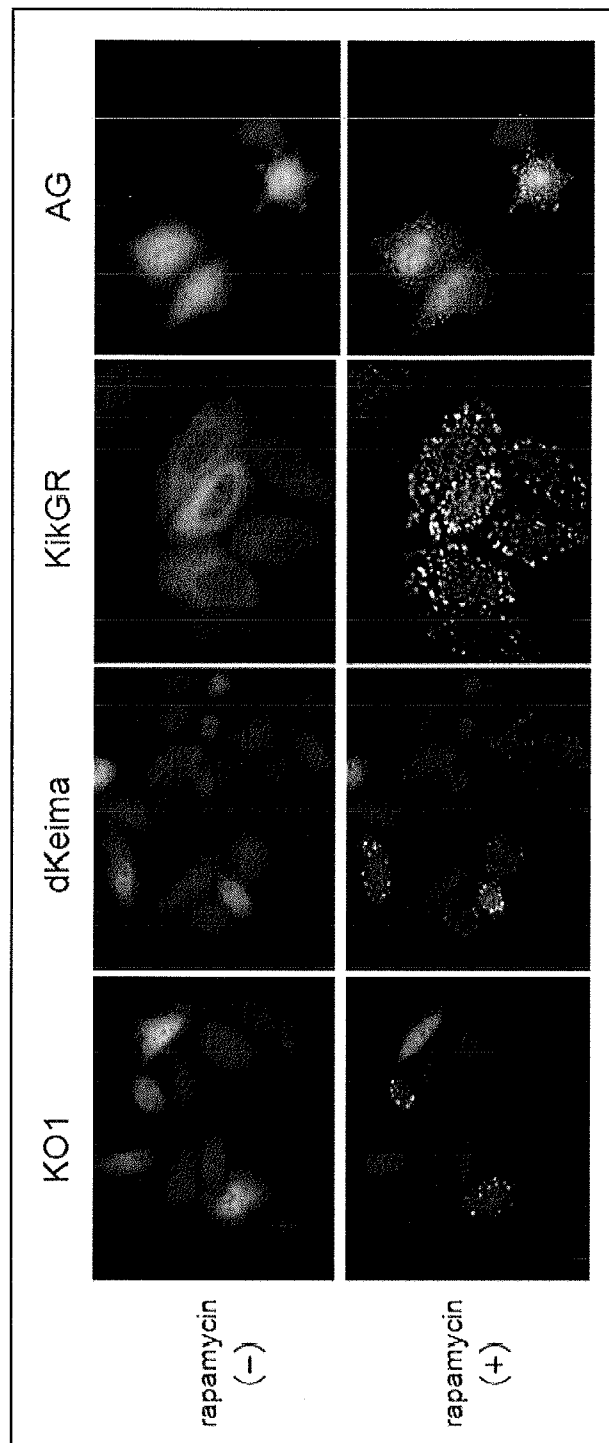


Fig. 18

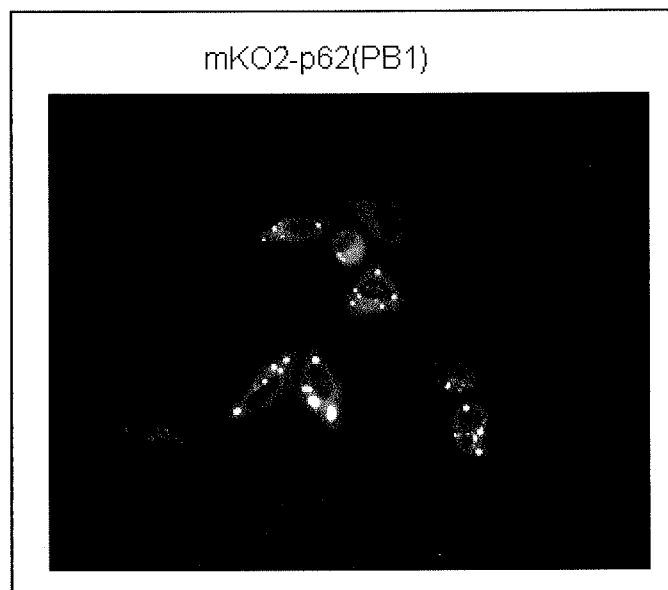


Fig. 19

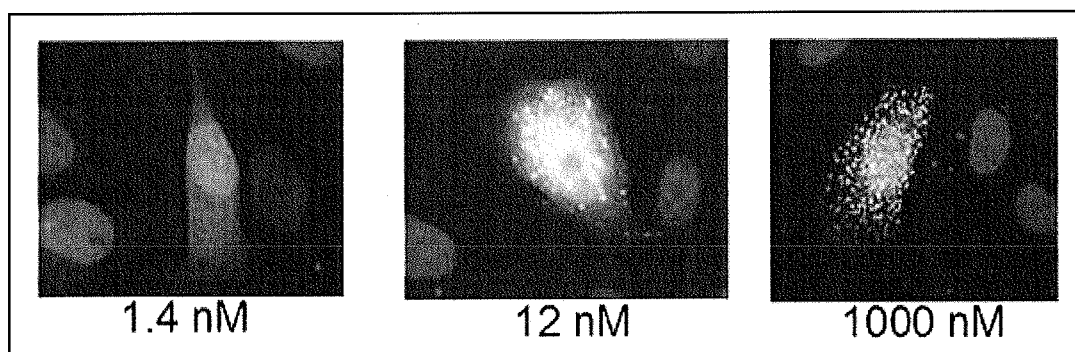


Fig. 20

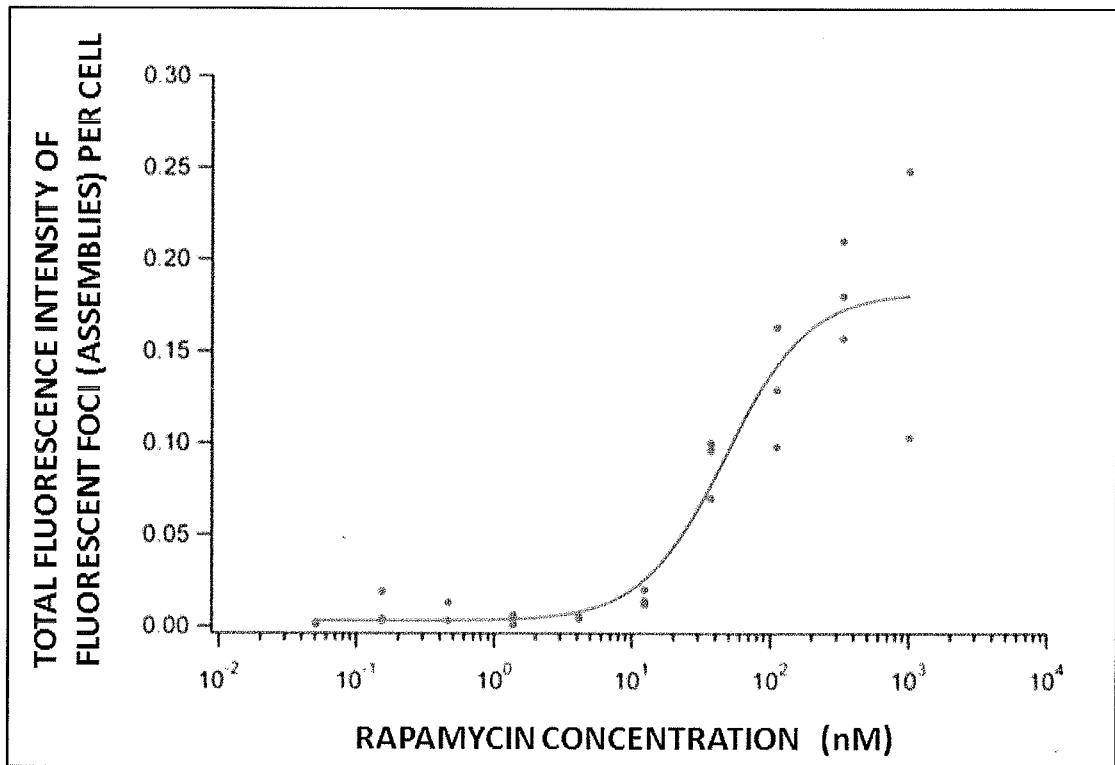


Fig. 21

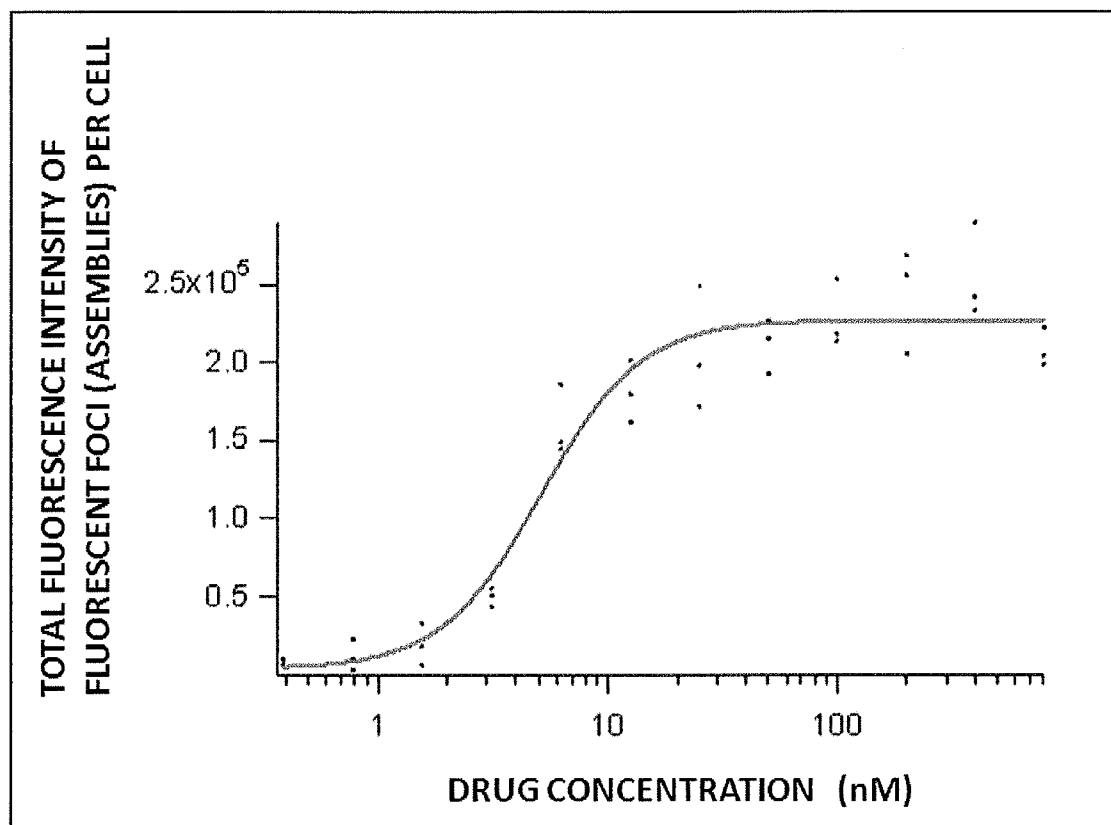


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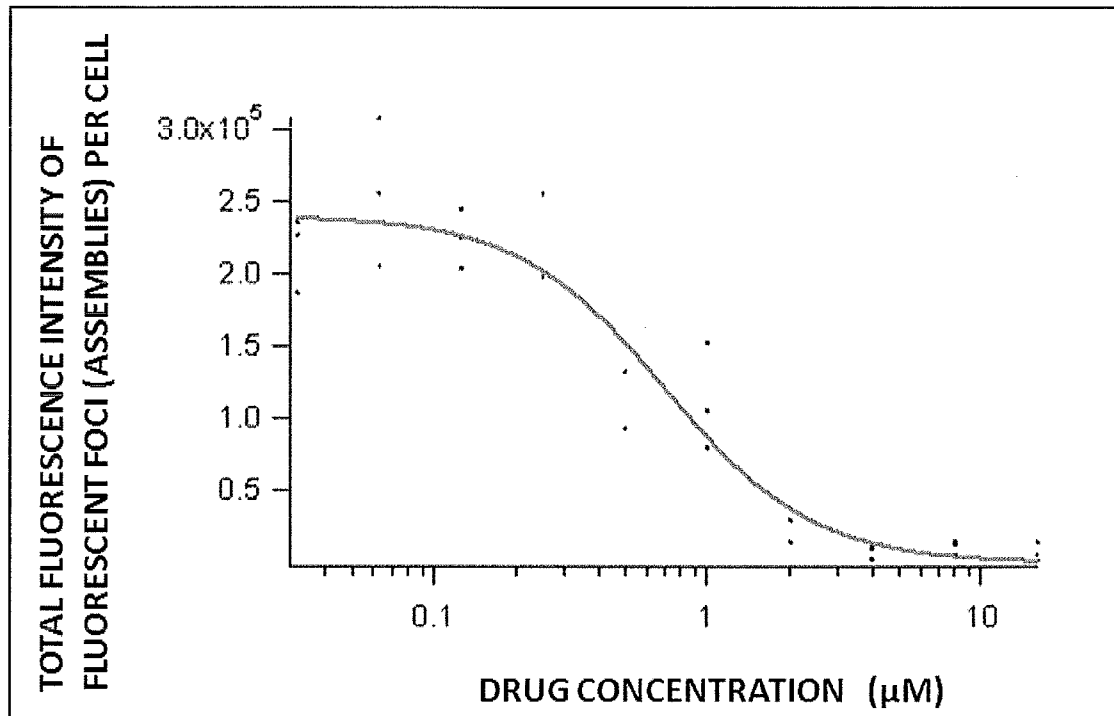


Fig. 23

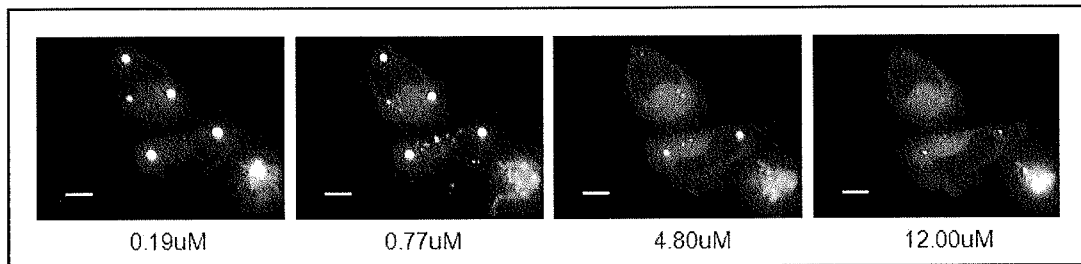


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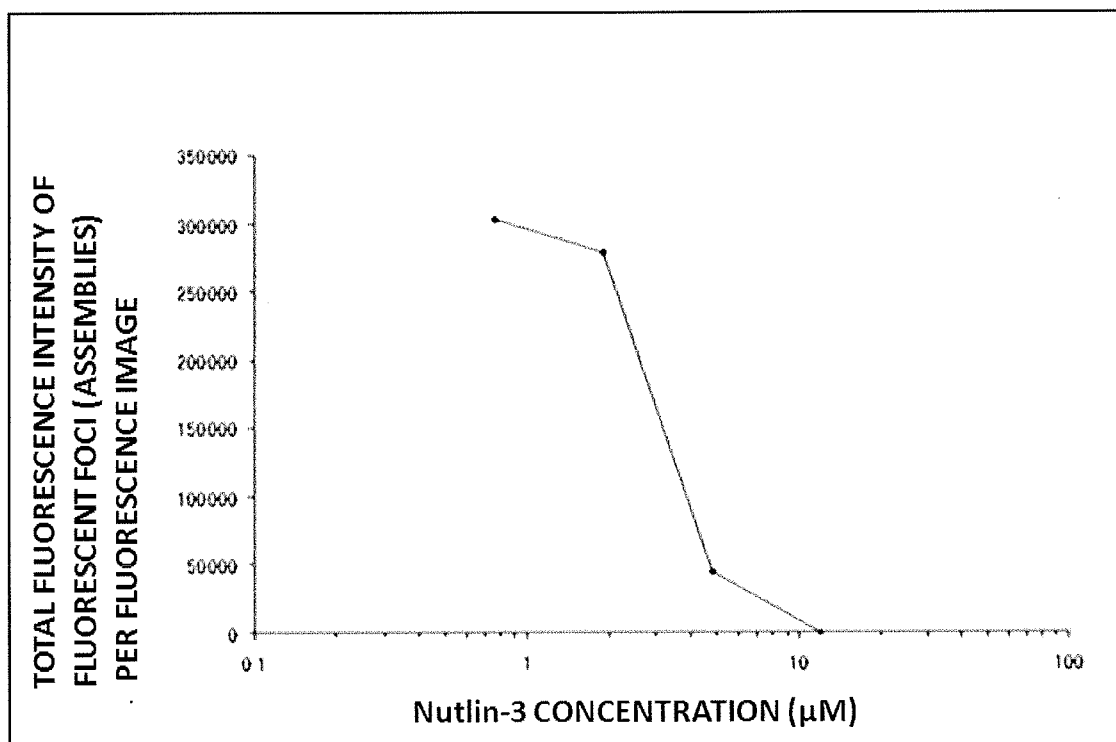


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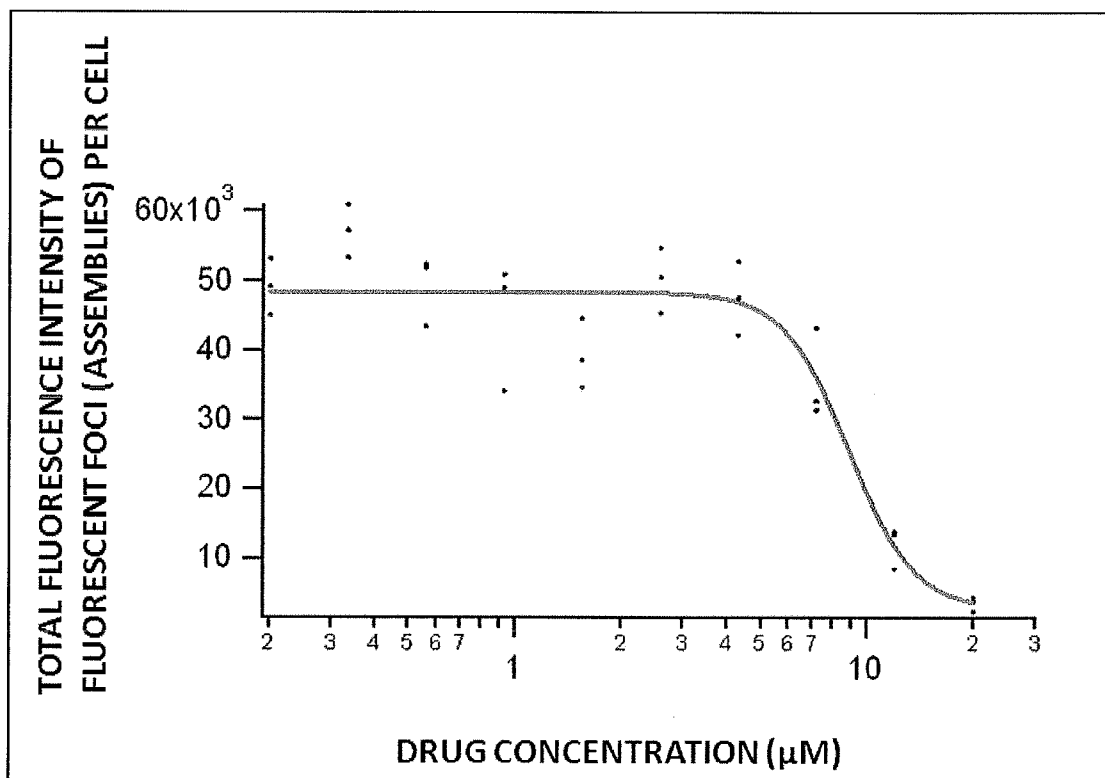


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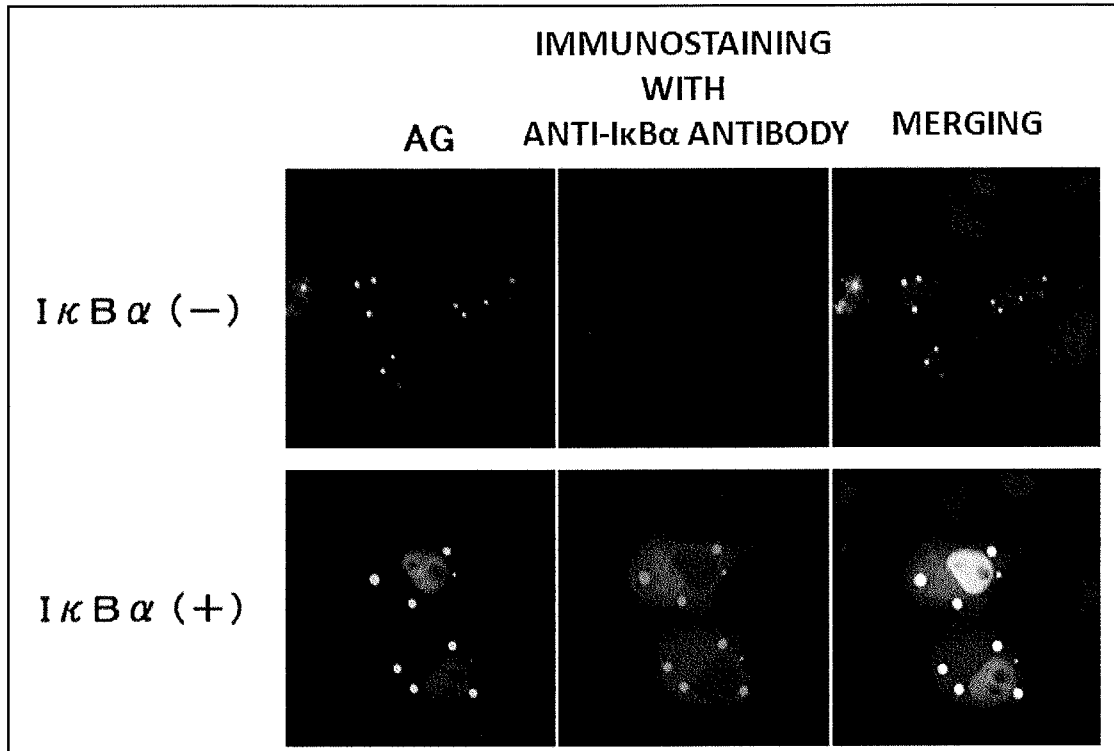


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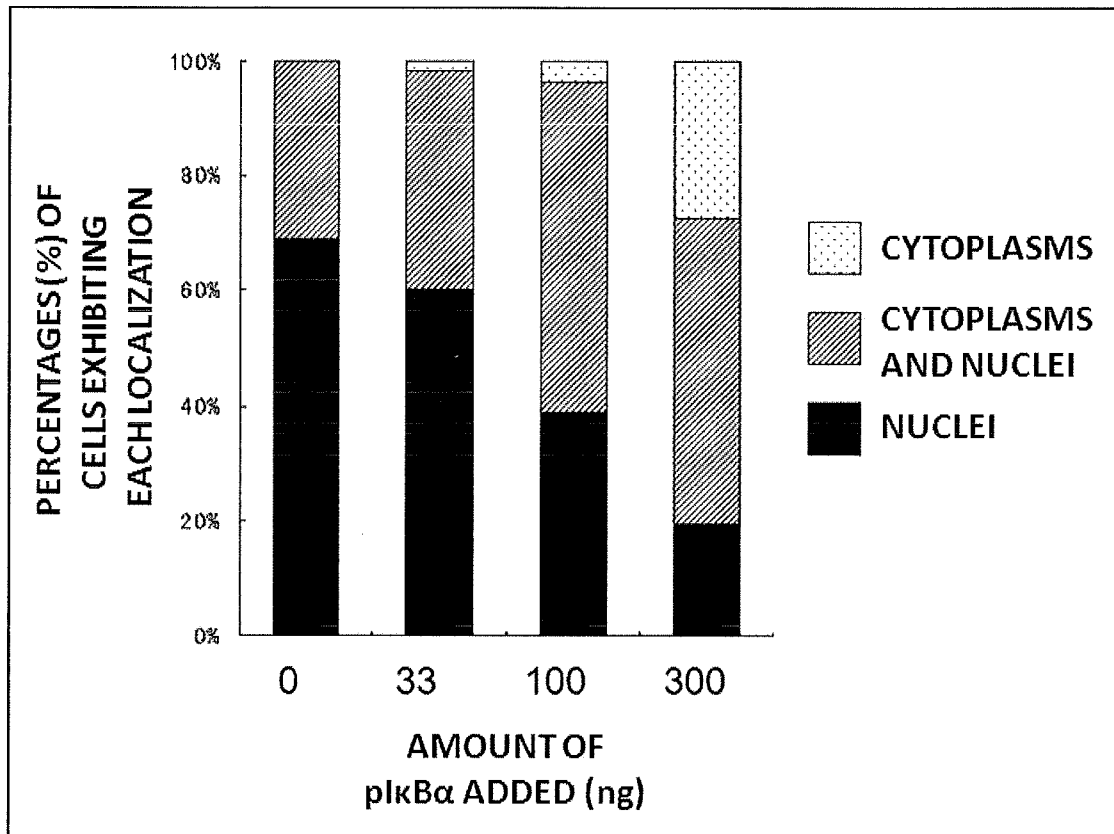


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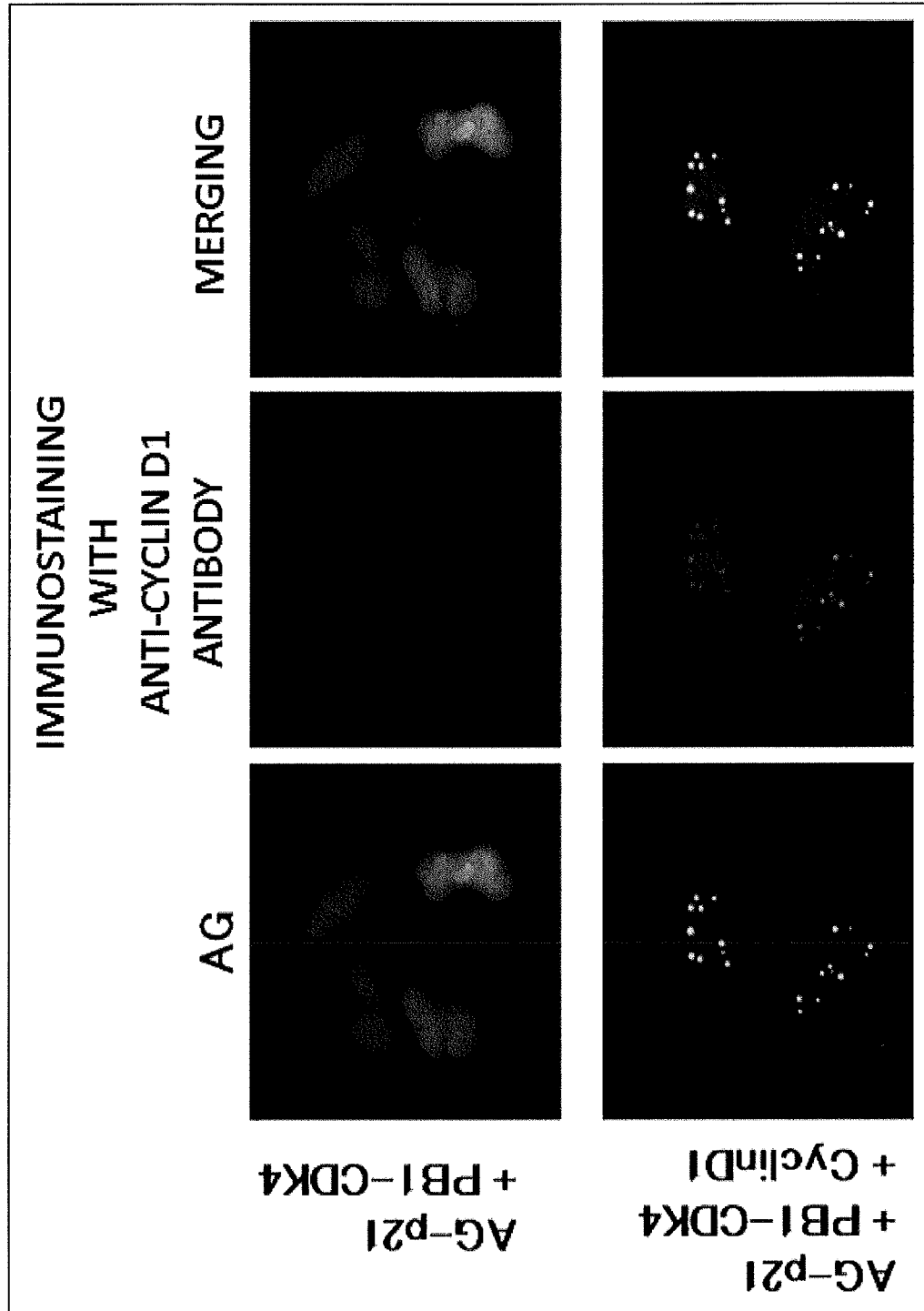


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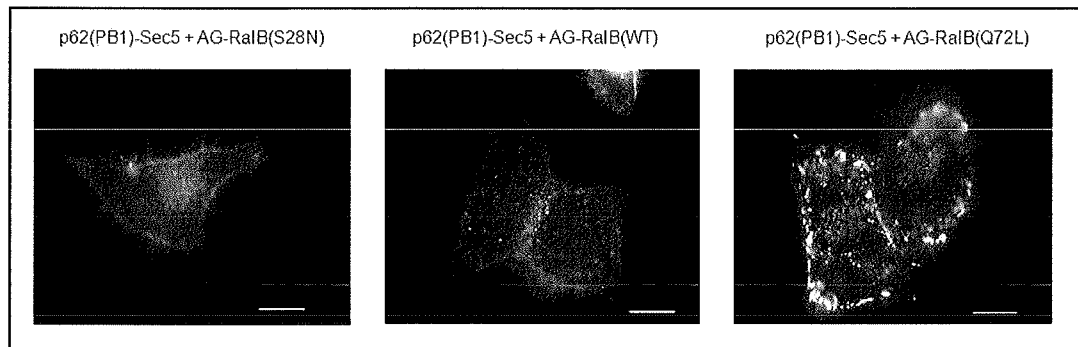


Fig. 30

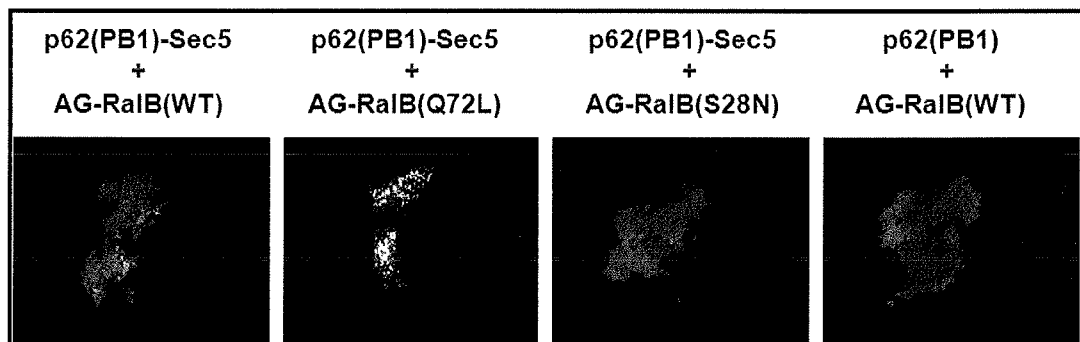


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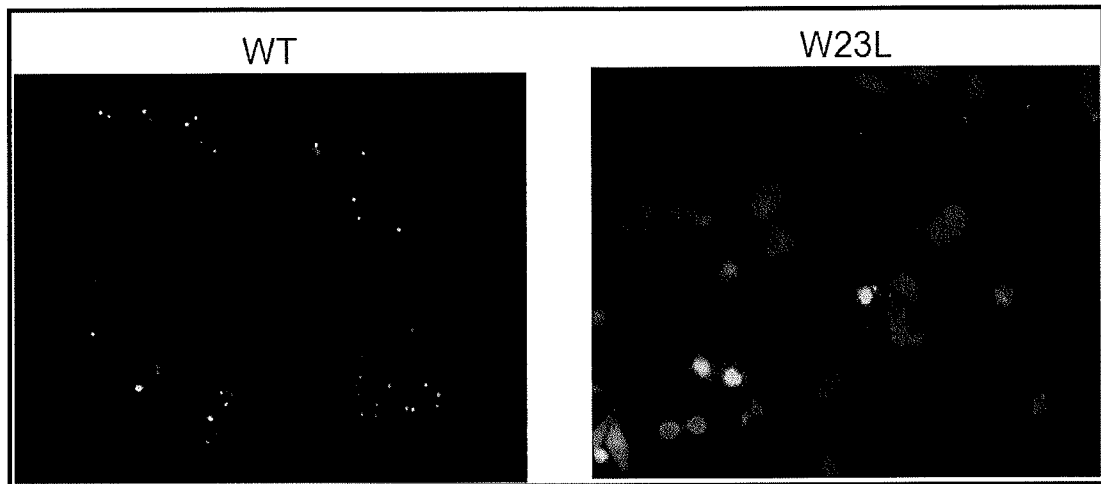


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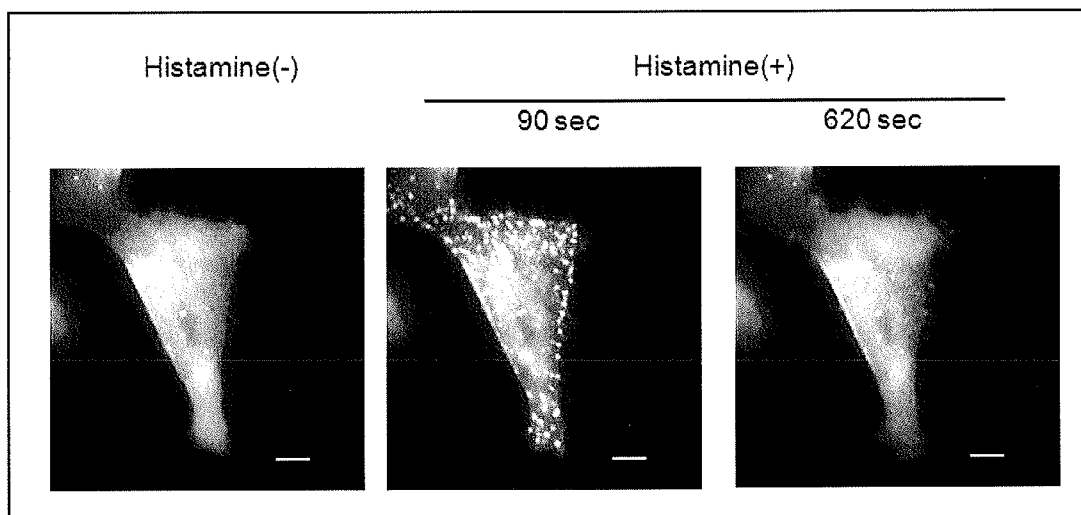


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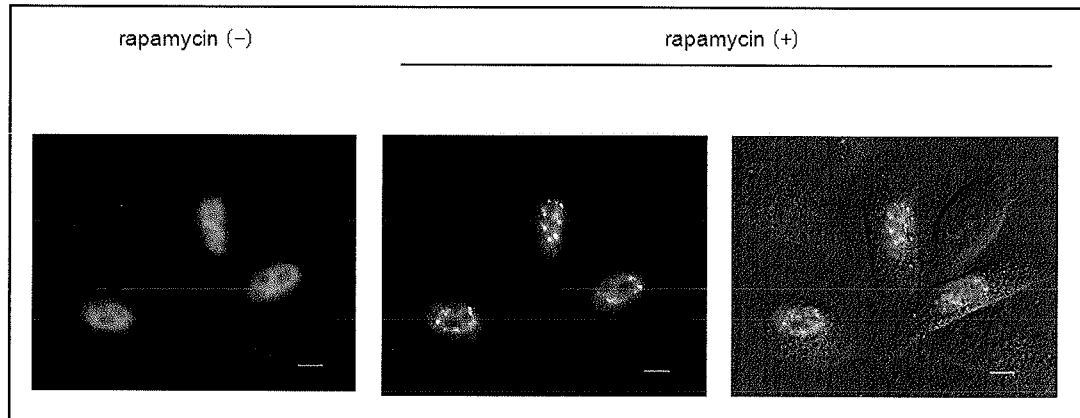


Fig. 34

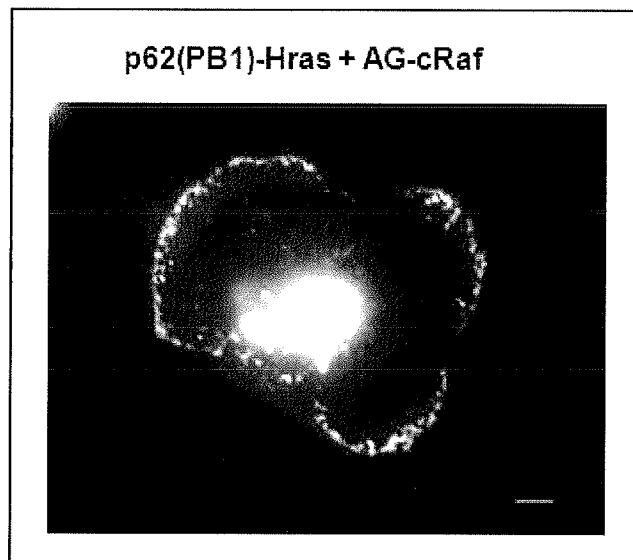


Fig. 35

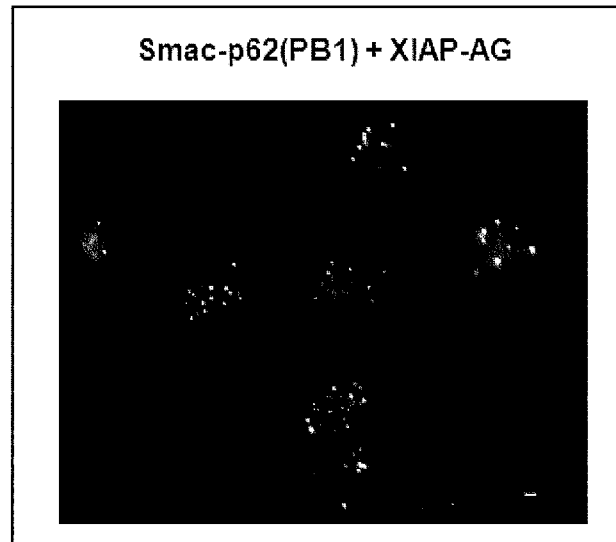


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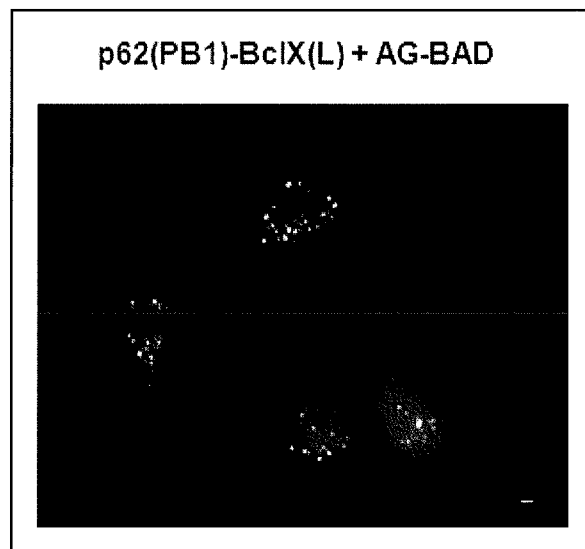


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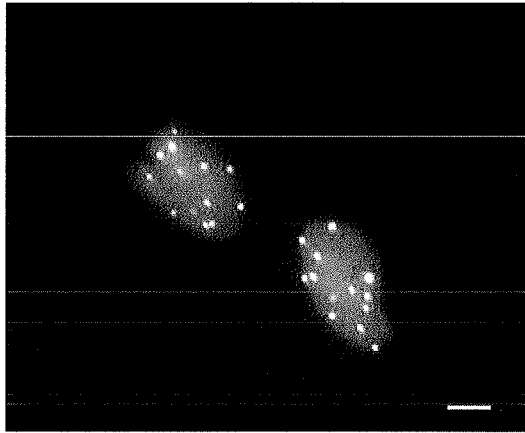


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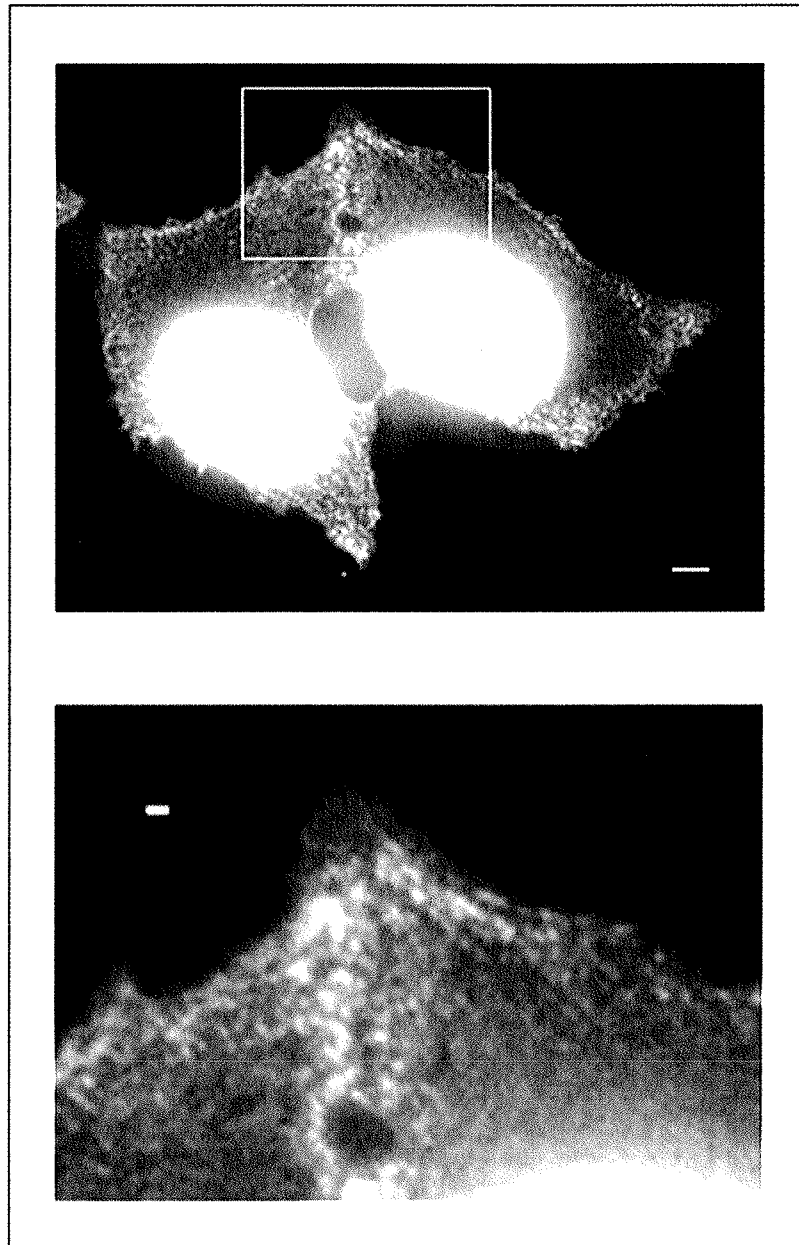


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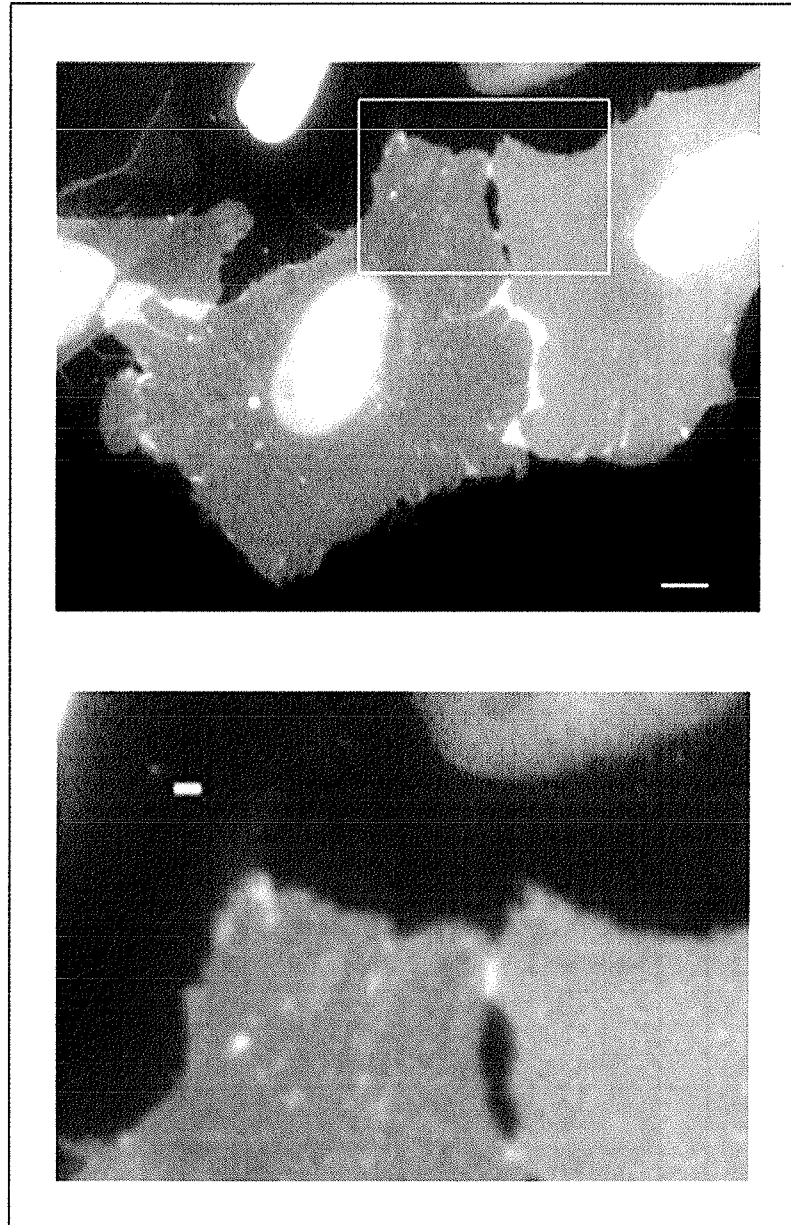


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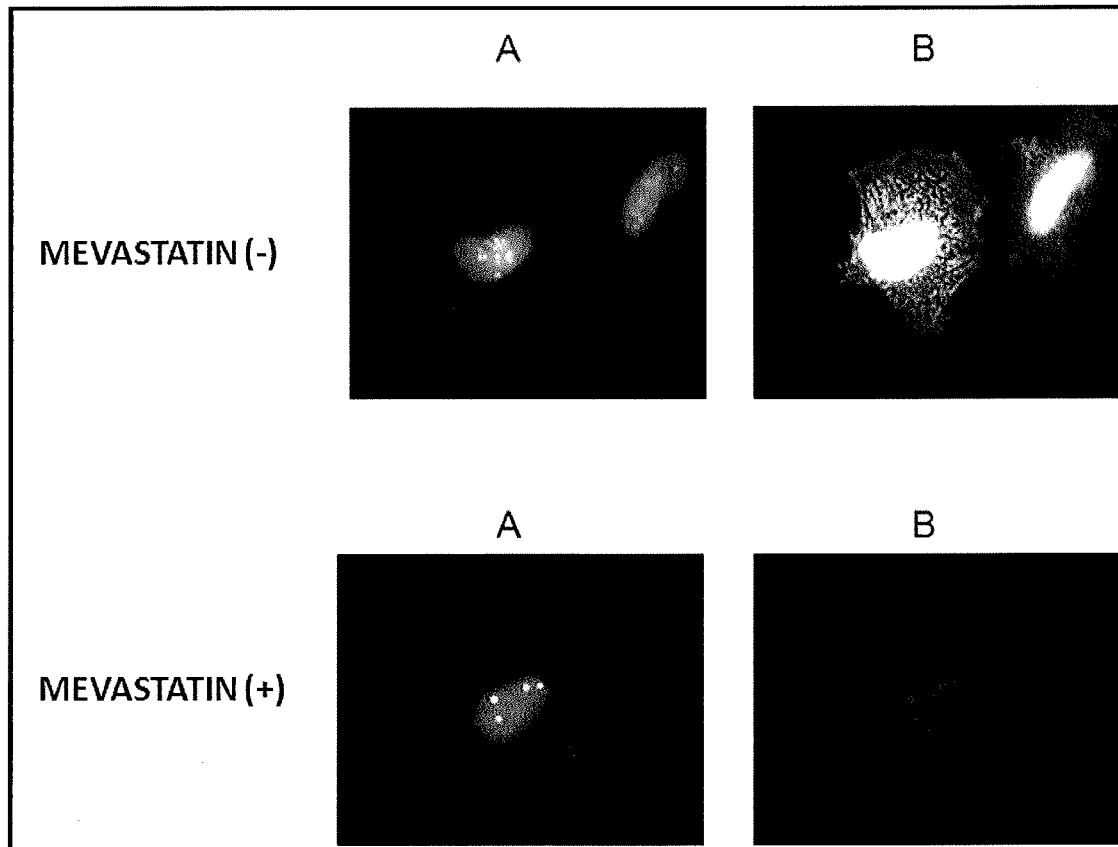


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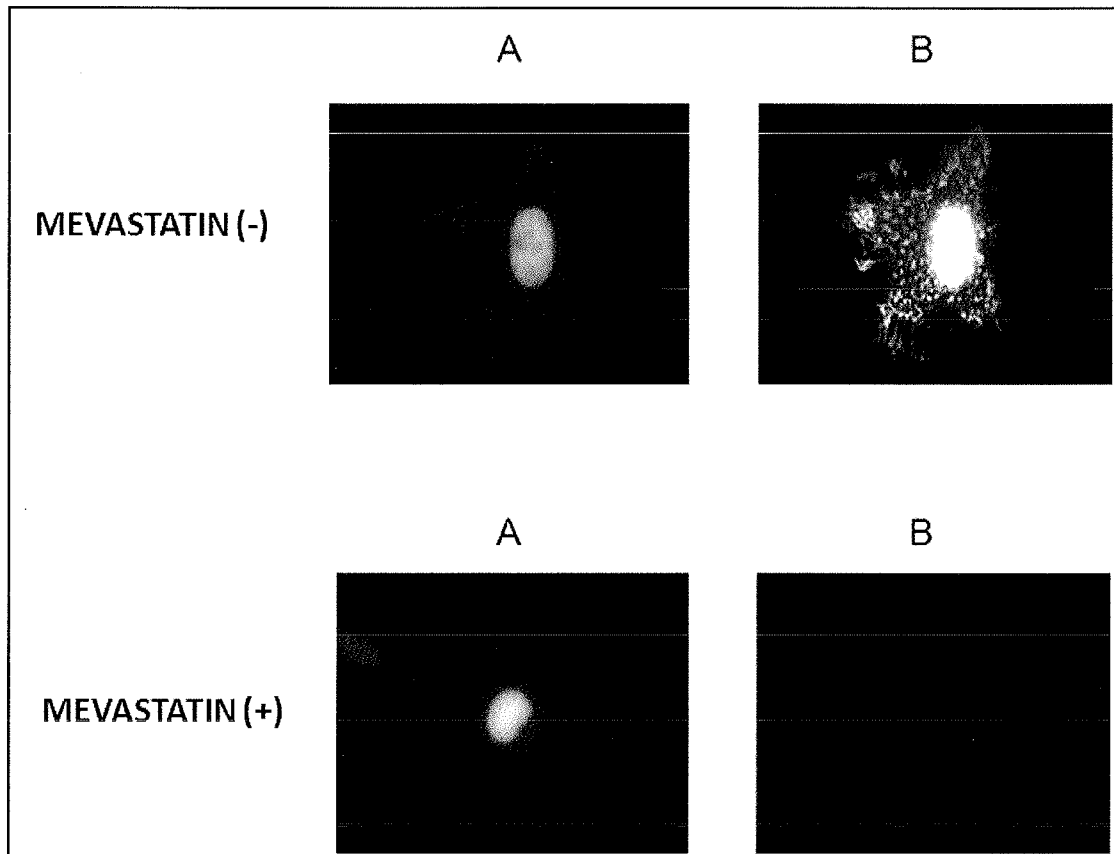


Fig. 42

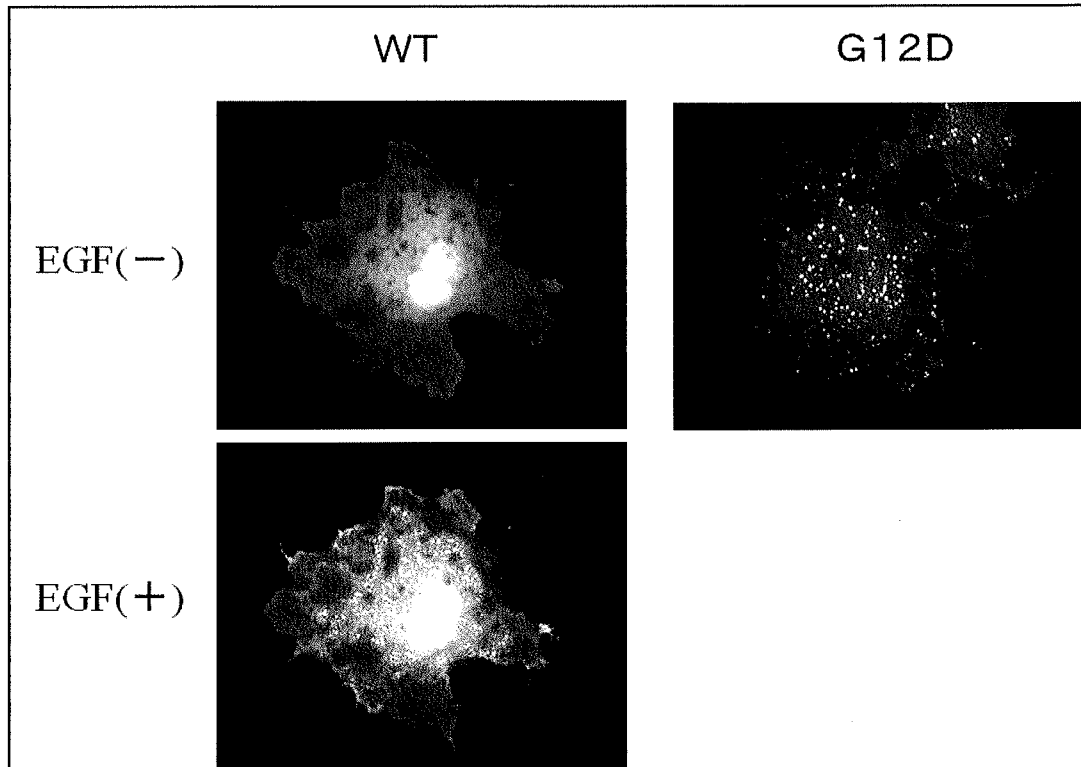


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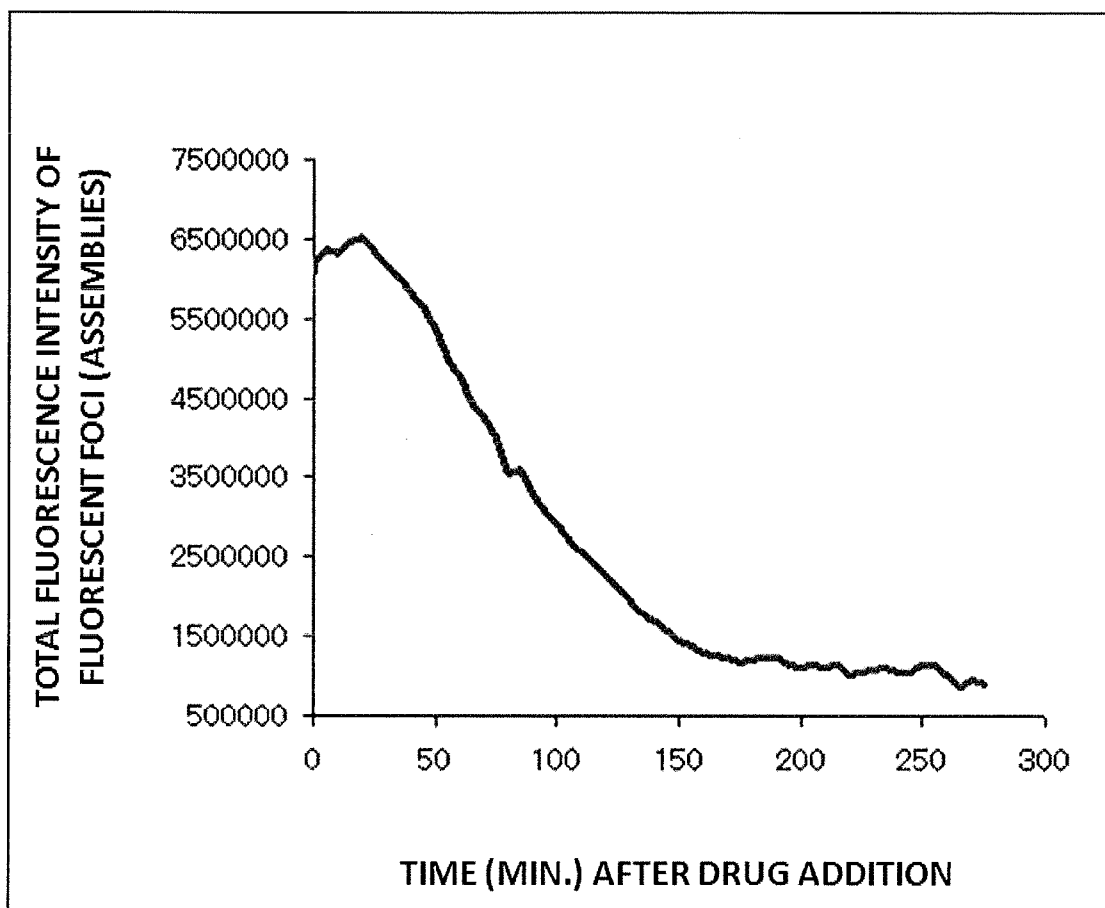


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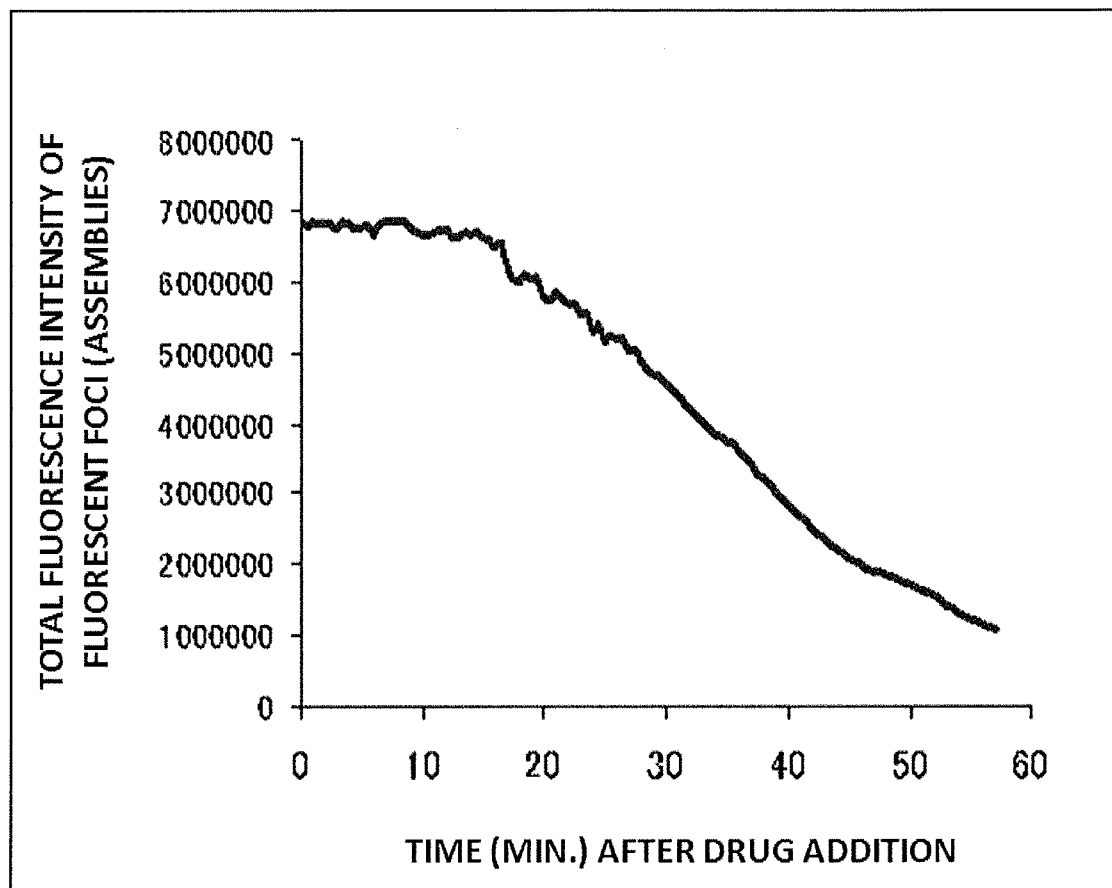


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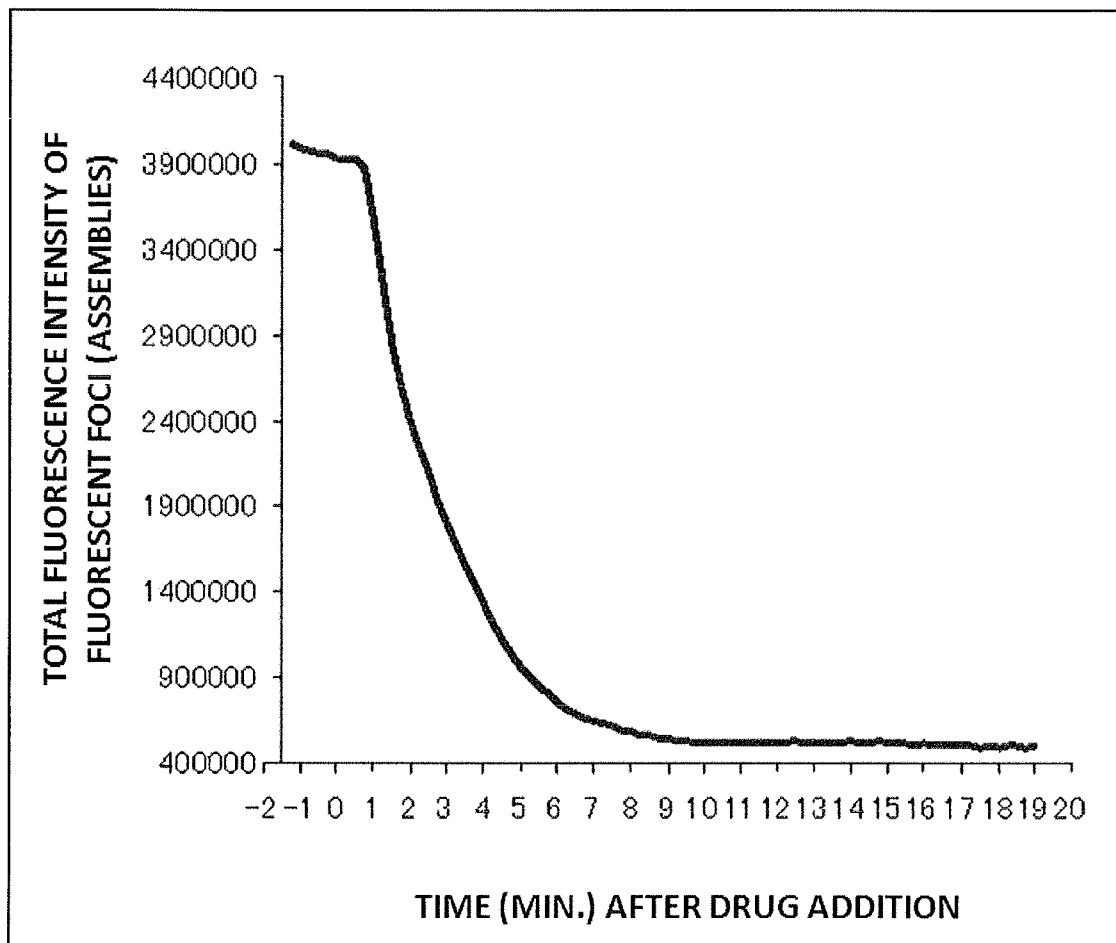


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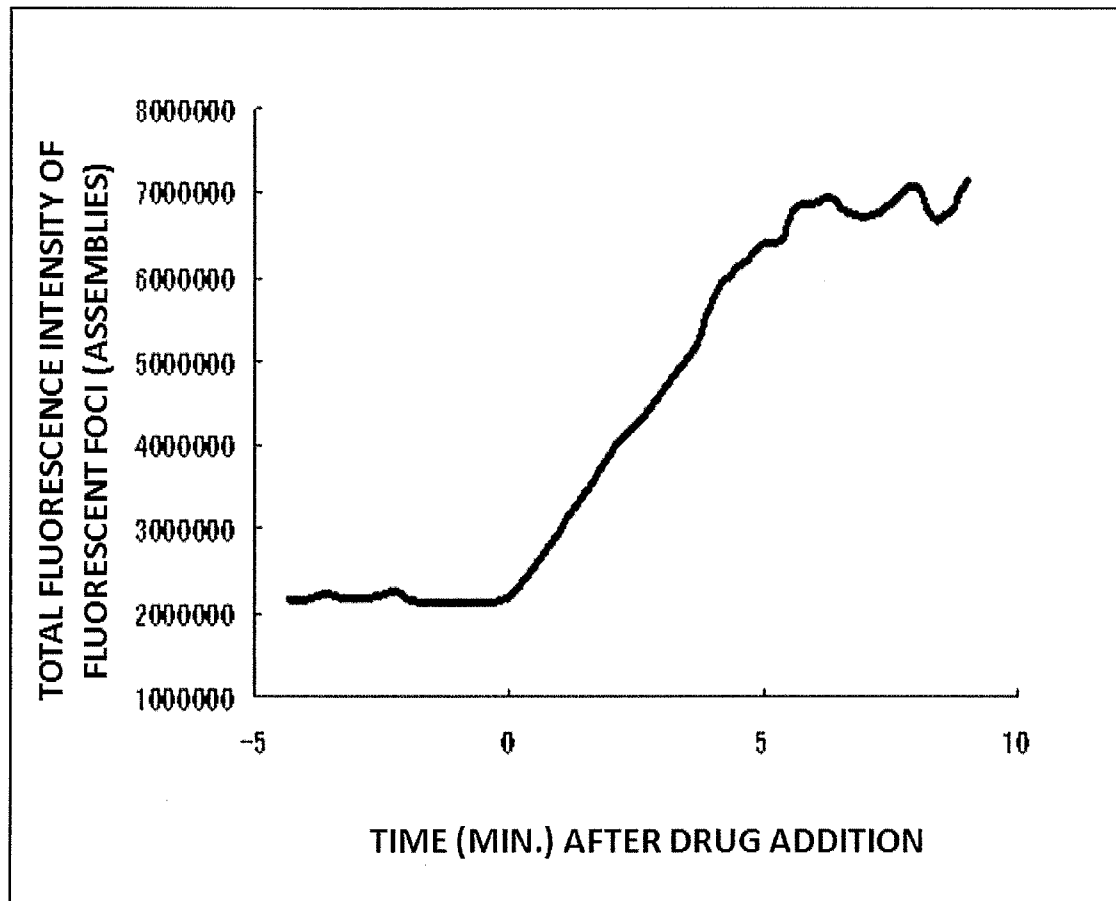


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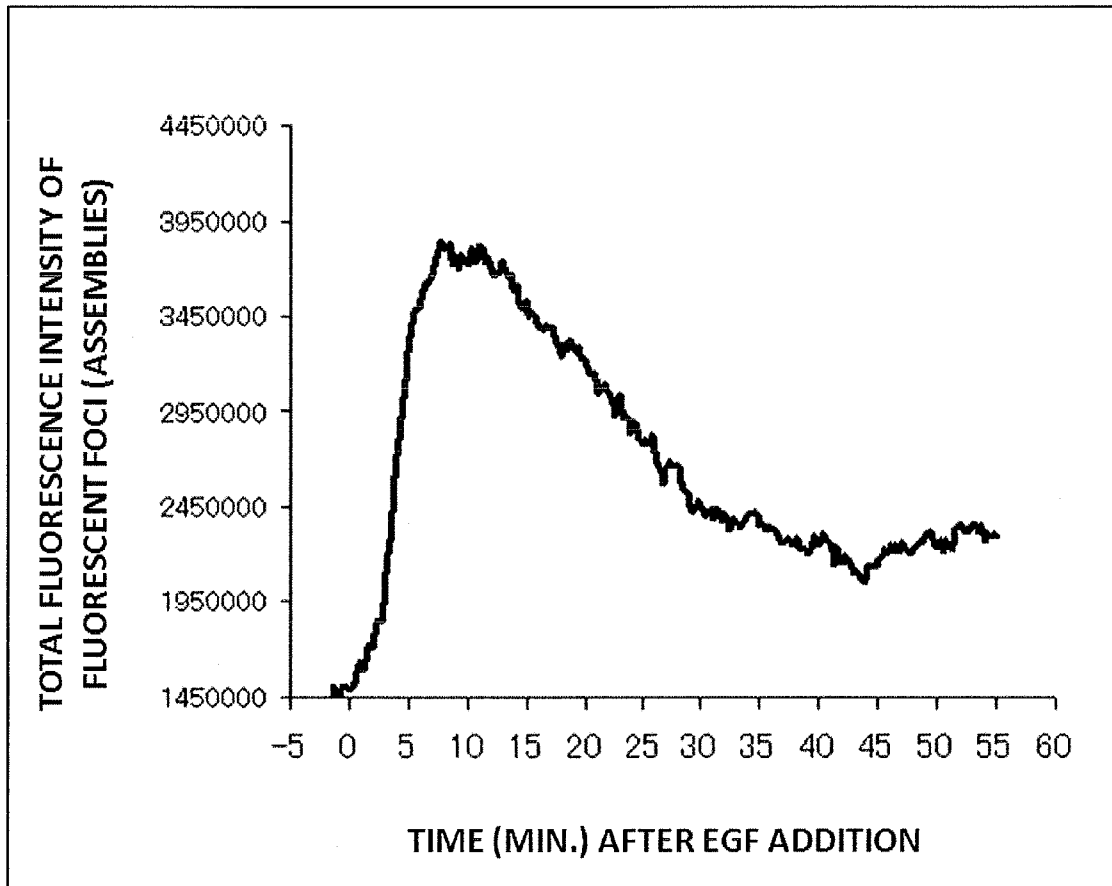


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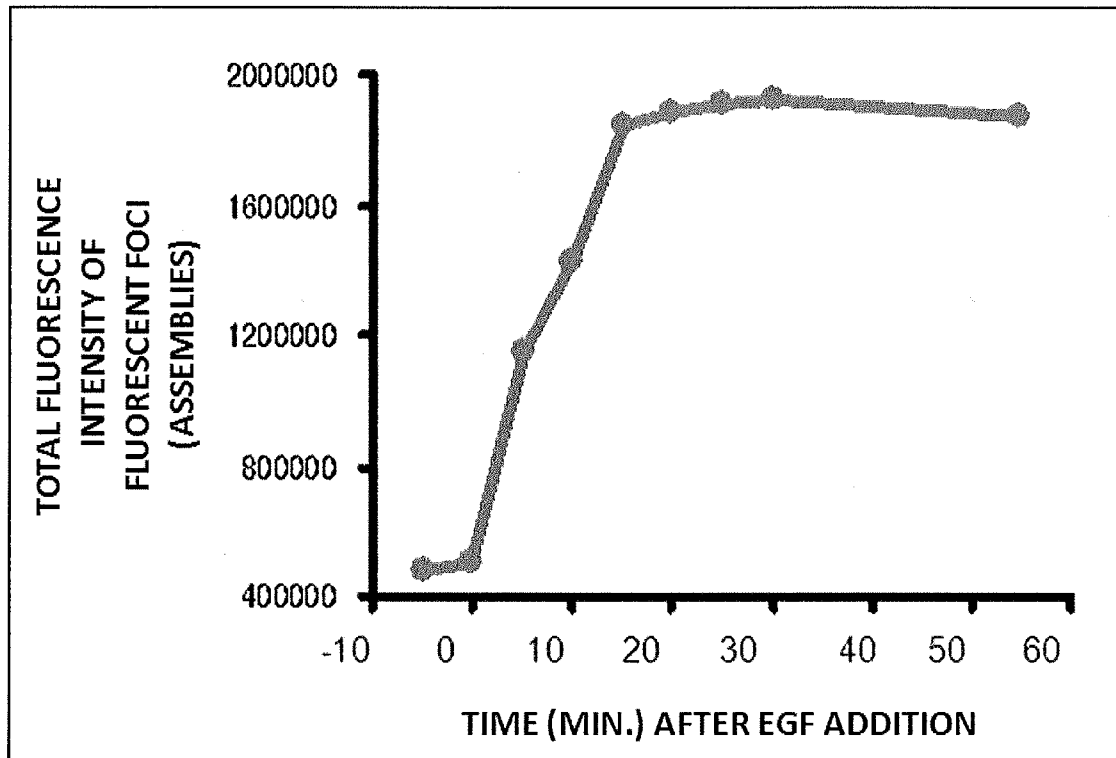
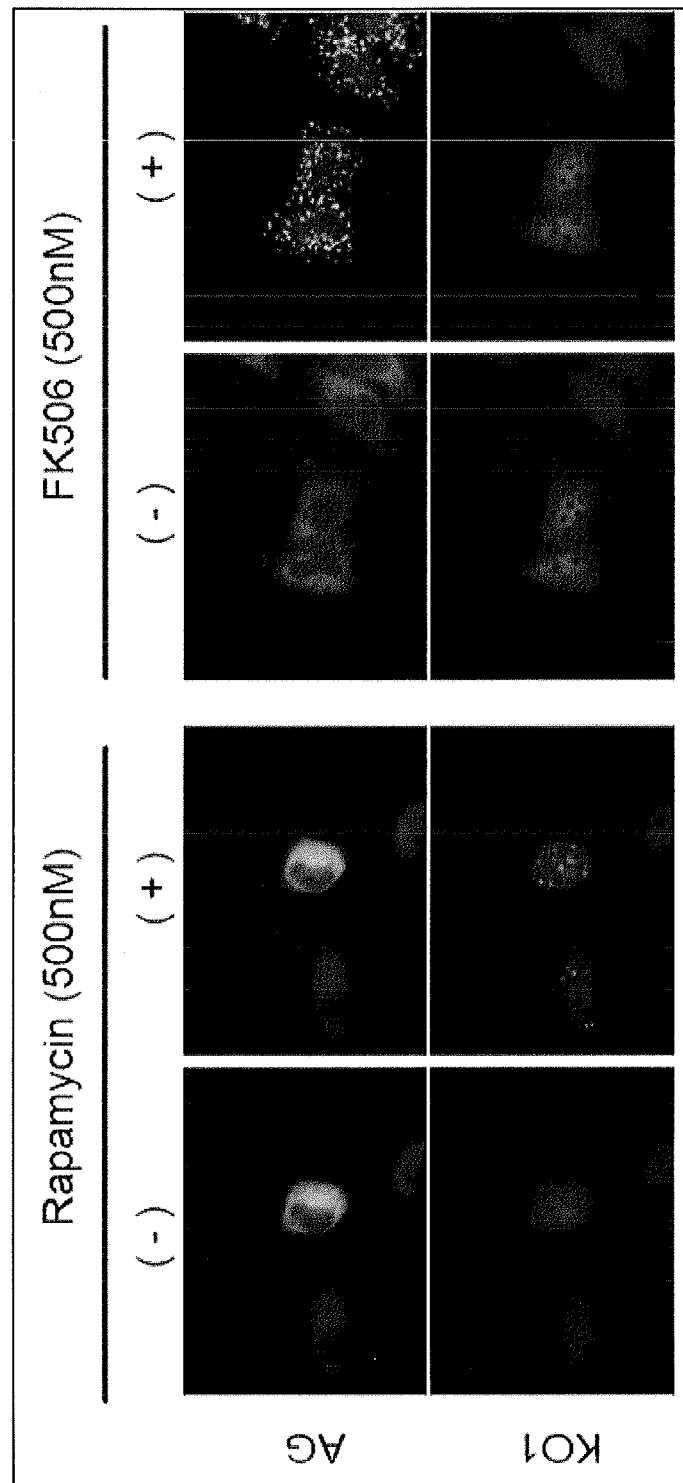


Fig. 49



IBPF12-538W0-E (seq) fin

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ggc	acc	gtg	aac	ggc	cac	aac	ttc	gtg	atc	gag	ggc	gag	ggc	aag	ggc	96
Gly	Thr	Val	Asn	Gly	His	Asn	Phe	Val	Ile	Glu	Gly	Glu	Gly	Lys	Gly	
			20				25					30				
aac	ccc	tac	gag	ggc	acc	cag	atc	ctg	gac	ctg	aac	gtg	acc	gag	ggc	144
Asn	Pro	Tyr	Glu	Gly	Thr	Gln	Ile	Leu	Asp	Leu	Asn	Val	Thr	Glu	Gly	
		35				40					45					
gcc	ccc	ctg	ccc	ttc	gcc	tac	gac	atc	ctg	acc	acc	gtg	ttc	cag	tac	192
Ala	Pro	Leu	Pro	Phe	Ala	Tyr	Asp	Ile	Leu	Thr	Thr	Val	Phe	Gln	Tyr	
		50			55					60						
ggc	aac	agg	gcc	ttc	acc	aag	tac	ccc	gcc	gac	atc	cag	gac	tac	ttc	240
Gly	Asn	Arg	Ala	Phe	Thr	Lys	Tyr	Pro	Ala	Asp	Ile	Gln	Asp	Tyr	Phe	
65				70				75						80		
aag	cag	acc	ttc	ccc	gag	ggc	tac	cac	tgg	gag	agg	agc	atg	acc	tac	288
Lys	Gln	Thr	Phe	Pro	Glu	Gly	Tyr	His	Trp	Glu	Arg	Ser	Met	Thr	Tyr	
			85					90				95				
gag	gac	cag	ggc	atc	tgc	acc	gcc	acc	agc	aac	atc	agc	atg	agg	ggc	336
Glu	Asp	Gln	Gly	Ile	Cys	Thr	Ala	Thr	Ser	Asn	Ile	Ser	Met	Arg	Gly	
		100					105					110				
gac	tgc	ttc	ttc	tac	gac	atc	agg	ttc	gac	ggc	gtg	aac	ttc	ccc	ccc	384
Asp	Cys	Phe	Phe	Tyr	Asp	Ile	Arg	Phe	Asp	Gly	Val	Asn	Phe	Pro	Pro	
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Asn	Gly	Pro	Val	Met	Gln	Lys	Lys	Thr	Leu	Lys	Trp	Glu	Pro	Ser	Thr	
		130			135						140					
gag	aag	atg	tac	gtg	agg	gac	ggc	gtg	ctg	aag	ggc	gac	gtg	aac	atg	480
Glu	Lys	Met	Tyr	Val	Arg	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val	Asn	Met	
145				150				155						160		
gcc	ctg	ctg	ctg	gag	ggc	ggc	ggc	cac	tac	agg	tgc	gac	ttc	aag	acc	528
Ala	Leu	Leu	Leu	Glu	Gly	Gly	Gly	His	Tyr	Arg	Cys	Asp	Phe	Lys	Thr	
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acc	tac	aag	gcc	aag	aag	gac	gtg	agg	ctg	ccc	gac	tac	cac	ttc	gtg	576
Thr	Tyr	Lys	Ala	Lys	Lys	Asp	Val	Arg	Leu	Pro	Asp	Tyr	His	Phe	Val	
		180				185						190				
gac	cac	agg	atc	gag	atc	ctg	aag	cac	gac	aag	gac	tac	aac	aag	gtg	624
Asp	His	Arg	Ile	Glu	Ile	Leu	Lys	His	Asp	Lys	Asp	Tyr	Asn	Lys	Val	
		195				200						205				
aag	ctg	tac	gag	aac	gcc	gtg	gcc	agg	tac	agc	atg	ctg	ccc	agc	cag	672
Lys	Leu	Tyr	Glu	Asn	Ala	Val	Ala	Arg	Tyr	Ser	Met	Leu	Pro	Ser	Gln	
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Ala	Lys															
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IBPF12-538W0-E (seq) fin

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<223> humanized codon Azami Green

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 35 40 45
 Ala Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Val Phe Gln Tyr
 50 55 60
 Gly Asn Arg Ala Phe Thr Lys Tyr Pro Ala Asp Ile Gln Asp Tyr Phe
 65 70 75 80
 Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ser Met Thr Tyr
 85 90 95
 Glu Asp Gln Gly Ile Cys Thr Ala Thr Ser Asn Ile Ser Met Arg Gly
 100 105 110
 Asp Cys Phe Phe Tyr Asp Ile Arg Phe Asp Gly Val Asn Phe Pro Pro
 115 120 125
 Asn Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp Glu Pro Ser Thr
 130 135 140
 Glu Lys Met Tyr Val Arg Asp Gly Val Leu Lys Gly Asp Val Asn Met
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 Ala Leu Leu Leu Glu Gly Gly Gly His Tyr Arg Cys Asp Phe Lys Thr
 165 170 175
 Thr Tyr Lys Ala Lys Lys Asp Val Arg Leu Pro Asp Tyr His Phe Val
 180 185 190
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 Ala Arg Glu Ile Arg Arg Phe Ser Phe Cys Cys Ser Pro Glu Pro Glu
 20 25 30
 gcg gaa gcc gag gct gcg gcg ggt ccg gga ccc tgc gag cgg ctg ctg 144
 Ala Glu Ala Glu Ala Ala Ala Gly Pro Gly Pro Cys Glu Arg Leu Leu
 35 40 45
 agc cgg gtg gcc gcc ctg ttc ccc gcg ctg cgg cct gcc ggc ttc cag 192
 Ser Arg Val Ala Ala Leu Phe Pro Ala Leu Arg Pro Gly Gly Phe Gln
 50 55 60
 gcg cac tac cgc gat gag gac ggg gac ttg gtt gcc ttt tcc agt gac 240
 Ala His Tyr Arg Asp Glu Asp Gly Asp Leu Val Ala Phe Ser Ser Asp
 65 70 75 80
 gag gaa ttg aca atg gcc atg tcc tac gtg aag gat gac atc ttc cga 288
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 35 40 45
 Ser Arg Val Ala Ala Leu Phe Pro Ala Leu Arg Pro Gly Gly Phe Gln
 50 55 60
 Ala His Tyr Arg Asp Glu Asp Gly Asp Leu Val Ala Phe Ser Ser Asp
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 aca gtg cac toc ggg ccg cag tta ctc ttc agg gat gtg ctg gat gtg 96
 Thr Val His Ser Gly Pro Gln Leu Leu Phe Arg Asp Val Leu Asp Val 30
 20 25 30
 ata ggc cag gtt ctg cct gaa gca aca act aca gca ttt gaa tat gaa 144
 Ile Gly Gln Val Leu Pro Glu Ala Thr Thr Thr Ala Phe Glu Tyr Glu 45
 35 40 45
 gat gaa gat ggt gat cga att aca gtg aga agt gat gag gaa atg aag 192
 Asp Glu Asp Gly Asp Arg Ile Thr Val Arg Ser Asp Glu Glu Met Lys 60
 50 55 60
 gca atg ctg tca tat tat tat tcc aca gta atg gaa cag caa gta aat 240
 Ala Met Leu Ser Tyr Tyr Tyr Ser Thr Val Met Glu Gln Gln Val Asn 80
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 35 40 45
 Asp Glu Asp Gly Asp Arg Ile Thr Val Arg Ser Asp Glu Glu Met Lys
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Val Ser Asp Pro Glu Asn Thr Thr Trp Ala Asp Ile Glu Ala Met Val	
20 25 30	
aaa gtt tca ttt gat ctg aat act att caa ata aaa tac ctg gat gag	144
Lys Val Ser Phe Asp Leu Asn Thr Ile Gln Ile Lys Tyr Leu Asp Glu	
35 40 45	
gaa aat gaa gag gta tcc atc aac agt caa gga gaa tat gaa gaa gcg	192
Glu Asn Glu Glu Val Ser Ile Asn Ser Gln Gly Glu Tyr Glu Glu Ala	
50 55 60	
ctt aag atg gca gtt aaa cag gga aac caa ctg cag atg caa gtc cac	240
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Glu Gly	

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Gln Val Thr Leu Asn Val Thr Phe Lys Asn Glu Ile Gln Ser Phe Leu	
1 5 10 15	
Val Ser Asp Pro Glu Asn Thr Thr Trp Ala Asp Ile Glu Ala Met Val	
20 25 30	
Lys Val Ser Phe Asp Leu Asn Thr Ile Gln Ile Lys Tyr Leu Asp Glu	
35 40 45	
Glu Asn Glu Glu Val Ser Ile Asn Ser Gln Gly Glu Tyr Glu Glu Ala	
50 55 60	
Leu Lys Met Ala Val Lys Gln Gly Asn Gln Leu Gln Met Gln Val His	
65 70 75 80	
Glu Gly	

<210> 9
 <211> 252
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1)..(252)
 <223> PKCiota(PB1)
 <400> 9

cag gtc cgg gtg aaa gcc tac tac cgc ggg gat atc atg ata aca cat	48
Gln Val Arg Val Lys Ala Tyr Tyr Arg Gly Asp Ile Met Ile Thr His	
1 5 10 15	
ttt gaa cct tcc atc tcc ttt gag gcc ctt tgc aat gag gtt cga gac	96
Phe Glu Pro Ser Ile Ser Phe Glu Gly Leu Cys Asn Glu Val Arg Asp	
20 25 30	
atg tgt tct ttt gac aac gaa cag ctc ttc acc atg aaa tgg ata gat	144
Met Cys Ser Phe Asp Asn Glu Gln Leu Phe Thr Met Lys Trp Ile Asp	
35 40 45	
gag gaa gga gac ccg tgt aca gta tca tct cag ttg gag tta gaa gaa	192
Glu Glu Gly Asp Pro Cys Thr Val Ser Ser Gln Leu Glu Leu Glu Glu	
50 55 60	
gcc ttt aga ctt tat gag cta aac aag gat tct gaa ctc ttg att cat	240

IBPF12-538W0-E (seq) fin
 Ala Phe Arg Leu Tyr Glu Leu Asn Lys Asp Ser Glu Leu Leu Ile His
 65 70 75 80
 gtg ttc cct tgt
 Val Phe Pro Cys

252

<210> 10
 <211> 84
 <212> PRT
 <213> Homo sapiens
 <223> PKCιota(PB1)
 <400> 10
 Gln Val Arg Val Lys Ala Tyr Tyr Arg Gly Asp Ile Met Ile Thr His
 1 5 10 15
 Phe Glu Pro Ser Ile Ser Phe Glu Gly Leu Cys Asn Glu Val Arg Asp
 20 25 30
 Met Cys Ser Phe Asp Asn Glu Gln Leu Phe Thr Met Lys Trp Ile Asp
 35 40 45
 Glu Glu Gly Asp Pro Cys Thr Val Ser Ser Gln Leu Glu Leu Glu Glu
 50 55 60
 Ala Phe Arg Leu Tyr Glu Leu Asn Lys Asp Ser Glu Leu Leu Ile His
 65 70 75 80
 Val Phe Pro Cys

<210> 11
 <211> 246
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1)..(246)
 <223> TFG(PB1)
 <400> 11
 aag cta atc atc aaa gct caa ctt ggg gag gat att cgg cga att cct 48
 Lys Leu Ile Ile Lys Ala Gln Leu Gly Glu Asp Ile Arg Arg Ile Pro
 1 5 10 15
 att cat aat gaa gat att act tat gat gaa tta gtg cta atg atg caa 96
 Ile His Asn Glu Asp Ile Thr Tyr Asp Glu Leu Val Leu Met Met Gln
 20 25 30
 cga gtt ttc aga gga aaa ctt ctg agt aat gat gaa gta aca ata aag 144
 Arg Val Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val Thr Ile Lys
 35 40 45
 tat aaa gat gaa gat gga gat ctt ata aca att ttt gat agt tct gac 192
 Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp Ser Ser Asp
 50 55 60
 ctt tcc ttt gca att cag tgc agt agg ata ctg aaa ctg aca tta ttt 240
 Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu Thr Leu Phe
 65 70 75 80
 gtt aat 246
 Val Asn

<210> 12
 <211> 82
 <212> PRT
 <213> Homo sapiens
 <223> TFG(PB1)
 <400> 12
 Lys Leu Ile Ile Lys Ala Gln Leu Gly Glu Asp Ile Arg Arg Ile Pro
 1 5 10 15
 Ile His Asn Glu Asp Ile Thr Tyr Asp Glu Leu Val Leu Met Met Gln
 20 25 30
 Arg Val Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val Thr Ile Lys
 35 40 45
 Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp Ser Ser Asp
 50 55 60
 Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu Thr Leu Phe

65
Val Asn

70

75

80

<210> 13
 <211> 261
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1)..(261)
 <223> TEL (SAM)
 <400> 13

cct cga gcg ctc agg atg gag gaa gac tcg atc cgc ctg cct gcg cac	48
Pro Arg Ala Leu Arg Met Glu Glu Asp Ser Ile Arg Leu Pro Ala His	
1 5 10 15	
ctg cgc ttg cag cca att tac tgg agc agg gat gac gta gcc cag tgg	96
Leu Arg Leu Gln Pro Ile Tyr Trp Ser Arg Asp Asp Val Ala Gln Trp	
20 25 30	
ctc aag tgg gct gaa aat gag ttt tct tta agg cca att gac agc aac	144
Leu Lys Trp Ala Glu Asn Glu Phe Ser Leu Arg Pro Ile Asp Ser Asn	
35 40 45	
acg ttt gaa atg aat ggc aaa gct ctc ctg ctg acc aaa gag gac	192
Thr Phe Glu Met Asn Gly Lys Ala Leu Leu Leu Leu Thr Lys Glu Asp	
50 55 60	
ttt cgc tat cga tct cct cat tca ggt gat gtg ctc tat gaa ctc ctt	240
Phe Arg Tyr Arg Ser Pro His Ser Gly Asp Val Leu Tyr Glu Leu Leu	
65 70 75 80	
cag cat att ctg aag cag agg	261
Gln His Ile Leu Lys Gln Arg	
85	

<210> 14
 <211> 87
 <212> PRT
 <213> Homo sapiens
 <223> TEL (SAM)
 <400> 14

Pro Arg Ala Leu Arg Met Glu Glu Asp Ser Ile Arg Leu Pro Ala His	
1 5 10 15	
Leu Arg Leu Gln Pro Ile Tyr Trp Ser Arg Asp Asp Val Ala Gln Trp	
20 25 30	
Leu Lys Trp Ala Glu Asn Glu Phe Ser Leu Arg Pro Ile Asp Ser Asn	
35 40 45	
Thr Phe Glu Met Asn Gly Lys Ala Leu Leu Leu Leu Thr Lys Glu Asp	
50 55 60	
Phe Arg Tyr Arg Ser Pro His Ser Gly Asp Val Leu Tyr Glu Leu Leu	
65 70 75 80	
Gln His Ile Leu Lys Gln Arg	
85	

<210> 15
 <211> 231
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1)..(231)
 <223> EphB2 (SAM)
 <400> 15

ctg gac cgc acg atc ccc gac tac acc agc ttt aac acg gtg gac gag	48
Leu Asp Arg Thr Ile Pro Asp Tyr Thr Ser Phe Asn Thr Val Asp Glu	
1 5 10 15	
tgg ctg gag gcc atc aag atg ggg cag tac aag gag agc ttc gcc aat	96
Trp Leu Glu Ala Ile Lys Met Gly Gln Tyr Lys Glu Ser Phe Ala Asn	
20 25 30	
gcc ggc ttc acc tcc ttt gac gtc gtg tct cag atg atg atg gag gac	144
Ala Gly Phe Thr Ser Phe Asp Val Val Ser Gln Met Met Met Glu Asp	

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35 40 45
 att ctc cgg gtt ggg gtc act ttg gct ggc cac cag aaa aaa atc ctg 192
 Ile Leu Arg Val Gly Val Thr Leu Ala Gly His Gln Lys Lys Ile Leu
 50 55 60
 aac agt atc cag gtg atg cgg gcg cag atg aac cag att 231
 Asn Ser Ile Gln Val Met Arg Ala Gln Met Asn Gln Ile
 65 70 75

<210> 16
 <211> 77
 <212> PRT
 <213> Homo sapiens
 <223> EphB2 (SAM)
 <400> 16

Leu Asp Arg Thr Ile Pro Asp Tyr Thr Ser Phe Asn Thr Val Asp Glu
 1 5 10 15
 Trp Leu Glu Ala Ile Lys Met Gly Gln Tyr Lys Glu Ser Phe Ala Asn
 20 25 30
 Ala Gly Phe Thr Ser Phe Asp Val Val Ser Gln Met Met Met Glu Asp
 35 40 45
 Ile Leu Arg Val Gly Val Thr Leu Ala Gly His Gln Lys Lys Ile Leu
 50 55 60
 Asn Ser Ile Gln Val Met Arg Ala Gln Met Asn Gln Ile
 65 70 75

<210> 17
 <211> 204
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1).. (204)
 <223> DGKdelta (SAM)
 <400> 17

ccg gtt cac ctc tgg ggg aca gag gag gtt gct gcc tgg ctg gag cac 48
 Pro Val His Leu Trp Gly Thr Glu Glu Val Ala Ala Trp Leu Glu His
 1 5 10 15
 ctc agt ctc tgt gag tat aag gac atc ttc aca cgg cac gac atc cgg 96
 Leu Ser Leu Cys Glu Tyr Lys Asp Ile Phe Thr Arg His Asp Ile Arg
 20 25 30
 ggc tct gag ctc ctg cac ctg gag cgg agg gac ctc aag gac ctg ggc 144
 Gly Ser Glu Leu Leu His Leu Glu Arg Arg Asp Leu Lys Asp Leu Gly
 35 40 45
 gtg acc aag gtg ggc cac atg aag agg atc ctg tgt ggc atc aag gag 192
 Val Thr Lys Val Gly His Met Lys Arg Ile Leu Cys Gly Ile Lys Glu
 50 55 60
 ctg agc cgc agc 204
 Leu Ser Arg Ser
 65

<210> 18
 <211> 68
 <212> PRT
 <213> Homo sapiens
 <223> DGKdelta (SAM)
 <400> 18

Pro Val His Leu Trp Gly Thr Glu Glu Val Ala Ala Trp Leu Glu His
 1 5 10 15
 Leu Ser Leu Cys Glu Tyr Lys Asp Ile Phe Thr Arg His Asp Ile Arg
 20 25 30
 Gly Ser Glu Leu Leu His Leu Glu Arg Arg Asp Leu Lys Asp Leu Gly
 35 40 45
 Val Thr Lys Val Gly His Met Lys Arg Ile Leu Cys Gly Ile Lys Glu
 50 55 60
 Leu Ser Arg Ser
 65

<210> 19

IBPF12-538W0-E (seq) fin

<211> 597
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1).. (597)
 <223> Tankyrase (SAM)
 <400> 19

ctg ata gat gcc atg ccc cca gag gcc tta cct acc tgt ttt aaa cct	48
Leu Ile Asp Ala Met Pro Pro Glu Ala Leu Pro Thr Cys Phe Lys Pro	
1 5 10 15	
cag gct act gta gtg agt gcc tct ctg atc tca cca gca tcc acc ccc	96
Gln Ala Thr Val Val Ser Ala Ser Leu Ile Ser Pro Ala Ser Thr Pro	
20 25 30	
tcc tgc ctc tcg gct gcc agc agc ata gac aac ctc act ggc cct tta	144
Ser Cys Leu Ser Ala Ala Ser Ser Ile Asp Asn Leu Thr Gly Pro Leu	
35 40 45	
gca gag ttg gcc gta gga gga gcc tcc aat gca ggg gat ggc gcc gcg	192
Ala Glu Leu Ala Val Gly Gly Ala Ser Asn Ala Gly Asp Gly Ala Ala	
50 55 60	
gga aca gaa agg aag gaa gga gaa gtt gct ggt ctt gac atg aat atc	240
Gly Thr Glu Arg Lys Glu Gly Glu Val Ala Gly Leu Asp Met Asn Ile	
65 70 75 80	
agc caa ttt cta aaa agc ctt ggc ctt gaa cac ctt cgg gat atc ttt	288
Ser Gln Phe Leu Lys Ser Leu Gly Leu Glu His Leu Arg Asp Ile Phe	
85 90 95	
gaa aca gaa cag att aca cta gat gtg ttg gct gat atg ggt cat gaa	336
Glu Thr Glu Gln Ile Thr Leu Asp Val Leu Ala Asp Met Gly His Glu	
100 105 110	
gag ttg aaa gaa ata ggc atc aat gca tat ggg cac cgc cac aaa tta	384
Glu Leu Lys Glu Ile Gly Ile Asn Ala Tyr Gly His Arg His Lys Leu	
115 120 125	
atc aaa gga gta gaa aga ctc tta ggt gga caa caa ggc acc aat cct	432
Ile Lys Gly Val Glu Arg Leu Leu Gly Gly Gln Gln Gly Thr Asn Pro	
130 135 140	
tat ttg act ttt cac tgt gtt aat cag gga acg att ttg ctg gat ctt	480
Tyr Leu Thr Phe His Cys Val Asn Gln Gly Thr Ile Leu Leu Asp Leu	
145 150 155 160	
gct cca gaa gat aaa gaa tat cag tca gtg gaa gaa gag atg caa agt	528
Ala Pro Glu Asp Lys Glu Tyr Gln Ser Val Glu Glu Glu Met Gln Ser	
165 170 175	
act att cga gaa cac aga gat ggt ggt aat gct ggc ggc atc ttc aac	576
Thr Ile Arg Glu His Arg Asp Gly Gly Asn Ala Gly Gly Ile Phe Asn	
180 185 190	
aga tac aat gtc att cga att	597
Arg Tyr Asn Val Ile Arg Ile	
195	

<210> 20
 <211> 199
 <212> PRT
 <213> Homo sapiens
 <223> Tankyrase (SAM)
 <400> 20

Leu Ile Asp Ala Met Pro Pro Glu Ala Leu Pro Thr Cys Phe Lys Pro
1 5 10 15
Gln Ala Thr Val Val Ser Ala Ser Leu Ile Ser Pro Ala Ser Thr Pro
20 25 30
Ser Cys Leu Ser Ala Ala Ser Ser Ile Asp Asn Leu Thr Gly Pro Leu
35 40 45
Ala Glu Leu Ala Val Gly Gly Ala Ser Asn Ala Gly Asp Gly Ala Ala
50 55 60
Gly Thr Glu Arg Lys Glu Gly Glu Val Ala Gly Leu Asp Met Asn Ile
65 70 75 80
Ser Gln Phe Leu Lys Ser Leu Gly Leu Glu His Leu Arg Asp Ile Phe
85 90 95
Glu Thr Glu Gln Ile Thr Leu Asp Val Leu Ala Asp Met Gly His Glu
100 105 110

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Glu	Leu	Lys	Glu	Ile	Gly	Ile	Asn	Ala	Tyr	Gly	His	Arg	His	Lys	Leu
		115					120					125			
Ile	Lys	Gly	Val	Glu	Arg	Leu	Leu	Gly	Gly	Gln	Gln	Gly	Thr	Asn	Pro
	130					135					140				
Tyr	Leu	Thr	Phe	His	Cys	Val	Asn	Gln	Gly	Thr	Ile	Leu	Leu	Asp	Leu
145					150					155					160
Ala	Pro	Glu	Asp	Lys	Glu	Tyr	Gln	Ser	Val	Glu	Glu	Glu	Met	Gln	Ser
				165					170					175	
Thr	Ile	Arg	Glu	His	Arg	Asp	Gly	Gly	Asn	Ala	Gly	Gly	Ile	Phe	Asn
			180					185					190		
Arg	Tyr	Asn	Val	Ile	Arg	Ile									
		195													

<210> 21
 <211> 270
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1)..(270)
 <223> mTOR (FRB)
 <400> 21

gag	atg	tgg	cat	gaa	ggc	ctg	gaa	gag	gca	tct	cgt	ttg	tac	ttt	ggg	48
Glu	Met	Trp	His	Glu	Gly	Leu	Glu	Glu	Ala	Ser	Arg	Leu	Tyr	Phe	Gly	
1				5					10					15		
gaa	agg	aac	gtg	aaa	ggc	atg	ttt	gag	gtg	ctg	gag	ccc	ttg	cat	gct	96
Glu	Arg	Asn	Val	Lys	Gly	Met	Phe	Glu	Val	Leu	Glu	Pro	Leu	His	Ala	
			20					25					30			
atg	atg	gaa	cgg	ggc	ccc	cag	act	ctg	aag	gaa	aca	tcc	ttt	aat	cag	144
Met	Met	Glu	Arg	Gly	Pro	Gln	Thr	Leu	Lys	Glu	Thr	Ser	Phe	Asn	Gln	
		35					40					45				
gcc	tat	ggt	cga	gat	tta	atg	gag	gcc	caa	gag	tgg	tgc	agg	aag	tac	192
Ala	Tyr	Gly	Arg	Asp	Leu	Met	Glu	Ala	Gln	Glu	Trp	Cys	Arg	Lys	Tyr	
	50					55					60					
atg	aaa	tca	ggg	aat	gtc	aag	gac	ctc	acc	caa	gcc	tgg	gac	ctc	tat	240
Met	Lys	Ser	Gly	Asn	Val	Lys	Asp	Leu	Thr	Gln	Ala	Trp	Asp	Leu	Tyr	
65				70						75				80		
tat	cat	gtg	ttc	cga	cga	atc	tca	aag	cag							270
Tyr	His	Val	Phe	Arg	Arg	Ile	Ser	Lys	Gln							
				85					90							

<210> 22
 <211> 90
 <212> PRT
 <213> Homo sapiens
 <223> mTOR (FRB)
 <400> 22

Glu	Met	Trp	His	Glu	Gly	Leu	Glu	Glu	Ala	Ser	Arg	Leu	Tyr	Phe	Gly
1				5					10					15	
Glu	Arg	Asn	Val	Lys	Gly	Met	Phe	Glu	Val	Leu	Glu	Pro	Leu	His	Ala
			20					25					30		
Met	Met	Glu	Arg	Gly	Pro	Gln	Thr	Leu	Lys	Glu	Thr	Ser	Phe	Asn	Gln
		35					40					45			
Ala	Tyr	Gly	Arg	Asp	Leu	Met	Glu	Ala	Gln	Glu	Trp	Cys	Arg	Lys	Tyr
	50					55					60				
Met	Lys	Ser	Gly	Asn	Val	Lys	Asp	Leu	Thr	Gln	Ala	Trp	Asp	Leu	Tyr
65				70						75				80	
Tyr	His	Val	Phe	Arg	Arg	Ile	Ser	Lys	Gln						
				85					90						

<210> 23
 <211> 324
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1)..(324)
 <223> FKBP12

IBPF12-538W0-E (seq) fin

<400> 23

atg gga gtg cag gtg gaa acc atc tcc cca gga gac ggg cgc acc ttc	48
Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe	
1 5 10 15	
ccc aag cgc ggc cag acc tgc gtg gtg cac tac acc ggg atg ctt gaa	96
Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu	
20 25 30	
gat gga aag aaa ttt gat tcc tcc cgg gac aga aac aag ccc ttt aag	144
Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys	
35 40 45	
ttt atg cta ggc aag cag gag gtg atc cga ggc tgg gaa gaa ggg gtt	192
Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val	
50 55 60	
gcc cag atg agt gtg ggt cag aga gcc aaa ctg act ata tct cca gat	240
Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp	
65 70 75 80	
tat gcc tat ggt gcc act ggg cac cca ggc atc atc cca cca cat gcc	288
Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala	
85 90 95	
act ctc gtc ttc gat gtg gag ctt cta aaa ctg gaa	324
Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu	
100 105	

<210> 24

<211> 108

<212> PRT

<213> Homo sapiens

<223> FKBP12

<400> 24

Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe	
1 5 10 15	
Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu	
20 25 30	
Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys	
35 40 45	
Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val	
50 55 60	
Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp	
65 70 75 80	
Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala	
85 90 95	
Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu	
100 105	

<210> 25

<211> 210

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(210)

<223> p53

<400> 25

atg gag gag ccg cag tca gat cct agc gtc gag ccc cct ctg agt cag	48
Met Glu Glu Pro Gln Ser Asp Pro Ser Val Glu Pro Pro Leu Ser Gln	
1 5 10 15	
gaa aca ttt tca gac cta tgg aaa cta ctt cct gaa aac aac gtt ctg	96
Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro Glu Asn Asn Val Leu	
20 25 30	
tcc ccc ttg ccg tcc caa gca atg gat gat ttg atg ctg tcc ccg gac	144
Ser Pro Leu Pro Ser Gln Ala Met Asp Asp Leu Met Leu Ser Pro Asp	
35 40 45	
gat att gaa caa tgg ttc act gaa gac cca ggt cca gat gaa gct ccc	192
Asp Ile Glu Gln Trp Phe Thr Glu Asp Pro Gly Pro Asp Glu Ala Pro	
50 55 60	
aga atg cca gag gct gct	210
Arg Met Pro Glu Ala Ala	
65 70	

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<210> 26
 <211> 70
 <212> PRT
 <213> Homo sapiens
 <223> p53
 <400> 26
 Met Glu Glu Pro Gln Ser Asp Pro Ser Val Glu Pro Pro Leu Ser Gln
 1 5 10 15
 Glu Thr Phe Ser Asp Leu Trp Lys Leu Pro Glu Asn Asn Val Leu
 20 25 30
 Ser Pro Leu Pro Ser Gln Ala Met Asp Asp Leu Met Leu Ser Pro Asp
 35 40 45
 Asp Ile Glu Gln Trp Phe Thr Glu Asp Pro Gly Pro Asp Glu Ala Pro
 50 55 60
 Arg Met Pro Glu Ala Ala
 65 70

<210> 27
 <211> 357
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1).. (357)
 <223> MDM2
 <400> 27

atg tgc aat acc aac atg tct gta cct act gat ggt gct gta acc acc 48
 Met Cys Asn Thr Asn Met Ser Val Pro Thr Asp Gly Ala Val Thr Thr
 1 5 10 15
 tca cag att cca gct tcg gaa caa gag acc ctg gtt aga cca aag cca 96
 Ser Gln Ile Pro Ala Ser Glu Gln Glu Thr Leu Val Arg Pro Lys Pro
 20 25 30
 ttg ctt ttg aag tta tta aag tct gtt ggt gca caa aaa gac act tat 144
 Leu Leu Leu Lys Leu Leu Lys Ser Val Gly Ala Gln Lys Asp Thr Tyr
 35 40 45
 act atg aaa gag gtt ctt ttt tat ctt ggc cag tat att atg act aaa 192
 Thr Met Lys Glu Val Leu Phe Tyr Leu Gly Gln Tyr Ile Met Thr Lys
 50 55 60
 cga tta tat gat gag aag caa caa cat att gta tat tgt tca aat gat 240
 Arg Leu Tyr Asp Glu Lys Gln Gln His Ile Val Tyr Cys Ser Asn Asp
 65 70 75 80
 ctt cta gga gat ttg ttt ggc gtg cca agc ttc tct gtg aaa gag cac 288
 Leu Leu Gly Asp Leu Phe Gly Val Pro Ser Phe Ser Val Lys Glu His
 85 90 95
 agg aaa ata tat acc atg atc tac agg aac ttg gta gta gtc aat cag 336
 Arg Lys Ile Tyr Thr Met Ile Tyr Arg Asn Leu Val Val Val Asn Gln
 100 105 110
 cag gaa tca tcg gac tca ggt 357
 Gln Glu Ser Ser Asp Ser Gly
 115

<210> 28
 <211> 119
 <212> PRT
 <213> Homo sapiens
 <223> MDM2
 <400> 28
 Met Cys Asn Thr Asn Met Ser Val Pro Thr Asp Gly Ala Val Thr Thr
 1 5 10 15
 Ser Gln Ile Pro Ala Ser Glu Gln Glu Thr Leu Val Arg Pro Lys Pro
 20 25 30
 Leu Leu Leu Lys Leu Leu Lys Ser Val Gly Ala Gln Lys Asp Thr Tyr
 35 40 45
 Thr Met Lys Glu Val Leu Phe Tyr Leu Gly Gln Tyr Ile Met Thr Lys
 50 55 60
 Arg Leu Tyr Asp Glu Lys Gln Gln His Ile Val Tyr Cys Ser Asn Asp
 65 70 75 80

IBPF12-538W0-E (seq) fin

Leu Leu Gly Asp Leu Phe Gly Val Pro Ser Phe Ser Val Lys Glu His
 85 90 95
 Arg Lys Ile Tyr Thr Met Ile Tyr Arg Asn Leu Val Val Val Asn Gln
 100 105 110
 Gln Glu Ser Ser Asp Ser Gly
 115

<210> 29
 <211> 297
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1).. (297)
 <223> Sec5
 <400> 29

atg tct cga tca cga caa ccc ccc ctt gtg acc ggc atc tct cca aat	48
Met Ser Arg Ser Arg Gln Pro Pro Leu Val Thr Gly Ile Ser Pro Asn	
1 5 10 15	
gaa ggg ata cca tgg acg aag gtc aca atc agg gga gaa aat ctg ggg	96
Glu Gly Ile Pro Trp Thr Lys Val Thr Ile Arg Gly Glu Asn Leu Gly	
20 25 30	
act ggc ccc acc gac ctc ata ggc ttg acc att tgt gga cat aat tgc	144
Thr Gly Pro Thr Asp Leu Ile Gly Leu Thr Ile Cys Gly His Asn Cys	
35 40 45	
ctc ctg acg gca gaa tgg atg tct gca agt aaa ata gta tgt cga gtg	192
Leu Leu Thr Ala Glu Trp Met Ser Ala Ser Lys Ile Val Cys Arg Val	
50 55 60	
gga caa gcc aaa aat gac aaa gga gac att att gtc acc act aag tca	240
Gly Gln Ala Lys Asn Asp Lys Gly Asp Ile Ile Val Thr Thr Lys Ser	
65 70 75 80	
ggg ggc aga gga acc tca aca gtc tct ttc aag cta ctc aaa cct gag	288
Gly Gly Arg Gly Thr Ser Thr Val Ser Phe Lys Leu Leu Lys Pro Glu	
85 90 95	
aaa ata ggc	297
Lys Ile Gly	

<210> 30
 <211> 99
 <212> PRT
 <213> Homo sapiens
 <223> Sec5
 <400> 30

Met Ser Arg Ser Arg Gln Pro Pro Leu Val Thr Gly Ile Ser Pro Asn
1 5 10 15
Glu Gly Ile Pro Trp Thr Lys Val Thr Ile Arg Gly Glu Asn Leu Gly
20 25 30
Thr Gly Pro Thr Asp Leu Ile Gly Leu Thr Ile Cys Gly His Asn Cys
35 40 45
Leu Leu Thr Ala Glu Trp Met Ser Ala Ser Lys Ile Val Cys Arg Val
50 55 60
Gly Gln Ala Lys Asn Asp Lys Gly Asp Ile Ile Val Thr Thr Lys Ser
65 70 75 80
Gly Gly Arg Gly Thr Ser Thr Val Ser Phe Lys Leu Leu Lys Pro Glu
85 90 95
Lys Ile Gly

<210> 31
 <211> 621
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1).. (621)
 <223> Ra1B
 <400> 31

IBPF12-538W0-E (seq) fin

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Met Ala Ala Asn Lys Ser Lys Gly Gln Ser Ser Leu Ala Leu His Lys	
1 5 10 15	
gtg atc atg gtt ggc agc gga ggc gtt ggc aag tca gcc ctg acg ctt	96
Val Ile Met Val Gly Ser Gly Gly Val Gly Lys Ser Ala Leu Thr Leu	
20 25 30	
cag ttc atg tat gac gag ttt gta gaa gac tat gaa cct acc aaa gct	144
Gln Phe Met Tyr Asp Glu Phe Val Glu Asp Tyr Glu Pro Thr Lys Ala	
35 40 45	
gac agt tat aga aag aaa gtg gtt ctt gat ggg gaa gaa gtt cag ata	192
Asp Ser Tyr Arg Lys Lys Val Leu Asp Gly Glu Glu Val Gln Ile	
50 55 60	
gat att ctg gac acc gct ggg caa gag gac tac gca gcc att cga gat	240
Asp Ile Leu Asp Thr Ala Gly Gln Glu Asp Tyr Ala Ala Ile Arg Asp	
65 70 75 80	
aac tac ttt cgg agt ggg gaa ggg ttt ctt ctt gtg ttc tca atc aca	288
Asn Tyr Phe Arg Ser Gly Glu Gly Phe Leu Leu Val Phe Ser Ile Thr	
85 90 95	
gaa cat gaa tcc ttt aca gca act gcc gaa ttc agg gaa cag att ctc	336
Glu His Glu Ser Phe Thr Ala Thr Ala Glu Phe Arg Glu Gln Ile Leu	
100 105 110	
cgt gtg aag gct gaa gaa gat aaa att cca ctg ctc gtc gtg gga aac	384
Arg Val Lys Ala Glu Glu Asp Lys Ile Pro Leu Leu Val Val Gly Asn	
115 120 125	
aag tct gac cta gag gag cgg agg cag gtg cct gtg gag gag gcc agg	432
Lys Ser Asp Leu Glu Glu Arg Arg Gln Val Pro Val Glu Glu Ala Arg	
130 135 140	
agt aaa gcc gaa gag tgg ggc gtg cag tac gtg gag acg tca gcg aag	480
Ser Lys Ala Glu Glu Trp Gly Val Gln Tyr Val Glu Thr Ser Ala Lys	
145 150 155 160	
acc cgg gcc aac gtg gac aag gtg ttc ttt gac cta atg aga gaa atc	528
Thr Arg Ala Asn Val Asp Lys Val Phe Phe Asp Leu Met Arg Glu Ile	
165 170 175	
aga aca aag aag atg tca gaa aac aaa gac aag aat ggc aag aaa agc	576
Arg Thr Lys Lys Met Ser Glu Asn Lys Asp Lys Asn Gly Lys Lys Ser	
180 185 190	
agc aag aac aag aaa agt ttt aaa gaa aga tgt tgc tta cta tga	621
Ser Lys Asn Lys Lys Ser Phe Lys Glu Arg Cys Cys Leu Leu	
195 200 205	

<210> 32
 <211> 206
 <212> PRT
 <213> Homo sapiens
 <223> Ra1B
 <400> 32

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

IBPF12-538W0-E (seq) fin

Arg	Thr	Lys	Lys	Met	Ser	Glu	Asn	Lys	Asp	Lys	Asn	Gly	Lys	Lys	Ser
			180					185					190		
Ser	Lys	Asn	Lys	Lys	Ser	Phe	Lys	Glu	Arg	Cys	Cys	Leu	Leu		
		195					200					205			

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<210> 33
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<220>
<223> Ra1B Protein Q72L mutant
<220>
<221> CDS
<222> (1)..(621)
<223> Ra1B(Q72L)
<400> 33

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<210>	34
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<212>	PRT
<213>	Artificial
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<223>	Ra1B Protein Q72L mutant
<400>	34

IBPF12-538W0-E (seq) fin

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

<210> 35
 <211> 621
 <212> DNA
 <213> Artificial
 <220>
 <223> RaIB Protein S28N mutant
 <220>
 <221> CDS
 <222> (1)..(621)
 <223> RaIB(S28N)
 <400> 35

atg gct gcc aac aag agt aag ggc cag agc tcc ttg gcc ctc cac aag 48
 Met Ala Ala Asn Lys Ser Lys Gly Gln Ser Leu Ala Leu His Lys
 1 5 10 15
 gtg atc atg gtt ggc agc gga ggc gtt ggc aag aac gcc ctg acg ctt 96
 Val Ile Met Val Gly Ser Gly Gly Val Gly Lys Asn Ala Leu Thr Leu
 20 25 30
 cag ttc atg tat gac gag ttt gta gaa gac tat gaa cct acc aaa gct 144
 Gln Phe Met Tyr Asp Glu Phe Val Glu Asp Tyr Glu Pro Thr Lys Ala
 35 40 45
 gac agt tat aga aag aaa gtg gtt ctt gat ggg gaa gaa gtt cag ata 192
 Asp Ser Tyr Arg Lys Lys Val Val Leu Asp Gly Glu Glu Val Gln Ile
 50 55 60
 gat att ctg gac acc gct ggg caa gag gac tac gca gcc att cga gat 240
 Asp Ile Leu Asp Thr Ala Gly Gln Glu Asp Tyr Ala Ala Ile Arg Asp
 65 70 75 80
 aac tac ttt cgg agt ggg gaa ggg ttt ctt ctt gtg ttc tca atc aca 288
 Asn Tyr Phe Arg Ser Gly Glu Gly Phe Leu Leu Val Phe Ser Ile Thr
 85 90 95
 gaa cat gaa tcc ttt aca gca act gcc gaa ttc agg gaa cag att ctc 336
 Glu His Glu Ser Phe Thr Ala Thr Ala Glu Phe Arg Glu Gln Ile Leu
 100 105 110
 cgt gtg aag gct gaa gaa gat aaa att cca ctg ctc gtc gtg gga aac 384
 Arg Val Lys Ala Glu Glu Asp Lys Ile Pro Leu Leu Val Val Gly Asn
 115 120 125
 aag tct gac cta gag gag cgg agg cag gtg cct gtg gag gag gcc agg 432
 Lys Ser Asp Leu Glu Glu Arg Arg Gln Val Pro Val Glu Glu Ala Arg
 130 135 140
 agt aaa gcc gaa gag tgg ggc gtg cag tac gtg gag acg tca gcg aag 480
 Ser Lys Ala Glu Glu Trp Gly Val Gln Tyr Val Glu Thr Ser Ala Lys
 145 150 155 160
 acc cgg gcc aac gtg gac aag gtg ttc ttt gac cta atg aga gaa atc 528
 Thr Arg Ala Asn Val Asp Lys Val Phe Phe Asp Leu Met Arg Glu Ile
 165 170 175
 aga aca aag aag atg tca gaa aac aaa gac aag aat ggc aag aaa agc 576
 Arg Thr Lys Lys Met Ser Glu Asn Lys Asp Lys Asn Gly Lys Lys Ser

IBPF12-538W0-E (seq) fin

180	185	190	
agc aag aac aag aaa agt ttt aaa gaa aga tgt tgc tta cta tga			621
Ser Lys Asn Lys Lys Ser Phe Lys Glu Arg Cys Cys Leu Leu			
195	200	205	

<210> 36
 <211> 206
 <212> PRT
 <213> Artificial
 <220>
 <223> RaIB Protein S28N mutant
 <400> 36

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

<210> 37
 <211> 441
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1)..(441)
 <223> Calmodulin
 <400> 37

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Asp	Gln	Leu	Thr	Glu	Glu	Gln	Ile	Ala	Glu	Phe	Lys	Glu	Ala	Phe	Ser	
1			5					10					15			
tta	ttc	gac	aag	gat	ggg	gac	ggc	acc	atc	acc	aca	aag	gaa	ctt	ggc	96
Leu	Phe	Asp	Lys	Asp	Gly	Asp	Gly	Thr	Ile	Thr	Thr	Lys	Glu	Leu	Gly	
			20				25						30			
acc	gtt	atg	agg	tcg	ctt	gga	caa	aac	cca	acg	gaa	gca	gaa	ttg	cag	144
Thr	Val	Met	Arg	Ser	Leu	Gly	Gln	Asn	Pro	Thr	Glu	Ala	Glu	Leu	Gln	
			35			40						45				
gat	atg	atc	aat	gaa	gtc	gat	gct	gat	ggc	aat	gga	acg	att	tac	ttt	192
Asp	Met	Ile	Asn	Glu	Val	Asp	Ala	Asp	Gly	Asn	Gly	Thr	Ile	Tyr	Phe	
			50			55					60					
cct	gaa	ttt	ctt	act	atg	atg	gct	aga	aaa	atg	aag	gac	aca	gac	agc	240
Pro	Glu	Phe	Leu	Thr	Met	Met	Ala	Arg	Lys	Met	Lys	Asp	Thr	Asp	Ser	
65					70					75				80		
gaa	gag	gaa	atc	cga	gaa	gca	ttc	cgt	gtt	ttt	gac	aag	gat	ggg	aac	288
Glu	Glu	Glu	Ile	Arg	Glu	Ala	Phe	Arg	Val	Phe	Asp	Lys	Asp	Gly	Asn	
			85					90						95		
ggc	tac	atc	agc	gct	gct	gaa	tta	cgt	cac	gtc	atg	aca	aac	ctc	ggg	336
Gly	Tyr	Ile	Ser	Ala	Ala	Glu	Leu	Arg	His	Val	Met	Thr	Asn	Leu	Gly	

IBPF12-538W0-E (seq) fin

100	105	110	
gag aag tta aca gat gaa gaa gtt gat gaa atg ata agg gaa gca gat			384
Glu Lys Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu Ala Asp			
115	120	125	
atc gat ggt gat ggc caa gta aac tat gaa gag ttt gta caa atg atg			432
Ile Asp Gly Asp Gly Gln Val Asn Tyr Glu Glu Phe Val Gln Met Met			
130	135	140	
aca gca aag			441
Thr Ala Lys			
145			

<210> 38
 <211> 147
 <212> PRT
 <213> Homo sapiens
 <223> Calmodulin
 <400> 38

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

<210> 39
 <211> 78
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1)..(78)
 <223> M13 peptide
 <400> 39

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Lys Arg Arg Trp Lys Lys Asn Phe Ile Ala Val Ser Ala Ala Asn Arg	
1 5 10 15	
ttc aag aag atc tcc agc tcc ggg gca ctg	78
Phe Lys Lys Ile Ser Ser Ser Gly Ala Leu	
20 25	

<210> 40
 <211> 26
 <212> PRT
 <213> Homo sapiens
 <223> M13 peptide
 <400> 40

Lys Arg Arg Trp Lys Lys Asn Phe Ile Ala Val Ser Ala Ala Asn Arg	
1 5 10 15	
Phe Lys Lys Ile Ser Ser Ser Gly Ala Leu	
20 25	

<210> 41
 <211> 594
 <212> DNA

IBPF12-538W0-E (seq) fin

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (594)

<223> HRas

<400> 41

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Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Val Gly Val Gly Lys
1      5      10      15
agt gcg ctg acc atc cag ctg atc cag aac cat ttt gtg gac gaa tac      96
Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
20      25      30
gac ccc act ata gag gat tcc tac cgg aag cag gtg gtc att gat ggg      144
Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
35      40      45
gag acg tgc ctg ttg gac atc ctg gat acc gcc ggc cag gag gag tac      192
Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
50      55      60
agc gcc atg cgg gac cag tac atg cgc acc ggg gag ggc ttc ctg tgt      240
Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
65      70      75      80
gtg ttt gcc atc aac aac acc aag tct ttt gag gac atc cac cag tac      288
Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr
85      90      95
agg gag cag atc aaa cgg gtg aag gac tcg gat gac gtg ccc atg gtg      336
Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val
100      105      110
ctg gtg ggg aac aag tgt gac ctg gct gca cgc act gtg gaa tct cgg      384
Leu Val Gly Asn Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg
115      120      125
cag gct cag gac ctc gcc cga agc tac ggc atc ccc tac atc gag acc      432
Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr
130      135      140
tcg gcc aag acc cgg cag gga gtg gag gat gcc ttc tac acg ttg gtg      480
Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val
145      150      155      160
cgt gag atc cgg cag cac aag ctg cgg aag ctg aac gtc tcc gga ggt      528
Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Val Ser Gly Gly
165      170      175
ctc gag aag atg agc aaa gat ggt aaa aag aag aaa aag aag tca aag      576
Leu Glu Lys Met Ser Lys Asp Gly Lys Lys Lys Lys Lys Ser Lys
180      185      190
aca aag tgt gta att atg
Thr Lys Cys Val Ile Met
195

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<210> 42

<211> 198

<212> PRT

<213> Homo sapiens

<223> HRas

<400> 42

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1      5      10      15
Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
20      25      30
Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
35      40      45
Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
50      55      60
Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
65      70      75      80
Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr
85      90      95
Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val
100      105      110
Leu Val Gly Asn Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg
115      120      125

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IBPF12-538W0-E (seq) fin

Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr
130 135 140
Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val
145 150 155
Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Val Ser Gly Gly
165 170 175
Leu Glu Lys Met Ser Lys Asp Gly Lys Lys Lys Lys Lys Ser Lys
180 185 190
Thr Lys Cys Val Ile Met
195

<210> 43
<211> 243
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (1).. (243)
<223> cRaf
<400> 43

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Pro Ser Lys Thr Ser Asn Thr Ile Arg Val Phe Leu Pro Asn Lys Gln	
1 5 10 15	
aga aca gtg gtc aat gtg cga aat gga atg agc ttg cat gac tgc ctt	96
Arg Thr Val Val Asn Val Arg Asn Gly Met Ser Leu His Asp Cys Leu	
20 25 30	
atg aaa gca ctc aag gtg agg ggc ctg caa cca gag tgc tgt gca gtg	144
Met Lys Ala Leu Lys Val Arg Gly Leu Gln Pro Glu Cys Cys Ala Val	
35 40 45	
ttc aga ctt ctc cac gaa cac aaa ggt aaa aaa gca cgc tta gat tgg	192
Phe Arg Leu Leu His Glu His Lys Gly Lys Lys Ala Arg Leu Asp Trp	
50 55 60	
aat act gat gct gcg tct ttg att gga gaa gaa ctt caa gta gat ttc	240
Asn Thr Asp Ala Ala Ser Leu Ile Gly Glu Glu Leu Gln Val Asp Phe	
65 70 75 80	
ctg	243
Leu	

<210> 44
<211> 81
<212> PRT
<213> Homo sapiens
<223> cRaf
<400> 44

Pro Ser Lys Thr Ser Asn Thr Ile Arg Val Phe Leu Pro Asn Lys Gln	
1 5 10 15	
Arg Thr Val Val Asn Val Arg Asn Gly Met Ser Leu His Asp Cys Leu	
20 25 30	
Met Lys Ala Leu Lys Val Arg Gly Leu Gln Pro Glu Cys Cys Ala Val	
35 40 45	
Phe Arg Leu Leu His Glu His Lys Gly Lys Lys Ala Arg Leu Asp Trp	
50 55 60	
Asn Thr Asp Ala Ala Ser Leu Ile Gly Glu Glu Leu Gln Val Asp Phe	
65 70 75 80	
Leu	

<210> 45
<211> 30
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (1).. (30)
<223> Smac
<400> 45

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1 5 10	

IBPF12-538W0-E (seq) fin

<210> 46
 <211> 10
 <212> PRT
 <213> Homo sapiens
 <223> Smac
 <400> 46

Met Ala Val Pro Ile Ala Gln Lys Ser Glu
 1 5 10

<210> 47
 <211> 342
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1).. (342)
 <223> XIAP
 <400> 47

gct gtg agt tct gat agg aat ttc cca aat tca aca aat ctt cca aga	48
Ala Val Ser Ser Asp Arg Asn Phe Pro Asn Ser Thr Asn Leu Pro Arg	
1 5 10 15	
aat cca tcc atg gca gat tat gaa gca cgg atc ttt act ttt ggg aca	96
Asn Pro Ser Met Ala Asp Tyr Glu Ala Arg Ile Phe Thr Phe Gly Thr	
20 25 30	
tgg ata tac tca gtt aac aag gag cag ctt gca aga gct gga ttt tat	144
Trp Ile Tyr Ser Val Asn Lys Glu Gln Leu Ala Arg Ala Gly Phe Tyr	
35 40 45	
gct tta ggt gaa ggt gat aaa gta aag tgc ttt cac tgt gga gga ggg	192
Ala Leu Gly Glu Gly Asp Lys Val Lys Cys Phe His Cys Gly Gly Gly	
50 55 60	
cta act gat tgg aag ccc agt gaa gac cct tgg gaa caa cat gct aaa	240
Leu Thr Asp Trp Lys Pro Ser Glu Asp Pro Trp Glu Gln His Ala Lys	
65 70 75 80	
tgg tat cca ggg tgc aaa tat ctg tta gaa cag aag gga caa gaa tat	288
Trp Tyr Pro Gly Cys Lys Tyr Leu Leu Glu Gln Lys Gly Gln Glu Tyr	
85 90 95	
ata aac aat att cat tta act cat tca ctt gag gag tgt ctg gta aga	336
Ile Asn Asn Ile His Leu Thr His Ser Leu Glu Glu Cys Leu Val Arg	
100 105 110	
act act	342
Thr Thr	

<210> 48
 <211> 114
 <212> PRT
 <213> Homo sapiens
 <223> XIAP
 <400> 48

Ala Val Ser Ser Asp Arg Asn Phe Pro Asn Ser Thr Asn Leu Pro Arg	
1 5 10 15	
Asn Pro Ser Met Ala Asp Tyr Glu Ala Arg Ile Phe Thr Phe Gly Thr	
20 25 30	
Trp Ile Tyr Ser Val Asn Lys Glu Gln Leu Ala Arg Ala Gly Phe Tyr	
35 40 45	
Ala Leu Gly Glu Gly Asp Lys Val Lys Cys Phe His Cys Gly Gly Gly	
50 55 60	
Leu Thr Asp Trp Lys Pro Ser Glu Asp Pro Trp Glu Gln His Ala Lys	
65 70 75 80	
Trp Tyr Pro Gly Cys Lys Tyr Leu Leu Glu Gln Lys Gly Gln Glu Tyr	
85 90 95	
Ile Asn Asn Ile His Leu Thr His Ser Leu Glu Glu Cys Leu Val Arg	
100 105 110	
Thr Thr	

<210> 49

IBPF12-538W0-E (seq) fin

<211> 627
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1)..(627)
 <223> BclIX(L)
 <400> 49

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Met Ser Gln Ser Asn Arg Glu Leu Val Val Asp Phe Leu Ser Tyr Lys	
1 5 10 15	
ctt tcc cag aaa gga tac agc tgg agt cag ttt agt gat gtg gaa gag	96
Leu Ser Gln Lys Gly Tyr Ser Trp Ser Gln Phe Ser Asp Val Glu Glu	
20 25 30	
aac agg act gag gcc cca gaa ggg act gaa tcg gag atg gag acc ccc	144
Asn Arg Thr Glu Ala Pro Glu Gly Thr Glu Ser Glu Met Glu Thr Pro	
35 40 45	
agt gcc atc aat ggc aac cca tcc tgg cac ctg gca gac agc ccc gcg	192
Ser Ala Ile Asn Gly Asn Pro Ser Trp His Leu Ala Asp Ser Pro Ala	
50 55 60	
gtg aat gga gcc act ggc cac agc agc agt ttg gat gcc cgg gag gtg	240
Val Asn Gly Ala Thr Gly His Ser Ser Ser Leu Asp Ala Arg Glu Val	
65 70 75 80	
atc ccc atg gca gca gta aag caa gcg ctg agg gag gca ggc gac gag	288
Ile Pro Met Ala Ala Val Lys Gln Ala Leu Arg Glu Ala Gly Asp Glu	
85 90 95	
ttt gaa ctg cgg tac cgg cgg gca ttc agt gac ctg aca tcc cag ctc	336
Phe Glu Leu Arg Tyr Arg Arg Ala Phe Ser Asp Leu Thr Ser Gln Leu	
100 105 110	
cac atc acc cca ggg aca gca tat cag agc ttt gaa cag gta gtg aat	384
His Ile Thr Pro Gly Thr Ala Tyr Gln Ser Phe Glu Gln Val Val Asn	
115 120 125	
gaa ctc ttc cgg gat ggg gta aac tgg ggt cgc att gtg gcc ttt ttc	432
Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe	
130 135 140	
tcc ttc ggc ggg gca ctg tgc gtg gaa agc gta gac aag gag atg cag	480
Ser Phe Gly Gly Ala Leu Cys Val Glu Ser Val Asp Lys Glu Met Gln	
145 150 155 160	
gta ttg gtg agt cgg atc gca gct tgg atg gcc act tac ctg aat gac	528
Val Leu Val Ser Arg Ile Ala Ala Trp Met Ala Thr Tyr Leu Asn Asp	
165 170 175	
cac cta gag cct tgg atc cag gag aac ggc tgg gat act ttt gtg	576
His Leu Glu Pro Trp Ile Gln Glu Asn Gly Gly Trp Asp Thr Phe Val	
180 185 190	
gaa ctc tat ggg aac aat gca gca gcc gag agc cga aag ggc cag gaa	624
Glu Leu Tyr Gly Asn Asn Ala Ala Ala Glu Ser Arg Lys Gly Gln Glu	
195 200 205	
cgc	627
Arg	

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

IBPF12-538W0-E (seq)															
85					90					95					
Phe	Glu	Leu	Arg	Tyr	Arg	Arg	Ala	Phe	Ser	Asp	Leu	Thr	Ser	Gln	Leu
			100					105						110	
His	Ile	Thr	Pro	Gly	Thr	Ala	Tyr	Gln	Ser	Phe	Glu	Gln	Val	Val	Asn
		115					120					125			
Glu	Leu	Phe	Arg	Asp	Gly	Val	Asn	Trp	Gly	Arg	Ile	Val	Ala	Phe	Phe
	130					135					140				
Ser	Phe	Gly	Gly	Ala	Leu	Cys	Val	Glu	Ser	Val	Asp	Lys	Glu	Met	Gln
					150					155					160
Val	Leu	Val	Ser	Arg	Ile	Ala	Ala	Trp	Met	Ala	Thr	Tyr	Leu	Asn	Asp
				165					170					175	
His	Leu	Glu	Pro	Trp	Ile	Gln	Glu	Asn	Gly	Gly	Trp	Asp	Thr	Phe	Val
			180					185					190		
Glu	Leu	Tyr	Gly	Asn	Asn	Ala	Ala	Ala	Glu	Ser	Arg	Lys	Gly	Gln	Glu
		195					200					205			
Arg															

IBPF12-538W0-E (seq) fin

65	70	75	80	
tgc ttt tcc ctt gtg agt cct gca tca ttt gaa aat gtc cgt gca aag				288
Cys Phe Ser Leu Val Ser Pro Ala Ser Phe Glu Asn Val Arg Ala Lys				
	85	90	95	
tgg tat cct gag gtg cgg cac cac tgt ccc aac act ccc atc atc cta				336
Trp Tyr Pro Glu Val Arg His His Cys Pro Asn Thr Pro Ile Ile Leu				
	100	105	110	
gtg gga act aaa ctt gat ctt agg gat gat aaa gac acg atc gag aaa				384
Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys Asp Thr Ile Glu Lys				
	115	120	125	
ctg aag gag aag aag ctg act ccc atc acc tat ccg cag ggt cta gcc				432
Leu Lys Glu Lys Lys Leu Thr Pro Ile Thr Tyr Pro Gln Gly Leu Ala				
	130	135	140	
atg gct aag gag att ggt gct gta aaa tac ctg gag tgc tcg gcg ctc				480
Met Ala Lys Glu Ile Gly Ala Val Lys Tyr Leu Glu Cys Ser Ala Leu				
	145	150	155	160
aca cag cga ggc ctc aag aca gtg ttt gac gaa gcg atc cga gca gtc				528
Thr Gln Arg Gly Leu Lys Thr Val Phe Asp Glu Ala Ile Arg Ala Val				
	165	170	175	
ctc tgc ccg cct ccc gtg aag aag agg aag aga aaa tgc ctg ctg ttg				576
Leu Cys Pro Pro Pro Val Lys Lys Arg Lys Arg Lys Cys Leu Leu Leu				
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taa				579

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20 25 30	
Ile Pro Thr Val Phe Asp Asn Tyr Ser Ala Asn Val Met Val Asp Gly	
35 40 45	
Lys Pro Val Asn Leu Gly Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr	
50 55 60	
Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe Leu Ile	
65 70 75 80	
Cys Phe Ser Leu Val Ser Pro Ala Ser Phe Glu Asn Val Arg Ala Lys	
85 90 95	
Trp Tyr Pro Glu Val Arg His His Cys Pro Asn Thr Pro Ile Ile Leu	
100 105 110	
Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys Asp Thr Ile Glu Lys	
115 120 125	
Leu Lys Glu Lys Lys Leu Thr Pro Ile Thr Tyr Pro Gln Gly Leu Ala	
130 135 140	
Met Ala Lys Glu Ile Gly Ala Val Lys Tyr Leu Glu Cys Ser Ala Leu	
145 150 155 160	
Thr Gln Arg Gly Leu Lys Thr Val Phe Asp Glu Ala Ile Arg Ala Val	
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Lys Lys Glu Lys Glu Arg Pro Glu Ile Ser Leu Pro Ser Asp Phe Glu	
1 5 10 15	
cac aca att cat gtc ggt ttt gat gct gtc aca ggg gag ttt acg gga	96

IBPF12-538W0-E (seq) fin

His	Thr	Ile	His	Val	Gly	Phe	Asp	Ala	Val	Thr	Gly	Glu	Phe	Thr	Gly	
		20						25				30				
atg	cca	gag	cag	tgg	gcc	cg	ttg	ctt	cag	aca	tca	aat	atc	act	aag	144
Met	Pro	Glu	Gln	Trp	Ala	Arg	Leu	Leu	Gln	Thr	Ser	Asn	Ile	Thr	Lys	
		35					40					45				
tcg	gag	cag	aag	aaa	aac	cgc	cag	gct	gtt	ctg	gat	gtg	ttg	gag	ttt	192
Ser	Glu	Gln	Lys	Lys	Asn	Pro	Gln	Ala	Val	Leu	Asp	Val	Leu	Glu	Phe	
		50				55					60					
tac	aac	tgc	aag	aag	aca	tcc	aac	agc	cag	aaa	tac	atg	agc	ttt	aca	240
Tyr	Asn	Ser	Lys	Lys	Thr	Ser	Asn	Ser	Gln	Lys	Tyr	Met	Ser	Phe	Thr	
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gat	aag	tca	gct													252
Asp	Lys	Ser	Ala													

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

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 <400> 58

actaccggtc ttggcctggc tgggcagcat gctgtacc 38

<210> 59
 <211> 45
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 <400> 59

aagaattcga tggcgtcgtc caccgtgaag gcctaccttc tgggc 45

<210> 60
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 <212> DNA
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IBPF12-538W0-E (seq) fin

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 ttcttagatc acttggcctg gctgggcagc atgc 34

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 <223> Artificially synthesized p62(PB1) forward primer 2 sequence
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 gggaccggta tggcgtcgt caccgtgaag gcctaccttc 40

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<210> 66
 <211> 37
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 <211> 54
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 <223> Artificially synthesized mTOR(FRB) forward primer sequence
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 gccgaattcg gccaccatgg agatgtggca tgaaggcctg gaagaggcat ctcg 54

<210> 68
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 <212> DNA
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IBPF12-538W0-E (seq) fin

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 <211> 31
 <212> DNA
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 <223> Artificially synthesized FKBP12 forward primer sequence
 <400> 69
 gccgaattcg atgggagtg c aggtggaac c 31
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 <223> Artificially synthesized FKBP12 reverse primer sequence
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 <210> 72
 <211> 35
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 <223> Artificially synthesized MEK(PB1) reverse primer sequence
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 ttctcgagtt agcaggtct tggaaatata tgcag 35
 <210> 73
 <211> 37
 <212> DNA
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 <223> Artificially synthesized Nbr1 (PB1) forward primer sequence
 <400> 73
 aagaattcgg caggttactc taaatgtgac ttttaaa 37
 <210> 74
 <211> 37
 <212> DNA
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 <223> Artificially synthesized Nbr1 (PB1) reverse primer sequence
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 <223> Artificially synthesized PKCιota(PB1) forward primer sequence
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IBPF12-538W0-E (seq) fin

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<210> 77
 <211> 39
 <212> DNA
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 <223> Artificially synthesized TFG(PB1) forward primer 1 sequence
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<210> 78
 <211> 38
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 <223> Artificially synthesized TFG(PB1) reverse primer 1 sequence
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 ttaagctttt aattaacaaa taatgtcagt ttcagtat 38

<210> 79
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 <223> Artificially synthesized TEL(SAM) forward primer sequence
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<210> 80
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 aaaaaagctt ttaaactctgg ttcactctgc cccg 34

<210> 83
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IBPF12-538W0-E (seq) fin

<223> Artificially synthesized DGKdelta(SAM) forward primer sequence
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<210> 84
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 <213> Artificial
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 aaaaaagctt ttagctgcgg ctcagctcct tgat 34

<210> 85
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 <223> Artificially synthesized Tankyrase(SAM) forward primer sequence
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<210> 86
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 aaaccggtaa gctaatacatc aaagctcaac tt 32

<210> 88
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 aaaaaccggt cctcgagcgc tcaggatgga ggaa 34

<210> 90
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IBPF12-538W0-E (seq) fin

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<400> 92
aaaatctaga ttagctgcgg ctcagctcct tgat                                     34

<210> 93
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<400> 93
aaaaaccggt ctgatatagc ccatgcccc aga                                     33

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<400> 94
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<220>
<223> Artificially synthesized hK01 forward primer sequence
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<210> 96
<211> 35
<212> DNA
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<223> Artificially synthesized hK01reverse primer sequence
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aaaatctaga ttagcagtgg gccacggcgt cctcc                                     35

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<210> 98
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<212> DNA
<213> Artificial
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IBPF12-538W0-E (seq) fin

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<210> 104
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<210> 105
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IBPF12-538W0-E (seq) fin

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 <223> Artificially synthesized Calmodulin forward primer sequence
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<210> 108
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 <212> DNA
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 <223> Artificially synthesized M13 peptide forward primer sequence
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<210> 110
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 <213> Artificial
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 <223> Artificially synthesized M13 peptide reverse primer sequence
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<210> 111
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 <223> Artificially synthesized AGNLS forward primer sequence
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 <223> Artificially synthesized HRas forward primer sequence
 <400> 113

IBPF12-538W0-E (seq) fin

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gc 62

<210> 114
<211> 63
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<223> Artificially synthesized HRas reverse primer sequence
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aac 63

<210> 115
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<223> Artificially synthesized KRas forward primer sequence
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<210> 116
<211> 60
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<210> 117
<211> 41
<212> DNA
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<223> Artificially synthesized HRas mutant primer sequence
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<210> 118
<211> 60
<212> DNA
<213> Artificial
<220>
<223> Artificially synthesized cRaf forward primer sequence
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<210> 119
<211> 52
<212> DNA
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<223> Artificially synthesized cRaf reverse primer sequence
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<210> 120
<211> 50
<212> DNA
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<220>
<223> Artificially synthesized Smac forward primer sequence
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<210> 121

IBPF12-538W0-E (seq) fin

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 <210> 122
 <211> 45
 <212> DNA
 <213> Artificial
 <220>
 <223> Artificially synthesized XIAP reverse primer sequence
 <400> 122
 ttgaattctc agtagttott accagacact cctcaagtga atgag 45

 <210> 123
 <211> 42
 <212> DNA
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 <223> Artificially synthesized BclX(L) forward primer sequence
 <400> 123
 ttctcgagga tgtctcagag caaccgggag ctggtggttg ac 42

 <210> 124
 <211> 44
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 <213> Artificial
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 <223> Artificially synthesized BclX(L) reverse primer sequence
 <400> 124
 ctaagcggcc gcttagcggt cctggccctt toggctctcg gctg 44

 <210> 125
 <211> 50
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 <213> Artificial
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 <212> DNA
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 <223> Artificially synthesized BAD reverse primer sequence
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 <210> 128
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 <212> DNA
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 <223> Artificially synthesized Rac1 forward primer sequence

IBPF12-538W0-E (seq) fin

<400> 128
 gagaattcga tgcaggccat caagtgtgtg gtgg 34
 <210> 129
 <211> 34
 <212> DNA
 <213> Artificial
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 ggctcgagtt acaacagcag gcattttctc ttcc 34
 <210> 130
 <211> 43
 <212> DNA
 <213> Artificial
 <220>
 <223> Artificially synthesized PBD forward primer sequence
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 <210> 131
 <211> 46
 <212> DNA
 <213> Artificial
 <220>
 <223> Artificially synthesized PBD reverse primer sequence
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 <210> 132
 <211> 654
 <212> DNA
 <213> Artificial
 <220>
 <223> base sequence of a monomeric version pf K0 (Kusabira-Orange)
 <220>
 <221> CDS
 <222> (1).. (654)
 <223>
 <400> 132
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 Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
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 ggc tcc gtc aat ggg cat gag ttc aca atc gag ggt gag ggc aca ggc 96
 Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
 20 25 30
 aga cct tac gag gga cat cag gag atg aca ctg cgc gtc aca atg gcc 144
 Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
 35 40 45
 gag ggc ggg cca atg cct ttc gcc ttc gac ctg gtg tcc cac gtg ttc 192
 Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
 50 55 60
 tgt tac ggc cac aga gtt ttt acc aag tac cca gaa gag atc cca gac 240
 Cys Tyr Gly His Arg Val Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
 65 70 75 80
 tat ttc aag cag gcc ttt cct gag ggc ctg tcc tgg gag agg tcc ctg 288
 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
 85 90 95
 gag ttc gag gac ggc ggc tcc gcc tcc gtg agc gcc cac atc agc ctg 336
 Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
 100 105 110
 agg ggc aac acc ttc tac cac aag tcc aag ttc acc ggc gtg aac ttc 384
 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
 115 120 125
 ccc gcc gac ggc ccc atc atg cag aac cag agc gtg gac tgg gag ccc 432
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro
 130 135 140

IBPF12-538W0-E (seq) fin

tcc acc gag aag atc acc gcc agc gac ggc gtg ctg aag ggc gac gtg	480
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val	
145 150 155 160	
acc atg tac ctg aag ctg gag ggc ggc ggc aac cac aag tgc cag atg	528
Thr Met Tyr Leu Lys Leu Glu Gly Gly Asn His Lys Cys Gln Met	
165 170 175	
aag acc acc tac aag gcc gcc aag gag atc ctg gag atg ccc ggc gac	576
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp	
180 185 190	
cac tac atc ggc cac agg ctg gtg agg aag acc gag ggc aac atc acc	624
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr	
195 200 205	
gag cag gtg gag gac gcc gtg gcc cac tcc	654
Glu Gln Val Glu Asp Ala Val Ala His Ser	
210 215	

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 <400> 133

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

<210> 134
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 <222> (1).. (678)
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1 5 10 15	
ggc acc gtg aac ggc cac aac ttc gtg atc gag ggc gag ggc aag ggc	96
Gly Thr Val Asn Gly His Asn Phe Val Ile Glu Gly Glu Gly Lys Gly	

IBPF12-538W0-E (seq) fin

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      20      25      30
aac ccc tac gag ggc acc cag atc ctg gac ctg aac gtg acc gag ggc 144
Asn Pro Tyr Glu Gly Thr Gln Ile Leu Asp Leu Asn Val Thr Glu Gly
      35      40      45
gcc ccc ctg ccc ttc gcc tac gac atc ctg acc acc gtg ttc cag tac 192
Ala Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Val Phe Gln Tyr
      50      55      60
ggc aac agg gcc ttc acc aag tac ccc gcc gac atc cag gac tac ttc 240
Gly Asn Arg Ala Phe Thr Lys Tyr Pro Ala Asp Ile Gln Asp Tyr Phe
      65      70      75      80
aag cag acc ttc ccc gag ggc tac cac tgg gag agg agc atg acc tac 288
Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ser Met Thr Tyr
      85      90      95
gag gac cag ggc atc tgc acc gcc acc agc aac atc agc atg agg ggc 336
Glu Asp Gln Gly Ile Cys Thr Ala Thr Ser Asn Ile Ser Met Arg Gly
      100      105      110
gac tgc ttc ttc tac gac atc agg ttc gac ggc acc aac ttc ccc ccc 384
Asp Cys Phe Phe Tyr Asp Ile Arg Phe Asp Gly Thr Asn Phe Pro Pro
      115      120      125
aac ggc ccc gtg atg cag aag aag acc ctg aag tgg gag ccc agc acc 432
Asn Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp Glu Pro Ser Thr
      130      135      140
gag aag atg tac gtg gag gac ggc gtg ctg aag ggc gac gtg aac atg 480
Glu Lys Met Tyr Val Glu Asp Gly Val Leu Lys Gly Asp Val Asn Met
      145      150      155      160
agg ctg ctg ctg gag ggc ggc ggc cac tac agg tgc gac ttc aag acc 528
Arg Leu Leu Leu Glu Gly Gly Gly His Tyr Arg Cys Asp Phe Lys Thr
      165      170      175
acc tac aag gcc aag aag gag gtg agg ctg ccc gac gcc cac aag atc 576
Thr Tyr Lys Ala Lys Lys Glu Val Arg Leu Pro Asp Ala His Lys Ile
      180      185      190
gac cac agg atc gag atc ctg aag cac gac aag gac tac aac aag gtg 624
Asp His Arg Ile Glu Ile Leu Lys His Asp Lys Asp Tyr Asn Lys Val
      195      200      205
aag ctg tac gag aac gcc gtg gcc agg tac tcc atg ctg ccc agc cag 672
Lys Leu Tyr Glu Asn Ala Val Ala Arg Tyr Ser Met Leu Pro Ser Gln
      210      215      220
gcc aag
Ala Lys
225

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<210> 135
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 <212> PRT
 <213> Artificial
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 <223> humanized mAG1
 <400> 135

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

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IBPF12-538W0-E (seq) fin

Arg	Leu	Leu	Leu	Glu	Gly	Gly	Gly	His	Tyr	Arg	Cys	Asp	Phe	Lys	Thr
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Thr	Tyr	Lys	Ala	Lys	Lys	Glu	Val	Arg	Leu	Pro	Asp	Ala	His	Lys	Ile
			180					185					190		
Asp	His	Arg	Ile	Glu	Ile	Leu	Lys	His	Asp	Lys	Asp	Tyr	Asn	Lys	Val
		195					200					205			
Lys	Leu	Tyr	Glu	Asn	Ala	Val	Ala	Arg	Tyr	Ser	Met	Leu	Pro	Ser	Gln
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Ala	Lys														
225															

<210> 136
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1				5					10					15		
tac	cgc	atg	gag	ggc	agc	gtg	aac	ggc	cac	gag	ttc	acc	atc	gag	ggc	96
Tyr	Arg	Met	Glu	Gly	Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	Glu	Gly	
			20				25					30				
gtg	ggc	acc	ggc	aac	ccc	tac	gag	ggc	aag	cag	acc	tcc	gag	ctg	gtg	144
Val	Gly	Thr	Gly	Asn	Pro	Tyr	Glu	Gly	Lys	Gln	Thr	Ser	Glu	Leu	Val	
		35				40					45					
atc	atc	aag	ccc	aag	ggc	aag	ccc	ctg	ccc	ttc	tcc	ttc	gac	atc	ctg	192
Ile	Ile	Lys	Pro	Lys	Gly	Lys	Pro	Leu	Pro	Phe	Ser	Phe	Asp	Ile	Leu	
		50			55					60						
tcc	acc	gtg	ttc	cag	tac	ggc	aac	agg	tgc	ttc	acc	aag	tac	ccc	gcc	240
Ser	Thr	Val	Phe	Gln	Tyr	Gly	Asn	Arg	Cys	Phe	Thr	Lys	Tyr	Pro	Ala	
		65			70				75					80		
gac	atg	ccc	gac	tac	ttc	aag	cag	gcc	ttc	ccc	gac	ggc	atg	tcc	tac	288
Asp	Met	Pro	Asp	Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Asp	Gly	Met	Ser	Tyr	
			85					90					95			
gag	agg	tcc	ttc	ctg	ttc	gag	gac	ggc	ggc	gtg	gcc	acc	gcc	agc	tgg	336
Glu	Arg	Ser	Phe	Leu	Phe	Glu	Asp	Gly	Gly	Val	Ala	Thr	Ala	Ser	Trp	
		100					105					110				
agc	atc	cgc	ctg	gag	ggc	aac	tgc	ttc	atc	cac	aac	tcc	atc	tac	cac	384
Ser	Ile	Arg	Leu	Glu	Gly	Asn	Cys	Phe	Ile	His	Asn	Ser	Ile	Tyr	His	
		115				120					125					
ggc	acc	aac	ttc	ccc	gcc	gac	ggc	ccc	gtg	atg	aag	aag	cag	acc	atc	432
Gly	Thr	Asn	Phe	Pro	Ala	Asp	Gly	Pro	Val	Met	Lys	Lys	Gln	Thr	Ile	
		130			135					140						
ggc	tgg	gac	aag	tcc	tcc	gag	aag	atg	agc	gtg	gcc	aag	gag	gtg	ctg	480
Gly	Trp	Asp	Lys	Ser	Ser	Glu	Lys	Met	Ser	Val	Ala	Lys	Glu	Val	Leu	
		145			150			155						160		
agg	ggc	gac	gtg	acc	cag	ttc	ctg	ctg	ctg	gag	ggc	ggc	ggc	tac	cag	528
Arg	Gly	Asp	Val	Thr	Gln	Phe	Leu	Leu	Leu	Glu	Gly	Gly	Gly	Tyr	Gln	
			165					170					175			
agg	tgc	cag	ctg	cac	tcc	acc	tac	aag	acc	gag	aag	ccc	gtg	gcc	atg	576
Arg	Cys	Gln	Leu	His	Ser	Thr	Tyr	Lys	Thr	Glu	Lys	Pro	Val	Ala	Met	
		180					185					190				
ccc	ccc	agc	cac	gtg	gtg	gag	cac	cag	atc	gtg	agg	acc	gac	ctg	ggc	624
Pro	Pro	Ser	His	Val	Val	Glu	His	Gln	Ile	Val	Arg	Thr	Asp	Leu	Gly	
		195				200					205					
cag	acc	gcc	aag	ggc	ttc	aag	gtg	aag	ctg	gag	gag	cac	gcc	gag	gcc	672
Gln	Thr	Ala	Lys	Gly	Phe	Lys	Val	Lys	Leu	Glu	Glu	His	Ala	Glu	Ala	
		210			215					220						
cac	gtg	aac	ccc	ctg	aag	gtg	aag									696
His	Val	Asn	Pro	Leu	Lys	Val	Lys									
225					230											

IBPF12-538W0-E (seq) fin

<210> 137
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 Val Gly Thr Gly Asn Pro Tyr Glu Gly Lys Gln Thr Ser Glu Leu Val
 35 40 45
 Ile Ile Lys Pro Lys Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu
 50 55 60
 Ser Thr Val Phe Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala
 65 70 75 80
 Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr
 85 90 95
 Glu Arg Ser Phe Leu Phe Glu Asp Gly Gly Val Ala Thr Ala Ser Trp
 100 105 110
 Ser Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Tyr His
 115 120 125
 Gly Thr Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile
 130 135 140
 Gly Trp Asp Lys Ser Ser Glu Lys Met Ser Val Ala Lys Glu Val Leu
 145 150 155 160
 Arg Gly Asp Val Thr Gln Phe Leu Leu Leu Glu Gly Gly Gly Tyr Gln
 165 170 175
 Arg Cys Gln Leu His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala Met
 180 185 190
 Pro Pro Ser His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly
 195 200 205
 Gln Thr Ala Lys Gly Phe Lys Val Lys Leu Glu Glu His Ala Glu Ala
 210 215 220
 His Val Asn Pro Leu Lys Val Lys
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<210> 138
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 ggc tct gta aac ggg cac aag ttc gtg att aca ggg aaa gga agt ggc 96
 Gly Ser Val Asn Gly His Lys Phe Val Ile Thr Gly Lys Gly Ser Gly
 20 25 30
 aga cct tac gag gga aca cag act gtg gac ctg aca gtc ata gag ggc 144
 Arg Pro Tyr Glu Gly Thr Gln Thr Val Asp Leu Thr Val Ile Glu Gly
 35 40 45
 gga cct ctt cct ttt gct ttc gat atc ctg aca aca gca ttc cat tac 192
 Gly Pro Leu Pro Phe Ala Phe Asp Ile Leu Thr Thr Ala Phe His Tyr
 50 55 60
 ggc aac cgg gta ttt gtc gaa tac cca gaa gaa ata gta gac tac ttc 240
 Gly Asn Arg Val Phe Val Glu Tyr Pro Glu Glu Ile Val Asp Tyr Phe
 65 70 75 80
 aag cag tcg ttt cct gag ggt tat tot tgg gaa cga agc atg agt tac 288
 Lys Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Ser Met Ser Tyr
 85 90 95
 gaa gac ggg gga att tgc ctc gcc aca aac aat ata acg atg aag aaa 336

IBPF12-538W0-E (seq) fin

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			100					105					110				
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Asp	Gly	Ser	Asn	Thr	Phe	Val	Asn	Glu	Ile	Arg	Phe	Asp	Gly	Thr	Asn		
			115				120					125					
ttt	cct	gcc	aat	ggt	cca	ggt	atg	cag	agg	aag	acc	gtc	aaa	tgg	gag		432
Phe	Pro	Ala	Asn	Gly	Pro	Val	Met	Gln	Arg	Lys	Thr	Val	Lys	Trp	Glu		
			130				135					140					
cca	tcc	act	gag	aaa	atg	tat	gtg	cgt	gat	gga	gtg	ctg	aag	ggt	gat		480
Pro	Ser	Thr	Glu	Lys	Met	Tyr	Val	Arg	Asp	Gly	Val	Leu	Lys	Gly	Asp		
			145				150				155				160		
ggt	gaa	atg	gct	ctg	ttg	ctt	gaa	gga	ggt	ggc	cat	tac	cga	tgt	gac		528
Val	Glu	Met	Ala	Leu	Leu	Glu	Gly	Gly	Gly	His	Tyr	Arg	Cys	Asp			
			165					170					175				
ttc	aga	act	act	tac	aaa	gca	aag	aag	ggt	gtc	cag	ttg	cca	gac	tat		576
Phe	Arg	Thr	Thr	Tyr	Lys	Ala	Lys	Lys	Val	Val	Gln	Leu	Pro	Asp	Tyr		
			180					185				190					
cac	tac	gtg	gat	cat	caa	atg	gag	ata	aca	agc	cat	gac	aag	gat	tac		624
His	Tyr	Val	Asp	His	Gln	Met	Glu	Ile	Thr	Ser	His	Asp	Lys	Asp	Tyr		
			195				200					205					
aac	aag	ggt	aag	gcg	tat	gaa	cat	gct	aag	gct	tat	tcc	ggg	acc	tac		672
Asn	Lys	Val	Lys	Ala	Tyr	Glu	His	Ala	Lys	Ala	Tyr	Ser	Gly	Thr	Tyr		
			210				215				220						
agg	ggc	gcc	aag	tat	gaa	ttt	gaa	gcc	taa								702
Arg	Gly	Ala	Lys	Tyr	Glu	Phe	Glu	Ala									
						230											

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

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 <212> DNA

IBPF12-538W0-E (seq) fin

<213> Artificial

<220>

<223> KCy1

<220>

<221> CDS

<222> (1).. (663)

<223>

<400> 140

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ggc tcc gtc aat ggg cat gag ttc aca gtt gaa ggt gaa ggc aca ggc      96
Gly Ser Val Asn Gly His Glu Phe Thr Val Glu Gly Glu Gly Thr Gly
20      25      30
aga cct tac gag gga aag cac aaa ata aca ctt gac gtc acc aag ggt      144
Arg Pro Tyr Glu Gly Lys His Lys Ile Thr Leu Asp Val Thr Lys Gly
35      40      45
ggg cca ctg cct ttt gcg ttt gac ttg ttg tct aca gtg ttc tct tat      192
Gly Pro Leu Pro Phe Ala Phe Asp Leu Leu Ser Thr Val Phe Ser Tyr
50      55      60
ggc aac aga gcc ctt act aaa tat cct gac gat atc ccc gac tat ttc      240
Gly Asn Arg Ala Leu Thr Lys Tyr Pro Asp Asp Ile Pro Asp Tyr Phe
65      70      75      80
aaa caa tgc ttt cct gga ggc tat tca tgg gaa aga aag ttt gag ttc      288
Lys Gln Cys Phe Pro Gly Gly Tyr Ser Trp Glu Arg Lys Phe Glu Phe
85      90      95
gaa gat ggc ggg ttg gcg ata gcc aaa gcg gaa ata agc ctt aaa gga      336
Glu Asp Gly Gly Leu Ala Ile Ala Lys Ala Glu Ile Ser Leu Lys Gly
100      105      110
aac tgc ttc gaa cac aaa tcc acc att gaa ggc act ttt ccc gat agc      384
Asn Cys Phe Glu His Lys Ser Thr Ile Glu Gly Thr Phe Pro Asp Ser
115      120      125
agt cct att atg caa aac aag acg cta gga tgg gaa cca tcc acc gag      432
Ser Pro Ile Met Gln Asn Lys Thr Leu Gly Trp Glu Pro Ser Thr Glu
130      135      140
aag atg acc gtc cgc gac gga tca atg aag ggt gat gat gcg gcc tac      480
Lys Met Thr Val Arg Asp Gly Ser Met Lys Gly Asp Asp Ala Ala Tyr
145      150      155      160
ctc aaa ttg gtg gga ggc ggc aat cac aaa tgc tac ttt aca act acc      528
Leu Lys Leu Val Gly Gly Gly Asn His Lys Cys Tyr Phe Thr Thr Thr
165      170      175
tac aca gcg aag aaa aag att cct aac ctg cca gga agc cat ttc att      576
Tyr Thr Ala Lys Lys Ile Pro Asn Leu Pro Gly Ser His Phe Ile
180      185      190
ggc cat cgc atc tcc agt gtc gtc gag ggc act aaa att aaa gtg atg      624
Gly His Arg Ile Ser Ser Val Val Glu Gly Thr Lys Ile Lys Val Met
195      200      205
gaa gat gca att gct cat ctt tac cct ttt aat ggc agc      663
Glu Asp Ala Ile Ala His Leu Tyr Pro Phe Asn Gly Ser
210      215      220

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<210> 141

<211> 221

<212> PRT

<213> Artificial

<220>

<223> KCy1

<400> 141

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Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
1      5      10      15
Gly Ser Val Asn Gly His Glu Phe Thr Val Glu Gly Glu Gly Thr Gly
20      25      30
Arg Pro Tyr Glu Gly Lys His Lys Ile Thr Leu Asp Val Thr Lys Gly
35      40      45
Gly Pro Leu Pro Phe Ala Phe Asp Leu Leu Ser Thr Val Phe Ser Tyr
50      55      60
Gly Asn Arg Ala Leu Thr Lys Tyr Pro Asp Asp Ile Pro Asp Tyr Phe
65      70      75      80

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IBPF12-538W0-E (seq) fin

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

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

IBPF12-538W0-E (seq) fin

195 200 205
aag ctc tat gag aat gcc gtt gct cgc tat tct atg ctg ccg agt cag
Lys Leu Tyr Glu Asn Ala Val Ala Arg Tyr Ser Met Leu Pro Ser Gln
210 215 220
gcc aag
Ala Lys
225

672

678

<210> 143
<211> 226
<212> PRT
<213> Artificial
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<223> dAG (AB)
<400> 143

Met Val Ser Val Ile Lys Pro Glu Met Lys Ile Lys Leu Cys Met Arg
1 5 10 15
Gly Thr Val Asn Gly His Asn Phe Val Ile Glu Gly Glu Gly Lys Gly
20 25 30
Asn Pro Tyr Glu Gly Thr Gln Ile Leu Asp Leu Asn Val Thr Glu Gly
35 40 45
Ala Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Val Phe Gln Tyr
50 55 60
Gly Asn Arg Ala Phe Thr Lys Tyr Pro Ala Asp Ile Gln Asp Tyr Phe
65 70 75 80
Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ser Met Thr Tyr
85 90 95
Glu Asp Gln Gly Ile Cys Thr Ala Thr Ser Asn Ile Ser Met Arg Gly
100 105 110
Asp Cys Phe Phe Tyr Asp Ile Arg Phe Asp Gly Val Asn Phe Pro Pro
115 120 125
Asn Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp Glu Pro Ser Thr
130 135 140
Glu Lys Met Tyr Val Arg Asp Gly Val Leu Lys Gly Asp Val Asn Met
145 150 155 160
Ala Leu Leu Leu Glu Gly Gly Gly His Tyr Arg Cys Asp Phe Lys Thr
165 170 175
Thr Tyr Lys Ala Lys Lys Asp Val Arg Leu Pro Asp Ala His Lys Val
180 185 190
Asp His Arg Ile Glu Ile Leu Lys His Asp Lys Asp Tyr Asn Lys Val
195 200 205
Lys Leu Tyr Glu Asn Ala Val Ala Arg Tyr Ser Met Leu Pro Ser Gln
210 215 220
Ala Lys
225

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1 5 10 15
ggc act gta aac ggg cat aat ttc gtg att gaa gga gaa gga aaa gga
Gly Thr Val Asn Gly His Asn Phe Val Ile Glu Gly Glu Gly Lys Gly
20 25 30
aat cct tac gag gga acg cag att tta gac ctg aac gtc act gaa ggc
Asn Pro Tyr Glu Gly Thr Gln Ile Leu Asp Leu Asn Val Thr Glu Gly
35 40 45
gca cct ctg cct ttc gct tac gat atc ttg aca aca gtg ttc cag tac
Ala Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr Val Phe Gln Tyr
220

48

96

144

192

IBPF12-538W0-E (seq) fin

50	55	60	
ggc aac agg gca ttc acc aag tac cca gca gat att cag gac tat ttc			240
Gly Asn Arg Ala Phe Thr Lys Tyr Pro Ala Asp Ile Gln Asp Tyr Phe			
65	70	75	80
aag cag act ttt cct gag ggg tat cac tgg gaa aga agc atg act tat			288
Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Ser Met Thr Tyr			
85	90	95	
gaa gac cag ggc att tgc acc gcc aca agc aac ata agc atg cgt ggc			336
Glu Asp Gln Gly Ile Cys Thr Ala Thr Ser Asn Ile Ser Met Arg Gly			
100	105	110	
gac tgt ttt ttc tat gac att cgt ttt gat ggt acc aac ttt cct ccc			384
Asp Cys Phe Phe Tyr Asp Ile Arg Phe Asp Gly Thr Asn Phe Pro Pro			
115	120	125	
aat ggt ccg gtt atg cag aag aag act ctt aaa tgg gag cca tcc act			432
Asn Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp Glu Pro Ser Thr			
130	135	140	
gag aaa atg tac gta cgt gat gga gtg ctg aag ggt gat gtt aac atg			480
Glu Lys Met Tyr Val Arg Asp Gly Val Leu Lys Gly Asp Val Asn Met			
145	150	155	160
gct ctg ttg ctt gaa gga ggt ggc cat tat cga tgt gat ttc aaa act			528
Ala Leu Leu Leu Glu Gly Gly Gly His Tyr Arg Cys Asp Phe Lys Thr			
165	170	175	
act tac aaa gca aag aag gat gtc cgt ttg cca gac tat cac ttt gtg			576
Thr Tyr Lys Ala Lys Lys Asp Val Arg Leu Pro Asp Tyr His Phe Val			
180	185	190	
gac cac cgc att gag att ttg aag cat gac aaa gat tac aac aag gtc			624
Asp His Arg Ile Glu Ile Leu Lys His Asp Lys Asp Tyr Asn Lys Val			
195	200	205	
aag ctc tat gag aat gcc gtt gct cgc tat tct atg ctg ccg agt cag			672
Lys Leu Tyr Glu Asn Ala Val Ala Arg Tyr Ser Met Leu Pro Ser Gln			
210	215	220	
gcc aag			678
Ala Lys			
225			

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

IBPF12-538W0-E (seq) fin

Lys Leu Tyr Glu Asn Ala Val Ala Arg Tyr Ser Met Leu Pro Ser Gln
 210 215 220

Ala Lys
 225

<210> 146
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 <222> (1).. (672)
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1			5					10					15			
gga	tgt	gtc	aac	ggc	cac	tcc	ttc	aag	att	gag	ggt	gac	ggc	aaa	ggc	96
Gly	Cys	Val	Asn	Gly	His	Ser	Phe	Lys	Ile	Glu	Gly	Asp	Gly	Lys	Gly	
		20					25					30				
aaa	cgc	tac	gag	gga	gac	caa	act	gtg	aag	ctg	cgt	ggt	act	gaa	gga	144
Lys	Pro	Tyr	Glu	Gly	Asp	Gln	Thr	Val	Lys	Leu	Arg	Val	Thr	Glu	Gly	
		35				40					45					
ggg	ccc	tta	cca	ttc	gca	ttt	gac	atc	ttg	tca	gcc	tca	atg	tgt	tat	192
Gly	Pro	Leu	Pro	Phe	Ala	Phe	Asp	Ile	Leu	Ser	Ala	Ser	Met	Cys	Tyr	
	50				55						60					
gga	aac	agg	tgt	ttt	acc	aaa	tat	cgc	gca	gag	att	ccc	gac	att	ttc	240
Gly	Asn	Arg	Cys	Phe	Thr	Lys	Tyr	Pro	Ala	Glu	Ile	Pro	Asp	Ile	Phe	
65			70					75						80		
aag	cag	aca	ttt	cct	gaa	ggc	tac	tca	tgg	gaa	aga	gcc	ttg	aca	ttt	288
Lys	Gln	Thr	Phe	Pro	Glu	Gly	Tyr	Ser	Trp	Glu	Arg	Ala	Leu	Thr	Phe	
		85						90					95			
gaa	gat	gga	ggg	ttt	gct	tca	tca	agc	tgc	cac	atc	agt	gtc	cgt	ggc	336
Glu	Asp	Gly	Gly	Phe	Ala	Ser	Ser	Ser	Ser	His	Ile	Ser	Val	Arg	Gly	
		100					105						110			
aac	tgc	ttc	ttc	tac	gac	gtc	aaa	tat	cat	ggc	gta	aac	ttc	cct	tcc	384
Asn	Cys	Phe	Phe	Tyr	Asp	Val	Lys	Tyr	His	Gly	Val	Asn	Phe	Pro	Ser	
		115				120					125					
aat	gga	cca	att	atg	caa	aga	aag	aca	atc	ggc	tgg	caa	cca	tcc	aca	432
Asn	Gly	Pro	Ile	Met	Gln	Arg	Lys	Thr	Ile	Gly	Trp	Gln	Pro	Ser	Thr	
		130				135					140					
gag	aaa	ttg	tac	atc	gga	gag	gga	acg	ctg	aag	ggt	gat	gat	acg	atg	480
Glu	Lys	Leu	Tyr	Ile	Gly	Glu	Gly	Thr	Leu	Lys	Gly	Asp	Asp	Thr	Met	
145					150					155					160	
ttc	ctc	aag	ctc	gaa	gga	ggg	gga	act	cat	aaa	tgc	cac	gtc	cta	acc	528
Phe	Leu	Lys	Leu	Glu	Gly	Gly	Gly	Thr	His	Lys	Cys	His	Val	Leu	Thr	
			165					170					175			
act	tac	aaa	acg	aag	aaa	gat	gtc	cag	atg	cca	gac	agc	cac	ttc	att	576
Thr	Tyr	Lys	Thr	Lys	Lys	Asp	Val	Gln	Met	Pro	Asp	Ser	His	Phe	Ile	
		180						185					190			
gac	cat	cgt	ctc	ctg	acc	agc	cac	ctt	gat	aag	gaa	tgc	aac	aac	gtg	624
Asp	His	Arg	Leu	Leu	Thr	Ser	His	Leu	Asp	Lys	Glu	Cys	Asn	Asn	Val	
		195				200						205				
gaa	ttg	cgc	gag	cac	gca	gtt	gcg	cgt	aac	tca	agt	ctg	cct	tcc	cgt	672
Glu	Leu	Arg	Glu	His	Ala	Val	Ala	Arg	Asn	Ser	Ser	Leu	Pro	Ser	Arg	
	210					215						220				

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 <212> PRT
 <213> Artificial
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 <223> TGuv
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Met Val Ser Val Ile Gly Lys Asp Met Ile Met Lys Leu His Val Glu
 1 5 10 15

IBPF12-538W0-E (seq) fin

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

<210> 148
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 <213> Artificial
 <220>
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 <222> (1).. (687)
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Met	Val	Ser	Val	Ile	Lys	Asp	Glu	Met	Lys	Val	Asn	Leu	Arg	Met	Glu	
1			5					10				15				
ggc	agc	gtg	aac	ggc	cac	gac	ttc	gtg	atc	gac	ggc	ctg	ggc	tcc	ggc	96
Gly	Ser	Val	Asn	Gly	His	Asp	Phe	Val	Ile	Asp	Gly	Leu	Gly	Ser	Gly	
			20				25					30				
aag	ccc	aag	gag	ggc	acc	cag	acc	atc	gag	ctg	aag	gtg	gtg	aag	ggc	144
Lys	Pro	Lys	Glu	Gly	Thr	Gln	Thr	Ile	Glu	Leu	Lys	Val	Val	Lys	Gly	
		35				40					45					
ggc	ccc	ctg	ccc	ttc	gcc	tac	gac	atc	ctg	acc	acc	gcc	ttc	cac	tac	192
Gly	Pro	Leu	Pro	Phe	Ala	Tyr	Asp	Ile	Leu	Thr	Thr	Ala	Phe	His	Tyr	
	50				55						60					
ggc	aac	agg	gtg	ttc	gcc	aag	tac	ccc	aag	gac	atc	ccc	aac	tac	ttc	240
Gly	Asn	Arg	Val	Phe	Ala	Lys	Tyr	Pro	Lys	Asp	Ile	Pro	Asn	Tyr	Phe	
	65				70					75				80		
gag	cag	tcc	ttc	ccc	gag	ggc	tac	tcc	tgg	gag	agg	agc	atg	atc	ttc	288
Glu	Gln	Ser	Phe	Pro	Glu	Gly	Tyr	Ser	Trp	Glu	Arg	Ser	Met	Ile	Phe	
			85					90					95			
gag	gac	ggc	ggc	atc	tgc	atc	gcc	agg	aac	gac	atc	act	atg	gac	ggc	336
Glu	Asp	Gly	Gly	Ile	Cys	Ile	Ala	Arg	Asn	Asp	Ile	Thr	Met	Asp	Gly	
		100					105					110				
ggc	acc	ttc	tac	aac	aag	gtg	agg	ttc	tac	ggc	gtg	aac	ttc	ccc	ccc	384
Gly	Thr	Phe	Tyr	Asn	Lys	Val	Arg	Phe	Tyr	Gly	Val	Asn	Phe	Pro	Pro	
		115				120					125					
aac	ggc	ccc	gtg	atg	cag	aag	aag	acc	cag	aag	tgg	gag	cag	tcc	acc	432
Asn	Gly	Pro	Val	Met	Gln	Lys	Lys	Thr	Gln	Lys	Trp	Glu	Gln	Ser	Thr	
	130					135					140					
gag	aag	atg	tac	gcc	agg	gac	ggc	gtg	ctg	acc	ggc	gac	atc	aac	atg	480
Glu	Lys	Met	Tyr	Ala	Arg	Asp	Gly	Val	Leu	Thr	Gly	Asp	Ile	Asn	Met	
	145				150					155				160		

IBPF12-538W0-E (seq) fin

gcc ctg ctg ctg aag ggc ggc ggc cac tac agg tgc gac ttc agg acc	528
Ala Leu Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe Arg Thr	
165 170 175	
acc tac aag gcc aag gag aag ggc gtc aag ctg ccc ggc tac cac ttc	576
Thr Tyr Lys Ala Lys Glu Lys Gly Val Lys Leu Pro Gly Tyr His Phe	
180 185 190	
atc gac cac tgc atc gag atc ctg agc cac agg aac gac tac aac aac	624
Ile Asp His Cys Ile Glu Ile Leu Ser His Arg Asn Asp Tyr Asn Asn	
195 200 205	
gtg acc ctg ttc gag cac gcc gtg gcc agg tcc ggc ctg caa gac aag	672
Val Thr Leu Phe Glu His Ala Val Ala Arg Ser Gly Leu Gln Asp Lys	
210 215 220	
gag aag cag cag cag	687
Glu Lys Gln Gln Gln	
225	

<210> 149
 <211> 229
 <212> PRT
 <213> Artificial
 <220>
 <223> Momiji
 <400> 149

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

<210> 150
 <211> 696
 <212> DNA
 <213> Artificial
 <220>
 <223> COR3.01
 <220>
 <221> CDS
 <222> (1).. (696)
 <223>
 <400> 150

atg gcc ctg agc aag cac ggc ctg acc aag aac atg acc acc aag tac	48
Met Ala Leu Ser Lys His Gly Leu Thr Lys Asn Met Thr Thr Lys Tyr	
1 5 10 15	

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agg atg gag ggc tgc gtg gac ggc cac aag ttc gtg atc acc ggc gac	96
Arg Met Glu Gly Cys Val Asp Gly His Lys Phe Val Ile Thr Gly Asp	
20 25 30	
ggc atc ggc gac ccc ttc gag ggc aag cag acc agc atc gac ctg tgc	144
Gly Ile Gly Asp Pro Phe Glu Gly Lys Gln Thr Ser Ile Asp Leu Cys	
35 40 45	
gtg gtg gag ggc ggc ccc ctg ccc ttc agc gag gac atc ctg agc acc	192
Val Val Glu Gly Gly Pro Leu Pro Phe Ser Glu Asp Ile Leu Ser Thr	
50 55 60	
gtg ttc gac tac ggc aac agg gtg ttc acc aag tac ccc cag gac ctg	240
Val Phe Asp Tyr Gly Asn Arg Val Phe Thr Lys Tyr Pro Gln Asp Leu	
65 70 75 80	
gtg gac tac ttc aag aac agc tgc ccc gcc ggc tac acc tgg cag agg	288
Val Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Gln Arg	
85 90 95	
agc ttc ctg ttc gag gac ggc gcc gtg tgc acc gcc agc gcc gac atc	336
Ser Phe Leu Phe Glu Asp Gly Ala Val Cys Thr Ala Ser Ala Asp Ile	
100 105 110	
agg gtg agc gtg gag gag aac tgc ttc tac cac gag agc aag ttc cac	384
Arg Val Ser Val Glu Glu Asn Cys Phe Tyr His Glu Ser Lys Phe His	
115 120 125	
ggc gtg aac ttc ccc gcc gac ggc ccc gtg atg aag aag atg acc acc	432
Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Thr	
130 135 140	
aac tgg gag ccc agc tgc gag aag atc acc ccc atc ctg aac gag ggc	480
Asn Trp Glu Pro Ser Cys Glu Lys Ile Thr Pro Ile Leu Asn Glu Gly	
145 150 155 160	
atc ctg aag ggc gac gtg acc atg ttc ctg ctg ctg aag gac ggc ggc	528
Ile Leu Lys Gly Asp Val Thr Met Phe Leu Leu Leu Lys Asp Gly Gly	
165 170 175	
agg tac agg tgc cag ttc gac acc gtg tac aag gcc aag gcc gac gcc	576
Arg Tyr Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ala Asp Ala	
180 185 190	
aag aag atg ccc gag tgg cac ttc atc cag cac gag ctg acc agg gag	624
Lys Lys Met Pro Glu Trp His Phe Ile Gln His Glu Leu Thr Arg Glu	
195 200 205	
gac agg agc gac gcc aag cac cag aag tgg agg ctg gtg gag aac gcc	672
Asp Arg Ser Asp Ala Lys His Gln Lys Trp Arg Leu Val Glu Asn Ala	
210 215 220	
atc gcc tac agg agc acc ctg ccc	696
Ile Ala Tyr Arg Ser Thr Leu Pro	
225 230	

<210> 151
 <211> 232
 <212> PRT
 <213> Artificial
 <220>
 <223> COR3.01
 <400> 151

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

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Asn Trp Glu Pro Ser Cys Glu Lys Ile Thr Pro Ile Leu Asn Glu Gly
 145 150 155 160
 Ile Leu Lys Gly Asp Val Thr Met Phe Leu Leu Leu Lys Asp Gly Gly
 165 170 175
 Arg Tyr Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ala Asp Ala
 180 185 190
 Lys Lys Met Pro Glu Trp His Phe Ile Gln His Glu Leu Thr Arg Glu
 195 200 205
 Asp Arg Ser Asp Ala Lys His Gln Lys Trp Arg Leu Val Glu Asn Ala
 210 215 220
 Ile Ala Tyr Arg Ser Thr Leu Pro
 225 230

<210> 152
 <211> 678
 <212> DNA
 <213> Artificial
 <220>
 <223> DsRed2
 <220>
 <221> CDS
 <222> (1).. (678)
 <223>
 <400> 152

atg gcc tcc tcc gag aac gtc atc acc gag ttc atg cgc ttc aag gtg	48
Met Ala Ser Ser Glu Asn Val Ile Thr Glu Phe Met Arg Phe Lys Val	
1 5 10 15	
cgc atg gag ggc acc gtg aac ggc cac gag ttc gag atc gag ggc gag	96
Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu	
20 25 30	
ggc gag ggc cgc ccc tac gag ggc cac aac acc gtg aag ctg aag gtg	144
Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val	
35 40 45	
acc aag ggc ggc ccc ctg ccc ttc gcc tgg gac atc ctg tcc ccc cag	192
Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln	
50 55 60	
ttc cag tac ggc tcc aag gtg tac gtg aag cac ccc gcc gac atc ccc	240
Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro	
65 70 75 80	
gac tac aag aag ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg	288
Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val	
85 90 95	
atg aac ttc gag gac ggc ggc gtg gcg acc gtg acc cag gac tcc tcc	336
Met Asn Phe Glu Asp Gly Gly Val Ala Thr Val Thr Gln Asp Ser Ser	
100 105 110	
ctg cag gac ggc tgc ttc atc tac aag gtg aag ttc atc ggc gtg aac	384
Leu Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn	
115 120 125	
ttc ccc tcc gac ggc ccc gtg atg cag aag aag acc atg ggc tgg gag	432
Phe Pro Val Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu	
130 135 140	
gcc tcc acc gag cgc ctg tac ccc cgc gac ggc gtg ctg aag ggc gag	480
Ala Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu	
145 150 155 160	
acc cac aag gcc ctg aag ctg aag gac ggc ggc cac tac ctg gtg gag	528
Thr His Lys Ala Leu Lys Leu Lys Asp Gly Gly His Tyr Leu Val Glu	
165 170 175	
ttc aag tct atc tac atg gcc aag aag ccc gtg cag ctg ccc ggc tac	576
Phe Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr	
180 185 190	
tac tac gtg gac gcc aag ctg gac atc acc tcc cac aac gag gac tac	624
Tyr Tyr Val Asp Ala Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr	
195 200 205	
acc atc gtg gag cag tac gag cgc acc gag ggc cgc cac cac ctg ttc	672
Thr Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe	
210 215 220	
ctg tag	678
Leu	

225

<210> 153
 <211> 225
 <212> PRT
 <213> Artificial
 <220>
 <223> DsRed2
 <400> 153
 Met Ala Ser Ser Glu Asn Val Ile Thr Glu Phe Met Arg Phe Lys Val
 1 5 10 15
 Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu
 20 25 30
 Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val
 35 40 45
 Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln
 50 55 60
 Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro
 65 70 75 80
 Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val
 85 90 95
 Met Asn Phe Glu Asp Gly Gly Val Ala Thr Val Thr Gln Asp Ser Ser
 100 105 110
 Leu Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn
 115 120 125
 Phe Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu
 130 135 140
 Ala Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu
 145 150 155 160
 Thr His Lys Ala Leu Lys Leu Lys Asp Gly Gly His Tyr Leu Val Glu
 165 170 175
 Phe Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr
 180 185 190
 Tyr Tyr Val Asp Ala Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr
 195 200 205
 Thr Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe
 210 215 220
 Leu
 225

<210> 154
 <211> 49
 <212> DNA
 <213> Artificial
 <220>
 <223> Artificially synthesized primer sequence
 <400> 154
 gcttccaggc gcactaccgc gctgagcgcg gggacttggt tgccttttc

49

<210> 155
 <211> 372
 <212> DNA
 <213> Artificial
 <220>
 <223> Artificially synthesized polynucleotide sequence
 <220>
 <221> CDS
 <222> (1)..(372)
 <223>
 <400> 155

aat gca tcc aac ttg aaa att gta aga atg gac agg aca gct gga tgt
 Asn Ala Ser Asn Leu Lys Ile Val Arg Met Asp Arg Thr Ala Gly Cys
 1 5 10 15
 gtg act gga ggg gag gaa att tat ctt ctt tgt gac aaa gtt cag aaa
 Val Thr Gly Gly Glu Glu Ile Tyr Leu Leu Cys Asp Lys Val Gln Lys
 20 25 30
 gat gac atc cag att cga ttt tat gaa gag gaa gaa aat ggt gga gtc
 Asp Asp Ile Gln Ile Arg Phe Tyr Glu Glu Glu Glu Asn Gly Gly Val
 35 40 45 50

48

96

144

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35	40	45	
tgg gaa gga ttt gga gat ttt tcc ccc aca gat gtt cat aga caa ttt			192
Trp Glu Gly Phe Gly Asp Phe Ser Pro Thr Asp Val His Arg Gln Phe			
50	55	60	
gcc att gtc ttc aaa act cca aag tat aaa gat att aat att aca aaa			240
Ala Ile Val Phe Lys Thr Pro Lys Tyr Lys Asp Ile Asn Ile Thr Lys			
65	70	75	
cca gcc tct gtg ttt gtc cag ctt cgg agg aaa tct gac ttg gaa act			288
Pro Ala Ser Val Phe Val Gln Leu Arg Arg Lys Ser Asp Leu Glu Thr			
85	90	95	
agt gaa cca aaa cct ttc ctc tac tat cct gaa atc aaa gat aaa gaa			336
Ser Glu Pro Lys Pro Phe Leu Tyr Tyr Pro Glu Ile Lys Asp Lys Glu			
100	105	110	
gaa gtg cag agg aaa cgt cag aag ggc tcg aga taa			372
Glu Val Gln Arg Lys Arg Gln Lys Gly Ser Arg			
115	120		

<210> 156
 <211> 123
 <212> PRT
 <213> Artificial
 <220>
 <223> Artificially synthesized polypeptide sequence
 <400> 156
 Asn Ala Ser Asn Leu Lys Ile Val Arg Met Asp Arg Thr Ala Gly Cys
 1 5 10 15
 Val Thr Gly Gly Glu Glu Ile Tyr Leu Leu Cys Asp Lys Val Gln Lys
 20 25 30
 Asp Asp Ile Gln Ile Arg Phe Tyr Glu Glu Glu Glu Asn Gly Gly Val
 35 40 45
 Trp Glu Gly Phe Gly Asp Phe Ser Pro Thr Asp Val His Arg Gln Phe
 50 55 60
 Ala Ile Val Phe Lys Thr Pro Lys Tyr Lys Asp Ile Asn Ile Thr Lys
 65 70 75 80
 Pro Ala Ser Val Phe Val Gln Leu Arg Arg Lys Ser Asp Leu Glu Thr
 85 90 95
 Ser Glu Pro Lys Pro Phe Leu Tyr Tyr Pro Glu Ile Lys Asp Lys Glu
 100 105 110
 Glu Val Gln Arg Lys Arg Gln Lys Gly Ser Arg
 115 120

<210> 157
 <211> 393
 <212> DNA
 <213> Artificial
 <220>
 <223> Artificially synthesized polynucleotide sequence
 <220>
 <221> CDS
 <222> (1).. (393)
 <223>
 <400> 157

act gcc gag ctc aag atc tgc cga gtg aac cga aac tct ggc agc tgc	48
Thr Ala Glu Leu Lys Ile Cys Arg Val Asn Arg Asn Ser Gly Ser Cys	
1 5 10 15	
ctc ggt ggg gat gag atc ttc cta ctg tgt gac aag gtg cag aaa gag	96
Leu Gly Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys Val Gln Lys Glu	
20 25 30	
gac att gag gtg tat ttc acg gga cca ggc tgg gag gcc cga ggc tcc	144
Asp Ile Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu Ala Arg Gly Ser	
35 40 45	
ttt tcg caa gct gat gtg cac cga caa gtg gcc att gtg ttc cgg acc	192
Phe Ser Gln Ala Asp Val His Arg Gln Val Ala Ile Val Phe Arg Thr	
50 55 60	
cct ccc tac gca gac ccc agc ctg cag gct cct gtg cgt gtc tcc atg	240
Pro Pro Tyr Ala Asp Pro Ser Leu Gln Ala Pro Val Arg Val Ser Met	
65 70 75 80	
cag ctg cgg cgg cct tcc gac cgg gag ctc agt gag ccc atg gaa ttc	288

IBPF12-538W0-E (seq) fin
 Gln Leu Arg Arg Pro Ser Asp Arg Glu Leu Ser Glu Pro Met Glu Phe
 85 90 95
 cag tac ctg cca gat aca gac gat cgt cac cgg att gag gag aaa cgt 336
 Gln Tyr Leu Pro Asp Thr Asp Asp Arg His Arg Ile Glu Glu Lys Arg
 100 105 110
 aaa agg aca tat gag acc ttc aag agc atc atg aag aag agt cct ttc 384
 Lys Arg Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys Lys Ser Pro Phe
 115 120 125
 agc gga taa 393
 Ser Gly
 130

<210> 158
 <211> 130
 <212> PRT
 <213> Artificial
 <220>
 <223> Artificially synthesized polypeptide sequence
 <400> 158
 Thr Ala Glu Leu Lys Ile Cys Arg Val Asn Arg Asn Ser Gly Ser Cys
 1 5 10 15
 Leu Gly Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys Val Gln Lys Glu
 20 25 30
 Asp Ile Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu Ala Arg Gly Ser
 35 40 45
 Phe Ser Gln Ala Asp Val His Arg Gln Val Ala Ile Val Phe Arg Thr
 50 55 60
 Pro Pro Tyr Ala Asp Pro Ser Leu Gln Ala Pro Val Arg Val Ser Met
 65 70 75 80
 Gln Leu Arg Arg Pro Ser Asp Arg Glu Leu Ser Glu Pro Met Glu Phe
 85 90 95
 Gln Tyr Leu Pro Asp Thr Asp Asp Arg His Arg Ile Glu Glu Lys Arg
 100 105 110
 Lys Arg Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys Lys Ser Pro Phe
 115 120 125
 Ser Gly
 130

<210> 159
 <211> 41
 <212> DNA
 <213> Artificial
 <220>
 <223> Artificially synthesized primer sequence
 <400> 159
 acattttcag acctattgaa actacttcct gaaaacaacg t 41

<210> 160
 <211> 42
 <212> DNA
 <213> Artificial
 <220>
 <223> Artificially synthesized primer sequence
 <400> 160
 cttgtggtag ttggagctga cggcgtaggc aagagtgcct tg 42

<210> 161
 <211> 243
 <212> DNA
 <213> Artificial
 <220>
 <223> Artificially synthesized polynucleotide sequence
 <220>
 <221> CDS
 <222> (1).. (243)
 <223>
 <400> 161
 oct tct aag aca agc aac act atc got gtt ttc ttg ccg aac aag caa 48

IBPF12-538W0-E (seq) fin

Pro	Ser	Lys	Thr	Ser	Asn	Thr	Ile	Ala	Val	Phe	Leu	Pro	Asn	Lys	Gln	
1				5					10					15		
aga	aca	gtg	gtc	aat	gtg	cga	aat	gga	atg	agc	ttg	cat	gac	tgc	ctt	96
Arg	Thr	Val	Val	Asn	Val	Arg	Asn	Gly	Met	Ser	Leu	His	Asp	Cys	Leu	
		20						25					30			
atg	aaa	gca	ctc	aag	gtg	agg	ggc	ctg	caa	cca	gag	tgc	tgt	gca	gtg	144
Met	Lys	Ala	Leu	Lys	Val	Arg	Gly	Leu	Gln	Pro	Glu	Cys	Cys	Ala	Val	
		35					40					45				
ttc	aga	ctt	ctc	cac	gaa	cac	aaa	ggt	aaa	aaa	gca	cgc	tta	gat	tgg	192
Phe	Arg	Leu	Leu	His	Glu	His	Lys	Gly	Lys	Lys	Ala	Arg	Leu	Asp	Trp	
	50					55					60					
aat	act	gat	gct	gcg	tct	ttg	att	gga	gaa	gaa	ctt	caa	gta	gat	ttc	240
Asn	Thr	Asp	Ala	Ala	Ser	Leu	Ile	Gly	Glu	Glu	Leu	Gln	Val	Asp	Phe	
65					70				75					80		
ctg																243
Leu																

<210> 162
 <211> 81
 <212> PRT
 <213> Artificial
 <220>
 <223> Artificially synthesized polypeptide sequence
 <400> 162

Pro	Ser	Lys	Thr	Ser	Asn	Thr	Ile	Ala	Val	Phe	Leu	Pro	Asn	Lys	Gln	
1				5					10					15		
Arg	Thr	Val	Val	Asn	Val	Arg	Asn	Gly	Met	Ser	Leu	His	Asp	Cys	Leu	
		20						25					30			
Met	Lys	Ala	Leu	Lys	Val	Arg	Gly	Leu	Gln	Pro	Glu	Cys	Cys	Ala	Val	
		35					40					45				
Phe	Arg	Leu	Leu	His	Glu	His	Lys	Gly	Lys	Lys	Ala	Arg	Leu	Asp	Trp	
	50					55					60					
Asn	Thr	Asp	Ala	Ala	Ser	Leu	Ile	Gly	Glu	Glu	Leu	Gln	Val	Asp	Phe	
65					70				75					80		
Leu																

<210> 163
 <211> 48
 <212> DNA
 <213> Artificial
 <220>
 <223> Artificially synthesized polynucleotide sequence
 <220>
 <221> CDS
 <222> (1).. (48)
 <223>
 <400> 163

ggg	cag	gtg	gga	cgg	cag	ctc	gcc	atc	atc	ggg	gac	gac	atc	aac	cga	48
Gly	Gln	Val	Gly	Arg	Gln	Leu	Ala	Ile	Ile	Gly	Asp	Asp	Ile	Asn	Arg	
1				5					10					15		

<210> 164
 <211> 16
 <212> PRT
 <213> Artificial
 <220>
 <223> Artificially synthesized polypeptide sequence
 <400> 164

Gly	Gln	Val	Gly	Arg	Gln	Leu	Ala	Ile	Ile	Gly	Asp	Asp	Ile	Asn	Arg	
1				5					10					15		

<210> 165
 <211> 63
 <212> DNA
 <213> Artificial
 <220>

IBPF12-538W0-E (seq) fin

<223> Artificially synthesized polynucleotide sequence

<220>

<221> CDS

<222> (1).. (63)

<223>

<400> 165

cag gat gcg tcc acc aag aag ctg agc gag tgt ctc aag cgc atc ggg	48
Gln Asp Ala Ser Thr Lys Lys Leu Ser Glu Cys Leu Lys Arg Ile Gly	
1 5 10 15	
gac gaa ctg gac agt	63
Asp Glu Leu Asp Ser	
20	

<210> 166

<211> 21

<212> PRT

<213> Artificial

<220>

<223> Artificially synthesized polypeptide sequence

<400> 166

Gln Asp Ala Ser Thr Lys Lys Leu Ser Glu Cys Leu Lys Arg Ile Gly	
1 5 10 15	
Asp Glu Leu Asp Ser	
20	

<210> 167

<211> 1449

<212> DNA

<213> Artificial

<220>

<223> Artificially synthesized polynucleotide sequence

<220>

<221> CDS

<222> (1).. (1449)

<223>

<400> 167

atg gcg tcg ctc acc gtg aag gcc tac ctt ctg ggc aag gag gac gcg	48
Met Ala Ser Leu Thr Val Lys Ala Tyr Leu Leu Gly Lys Glu Asp Ala	
1 5 10 15	
gcg cgc gag att cgc cgc ttc agc ttc tgc tgc agc ccc gag cct gag	96
Ala Arg Glu Ile Arg Arg Phe Ser Phe Cys Cys Ser Pro Glu Pro Glu	
20 25 30	
gcg gaa gcc gag gct gcg gcg ggt ccg gga ccc tgc gag cgg ctg ctg	144
Ala Glu Ala Glu Ala Ala Ala Gly Pro Gly Pro Cys Glu Arg Leu Leu	
35 40 45	
agc cgg gtg gcc gcc ctg ttc ccc gcg ctg cgg cct ggc ggc ttc cag	192
Ser Arg Val Ala Ala Leu Phe Pro Ala Leu Arg Pro Gly Gly Phe Gln	
50 55 60	
gcg cac tac cgc gat gag gac ggg gac ttg gtt gcc ttt tcc agt gac	240
Ala His Tyr Arg Asp Glu Asp Gly Asp Leu Val Ala Phe Ser Ser Asp	
65 70 75 80	
gag gaa ttg aca atg gcc atg tcc tac gtg aag gat gac atc ttc cga	288
Glu Glu Leu Thr Met Ala Met Ser Tyr Val Lys Asp Asp Ile Phe Arg	
85 90 95	
atc tac att aaa gag aaa acc ggt aat tcc gct gac ggc ggc gga gga	336
Ile Tyr Ile Lys Glu Lys Thr Gly Asn Ser Ala Asp Gly Gly Gly Gly	
100 105 110	
tcg ggt ggt agt ggt ggt tca gga gga gga tcg acc caa gga gga tcc	384
Ser Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Thr Gln Gly Gly Ser	
115 120 125	
cca gat gtc cct aga act cca gtg ggc aaa ttc cag ttc cca gga agc	432
Pro Asp Val Pro Arg Thr Pro Val Gly Lys Phe Gln Phe Pro Gly Ser	
130 135 140	
gga gct act aac ttc agc ctg ctg aag cag gct gga gac gtg gag gag	480
Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu	
145 150 155 160	
aac cct gga cct atg gtg agc gtg atc aag ccc gag atg aag atc aag	528
Asn Pro Gly Pro Met Val Ser Val Ile Lys Pro Glu Met Lys Ile Lys	

IBPF12-538W0-E (seq) fin

ctg tgc atg agg ggc acc gtg aac ggc cac aac ttc gtg atc gag ggc	576
Leu Cys Met Arg Gly Thr Val Asn Gly His Asn Phe Val Ile Glu Gly	
165 170 175	
gag ggc aag ggc aac ccc tac gag ggc acc cag atc ctg gac ctg aac	624
Glu Gly Lys Gly Asn Pro Tyr Glu Gly Thr Gln Ile Leu Asp Leu Asn	
180 185 190	
gtg acc gag ggc gcc ccc ctg ccc ttc gcc tac gac atc ctg acc acc	672
Val Thr Glu Gly Ala Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr	
200 205	
gtg ttc cag tac ggc aac agg gcc ttc acc aag tac ccc gcc gac atc	720
Val Phe Gln Tyr Gly Asn Arg Ala Phe Thr Lys Tyr Pro Ala Asp Ile	
210 215 220	
cag gac tac ttc aag cag acc ttc ccc gag ggc tac cac tgg gag agg	768
Gln Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg	
230 235 240	
agc atg acc tac gag gac cag ggc atc tgc acc gcc acc agc aac atc	816
Ser Met Thr Tyr Glu Asp Gln Gly Ile Cys Thr Ala Thr Ser Asn Ile	
245 250 255	
agc atg agg ggc gac tgc ttc ttc tac gac atc agg ttc gac ggc gtg	864
Ser Met Arg Gly Asp Cys Phe Phe Tyr Asp Ile Arg Phe Asp Gly Val	
260 265 270	
aac ttc ccc ccc aac ggc ccc gtg atg cag aag aag acc ctg aag tgg	912
Asn Phe Pro Pro Asn Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp	
275 280 285	
gag ccc agc acc gag aag atg tac gtg agg gac ggc gtg ctg aag ggc	960
Glu Pro Ser Thr Glu Lys Met Tyr Val Arg Asp Gly Val Leu Lys Gly	
290 295 300	
gac gtg aac atg gcc ctg ctg ctg gag ggc ggc ggc cac tac agg tgc	1008
Asp Val Asn Met Ala Leu Leu Leu Glu Gly Gly Gly His Tyr Arg Cys	
305 310 315 320	
gac ttc aag acc acc tac aag gcc aag aag gac gtg agg ctg ccc gac	1056
Asp Phe Lys Thr Thr Tyr Lys Ala Lys Lys Asp Val Arg Leu Pro Asp	
325 330 335 340	
tac cac ttc gtg gac cac agg atc gag atc ctg aag cac gac aag gac	1104
Tyr His Phe Val Asp His Arg Ile Glu Ile Leu Lys His Asp Lys Asp	
345 350 355 360	
tac aac aag gtg aag ctg tac gag aac gcc gtg gcc agg tac agc atg	1152
Tyr Asn Lys Val Lys Leu Tyr Glu Asn Ala Val Ala Arg Tyr Ser Met	
365 370 375 380	
ctg ccc agc cag gcc aag acc ggt aat tcc gct gac ggc ggc gga gga	1200
Leu Pro Ser Gln Ala Lys Thr Gly Asn Ser Ala Asp Gly Gly Gly Gly	
385 390 395 400	
tcg ggt ggt agt ggt ggt tca gga gga gga tcg acc caa gga gga tcc	1248
Ser Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Thr Gln Gly Gly Ser	
405 410 415	
atg gcg gac gag gag aag ctg ccg ccc ggc tgg gag aag cgc atg agc	1296
Met Ala Asp Glu Glu Lys Leu Pro Pro Gly Trp Glu Lys Arg Met Ser	
420 425 430	
cgc agc tca ggc cga gtg tac tac ttc aac cac atc act aac gcc agc	1344
Arg Ser Ser Gly Arg Val Tyr Tyr Phe Asn His Ile Thr Asn Ala Ser	
435 440 445	
cag tgg gag cgg ccc agc ggc aac agc agc agt ggt ggc aaa aac ggg	1392
Gln Trp Glu Arg Pro Ser Gly Asn Ser Ser Ser Gly Gly Lys Asn Gly	
450 455 460	
cag ggg gag cct gcc agg ctt cag aag aaa ctc gag gaa ctt gag ctt	1440
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IBPF12-538W0-E (seq) fin

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 35 40 45
 Ser Arg Val Ala Ala Leu Phe Pro Ala Leu Arg Pro Gly Gly Phe Gln
 50 55 60
 Ala His Tyr Arg Asp Glu Asp Gly Asp Leu Val Ala Phe Ser Ser Asp
 65 70 75 80
 Glu Glu Leu Thr Met Ala Met Ser Tyr Val Lys Asp Asp Ile Phe Arg
 85 90 95
 Ile Tyr Ile Lys Glu Lys Thr Gly Asn Ser Ala Asp Gly Gly Gly Gly
 100 105 110
 Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Thr Gln Gly Gly Ser
 115 120 125
 Pro Asp Val Pro Arg Thr Pro Val Gly Lys Phe Gln Phe Pro Gly Ser
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 Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu
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 Asn Pro Gly Pro Met Val Ser Val Ile Lys Pro Glu Met Lys Ile Lys
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 Leu Cys Met Arg Gly Thr Val Asn Gly His Asn Phe Val Ile Glu Gly
 180 185 190
 Glu Gly Lys Gly Asn Pro Tyr Glu Gly Thr Gln Ile Leu Asp Leu Asn
 195 200 205
 Val Thr Glu Gly Ala Pro Leu Pro Phe Ala Tyr Asp Ile Leu Thr Thr
 210 215 220
 Val Phe Gln Tyr Gly Asn Arg Ala Phe Thr Lys Tyr Pro Ala Asp Ile
 225 230 235 240
 Gln Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg
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 Ser Met Thr Tyr Glu Asp Gln Gly Ile Cys Thr Ala Thr Ser Asn Ile
 260 265 270
 Ser Met Arg Gly Asp Cys Phe Phe Tyr Asp Ile Arg Phe Asp Gly Val
 275 280 285
 Asn Phe Pro Pro Asn Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp
 290 295 300
 Glu Pro Ser Thr Glu Lys Met Tyr Val Arg Asp Gly Val Leu Lys Gly
 305 310 315 320
 Asp Val Asn Met Ala Leu Leu Leu Glu Gly Gly His Tyr Arg Cys
 325 330 335
 Asp Phe Lys Thr Thr Tyr Lys Ala Lys Lys Asp Val Arg Leu Pro Asp
 340 345 350
 Tyr His Phe Val Asp His Arg Ile Glu Ile Leu Lys His Asp Lys Asp
 355 360 365
 Tyr Asn Lys Val Lys Leu Tyr Glu Asn Ala Val Ala Arg Tyr Ser Met
 370 375 380
 Leu Pro Ser Gln Ala Lys Thr Gly Asn Ser Ala Asp Gly Gly Gly Gly
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 405 410 415
 Met Ala Asp Glu Glu Lys Leu Pro Pro Gly Trp Glu Lys Arg Met Ser
 420 425 430
 Arg Ser Ser Gly Arg Val Tyr Tyr Phe Asn His Ile Thr Asn Ala Ser
 435 440 445
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IBPF12-538W0-E (seq) fin

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tcc ctt cca ttt gtt ggg gaa aaa gtg act gag atg ctg gta aat gtc      96
Ser Leu Pro Phe Val Gly Glu Lys Val Thr Glu Met Leu Val Asn Val
20     25     30
ctc aac atc tgc tca gat gat gaa cta ggg tca gaa gaa gat gga ttt      144
Leu Asn Ile Cys Ser Asp Asp Glu Leu Gly Ser Glu Glu Asp Gly Phe
35     40     45
gat ggt gca aca gct gca gcc cgg aaa gag gtc gag gag gca agt tat      192
Asp Gly Ala Thr Ala Ala Arg Lys Glu Val Glu Glu Ala Ser Tyr
50     55     60
cct ttg gaa atg tgc tca cac ttt gat gcg gat gaa att aaa agg cta      240
Pro Leu Glu Met Cys Ser His Phe Asp Ala Asp Glu Ile Lys Arg Leu
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gga aag aga ttt aag aag ctt gat ttg gac aat tct ggt tct ttg agt      288
Gly Lys Arg Phe Lys Lys Leu Asp Leu Asn Ser Gly Ser Leu Ser
85     90     95
gtg gaa gag ttc atg tct ctg cct gag tta caa cag aat cct tta gta      336
Val Glu Glu Phe Met Ser Leu Pro Glu Leu Gln Gln Asn Pro Leu Val
100    105    110
cag cga gta ata gat ata ttc gac aca gat ggg aat gga gaa gta gac      384
Gln Arg Val Ile Asp Ile Phe Asp Thr Asp Gly Asn Gly Glu Val Asp
115    120    125
ttt aaa gaa ttc att gag ggc gtc tct cag ttc agt gtc aaa gga gat      432
Phe Lys Glu Phe Ile Glu Gly Val Ser Gln Phe Ser Val Lys Gly Asp
130    135    140
aag gag cag aaa ttg agg ttt gct ttc cgt atc tat gac atg gat aaa      480
Lys Glu Gln Lys Leu Phe Ala Phe Arg Ile Tyr Asp Met Asp Lys
145    150    155    160
gat ggc tat att tcc aat ggg gaa ctc ttc cag gta ttg aag atg atg      528
Asp Gly Tyr Ile Ser Asn Gly Glu Leu Phe Gln Val Leu Lys Met Met
165    170    175
gtg ggg aac aat ctg aaa gat aca cag tta cag caa att gta gac aaa      576
Val Gly Asn Asn Leu Lys Asp Thr Gln Leu Gln Gln Ile Val Asp Lys
180    185    190
acc ata ata aat gca gat aag gat gga gat gga aga ata tcc ttt gaa      624
Thr Ile Ile Asn Ala Asp Lys Asp Gly Asp Gly Arg Ile Ser Phe Glu
195    200    205
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Leu Asn Ile Cys Ser Asp Asp Glu Leu Gly Ser Glu Glu Asp Gly Phe
35     40     45
Asp Gly Ala Thr Ala Ala Ala Arg Lys Glu Val Glu Glu Ala Ser Tyr
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IBPF12-538W0-E (seq) fin

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Gly Lys Arg Phe Lys Lys Leu Asp Leu Asp Asn Ser Gly Ser Leu Ser
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Val Glu Glu Phe Met Ser Leu Pro Glu Leu Gln Gln Asn Pro Leu Val
100 105 110
Gln Arg Val Ile Asp Ile Phe Asp Thr Asp Gly Asn Gly Glu Val Asp
115 120 125
Phe Lys Glu Phe Ile Glu Gly Val Ser Gln Phe Ser Val Lys Gly Asp
130 135 140
Lys Glu Gln Lys Leu Arg Phe Ala Phe Arg Ile Tyr Asp Met Asp Lys
145 150 155 160
Asp Gly Tyr Ile Ser Asn Gly Glu Leu Phe Gln Val Leu Lys Met Met
165 170 175
Val Gly Asn Asn Leu Lys Asp Thr Gln Leu Gln Gln Ile Val Asp Lys
180 185 190
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Arg Met Glu Gly Cys Val Asp Gly His Lys Phe Val Ile Thr Gly Asp	
20 25 30	
ggc atc ggc gac ccc ttc gag ggc aag cag acc agc atc gac ctg tgc	144
Gly Ile Gly Asp Pro Phe Glu Gly Lys Gln Thr Ser Ile Asp Leu Cys	
35 40 45	
gtg gtg gag ggc ggc ccc ctg ccc ttc agc gag gac atc ctg agc acc	192
Val Val Glu Gly Gly Pro Leu Pro Phe Ser Glu Asp Ile Leu Ser Thr	
50 55 60	
gtg ttc gac tac ggc aac agg gtg ttc acc aag tac ccc cag gac ctg	240
Val Phe Asp Tyr Gly Asn Arg Val Phe Thr Lys Tyr Pro Gln Asp Leu	
65 70 75 80	
gtg gac tac ttc aag aac agc tgc ccc gcc ggc tac acc tgg cag agg	288
Val Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Gln Arg	
85 90 95	
agc ttc ctg ttc gag gac ggc gcc gtg tgc acc gcc agc gcc gac atc	336
Ser Phe Leu Phe Glu Asp Gly Ala Val Cys Thr Ala Ser Ala Asp Ile	
100 105 110	
agg gtg agc gtg gag gag aac tgc ttc tac cac gag agc aag ttc cac	384
Arg Val Ser Val Glu Glu Asn Cys Phe Tyr His Glu Ser Lys Phe His	
115 120 125	
ggc gtg aac ttc ccc gcc gac ggc cca gtg atg aag aag atg acc acc	432
Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Thr	
130 135 140	
aac tgg gag ccc agc tgc gag aag atc acc ccc atc ctg aac gag ggc	480
Asn Trp Glu Pro Ser Cys Glu Lys Ile Thr Pro Ile Leu Asn Glu Gly	
145 150 155 160	
atc ctg aag ggc gac gtg acc atg ttc ctg ctg ctg aag gac ggc ggc	528
Ile Leu Lys Gly Asp Val Thr Met Phe Leu Leu Leu Lys Asp Gly Gly	
165 170 175	
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IBPF12-538W0-E (seq) fin

Arg	Tyr	Arg	Cys	Gln	Phe	Asp	Thr	Val	Tyr	Lys	Ala	Lys	Ala	Asp	Ala		
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Lys	Asp	Met	Pro	Glu	Met	His	Phe	Ile	Gln	His	Glu	Leu	Thr	Arg	Glu		
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gac	agg	agc	gac	gcc	aag	cac	cag	aag	tgg	agg	ctg	gtg	gag	agc	gcc		672
Asp	Arg	Ser	Asp	Ala	Lys	His	Gln	Lys	Trp	Arg	Leu	Val	Glu	Ser	Ala		
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Gly	Ile	Gly	Asp	Pro	Phe	Glu	Gly	Lys	Gln	Thr	Ser	Ile	Asp	Leu	Cys		
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Val	Val	Glu	Gly	Gly	Pro	Leu	Pro	Phe	Ser	Glu	Asp	Ile	Leu	Ser	Thr		
	50					55					60						
Val	Phe	Asp	Tyr	Gly	Asn	Arg	Val	Phe	Thr	Lys	Tyr	Pro	Gln	Asp	Leu		
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Val	Asp	Tyr	Phe	Lys	Asn	Ser	Cys	Pro	Ala	Gly	Tyr	Thr	Trp	Gln	Arg		
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Ser	Phe	Leu	Phe	Glu	Asp	Gly	Ala	Val	Cys	Thr	Ala	Ser	Ala	Asp	Ile		
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Arg	Val	Ser	Val	Glu	Glu	Asn	Cys	Phe	Tyr	His	Glu	Ser	Lys	Phe	His		
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Gly	Val	Asn	Phe	Pro	Ala	Asp	Gly	Pro	Val	Met	Lys	Lys	Met	Thr	Thr		
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Asn	Trp	Glu	Pro	Ser	Cys	Glu	Lys	Ile	Thr	Pro	Ile	Leu	Asn	Glu	Gly		
145					150					155				160			
Ile	Leu	Lys	Gly	Asp	Val	Thr	Met	Phe	Leu	Leu	Leu	Lys	Asp	Gly	Gly		
			165					170						175			
Arg	Tyr	Arg	Cys	Gln	Phe	Asp	Thr	Val	Tyr	Lys	Ala	Lys	Ala	Asp	Ala		
		180						185					190				
Lys	Asp	Met	Pro	Glu	Met	His	Phe	Ile	Gln	His	Glu	Leu	Thr	Arg	Glu		
	195					200						205					
Asp	Arg	Ser	Asp	Ala	Lys	His	Gln	Lys	Trp	Arg	Leu	Val	Glu	Ser	Ala		
	210					215					220						
Ile	Ala	Tyr	Arg	Ser	Thr	Pro	Pro										
225					230												