

LISTADO DE SECUENCIAS

<110> DAIICHI SANKYO COMPANY, LIMITED

<120> ANTICUERPO ANTI-CD3 Y MOLÉCULAS QUE COMPRENDEN EL ANTICUERPO

<130> FP1729

<150> JP2016-249148

<151> 2016-12-22

<160> 103

<170> PatentIn version 3.5

<210> SEQ ID NO: 1

<211> 207

<212> PRT

<213> *Homo sapiens*

<400> 1

Met	Gln	Ser	Gly	Thr	His	Trp	Arg	Val	Leu	Gly	Leu	Cys	Leu	Leu	Ser
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Val	Gly	Val	Trp	Gly	Gln	Asp	Gly	Asn	Glu	Glu	Met	Gly	Gly	Ile	Thr
			20					25					30		

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

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

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

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

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

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

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

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

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

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

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

<210> SEQ ID NO: 2

<211> 171

<212> PRT

<213> *Homo sapiens*

<400> 2

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

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

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

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

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

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

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

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

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

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

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

<210> SEQ ID NO: 3

<211> 182

<212> PRT

<213> *Homo sapiens*

<400> 3

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

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

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

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

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

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

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

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

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

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

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

Asn Gln Leu Arg Arg Asn
180

<210> SEQ ID NO: 4

<211> 657

<212> ADN

<213> Secuencia artificial

<220>

<223> ADN de CD3 epsilon gamma

<400> 4

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gtgaaagtgt atgactatca agaagatggg agcgttctgc tgacctgtga tgcagaagca 120

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aaaaacatta cctggttcaa agacggcaaa atgattgggtt ttctgaccga agataaaaaa 180
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cagaataaaa gcaaaccgct gcaggtttat tatcgtatgg gtagcgcaga tgatgcaaaa 300
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ctgaaagaat tcagcgaact ggaacagagc ggttattatg ttgttatcc tcgtggtagc 600
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<210> SEQ ID NO: 5

<211> 219

<212> PRT

<213> Secuencia artificial

<220>

<223> His-scCD3 AA

<400> 5

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Met Arg Gly Ser His His His His His His Gly Ser Gln Ser Ile Lys
1           5           10           15

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

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Leu Leu Thr Cys Asp Ala Glu Ala Lys Asn Ile Thr Trp Phe Lys Asp
          35           40           45

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

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Gly Ser Asn Ala Lys Asp Pro Arg Gly Met Tyr Gln Cys Lys Gly Ser
65           70           75           80

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```

Gln Asn Lys Ser Lys Pro Leu Gln Val Tyr Tyr Arg Met Gly Ser Ala
          85           90           95

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Asp Asp Ala Lys Lys Asp Ala Ala Lys Lys Asp Asp Ala Lys Lys Asp
100           105           110

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Asp Ala Lys Lys Asp Gly Ser Asp Gly Asn Glu Glu Met Gly Gly Ile
115           120           125

```

Thr Gln Thr Pro Tyr Lys Val Ser Ile Ser Gly Thr Thr Val Ile Leu
130 135 140

Thr Cys Pro Gln Tyr Pro Gly Ser Glu Ile Leu Trp Gln His Asn Asp
145 150 155 160

Lys Asn Ile Gly Gly Asp Glu Asp Asp Lys Asn Ile Gly Ser Asp Glu
165 170 175

Asp His Leu Ser Leu Lys Glu Phe Ser Glu Leu Glu Gln Ser Gly Tyr
180 185 190

Tyr Val Cys Tyr Pro Arg Gly Ser Lys Pro Glu Asp Ala Asn Phe Tyr
195 200 205

Leu Tyr Leu Arg Ala Arg Val Gly Lys Leu Asn
210 215

<210> SEQ ID NO: 6

<211> 354

<212> ADN

<213> *Rutilus rutilus*

<400> 6

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tcctgtgtag tctctggagt cacattcaat tactacggga tgagctggat ccgccaggct 120

ccaggaagg ggctggagtg ggttgcattc attactaatt ctggtggtag aatttactat 180

ccagactctg tgaagggccg attcactatc tccagagaaa atacacaaaa gaccctatac 240

ctacaaatga acagtctgag gtctgaggac acggccactt attactgtac tctcgatggt 300

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<210> SEQ ID NO: 7

<211> 118

<212> PRT

<213> *Rutilus rutilus*

<400> 7

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

Ala Leu Lys Leu Ser Cys Val Val Ser Gly Val Thr Phe Asn Tyr Tyr
20 25 30

Gly Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Ser Ile Thr Asn Ser Gly Gly Arg Ile Tyr Tyr Pro Asp Ser Val
 50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Thr Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
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<210> SEQ ID NO: 8

<211> 327

<212> ADN

<213> *Rutilus rutilus*

<400> 8

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gaggggaagat ctcccaccac tattatttat agggatgata agagaccaga tggagtttct 180

gacaggttct ctgggtccat tgacagatct tccaagtcag ccctcctgac aatcaataat 240

gtgcagactg aagatgaagc tgactacttc tgtcagtctt acagtagtgg ttttattttc 300

ggcgggtggaa ccaagctcac tgtccta 327

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<211> 109

<212> PRT

<213> Secuencia artificial

<220>

<223> C3-147_VL AA

<400> 9

Gln Phe Val Leu Thr Gln Pro Asn Ser Val Ser Thr Asn Leu Gly Thr
 1 5 10 15

Thr Val Glu Leu Ser Cys Lys Arg Asn Thr Gly Asn Ile Gly Ser Asn
 20 25 30

Tyr Val Asn Trp Tyr Gln Gln His Glu Gly Arg Ser Pro Thr Thr Ile
 35 40 45

Ile Tyr Arg Asp Asp Lys Arg Pro Asp Gly Val Ser Asp Arg Phe Ser
50 55 60

Gly Ser Ile Asp Arg Ser Ser Lys Ser Ala Leu Leu Thr Ile Asn Asn
65 70 75 80

Val Gln Thr Glu Asp Glu Ala Asp Tyr Phe Cys Gln Ser Tyr Ser Ser
85 90 95

Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> SEQ ID NO: 10

<211> 75

<212> ADN

<213> Secuencia artificial

<220>

<223> Ligador sentido G4S

<400> 10

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cagtttgtgc ttact 75

<210> SEQ ID NO: 11

<211> 75

<212> ADN

<213> Secuencia artificial

<220>

<223> Ligador antientido G4S

<400> 11

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tgaagagaca gtgac 75

<210> SEQ ID NO: 12

<211> 118

<212> PRT

<213> *Rutilus rutilus*

<400> 12

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

Ala Leu Lys Leu Ser Cys Val Val Ser Gly Val Thr Phe Asn Tyr Tyr
20 25 30

Gly Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Ser Ile Thr Asn Ser Gly Gly Arg Ile Tyr Tyr Pro Asp Ser Val
 50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95

Thr Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> SEQ ID NO: 13

<211> 109

<212> PRT

<213> *Rutilus rutilus*

<400> 13

Gln Phe Val Leu Thr Gln Pro Asn Ser Val Ser Thr Asn Leu Gly Thr
 1 5 10 15

Thr Val Glu Leu Ser Cys Lys Arg Asn Thr Gly Asn Ile Gly Ser Asn
 20 25 30

Tyr Val Asn Trp Tyr Gln Gln His Glu Gly Arg Ser Pro Thr Thr Ile
 35 40 45

Ile Tyr Arg Asp Asp Lys Arg Pro Asp Gly Val Ser Asp Arg Phe Ser
 50 55 60

Gly Ser Ile Asp Arg Ser Ser Lys Ser Ala Leu Leu Thr Ile Asn Asn
 65 70 75 80

Val Gln Thr Glu Asp Glu Ala Asp Tyr Phe Cys Gln Ser Tyr Ser Ser
 85 90 95

Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
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<210> SEQ ID NO: 14

<211> 867

<212> ADN

<213> Secuencia artificial

<220>

<223> C3E-7000 ORF

<400> 14

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tgtgtagtct ctggagtcac attcaattac tacgggatga gctggatccg ccaggctcca      180
gggaaggggc tggagtgggt tgcattccatt actaattctg gtggtagaat ttactatcca      240
gactctgtga agggccgatt cactatctcc agagaaaata cacaaaagac cctataccta      300
caaatgaaca gtctgaggtc tgaggacacg gccacttatt actgtactct cgatggctgc      360
gatggttggg ttgcttactg gggccaaggc actctggtca ctgtctcttc aggtggaggc      420
ggttcaggcg gaggtggcag cggcgggtggc gggagtcagt ttgtgcttac tcagccaaac      480
tctgtgtcta cgaatctcgg aaccacagtc gaactgtctt gcaagcgcaa cactgggaac      540
attggaagca attatgtgaa ctggtaccag cagcatgagg gaagatctcc caccactatt      600
atztataggg atgataagag accagatgga gtttctgaca ggttctctgg gtccattgac      660
agatcttcca agtcagccct cctgacaatc aataatgtgc agactgaaga tgaagctgac      720
tacttctgtc agtcttacag tagtggtttt attttcggcg gtggaaccaa gctcactgtc      780
ctaggcgcggt ctgcggccgc aggatccggt ggtgattaca aagatgatga cgataaaggt      840
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<210> SEQ ID NO: 15

<211> 270

<212> PRT

<213> Secuencia artificial

<220>

<223> C3E-7000 AA

<400> 15

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

Ala Leu Lys Leu Ser Cys Val Val Ser Gly Val Thr Phe Asn Tyr Tyr
          20           25           30

Gly Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35           40           45

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Ala Ser Ile Thr Asn Ser Gly Gly Arg Ile Tyr Tyr Pro Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ser Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Thr Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gln Phe Val Leu Thr Gln Pro Asn Ser Val Ser
130 135 140

Thr	Asn	Leu	Gly	Thr	Thr	Val	Glu	Leu	Ser	Cys	Lys	Arg	Asn	Thr	Gly
145					150					155					160

Asn Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln His Glu Gly Arg
165 170 175

Ser Pro Thr Thr Ile Ile Tyr Arg Asp Asp Lys Arg Pro Asp Gly Val
180 185 190

Ser Asp Arg Phe Ser Gly Ser Ile Asp Arg Ser Ser Lys Ser Ala Leu
195 200 205

Leu Thr Ile Asn Asn Val Gln Thr Glu Asp Glu Ala Asp Tyr Phe Cys
210 215 220

Gln Ser Tyr Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr
225 230 235 240

Val Leu Gly Ala Ser Ala Ala Ala Gly Ser Gly Gly Asp Tyr Lys Asp
245 250 255

Asp Asp Asp Lys Gly Ala Ala Ala His His His His His His
260 265 270

<210> SEO ID NO: 16

<211> 118

<212> PRT

<213> Secuencia artificial

 $\langle 220 \rangle$

<223> C3E-7034 VH AA

<400> 16

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

<210> SEQ ID NO: 17
 <211> 109
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> C3E-7034_VL AA

<400> 17

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

Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 100 105

<210> SEQ ID NO: 18
 <211> 864
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> C3E-7034 ORF

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 gaagtgcagc tgggtggaatc cggggggggc ctggtgcagc ctgggggggag cctgagactg 120
 agttgtgccg cctctgggggt gacatttaac tactatggca tgtcttgat cgcgcaggca 180
 cctggaaagg gcctggagtg ggtggccagc atcactaatt ccggcgggag aatctactat 240
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 ctgcagatga atagcctgag agccgaagat acagctgtgt actattgcac tctggacggc 360
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 aatattggca gtaactacgt gaattggtat cagcagcatg aagggtctag tccaaccaca 600
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 gattactttt gccagtccta ttctctggc ttcatctttg gaggcgggac taaactgacc 780
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<210> SEQ ID NO: 19
 <211> 269
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> C3E-7034 AA

<400> 19

Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
 1 5 10 15
 Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr
 20 25 30
 Tyr Gly Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
 35 40 45
 Val Ala Ser Ile Thr Asn Ser Gly Gly Arg Ile Tyr Tyr Pro Asp Ser
 50 55 60
 Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu
 65 70 75 80
 Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
 85 90 95
 Cys Thr Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly
 115 120 125
 Ser Gly Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro His Ser Val
 130 135 140
 Ser Glu Ser Pro Gly Lys Thr Val Thr Ile Ser Cys Lys Arg Asn Thr
 145 150 155 160
 Gly Asn Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln His Glu Gly
 165 170 175
 Ser Ser Pro Thr Thr Ile Ile Tyr Arg Asp Asp Lys Arg Pro Asp Gly
 180 185 190
 Val Ser Asp Arg Phe Ser Gly Ser Ile Asp Arg Ser Ser Lys Ser Ala
 195 200 205
 Ser Leu Thr Ile Ser Asn Leu Lys Thr Glu Asp Glu Ala Asp Tyr Phe
 210 215 220
 Cys Gln Ser Tyr Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu
 225 230 235 240
 Thr Val Leu Gly Ala Ala Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp
 245 250 255
 Asp Asp Lys Gly Ala Ala Ala His His His His His His
 260 265

<210> SEQ ID NO: 20

<211> 107
 <212> PRT
 <213> Secuencia artificial

<220>

<223> C3E-7035_VL AA

<400> 20

Gln Ala Val Leu Thr Gln Pro Ser Ser Val Ser Gly Val Pro Gly Gln
 1 5 10 15

Arg Val Thr Ile Ser Cys Lys Arg Asn Thr Gly Asn Ile Gly Ser Asn
 20 25 30

Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
 35 40 45

Ile Tyr Arg Asp Asp Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Phe Gln
 65 70 75 80

Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Ser Ser Gly Phe
 85 90 95

Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 100 105

<210> SEQ ID NO: 21
 <211> 864
 <212> ADN
 <213> Secuencia artificial

<220>

<223> C3E-7035 ORF

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 cctggaaagg gcctggagtg ggtggccagc atcactaatt ccggcggggc aatctactat 240
 cccgacagcg tcaagggcag gttcacaatt tcccgcgaga acacacagaa aactctgtac 300
 ctgcagatga atagcctgag agccgaagat acagctgtgt actattgcac tctggacggc 360
 agggatgggt gggtcgccta ttggggggcag ggaaccctgg tgacagtcag ctccggagga 420

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ggaggatctg gcggaggagg cagtggggga ggcgggtcaa tggcccaggc tgtgctcact      480
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accgggaata tcgggtctaa ctacgtgaac tggatcagc agcttccagg gacagctccc      600
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gactactatt gccagtcata ttccagcggc ttcattctcg gaggcggaac taagctgaca      780
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gcggcgcata accatcatca ccac                                             864

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<210> SEQ ID NO: 22

<211> 269

<212> PRT

<213> Secuencia artificial

<220>

<223> C3E-7035 AA

<400> 22

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Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1              5              10              15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr
              20              25              30

Tyr Gly Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
              35              40              45

Val Ala Ser Ile Thr Asn Ser Gly Gly Arg Ile Tyr Tyr Pro Asp Ser
              50              55              60

Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu
65              70              75              80

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

Cys Thr Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly
              100             105             110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
              115             120             125

Ser Gly Gly Gly Gly Ser Met Ala Gln Ala Val Leu Thr Gln Pro Ser
130             135             140

```

Ser Val Ser Gly Val Pro Gly Gln Arg Val Thr Ile Ser Cys Lys Arg
145 150 155 160

Asn Thr Gly Asn Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln Leu
165 170 175

Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Arg Asp Asp Lys Arg Pro
180 185 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala
195 200 205

Ser Leu Ala Ile Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr Tyr
210 215 220

Cys Gln Ser Tyr Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Thr Val Leu Gly Ala Ala Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp
245 250 255

Asp Asp Lys Gly Ala Ala Ala His His His His His
260 265

<210> SEQ ID NO: 23

<211> 107

<212> PRT

<213> Secuencia artificial

<220>

<223> C3E-7036_VL AA

<400> 23

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

Arg Val Thr Ile Ser Cys Thr Gly Asn Thr Gly Asn Ile Gly Ser Asn
20 25 30

Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Arg Asp Asp Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Phe Gln
65 70 75 80

Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Ser Ser Gly Phe
85 90 95

Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 100 105

<210> SEQ ID NO: 24
 <211> 858
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> C3E-7036 ORF

<400> 24
 atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcggg 60
 gaagtgcagc tgggtggaatc cggggggggc ctggtgcagc ctgggggggag cctgagactg 120
 agttgtgccg cctctgggggt gacatttaac tactatggca tgtcttgat cgcaggca 180
 cctggaaagg gcctggagtg ggtggccagc atcactaatt ccggcgggag aatctactat 240
 cccgacagcg tcaagggcag gttcacaatt tcccgcgaga acacacagaa aactctgtac 300
 ctgcagatga atagcctgag agccgaagat acagctgtgt actattgcac tctggacggc 360
 agggatgggt gggtcgccta ttggggggcag ggaaccctgg tgacagtcag ctccggagga 420
 ggaggatctg gcggaggagg cagtggggga ggcggtcaa actttatgct cactcagccg 480
 tcctctgttt ctggcggtacc tggccaacgg gtgaccatta gctgtacggg taataccggg 540
 aatatcgggt ctaactacgt gaactgggtat cagcagcttc caggacagc tccaagttg 600
 ctgatctatc gcgacgacaa aagaccctca ggggtccctg accgatttag tggcagcaaa 660
 agcgggtactt ccgcttccct ggcgataacc ggctttcagg ccgaagatga ggcagactac 720
 tattgccagt catattccag cggcttcac ttccggaggcg gaactaagct gacagtgttg 780
 ggtgcggccg caggtgcagg tgggtgattac aaagatgatg acgataaagg tgcagcggcg 840
 catcaccatc atcaccac 858

<210> SEQ ID NO: 25
 <211> 267
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> C3E-7036 AA

<400> 25

Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
 1 5 10 15
 Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr
 20 25 30
 Tyr Gly Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
 35 40 45
 Val Ala Ser Ile Thr Asn Ser Gly Gly Arg Ile Tyr Tyr Pro Asp Ser
 50 55 60
 Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu
 65 70 75 80
 Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
 85 90 95
 Cys Thr Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly
 115 120 125
 Ser Gly Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Ser Ser Val
 130 135 140
 Ser Gly Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Asn Thr
 145 150 155 160
 Gly Asn Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly
 165 170 175
 Thr Ala Pro Lys Leu Leu Ile Tyr Arg Asp Asp Lys Arg Pro Ser Gly
 180 185 190
 Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu
 195 200 205
 Ala Ile Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln
 210 215 220
 Ser Tyr Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val
 225 230 235 240
 Leu Gly Ala Ala Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp Asp Asp
 245 250 255
 Lys Gly Ala Ala Ala His His His His His His
 260 265

<210> SEQ ID NO: 26

<211> 8
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 7000_CDR-H1

<400> 26

Gly Val Thr Phe Asn Tyr Tyr Gly
 1 5

<210> SEQ ID NO: 27
 <211> 8
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 7000_CDR-H2

<400> 27

Ile Thr Asn Ser Gly Gly Arg Ile
 1 5

<210> SEQ ID NO: 28
 <211> 11
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 7000_CDR-H3

<400> 28

Thr Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr
 1 5 10

<210> SEQ ID NO: 29
 <211> 8
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 7000_CDR-L1

<400> 29

Thr Gly Asn Ile Gly Ser Asn Tyr
 1 5

<210> SEQ ID NO: 30

<211> 3
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 7000_CDR-L2

<400> 30

Arg Asp Asp
 1

<210> SEQ ID NO: 31
 <211> 8
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> 7000_CDR-L3

<400> 31

Gln Ser Tyr Ser Ser Gly Phe Ile
 1 5

<210> SEQ ID NO: 32
 <211> 864
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> C3E-3000 ORF

<400> 32
 atgaagcacc tgtggttctt tctgctgctg gtggccgctc ccagatgggt gctgtctcag 60
 gtgcagctgc agcagtctgg cgccgaactg gctagacctg ggcctccgt gaagatgagc 120
 tgcaaggcca gcggctacac cttcaccggt tacacatgc actgggtcaa gcagaggcct 180
 ggacagggcc tggaatggat cggctacatc aaccccagcc ggggctacac caactacaac 240
 cagaagttca aggacaaggc caccctgacc accgacaaga gcagcagcac cgcctacatg 300
 cagctgtcca gcctgaccag cgaggacagc gccgtgtact actgcgcccg gtactacgac 360
 gaccactact gcctggacta ctggggccag ggcaccacac tgaccgtgtc tagtggtgga 420
 ggcgggttcag gcggaggtgg cagcggcggt ggcgggagtc agatcgtgct gacacagagc 480
 cccgccatca tgtctgccag ccctggcgag aaagtgacca tgacctgtag cgccagcagc 540

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agcgtgtcct acatgaactg gtatcagcag aagtccggca ccagcccca gcggtggatc      600
tacgacacaa gcaagctggc ctctggcgtg cccgccact ttagaggctc tggcagcggc      660
acaagctaca gcctgaccat cagcggcatg gaagccgagg atgccgccac ctactactgc      720
cagcagtggg ccagcaaccc cttcaccttt ggctccggca caaagctgga aatcaagcgg      780
ggcgcgtctg cggccgcagg tagcgggtgg gattacaaag atgatgacga taaaggtgca      840
gcggcgcata accatcatca ccac                                             864

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<210> SEQ ID NO: 33

<211> 269

<212> PRT

<213> Secuencia artificial

<220>

<223> C3E-3000 AA

<400> 33

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
          20           25           30

Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
          35           40           45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
          50           55           60

Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr
65           70           75           80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
          85           90           95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
          100          105          110

Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
          115          120          125

Ser Gly Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser Pro Ala Ile
          130          135          140

Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser
145          150          155          160

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Ser Ser Val Ser Tyr Met Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser
165 170 175

Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro
180 185 190

Ala His Phe Arg Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
195 200 205

Ser Gly Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
210 215 220

Ser Ser Asn Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
225 230 235 240

Arg Gly Ala Ser Ala Ala Ala Gly Ser Gly Gly Asp Tyr Lys Asp Asp
245 250 255

Asp Asp Lys Gly Ala Ala Ala His His His His His His
260 265

<210> SEQ ID NO: 34

<211> 864

<212> ADN

<213> Secuencia artificial

<220>

<223> C3E-3007 ORF

<400> 34

atgaagcacc tgtggttctt tctgctgctg gtggccgctc ccagatgggt gctgtctcag	60
gtgcagctgg tgcagtctgg cgccgagagc aaaaagcctg ggcctccgt gaaggtgtcc	120
tgcaaggcca gcggctacac ctttaccggt tacaccatgc actgggtgcg ccaggcacct	180
ggacagggcc tggaatggat gggctacatc aacccagcc ggggctacac caactacaac	240
cagaaattca aggaccgct gaccatcacc gccgacaaga gcaccagcac cgcctacatg	300
gaactgagca gcctgcggag cgaggacacc gccgtgtact actgtgcccgt gtactacgac	360
gaccactact gcctggacta ctggggccag ggcacactcg tgaccgtgtc tagtggtgga	420
ggcggttcag gcggaggtgg cagcggcggt ggcgggagtc agatccagat gaccagagc	480
cctagcagcc tggccgtgtc tctgggagag agagccacca tcacctgtag cgccagcagc	540
agcgtgtcct acatgaactg gtatcagcag aagcccggca agcccccaa gcggtggatc	600
tacgatacca gcaagctggc ctccggcggtg cccgatagat tttctggcag cggctccggc	660

accgacttca ccctgacaat cagctccctg caggccgagg acgtggccac ctactactgt 720
 cagcagtggg ccagcaaccc cttcaccttc ggccagggca ccaaggtgga aatcaagcgg 780
 ggcgcgtctg cggccgcagg tagcgggtggg gattacaaag atgatgacga taaaggtgca 840
 gcggcgcata accatcatca ccac 864

<210> SEQ ID NO: 35
 <211> 269
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> C3E-3007 AA

<400> 35

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

Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro
 180 185 190

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
 195 200 205

Ser Ser Leu Gln Ala Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Trp
 210 215 220

Ser Ser Asn Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 225 230 235 240

Arg Gly Ala Ser Ala Ala Ala Gly Ser Gly Gly Asp Tyr Lys Asp Asp
 245 250 255

Asp Asp Lys Gly Ala Ala Ala His His His His His His
 260 265

<210> SEQ ID NO: 36

<211> 119

<212> PRT

<213> Secuencia artificial

<220>

<223> C3E-3000_VH AA

<400> 36

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
 50 55 60

Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Leu Thr Val Ser Ser
 115

<210> SEQ ID NO: 37
 <211> 106
 <212> PRT
 <213> Secuencia artificial

<220>

<223> C3E-3000_VL AA

<400> 37

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

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30

Asn Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala His Phe Arg Gly Ser
 50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Gly Met Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr
 85 90 95

Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> SEQ ID NO: 38
 <211> 119
 <212> PRT
 <213> Secuencia artificial

<220>

<223> C3E-3007_VH AA

<400> 38

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Ser Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
 50 55 60

Lys Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO: 39

<211> 106

<212> PRT

<213> Secuencia artificial

<220>

<223> C3E-3007_VL AA

<400> 39

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

Glu Arg Ala Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Trp Ile Tyr
35 40 45

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

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu
65 70 75 80

Asp Val Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Phe Thr
85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO: 40

<211> 822

<212> ADN

<213> Secuencia artificial

<220>

<223> HT1-11 scFv ORF

<400> 40

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atgaagcacc tgtggttctt tctgctgctg gtggccgctc ccagatgggt gctgtctcag      60
gtgcagctgg tgcagtctgg cgccgaagtg aagaaaccag ggcgcagcgt gaaggtgtcc      120
tgcaaggcca gcggctacac ctttaccacc gccggcatgc agtgggtgcg ccaggctcct      180
ggacagggcc tggaatggat gggctggatc aacaccacac gcggcggtgcc caaatacgcc      240
gaggacttca agggcagagt gaccatcagc gccgacacca gcacctccac agcctacctg      300
cagctgagca gcctgaagtc cgaggacacc gccgtgtact actgcgccag aagcggcttc      360
ggcagcagct actggtactt cgacgtgtgg ggccagggca ccctcgtgac agtgtctagc      420
ggaggcggag gatctggcgg cggaggaagt ggcggagggg gatccgatat ccagatgacc      480
cagagcccca gcagcctgtc tgccagcgtg ggcgacagag tgacaattac atgcaaggcc      540
tcccaggacg tgtccacagc cgtggcctgg tatcagcaga agcctggcaa ggcccccaag      600
ctgctgatct acagcgccag ctaccggtac accggcgtgc caagcagatt ttccggcagc      660
ggctccggca ccgacttcac cctgacaatc agctccctgc agcccgagga tttcgccgtg      720
tattattgcc agcagcacta catcaccccc ctgaccttcg gccagggggac caagctggaa      780
atcaagagaa caggcgccgc tgcccaccac caccatcacc at                          822

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<210> SEQ ID NO: 41
<211> 255
<212> PRT
<213> Secuencia artificial

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<220>
<223> HT1-11 scFv AA

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<400> 41

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1              5              10              15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Ala
              20              25              30

Gly Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
              35              40              45

Gly Trp Ile Asn Thr His Ser Gly Val Pro Lys Tyr Ala Glu Asp Phe
              50              55              60

Lys Gly Arg Val Thr Ile Ser Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65              70              75              80

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Leu Gln Leu Ser Ser Leu Lys Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Ser Gly Phe Gly Ser Ser Tyr Trp Tyr Phe Asp Val Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
 115 120 125
 Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
 130 135 140
 Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys
 145 150 155 160
 Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro
 165 170 175
 Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Thr
 180 185 190
 Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 195 200 205
 Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Val Tyr Tyr Cys
 210 215 220
 Gln Gln His Tyr Ile Thr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu
 225 230 235 240
 Glu Ile Lys Arg Thr Gly Ala Ala Ala His His His His His His
 245 250 255

<210> SEQ ID NO: 42

<211> 1614

<212> ADN

<213> Secuencia artificial

<220>

<223> T2C-0001 ORF

<400> 42

atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgga 60

caggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac caggcgccag cgtgaagggtg 120

tcctgcaagg ccagcggcta cacctttacc accgccggca tgcagtgggt gcgccaggct 180

cctggacagg gcctggaatg gatgggctgg atcaacaccc acagcggcgt gcccaaatac 240

gccgaggact tcaagggcag agtgaccatc agcgccgaca ccagcacctc cacagcctac 300

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ctgcagctga gcagcctgaa gtccgaggac accgccgtgt actactgcgc cagaagcggc      360
ttcggcagca gctactggta cttcgacgtg tggggccagg gcaccctcgt gacagtgtct      420
agcggaggcg gaggatctgg cggcggagga agtggcggag ggggatccga tatccagatg      480
accagagacc ccagcagcct gtctgccagc gtgggcgaca gagtgacaat tacatgcaag      540
gcctcccagg acgtgtccac agccgtggcc tggatatcagc agaagcctgg caaggccccc      600
aagctgctga tctacagcgc cagctaccgg tacaccggcg tgccaagcag attttccggc      660
agcggctccg gcaccgactt caccctgaca atcagctccc tgacagcccga ggatttcgcc      720
gtgtattatt gccagcagca ctacatcacc cccctgacct tcggccaggg gaccaagctg      780
gaaatcaaga gaacaggggg aggcgggttca gaagtgcagc tggtggaatc cggggggggc      840
ctggtgcagc ctggggggag cctgagactg agttgtgccg cctctggggg gacatttaac      900
tactatggca tgtcttggat ccgccaggca cctggaaagg gcctggagtg ggtggccagc      960
atcactaatt ccggcggggc aatctactat cccgacagcg tcaagggcag gttcacaatt     1020
tcccgcgaga acacacagaa aactctgtac ctgcagatga atagcctgag agccgaagat     1080
acagctgtgt actattgcac tctggacggc agggatgggt gggtcgccta ttgggggcag     1140
ggaaccctgg tgacagtcag ctccggagga ggaggatctg gcggaggagg cagtggggga     1200
ggcgggtcaa actttatgct gaccagccc cacagtgtgt cagagagccc tggcaagact     1260
gtcaccatct cttgtaaaag gaacaccgga aatattggca gtaactacgt gaattggtat     1320
cagcagcatg aagggtctag tccaaccaca atcatctacc gggacgataa gagacccgac     1380
ggggtgtccg atcgattctc cggatctatc gaccggtcaa gcaagagtgc ttcactgacc     1440
attagcaatc tgaaaacaga ggacgaagca gattactttt gccagtccta ttcctctggc     1500
ttcatctttg gaggcgggac taaactgacc gtgctgggcg cggccgcagg tgcaggtggt     1560
gattacaaag atgatgacga taaaggtgca gcggcgcac accatcatca ccac           1614

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<210> SEQ ID NO: 43

<211> 519

<212> PRT

<213> Secuencia artificial

<220>

<223> T2C-0001 AA

<400> 43

Gly	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	1	5	10	15
Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Thr	20	25	30	
Ala	Gly	Met	Gln	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	35	40	45	
Met	Gly	Trp	Ile	Asn	Thr	His	Ser	Gly	Val	Pro	Lys	Tyr	Ala	Glu	Asp	50	55	60	
Phe	Lys	Gly	Arg	Val	Thr	Ile	Ser	Ala	Asp	Thr	Ser	Thr	Ser	Thr	Ala	65	70	75	80
Tyr	Leu	Gln	Leu	Ser	Ser	Leu	Lys	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	85	90	95	
Cys	Ala	Arg	Ser	Gly	Phe	Gly	Ser	Ser	Tyr	Trp	Tyr	Phe	Asp	Val	Trp	100	105	110	
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	115	120	125	
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Gln	Met	Thr	Gln	Ser	130	135	140	
Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	145	150	155	160
Lys	Ala	Ser	Gln	Asp	Val	Ser	Thr	Ala	Val	Ala	Trp	Tyr	Gln	Gln	Lys	165	170	175	
Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ser	Ala	Ser	Tyr	Arg	Tyr	180	185	190	
Thr	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	195	200	205	
Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	210	215	220	
Cys	Gln	Gln	His	Tyr	Ile	Thr	Pro	Leu	Thr	Phe	Gly	Gln	Gly	Thr	Lys	225	230	235	240
Leu	Glu	Ile	Lys	Arg	Thr	Gly	Gly	Gly	Gly	Ser	Glu	Val	Gln	Leu	Val	245	250	255	
Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	260	265	270	

Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr Tyr Gly Met Ser Trp Ile
 275 280 285
 Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Ser Ile Thr Asn
 290 295 300
 Ser Gly Gly Arg Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr
 305 310 315 320
 Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu Tyr Leu Gln Met Asn Ser
 325 330 335
 Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Leu Asp Gly Arg
 340 345 350
 Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 355 360 365
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 370 375 380
 Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
 385 390 395 400
 Thr Val Thr Ile Ser Cys Lys Arg Asn Thr Gly Asn Ile Gly Ser Asn
 405 410 415
 Tyr Val Asn Trp Tyr Gln Gln His Glu Gly Ser Ser Pro Thr Thr Ile
 420 425 430
 Ile Tyr Arg Asp Asp Lys Arg Pro Asp Gly Val Ser Asp Arg Phe Ser
 435 440 445
 Gly Ser Ile Asp Arg Ser Ser Lys Ser Ala Ser Leu Thr Ile Ser Asn
 450 455 460
 Leu Lys Thr Glu Asp Glu Ala Asp Tyr Phe Cys Gln Ser Tyr Ser Ser
 465 470 475 480
 Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala
 485 490 495
 Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala Ala
 500 505 510
 Ala His His His His His His
 515

<210> SEQ ID NO: 44

<211> 1647

<212> ADN

<213> Secuencia artificial

<220>

<223> T2C-0003 ORF

<400> 44

atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgga	60
caggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac caggcgccag cgtgaagggtg	120
tcctgcaagg ccagcggcta cacctttacc accgccggca tgcagtgggt gcgccaggct	180
cctggacagg gcctggaatg gatgggctgg atcaacaccc acagcggcgt gcccaaatac	240
gccgaggact tcaagggcag agtgaccatc agcgccgaca ccagcacctc cacagcctac	300
ctgcagctga gcagcctgaa gtccgaggac accgccgtgt actactgcgc cagaagcggc	360
ttcggcagca gctactggta cttcgacgtg tggggccagg gcaccctcgt gacagtgtct	420
agcggaggcg gaggatctgg cggcggagga agtggcggag ggggatccga tatccagatg	480
accagagcc ccagcagcct gtctgccagc gtgggcgaca gagtgacaat tacatgcaag	540
gcctcccagg acgtgtccac agccgtggcc tggatatcagc agaagcctgg caaggccccc	600
aagctgctga tctacagcgc cagctaccgg tacaccggcg tgccaagcag attttccggc	660
agcggctccg gcaccgactt caccctgaca atcagctccc tgcagcccga ggatttcgcc	720
gtgtattatt gccagcagca ctacatcacc cccctgacct tcggccaggg gaccaagctg	780
gaaatcaaga gaacaggggg aggcgggttca gaagtgcagc tggtggaatc cggcggaggc	840
ctggtccagc ctggcggcag cctgaaactg agctgcgccg ccagcggctt caccttcaac	900
aaatacgcca tgaactgggt ccgccaggct cctggaaagg gactcgagtg ggtggcccgg	960
atcagaagca agtacaacaa ctacgccacc tactacgccg acagcgtgaa ggaccggttc	1020
accatcagcc gggacgacag caagaacacc gcctacctgc agatgaacaa cctgaaaacc	1080
gaggacacag ccgtgtacta ctgcgtgcgg cacggcaact tcggcaacag ctacatcagc	1140
tactgggcct attggggaca gggaacactc gtgacagtgt ccagtggcgg aggcggcagt	1200
ggtgggggag gaagcggagg tggcggatct cagaccgtgg tcaccagga acccagcctg	1260
acagtcagcc ctggaggcac cgtgaccctg acctgtggaa gcagcacagg cgccgtgacc	1320
agcggctact accccaactg ggtgcagcag aagcccggcc aggctcctag aggcctgac	1380

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ggcggcacca agtttctggc ccctggcacc cctgcccggg tctctggatc tctgctgggc 1440
ggcaaggccg ccctgacact gagcggagtg cagcccaggg acgaggccga gtactactgt 1500
gccctgtggt acagcaacag atgggtgttc ggcggaggga ccaagctgac cgtgctgggc 1560
agcggcgcggt ctgcggccgc aggtagcggg ggtgattaca aagatgatga cgataaaggt 1620
gcagcggcgc atcaccatca tcaccac 1647

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<210> SEQ ID NO: 45
<211> 530
<212> PRT
<213> Secuencia artificial

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<220>
<223> T2C-0003 AA

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<400> 45

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

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

Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala
 450 455 460

Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr
 465 470 475 480

Cys Ala Leu Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys
 485 490 495

Leu Thr Val Leu Gly Ser Gly Ala Ser Ala Ala Ala Gly Ser Gly Gly
 500 505 510

Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala Ala Ala His His His His
 515 520 525

His His
 530

<210> SEQ ID NO: 46

<211> 1614

<212> ADN

<213> Secuencia artificial

<220>

<223> T2C-0005 ORF

<400> 46

atgaagcacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgga	60
caggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac caggcgccag cgtgaagggtg	120
tcctgcaagg ccagcggcta cacctttacc accgccggca tgcagtgggt gcgccaggct	180
cctggacagg gcctggaatg gatgggctgg atcaacaccc acagcggcgt gcccaaatac	240
gccgaggact tcaagggcag agtgaccatc agcgccgaca ccagcacctc cacagcctac	300
ctgcagctga gcagcctgaa gtccgaggac accgccgtgt actactgcgc cagaagcggc	360
ttcggcagca gctactggta cttcgacgtg tggggccagg gcaccctcgt gacagtgtct	420
agcggaggcg gaggatctgg cggcgaggga agtggcggag ggggatccga tatccagatg	480
accagagcc ccagcagcct gtctgccagc gtgggcgaca gaggacaaat tacatgcaag	540
gcctcccagg acgtgtccac agccgtggcc tggtatcagc agaagcctgg caaggccccc	600
aagctgctga tctacagcgc cagctaccgg tacaccggcg tgccaagcag attttcgggc	660
agcggctccg gcaccgactt caccctgaca atcagctccc tgcagcccga ggatttcgcc	720
gtgtattatt gccagcagca ctacatcacc ccctgacct tcggccaggg gaccaagctg	780

gaaatcaaga gaacagggggg aggcgggttca gaagtgcagc tgggtggaatc cgggggggggc 840
 ctggtgcagc ctgggggggag cctgagactg agttgtgccg cctctgggggt gacattttaac 900
 tactatggca tgtcttggat cgcgcaggca cctggaaagg gcctggagtg ggtggccagc 960
 atcactaatt ccggcggggcg aatctactat cccgacagcg tcaagggcag gttcacaatt 1020
 tcccgcgaga acacacagaa aactctgtac ctgcagatga atagcctgag agccgaagat 1080
 acagctgtgt actattgcac tctggacggc agggatgggt gggtcgccta ttggggggcag 1140
 ggaaccctgg tgacagtcag ctccggagga ggaggatctg gcggaggagg cagtggggga 1200
 ggcgggtcaa tggcccaggc tgtgctcact cagccgtcct ctgtttctgg cgtacctggc 1260
 caacgggtga ccattagctg taaaaggaat accgggaata tcgggtctaa ctacgtgaac 1320
 tggatatcagc agcttccagg gacagctccc aagttgctga tctatcgca cgacaaaaga 1380
 ccctcagggg tccctgaccg atttagtggc agcaaaagcg gtacttccgc ttccctggcg 1440
 ataaccggct ttcaggccga agatgaggca gactactatt gccagtcata ttccagcggc 1500
 ttcattcttcg gaggcggaac taagctgaca gtgttggggc cggccgcagg tgcaggtggt 1560
 gattacaaag atgatgacga taaaggtgca gcggcgcac accatcatca ccac 1614

<210> SEQ ID NO: 47
 <211> 519
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> T2C-0005 AA

<400> 47

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

Tyr	Leu	Gln	Leu	Ser	Ser	Leu	Lys	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	
				85					90					95		
Cys	Ala	Arg	Ser	Gly	Phe	Gly	Ser	Ser	Tyr	Trp	Tyr	Phe	Asp	Val	Trp	
			100					105					110			
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	
		115					120					125				
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Gln	Met	Thr	Gln	Ser	
	130					135					140					
Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	
145					150					155					160	
Lys	Ala	Ser	Gln	Asp	Val	Ser	Thr	Ala	Val	Ala	Trp	Tyr	Gln	Gln	Lys	
				165					170					175		
Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ser	Ala	Ser	Tyr	Arg	Tyr	
			180					185					190			
Thr	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	
		195					200					205				
Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	
	210					215					220					
Cys	Gln	Gln	His	Tyr	Ile	Thr	Pro	Leu	Thr	Phe	Gly	Gln	Gly	Thr	Lys	
225					230					235					240	
Leu	Glu	Ile	Lys	Arg	Thr	Gly	Gly	Gly	Gly	Ser	Glu	Val	Gln	Leu	Val	
				245				250						255		
Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	
			260					265					270			
Cys	Ala	Ala	Ser	Gly	Val	Thr	Phe	Asn	Tyr	Tyr	Gly	Met	Ser	Trp	Ile	
		275					280					285				
Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Ser	Ile	Thr	Asn	
	290					295					300					
Ser	Gly	Gly	Arg	Ile	Tyr	Tyr	Pro	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	
305					310					315					320	
Ile	Ser	Arg	Glu	Asn	Thr	Gln	Lys	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	
				325					330					335		
Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Thr	Leu	Asp	Gly	Arg	
			340					345					350			

Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 355 360 365

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 370 375 380

Met Ala Gln Ala Val Leu Thr Gln Pro Ser Ser Val Ser Gly Val Pro
 385 390 395 400

Gly Gln Arg Val Thr Ile Ser Cys Lys Arg Asn Thr Gly Asn Ile Gly
 405 410 415

Ser Asn Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys
 420 425 430

Leu Leu Ile Tyr Arg Asp Asp Lys Arg Pro Ser Gly Val Pro Asp Arg
 435 440 445

Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly
 450 455 460

Phe Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Ser Ser
 465 470 475 480

Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala
 485 490 495

Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala Ala
 500 505 510

Ala His His His His His His
 515

<210> SEQ ID NO: 48

<211> 1608

<212> ADN

<213> Secuencia artificial

<220>

<223> T2C-0006 ORF

<400> 48

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caggtgcagc tggtgcagtc tggcgccgaa gtgaagaaac caggcgccag cgtgaaggtg 120

tcctgcaagg ccagcggcta cacctttacc accgccggca tgcagtgggt gcgccaggct 180

cctggacagg gcctggaatg gatgggctgg atcaacaccc acagcggcgt gcccaaatac 240

gccgaggact tcaagggcag agtgaccatc agcgccgaca ccagcacctc cacagcctac 300

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ctgcagctga gcagcctgaa gtccgaggac accgccgtgt actactgcgc cagaagcggc      360
ttcggcagca gctactggta cttcgacgtg tggggccagg gcaccctcgt gacagtgtct      420
agcggaggcg gaggatctgg cggcggagga agtggcggag ggggatccga tatccagatg      480
accagagacc ccagcagcct gtctgccagc gtgggcgaca gagtgacaat tacatgcaag      540
gcctcccagg acgtgtccac agccgtggcc tggatatcagc agaagcctgg caaggccccc      600
aagctgctga tctacagcgc cagctaccgg tacaccggcg tgccaagcag attttccggc      660
agcggctccg gcaccgactt caccctgaca atcagctccc tgacgcccga ggatttcgcc      720
gtgtattatt gccagcagca ctacatcacc cccctgacct tcggccaggg gaccaagctg      780
gaaatcaaga gaacaggggg aggcgggttca gaagtgcagc tggtggaatc cggggggggc      840
ctggtgcagc ctgggggggag cctgagactg agttgtgccg cctctggggg gacatttaac      900
tactatggca tgtcttggat ccgccaggca cctggaaagg gcctggagtg ggtggccagc      960
atcactaatt ccggcggggc aatctactat cccgacagcg tcaagggcag gttcacaatt     1020
tcccgcgaga acacacagaa aactctgtac ctgcagatga atagcctgag agccgaagat     1080
acagctgtgt actattgcac tctggacggc agggatgggt gggtcgccta ttgggggcag     1140
ggaaccctgg tgacagtcag ctccggagga ggaggatctg gcggaggagg cagtggggga     1200
ggcgggtcaa actttatgct cactcagccg tcctctgttt ctggcgtacc tggccaacgg     1260
gtgaccatta gctgtacggg taataccggg aatatcgggt ctaactacgt gaactggtat     1320
cagcagcttc cagggacagc tcccaagttg ctgatctatc gcgacgacaa aagaccctca     1380
ggggtccctg accgatttag tggcagcaaa agcgg tactt ccgcttccct ggcgataacc     1440
ggctttcagg ccgaagatga ggcagactac tattgccagt catattccag cggcttcac     1500
ttcggaggcg gaactaagct gacagtgttg ggcgcggccg caggtgcagg tggtgattac     1560
aaagatgatg acgataaagg tgcagcggcg catcaccatc atcaccac                     1608

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<210> SEQ ID NO: 49

<211> 517

<212> PRT

<213> Secuencia artificial

<220>

<223> T2C-0006 AA

<400> 49

Gly	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	1	5	10	15
Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Thr	20	25	30	
Ala	Gly	Met	Gln	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	35	40	45	
Met	Gly	Trp	Ile	Asn	Thr	His	Ser	Gly	Val	Pro	Lys	Tyr	Ala	Glu	Asp	50	55	60	
Phe	Lys	Gly	Arg	Val	Thr	Ile	Ser	Ala	Asp	Thr	Ser	Thr	Ser	Thr	Ala	65	70	75	80
Tyr	Leu	Gln	Leu	Ser	Ser	Leu	Lys	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	85	90	95	
Cys	Ala	Arg	Ser	Gly	Phe	Gly	Ser	Ser	Tyr	Trp	Tyr	Phe	Asp	Val	Trp	100	105	110	
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	115	120	125	
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Gln	Met	Thr	Gln	Ser	130	135	140	
Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	145	150	155	160
Lys	Ala	Ser	Gln	Asp	Val	Ser	Thr	Ala	Val	Ala	Trp	Tyr	Gln	Gln	Lys	165	170	175	
Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ser	Ala	Ser	Tyr	Arg	Tyr	180	185	190	
Thr	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	195	200	205	
Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	210	215	220	
Cys	Gln	Gln	His	Tyr	Ile	Thr	Pro	Leu	Thr	Phe	Gly	Gln	Gly	Thr	Lys	225	230	235	240
Leu	Glu	Ile	Lys	Arg	Thr	Gly	Gly	Gly	Gly	Ser	Glu	Val	Gln	Leu	Val	245	250	255	
Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	260	265	270	

Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr Tyr Gly Met Ser Trp Ile
 275 280 285
 Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Ser Ile Thr Asn
 290 295 300
 Ser Gly Gly Arg Ile Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr
 305 310 315 320
 Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu Tyr Leu Gln Met Asn Ser
 325 330 335
 Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Leu Asp Gly Arg
 340 345 350
 Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 355 360 365
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 370 375 380
 Asn Phe Met Leu Thr Gln Pro Ser Ser Val Ser Gly Val Pro Gly Gln
 385 390 395 400
 Arg Val Thr Ile Ser Cys Thr Gly Asn Thr Gly Asn Ile Gly Ser Asn
 405 410 415
 Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
 420 425 430
 Ile Tyr Arg Asp Asp Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
 435 440 445
 Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Phe Gln
 450 455 460
 Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Ser Ser Gly Phe
 465 470 475 480
 Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala Ala Gly
 485 490 495
 Ala Gly Gly Asp Tyr Lys Asp Asp Asp Lys Gly Ala Ala Ala His
 500 505 510
 His His His His His
 515

<210> SEQ ID NO: 50

<211> 37

<212> ADN

<213> Secuencia artificial

<220>
 <223> Nhe-poliC-S

<220>
 <221> misc_feature
 <222> (37)..(37)
 <223> n es a, c, g o t

<400> 50
 gctagcgcta ccggactcag atcccccccc cccccdn 37

<210> SEQ ID NO: 51
 <211> 28
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> rIg gamma-AS1

<400> 51
 tcactgagct ggtgagagt tagagccc 28

<210> SEQ ID NO: 52
 <211> 28
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> rIg gamma-AS2

<400> 52
 tcaccgagct gctgaggggtg tagagccc 28

<210> SEQ ID NO: 53
 <211> 37
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Nhe-poliC-S2

<220>
 <221> misc_feature
 <222> (37)..(37)
 <223> n es a, c, g o t

<400> 53
 gctagcgcta ccggactcag atcccccccc cccccdn 37

<210> SEQ ID NO: 54
 <211> 26
 <212> ADN

<213> Secuencia artificial
 <220>
 <223> rIgL-AS1
 <400> 54
 ttccacatca ctcggtaga aatcag 26
 <210> SEQ ID NO: 55
 <211> 28
 <212> ADN
 <213> Secuencia artificial
 <220>
 <223> rIgL-AS2
 <400> 55
 taacaccagg gtagaatct gtcacat 28
 <210> SEQ ID NO: 56
 <211> 19
 <212> ADN
 <213> Secuencia artificial
 <220>
 <223> rIg gamma-seq
 <400> 56
 ctggctcagg gaaatagcc 19
 <210> SEQ ID NO: 57
 <211> 18
 <212> ADN
 <213> Secuencia artificial
 <220>
 <223> rIgL-seq1
 <400> 57
 tccctggagc tcctcagt 18
 <210> SEQ ID NO: 58
 <211> 18
 <212> ADN
 <213> Secuencia artificial
 <220>
 <223> rIgL-seq2
 <400> 58
 gccttgtagc tcttgagc 18

<210> SEQ ID NO: 59
 <211> 864
 <212> ADN
 <213> Secuencia artificial

<220>

<223> C3E-7078 ORF

<400> 59

atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgga	60
gaagtgcagc tgggtggaatc cggggggggc ctgggtgcagc ctgggggggag cctgagactg	120
agttgtgccg cctctgggggt gacatttaac tactatggca tgtcttggat ccgccaggca	180
cctggaaagg gcctggagtg ggtggccagc atcactaggt ccggcgggcg aatctactat	240
cccgacagcg tcaagggcag gttcacaatt tcccgcgaga acacacagaa aactctgtac	300
ctgcagatga atagcctgag agccgaagat acagctgtgt actattgcac tctggacggc	360
agggatgggt gggtcgccta ttggggggcag ggaaccctgg tgacagtcag ctccggagga	420
ggaggatctg gcggaggagg cagtggggga ggcggtcaa actttatgct gaccagccc	480
cacagtgtgt cagagagccc tggcaagact gtcacatct cttgtaaaag gaacaccgga	540
aatattggca gtaactacgt gaattggtat cagcagcatg aagggtctag tccaaccaca	600
atcatctacc gggacgataa gagacccgac ggggtgtccg atcgattctc cggatctatc	660
gaccggtcaa gcaagagtgc ttactgacc attagcaatc tgaaaacaga ggacgaagca	720
gattactttt gccagtccta ttctctggc ttcatctttg gaggcgggac taaactgacc	780
gtgctgggcg cggccgcagg tgcaggtggg gattacaaag atgatgacga taaaggtgca	840
gcggcgcatc accatcatca ccac	864

<210> SEQ ID NO: 60
 <211> 269
 <212> PRT
 <213> Secuencia artificial

<220>

<223> C3E-7078 AA

<400> 60

Gly	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly
1				5				10					15		

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

<210> SEQ ID NO: 61

<211> 864

<212> ADN

<213> Secuencia artificial

<220>

<223> C3E-7079 ORF

<400> 61

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atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcggg      60
gaagtgcagc tggtggaatc cggggggggc ctggtgcagc ctgggggggag cctgagactg      120
agttgtgccg cctctggggg gacatttaac tactatggca tgtcttggat ccgccaggca      180
cctggaaagg gcctggagtg ggtggccagc atcacttctt ccggcgggcg aatctactat      240
cccgacagcg tcaagggcag gttcacaatt tcccgcgaga acacacagaa aactctgtac      300
ctgcagatga atagcctgag agccgaagat acagctgtgt actattgcac tctggacggc      360
agggatgggt gggtcgccta ttggggggcag ggaaccctgg tgacagtcag ctccggagga      420
ggaggatctg gcggaggagg cagtggggga ggcgggtcaa actttatgct gaccagccc      480
cacagtgtgt cagagagccc tggcaagact gtcaccatct cttgtaaaag gaacaccgga      540
aatattggca gtaactacgt gaattggtat cagcagcatg aagggtctag tccaaccaca      600
atcatctacc gggacgataa gagacccgac ggggtgtccg atcgattctc cggatctatc      660
gaccggtcaa gcaagagtgc ttactgacc attagcaatc tgaaaacaga ggacgaagca      720
gattactttt gccagtccta ttctctggc ttcatctttg gaggcgggac taaactgacc      780
gtgctgggcg cggccgcagg tgcaggtggg gattacaaag atgatgacga taaaggtgca      840
gcggcgcata accatcatca ccac                                             864

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<210> SEQ ID NO: 62

<211> 269

<212> PRT

<213> Secuencia artificial

<220>

<223> C3E-7079 AA

<400> 62

```

Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1           5           10          15
Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr
          20          25          30
Tyr Gly Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
          35          40          45

```

Val Ala Ser Ile Thr Ser Ser Gly Gly Arg Ile Tyr Tyr Pro Asp Ser
50 55 60

Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu
65 70 75 80

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

Cys Thr Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro His Ser Val
130 135 140

Ser Glu Ser Pro Gly Lys Thr Val Thr Ile Ser Cys Lys Arg Asn Thr
145 150 155 160

Gly Asn Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln His Glu Gly
165 170 175

Ser Ser Pro Thr Thr Ile Ile Tyr Arg Asp Asp Lys Arg Pro Asp Gly
180 185 190

Val Ser Asp Arg Phe Ser Gly Ser Ile Asp Arg Ser Ser Lys Ser Ala
195 200 205

Ser Leu Thr Ile Ser Asn Leu Lys Thr Glu Asp Glu Ala Asp Tyr Phe
210 215 220

Cys Gln Ser Tyr Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Thr Val Leu Gly Ala Ala Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp
245 250 255

Asp Asp Lys Gly Ala Ala Ala His His His His His His
260 265

<210> SEQ ID NO: 63

<211> 858

<212> ADN

<213> Secuencia artificial

<220>

<223> C3E-7085 ORF

<400> 63

atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgga

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gaagtgcagc tgggtggaatc cgggggggggc ctggtgcagc ctgggggggag cctgagactg      120
agtttgtgccg cctctgggggt gacattttaac tactatggca tgtcttggat ccgccaggca      180
cctggaaagg gcctggagtg ggtggccagc atcactaggt ccggcgggcg aatctactat      240
cccgacagcg tcaagggcag gttcacaatt tcccgcgaga acacacagaa aactctgtac      300
ctgcagatga atagcctgag agccgaagat acagctgtgt actattgcac tctggacggc      360
agggatgggt gggtcgccta ttggggggcag ggaaccctgg tgacagtcag ctccggagga      420
ggaggatctg gcggaggagg cagtggggga ggcgggtcaa actttatgct cactcagccg      480
tcctctgttt ctggcgtacc tggccaacgg gtgaccatta gctgtacggg taataccggg      540
aatatcgggt ctaactacgt gaactggtat cagcagcttc caggacagc tccaagttg      600
ctgatctatc gcgacgaaa aagaccctca ggggtccctg accgatttag tggcagcaaa      660
agcgggtactt ccgcttcctt ggcgataacc ggctttcagg ccgaagatga ggcagactac      720
tattgccagt catattccag cggcttcatc ttccggaggcg gaactaagct gacagtgttg      780
ggcgcgggccg caggtgcagg tggtgattac aaagatgatg acgataaagg tgcagcggcg      840
catcaccatc atcaccac                                     858

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<210> SEQ ID NO: 64
<211> 267
<212> PRT
<213> Secuencia artificial

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<220>
<223> C3E-7085 AA

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<400> 64

```

```

Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1              5              10              15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr
              20              25              30

Tyr Gly Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
              35              40              45

Val Ala Ser Ile Thr Arg Ser Gly Gly Arg Ile Tyr Tyr Pro Asp Ser
              50              55              60

Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu
65              70              75              80

```

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

Cys Thr Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro Ser Ser Val
130 135 140

Ser Gly Val Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Asn Thr
145 150 155 160

Gly Asn Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly
165 170 175

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

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

Ala Ile Thr Gly Phe Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln
210 215 220

Ser Tyr Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val
225 230 235 240

Leu Gly Ala Ala Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp Asp Asp
245 250 255

Lys Gly Ala Ala Ala His His His His His His
260 265

<210> SEQ ID NO: 65

<211> 864

<212> ADN

<213> Secuencia artificial

<220>

<223> C3E-7086 ORF

<400> 65

atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgga 60

gaagtgcagc tgggtggaatc cggggggggc ctggtgcagc ctgggggggag cctgagactg 120

agttgtgccg cctctgggggt gacatttaac tactatggca tgtcttggat ccgccaggca 180

cctggaaagg gcctggagtg ggtggccagc atcactaggt ccggcggggc aatctactat 240

```

cccgacagcg tcaagggcag gttcacaatt tccgcgaga acacacagaa aactctgtac      300
ctgcagatga atagcctgag agccgaagat acagctgtgt actattgcac tctggacggc      360
agggatgggt gggtcgccta ttgggggcag ggaaccctgg tgacagtcag ctccggagga      420
ggaggatctg gcggaggagg cagtggggga ggcggtcaa actttatgct gaccagccc      480
cacagtgtgt cagagagccc tggcaagact gtcaccatct cttgtaaaag gaacaccgga      540
aatattggca gtaactacgt gaattggtat cagcagcatg aagggtctag tccaaccaca      600
atcatctacc ggggcgataa gagacccgac ggggtgtccg atcgattctc cggatctatc      660
gaccggtcaa gcaagagtgc ttcactgacc attagcaatc tgaaaacaga ggacgaagca      720
gattactttt gccagtccta ttcctctggc ttcacttttg gaggcgggac taaactgacc      780
gtgctgggcg cggccgcagg tgcaggtggg gattacaaag atgatgacga taaaggtgca      840
gcggcgcac accatcatca ccac                                             864

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<210> SEQ ID NO: 66
<211> 269
<212> PRT
<213> Secuencia artificial

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<220>
<223> C3E-7086 AA

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<400> 66

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```

Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1              5              10              15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr
                20              25              30

Tyr Gly Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
        35              40              45

Val Ala Ser Ile Thr Arg Ser Gly Gly Arg Ile Tyr Tyr Pro Asp Ser
        50              55              60

Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu
65              70              75              80

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

Cys Thr Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly
        100              105              110

```

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

<210> SEQ ID NO: 67
 <211> 864
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> C3E-7087 ORF

<400> 67
 atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgga 60
 gaagtgcagc tggtggaatc cggggggggc ctggtgcagc ctggggggag cctgagactg 120
 agttgtgccg cctctggggg gacatttaac tactatggca tgtcttggat ccgccaggca 180
 cctggaaagg gcctggagtg ggtggccagc atcactaggt ccggcgggag aatctactat 240
 cccgacagcg tcaagggcag gttcacaatt tcccgcgaga acacacagaa aactctgtac 300
 ctgcagatga atagcctgag agccgaagat acagctgtgt actattgcac tctggacggc 360
 agggatgggt gggtcgccta ttggggggcag ggaaccctgg tgacagtcag ctccggagga 420

```

ggaggatctg gcggaggagg cagtggggga ggcgggtcaa actttatgct gaccagccc      480
cacagtgtgt cagagagccc tggcaagact gtcaccatct cttgtaaaag gaacaccgga      540
aatattggca gtaactacgt gaattggtat cagcagcatg aagggcttag tccaaccaca      600
atcatctacc ggcaggataa gagacccgac ggggtgtccg atcgattctc cggatctatc      660
gaccggtcaa gcaagagtgc ttactgacc attagcaatc tgaaaacaga ggacgaagca      720
gattactttt gccagtccta ttcctctggc ttcacttttg gaggcgggac taaactgacc      780
gtgctgggcg cggccgcagg tgcaggtggt gattacaaag atgatgacga taaaggtgca      840
gcggcgcata accatcatca ccac                                             864

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<210> SEQ ID NO: 68

<211> 269

<212> PRT

<213> Secuencia artificial

<220>

<223> C3E-7087 AA

<400> 68

```

Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1              5              10              15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr
              20              25              30

Tyr Gly Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
              35              40              45

Val Ala Ser Ile Thr Arg Ser Gly Gly Arg Ile Tyr Tyr Pro Asp Ser
              50              55              60

Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu
65              70              75              80

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

Cys Thr Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly
              100             105             110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
              115             120             125

Ser Gly Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro His Ser Val
130             135             140

```

Ser Glu Ser Pro Gly Lys Thr Val Thr Ile Ser Cys Lys Arg Asn Thr
145 150 155 160

Gly Asn Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln His Glu Gly
165 170 175

Ser Ser Pro Thr Thr Ile Ile Tyr Arg Gln Asp Lys Arg Pro Asp Gly
180 185 190

Val Ser Asp Arg Phe Ser Gly Ser Ile Asp Arg Ser Ser Lys Ser Ala
195 200 205

Ser Leu Thr Ile Ser Asn Leu Lys Thr Glu Asp Glu Ala Asp Tyr Phe
210 215 220

Cys Gln Ser Tyr Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Thr Val Leu Gly Ala Ala Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp
245 250 255

Asp Asp Lys Gly Ala Ala Ala His His His His His His
260 265

<210> SEQ ID NO: 69

<211> 864

<212> ADN

<213> Secuencia artificial

<220>

<223> C3E-7088 ORF

<400> 69

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atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgga      60
gaagtgcagc tgggtggaatc cggggggggc ctggtgcagc ctgggggggag cctgagactg      120
agttgtgccg cctctgggggt gacatttaac tactatggca tgtcttggat ccgccaggca      180
cctggaaagg gcctggagtg ggtggccagc atcactaggt ccggcggggcg aatctactat      240
cccgacagcg tcaagggcag gttcacaatt tcccgcgaga acacacagaa aactctgtac      300
ctgcagatga atagcctgag agccgaagat acagctgtgt actattgcac tctggacggc      360
agggatgggt gggtcgccta ttggggggcag ggaaccctgg tgacagtcag ctccggagga      420
ggaggatctg gcggaggagg cagtggggga ggcgggtcaa actttatgct gacccagccc      480
cacagtgtgt cagagagccc tggcaagact gtcaccatct cttgtaaaaag gaacaccgga      540
aatattggca gtaactacgt gaattggtat cagcagcatg aaggggtctag tccaaccaca      600

```

```

atcatctacc ggaacgataa gagacccgac ggggtgtccg atcgattctc cggatctatc      660
gaccggtcaa gcaagagtgc ttactgacc attagcaatc tgaaaacaga ggacgaagca      720
gattactttt gccagtccta ttctctggc ttcatctttg gaggcgggac taaactgacc      780
gtgctgggcg cggccgcagg tgcaggtggg gattacaaag atgatgacga taaaggtgca      840
gcggcgcatac accatcatca ccac                                             864

```

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<210> SEQ ID NO: 70
<211> 269
<212> PRT
<213> Secuencia artificial

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```

<220>
<223> C3E-7088 AA

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<400> 70

```

```

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

```

Ser Ser Pro Thr Thr Ile Ile Tyr Arg Asn Asp Lys Arg Pro Asp Gly
180 185 190

Val Ser Asp Arg Phe Ser Gly Ser Ile Asp Arg Ser Ser Lys Ser Ala
195 200 205

Ser Leu Thr Ile Ser Asn Leu Lys Thr Glu Asp Glu Ala Asp Tyr Phe
210 215 220

Cys Gln Ser Tyr Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Thr Val Leu Gly Ala Ala Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp
245 250 255

Asp Asp Lys Gly Ala Ala Ala His His His His His His
260 265

<210> SEQ ID NO: 71

<211> 864

<212> ADN

<213> Secuencia artificial

<220>

<223> C3E-7089 ORF

<400> 71

atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgga	60
gaagtgcagc tgggtggaatc cggggggggc ctggtgcagc ctgggggggag cctgagactg	120
agttgtgccg cctctgggggt gacatttaac tactatggca tgtcttggat ccgccaggca	180
cctggaaagg gcctggagtg ggtggccagc atcactaggt ccggcggggc aatctactat	240
cccgacagcg tcaagggcag gttcacaatt tcccgcgaga acacacagaa aactctgtac	300
ctgcagatga atagcctgag agccgaagat acagctgtgt actattgcac tctggacggc	360
agggatgggt gggtcgccta ttggggggcag ggaaccctgg tgacagtcag ctccggagga	420
ggaggatctg gcggaggagg cagtggggga ggcgggtcaa actttatgct gaccagccc	480
cacagtgtgt cagagagccc tggcaagact gtcacatct cttgtaaaag gaacaccgga	540
aatattggca gtaactacgt gaattggtat cagcagcatg aagggtctag tccaaccaca	600
atcatctacc ggagcgataa gagacccgac ggggtgtccg atcgattctc cgatctatc	660
gaccggtcaa gcaagagtgc ttactgacc attagcaatc tgaaaacaga ggacgaagca	720
gattactttt gccagtccta ttctcttggc ttcatctttg gaggcgggac taaactgacc	780

gtgctgggcg cggccgcagg tgcaggtggt gattacaaag atgatgacga taaaggtgca 840

gcggcgcatc accatcatca ccac 864

<210> SEQ ID NO: 72

<211> 269

<212> PRT

<213> Secuencia artificial

<220>

<223> C3E-7089 AA

<400> 72

Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr
20 25 30

Tyr Gly Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
35 40 45

Val Ala Ser Ile Thr Arg Ser Gly Gly Arg Ile Tyr Tyr Pro Asp Ser
50 55 60

Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu
65 70 75 80

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

Cys Thr Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro His Ser Val
130 135 140

Ser Glu Ser Pro Gly Lys Thr Val Thr Ile Ser Cys Lys Arg Asn Thr
145 150 155 160

Gly Asn Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln His Glu Gly
165 170 175

Ser Ser Pro Thr Thr Ile Ile Tyr Arg Ser Asp Lys Arg Pro Asp Gly
180 185 190

Val Ser Asp Arg Phe Ser Gly Ser Ile Asp Arg Ser Ser Lys Ser Ala
195 200 205

Ser Leu Thr Ile Ser Asn Leu Lys Thr Glu Asp Glu Ala Asp Tyr Phe
 210 215 220

Cys Gln Ser Tyr Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu
 225 230 235 240

Thr Val Leu Gly Ala Ala Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp
 245 250 255

Asp Asp Lys Gly Ala Ala Ala His His His His His His
 260 265

<210> SEQ ID NO: 73

<211> 864

<212> ADN

<213> Secuencia artificial

<220>

<223> C3E-7090 ORF

<400> 73

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atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcggg      60
gaagtgcagc tgggtggaatc cggggggggc ctggtgcagc ctgggggggag cctgagactg      120
agttgtgccg cctctggggg gacatttaac tactatggca tgtcttggat ccgccaggca      180
cctggaaagg gcctggagtg ggtggccagc atcactaggt ccggcggggc aatctactat      240
cccgacagcg tcaagggcag gttcacaatt tcccgcgaga acacacagaa aactctgtac      300
ctgcagatga atagcctgag agccgaagat acagctgtgt actattgcac tctggacggc      360
agggatgggt gggtcgccta ttggggggcag ggaaccctgg tgacagtcag ctccggagga      420
ggaggatctg gcggaggagg cagtggggga ggcggtcaa actttatgct gaccagccc      480
cacagtgtgt cagagagccc tggcaagact gtcacatct cttgtaaaag gaacaccgga      540
aatattggca gtaactacgt gaattggtat cagcagcatg aagggtctag tccaaccaca      600
atcatctacc gggccgataa gagacccgac ggggtgtccg atcgattctc cggatctatc      660
gaccggtcaa gcaagagtcg ttactgacc attagcaatc tgaaaacaga ggacgaagca      720
gattactttt gccagtccta ttcctctggc ttcatttttg gaggcgggac taaactgacc      780
gtgctgggcg cggccgcagg tgcaggtggg gattacaaag atgatgacga taaaggtgca      840
gcggcgcac accatcatca ccac      864

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<210> SEQ ID NO: 74
 <211> 269
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> C3E-7090 AA

<400> 74

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

Cys Gln Ser Tyr Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu
 225 230 235 240

Thr Val Leu Gly Ala Ala Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp
 245 250 255

Asp Asp Lys Gly Ala Ala Ala His His His His His His
 260 265

<210> SEQ ID NO: 75

<211> 864

<212> ADN

<213> Secuencia artificial

<220>

<223> C3E-7091 ORF

<400> 75

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atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcggg      60
gaagtgcagc tgggtggaatc cggggggggc ctggtgcagc ctggggggag cctgagactg      120
agttgtgccg cctctggggg gacatttaac tactatggca tgtcttggat ccgccaggca      180
cctggaaagg gcctggagtg ggtggccagc atcacttctt ccggcggggc aatctactat      240
cccgacagcg tcaagggcag gttcacaatt tccgcgaga acacacagaa aactctgtac      300
ctgcagatga atagcctgag agccgaagat acagctgtgt actattgcac tctggacggc      360
agggatgggt gggtcgccta ttggggggcag ggaaccctgg tgacagtcag ctccggagga      420
ggaggatctg gcggaggagg cagtggggga ggcggtcaa actttatgct gaccagccc      480
cacagtgtgt cagagagccc tggcaagact gtcaccatct cttgtaaaag gaacaccgga      540
aatattggca gtaactacgt gaattggtat cagcagcatg aagggcttag tccaaccaca      600
atcatctacc ggggcgataa gagacccgac ggggtgtccg atcgattctc cggatctatc      660
gaccggtcaa gcaagagtgc ttactgacc attagcaatc tgaaaacaga ggacgaagca      720
gattactttt gccagtccta ttctctggc ttcatctttg gaggcgggac taaactgacc      780
gtgctgggcg cggccgcagg tgcaggtggg gattacaaag atgatgacga taaaggtgca      840
gcggcgcatc accatcatca ccac      864

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<210> SEQ ID NO: 76

<211> 269

<212> PRT

<213> Secuencia artificial

<220>

<223> C3E-7091 AA

<400> 76

Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
 1 5 10 15
 Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr
 20 25 30
 Tyr Gly Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
 35 40 45
 Val Ala Ser Ile Thr Ser Ser Gly Gly Arg Ile Tyr Tyr Pro Asp Ser
 50 55 60
 Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu
 65 70 75 80
 Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
 85 90 95
 Cys Thr Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 115 120 125
 Ser Gly Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro His Ser Val
 130 135 140
 Ser Glu Ser Pro Gly Lys Thr Val Thr Ile Ser Cys Lys Arg Asn Thr
 145 150 155 160
 Gly Asn Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln His Glu Gly
 165 170 175
 Ser Ser Pro Thr Thr Ile Ile Tyr Arg Gly Asp Lys Arg Pro Asp Gly
 180 185 190
 Val Ser Asp Arg Phe Ser Gly Ser Ile Asp Arg Ser Ser Lys Ser Ala
 195 200 205
 Ser Leu Thr Ile Ser Asn Leu Lys Thr Glu Asp Glu Ala Asp Tyr Phe
 210 215 220
 Cys Gln Ser Tyr Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu
 225 230 235 240
 Thr Val Leu Gly Ala Ala Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp
 245 250 255

Asp Asp Lys Gly Ala Ala Ala His His His His His His
 260 265

<210> SEQ ID NO: 77
 <211> 864
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> C3E-7092 ORF

<400> 77
 atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcggg 60
 gaagtgcagc tgggtggaatc cggggggggc ctggtgcagc ctgggggggag cctgagactg 120
 agttgtgccg cctctgggggt gacatttaac tactatggca tgtcttgat cgcaggca 180
 cctggaaagg gcctggagtg ggtggccagc atcacttctt ccggcgggag aatctactat 240
 cccgacagcg tcaagggcag gttcacaatt tcccgcgaga acacacagaa aactctgtac 300
 ctgcagatga atagcctgag agccgaagat acagctgtgt actattgcac tctggacggc 360
 agggatgggt gggtcgccta ttggggggcag ggaaccctgg tgacagtcag ctccggagga 420
 ggaggatctg gcggaggagg cagtggggga ggcggtcaa actttatgct gaccagccc 480
 cacagtgtgt cagagagccc tggcaagact gtcaccatct cttgtaaaag gaacaccgga 540
 aatattggca gtaactacgt gaattggtat cagcagcatg aagggtctag tccaaccaca 600
 atcatctacc ggcaggataa gagacccgac ggggtgtccg atcgattctc cggatctatc 660
 gaccggtcaa gcaagagtgc ttactgacc attagcaatc tgaaaacaga ggacgaagca 720
 gattactttt gccagtccta ttctctggc ttcatctttg gaggcgggac taaactgacc 780
 gtgctgggag cggccgcagg tgcaggtggt gattacaaag atgatgacga taaaggtgca 840
 gcggcgcatc accatcatca ccac 864

<210> SEQ ID NO: 78
 <211> 269
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> C3E-7092 AA

<400> 78

Gly	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	1	5	10	15
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Val	Thr	Phe	Asn	Tyr	20	25	30	
Tyr	Gly	Met	Ser	Trp	Ile	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	35	40	45	
Val	Ala	Ser	Ile	Thr	Ser	Ser	Gly	Gly	Arg	Ile	Tyr	Tyr	Pro	Asp	Ser	50	55	60	
Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Glu	Asn	Thr	Gln	Lys	Thr	Leu	65	70	75	80
Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	85	90	95	
Cys	Thr	Leu	Asp	Gly	Arg	Asp	Gly	Trp	Val	Ala	Tyr	Trp	Gly	Gln	Gly	100	105	110	
Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	115	120	125	
Ser	Gly	Gly	Gly	Gly	Ser	Asn	Phe	Met	Leu	Thr	Gln	Pro	His	Ser	Val	130	135	140	
Ser	Glu	Ser	Pro	Gly	Lys	Thr	Val	Thr	Ile	Ser	Cys	Lys	Arg	Asn	Thr	145	150	155	160
Gly	Asn	Ile	Gly	Ser	Asn	Tyr	Val	Asn	Trp	Tyr	Gln	Gln	His	Glu	Gly	165	170	175	
Ser	Ser	Pro	Thr	Thr	Ile	Ile	Tyr	Arg	Gln	Asp	Lys	Arg	Pro	Asp	Gly	180	185	190	
Val	Ser	Asp	Arg	Phe	Ser	Gly	Ser	Ile	Asp	Arg	Ser	Ser	Lys	Ser	Ala	195	200	205	
Ser	Leu	Thr	Ile	Ser	Asn	Leu	Lys	Thr	Glu	Asp	Glu	Ala	Asp	Tyr	Phe	210	215	220	
Cys	Gln	Ser	Tyr	Ser	Ser	Gly	Phe	Ile	Phe	Gly	Gly	Gly	Thr	Lys	Leu	225	230	235	240
Thr	Val	Leu	Gly	Ala	Ala	Ala	Gly	Ala	Gly	Gly	Asp	Tyr	Lys	Asp	Asp	245	250	255	
Asp	Asp	Lys	Gly	Ala	Ala	Ala	His	His	His	His	His	His	His	His	His	260	265		

<210> SEQ ID NO: 79
 <211> 864
 <212> ADN
 <213> Secuencia artificial

<220>

<223> C3E-7093 ORF

<400> 79

atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcggg	60
gaagtgcagc tgggtggaatc cggggggggc ctggtgcagc ctgggggggag cctgagactg	120
agttgtgccg cctctgggggt gacatttaac tactatggca tgtcttggat ccgccaggca	180
cctggaaagg gcctggagtg ggtggccagc atcacttctt ccggcgggag aatctactat	240
cccgacagcg tcaagggcag gttcacaatt tcccgcgaga acacacagaa aactctgtac	300
ctgcagatga atagcctgag agccgaagat acagctgtgt actattgcac tctggacggc	360
agggatgggt gggtcgccta ttggggggcag ggaaccctgg tgacagtcag ctccggagga	420
ggaggatctg gcggaggagg cagtggggga ggcggtcaa actttatgct gaccagccc	480
cacagtgtgt cagagagccc tggcaagact gtcacatct cttgtaaaag gaacaccgga	540
aatattggca gtaactacgt gaattggtat cagcagcatg aagggtctag tccaaccaca	600
atcatctacc ggaacgataa gagacccgac ggggtgtccg atcgattctc cgatctatc	660
gaccggtcaa gcaagagtgc ttactgacc attagcaatc tgaaaacaga ggacgaagca	720
gattactttt gccagtccta ttctctggc ttcatctttg gaggcgggac taaactgacc	780
gtgctgggag cggccgcagg tgcaggtggt gattacaaag atgatgacga taaaggtgca	840
gcggcgcatc accatcatca ccac	864

<210> SEQ ID NO: 80
 <211> 269
 <212> PRT
 <213> Secuencia artificial

<220>

<223> C3E-7093 AA

<400> 80

Gly	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly
1				5				10					15		

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

<210> SEQ ID NO: 81

<211> 864

<212> ADN

<213> Secuencia artificial

<220>

<223> C3E-7094 ORF

<400> 81

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atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcggg      60
gaagtgcagc tgggtggaatc cggggggggc ctggtgcagc ctgggggggag cctgagactg      120
agttgtgccg cctctgggggt gacatttaac tactatggca tgtcttggat ccgccaggca      180
cctggaaagg gcctggagtg ggtggccagc atcacttctt ccggcgggag aatctactat      240
cccgacagcg tcaagggcag gttcacaatt tcccgcgaga acacacagaa aactctgtac      300
ctgcagatga atagcctgag agccgaagat acagctgtgt actattgcac tctggacggc      360
agggatgggt gggtcgccta ttggggggcag ggaaccctgg tgacagtcag ctccggagga      420
ggaggatctg gcggaggagg cagtggggga ggcgggtcaa actttatgct gaccagccc      480
cacagtgtgt cagagagccc tggcaagact gtcacatctt cttgtaaaag gaacaccgga      540
aatattggca gtaactacgt gaattggtat cagcagcatg aagggtctag tccaaccaca      600
atcatctacc ggagcgataa gagacccgac ggggtgtccg atcgattctc cggatctatc      660
gaccggtcaa gcaagagtgc ttactgacc attagcaatc tgaaaacaga ggacgaagca      720
gattactttt gccagtccta ttctctggc ttcatctttg gaggcgggac taaactgacc      780
gtgctgggag cggccgcagg tgcaggtggg gattacaaag atgatgacga taaaggtgca      840
gcggcgcata accatcatca ccac                                         864

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<210> SEQ ID NO: 82

<211> 269

<212> PRT

<213> Secuencia artificial

<220>

<223> C3E-7094 AA

<400> 82

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Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1           5           10           15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr
          20           25           30

Tyr Gly Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
          35           40           45

```

Val Ala Ser Ile Thr Ser Ser Gly Gly Arg Ile Tyr Tyr Pro Asp Ser
50 55 60

Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu
65 70 75 80

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

Cys Thr Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro His Ser Val
130 135 140

Ser Glu Ser Pro Gly Lys Thr Val Thr Ile Ser Cys Lys Arg Asn Thr
145 150 155 160

Gly Asn Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln His Glu Gly
165 170 175

Ser Ser Pro Thr Thr Ile Ile Tyr Arg Ser Asp Lys Arg Pro Asp Gly
180 185 190

Val Ser Asp Arg Phe Ser Gly Ser Ile Asp Arg Ser Ser Lys Ser Ala
195 200 205

Ser Leu Thr Ile Ser Asn Leu Lys Thr Glu Asp Glu Ala Asp Tyr Phe
210 215 220

Cys Gln Ser Tyr Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Thr Val Leu Gly Ala Ala Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp
245 250 255

Asp Asp Lys Gly Ala Ala Ala His His His His His His
260 265

<210> SEQ ID NO: 83

<211> 864

<212> ADN

<213> Secuencia artificial

<220>

<223> C3E-7095 ORF

<400> 83

atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgga

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gaagtgcagc tgggtggaatc cgggggggggc ctggtgcagc ctgggggggag cctgagactg      120
agtttgtgccg cctctgggggt gacatttaac tactatggca tgtcttggat ccgccaggca      180
cctggaaagg gcctggagtg ggtggccagc atcacttctt ccggcgggcg aatctactat      240
cccgacagcg tcaagggcag gttcacaatt tcccgcgaga acacacagaa aactctgtac      300
ctgcagatga atagcctgag agccgaagat acagctgtgt actattgcac tctggacggc      360
agggatgggt gggtcgccta ttggggggcag ggaaccctgg tgacagtcag ctccggagga      420
ggaggatctg gcggaggagg cagtggggga ggcgggtcaa actttatgct gaccagccc      480
cacagtgtgt cagagagccc tggcaagact gtcaccatct cttgtaaaag gaacaccgga      540
aatattggca gtaactacgt gaattggtat cagcagcatg aagggtctag tccaaccaca      600
atcatctacc gggccgataa gagacccgac ggggtgtccg atcgattctc cggatctatc      660
gaccggtcaa gcaagagtgc ttactgacc attagcaatc tgaaaacaga ggacgaagca      720
gattactttt gccagtccta ttctcttggc ttcatctttg gaggcgggac taaactgacc      780
gtgctgggcg cggccgcagg tgcaggtggg gattacaaag atgatgacga taaaggtgca      840
gcggcgcacac accatcatca ccac                                             864

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<210> SEQ ID NO: 84
<211> 269
<212> PRT
<213> Secuencia artificial

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<220>
<223> C3E-7095 AA

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<400> 84

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Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1              5              10              15

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr
              20              25              30

Tyr Gly Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
              35              40              45

Val Ala Ser Ile Thr Ser Ser Gly Gly Arg Ile Tyr Tyr Pro Asp Ser
              50              55              60

Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu
65              70              75              80

```

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
 85 90 95
 Cys Thr Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 115 120 125
 Ser Gly Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro His Ser Val
 130 135 140
 Ser Glu Ser Pro Gly Lys Thr Val Thr Ile Ser Cys Lys Arg Asn Thr
 145 150 155 160
 Gly Asn Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln His Glu Gly
 165 170 175
 Ser Ser Pro Thr Thr Ile Ile Tyr Arg Ala Asp Lys Arg Pro Asp Gly
 180 185 190
 Val Ser Asp Arg Phe Ser Gly Ser Ile Asp Arg Ser Ser Lys Ser Ala
 195 200 205
 Ser Leu Thr Ile Ser Asn Leu Lys Thr Glu Asp Glu Ala Asp Tyr Phe
 210 215 220
 Cys Gln Ser Tyr Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu
 225 230 235 240
 Thr Val Leu Gly Ala Ala Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp
 245 250 255
 Asp Asp Lys Gly Ala Ala Ala His His His His His His
 260 265

<210> SEQ ID NO: 85
 <211> 33
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> HN53R Fw

<400> 85
 gtggccagca tcactagggtc cggcggggcga atc

33

<210> SEQ ID NO: 86
 <211> 33
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> HN53R Rv

 <400> 86
 gattcgcccg ccggacctag tgatgctggc cac 33

 <210> SEQ ID NO: 87
 <211> 33
 <212> ADN
 <213> Secuencia artificial

 <220>
 <223> HN53S Fw

 <400> 87
 gtggccagca tcacttcttc cggcgggcca atc 33

 <210> SEQ ID NO: 88
 <211> 33
 <212> ADN
 <213> Secuencia artificial

 <220>
 <223> HN53S Rv

 <400> 88
 gattcgcccg ccggaagaag tgatgctggc cac 33

 <210> SEQ ID NO: 89
 <211> 1590
 <212> ADN
 <213> Secuencia artificial

 <220>
 <223> AXC-0001 ORF

 <400> 89
 atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgga 60
 gaagtgcagc tgcaggaatc tggccctggc ctcgtgaagc ctagccagac cctgagcctg 120
 acctgtaccg tgtccggcta cagcatcacc agcaactact ggggctggat cagaaagttc 180
 cccggcaaca agatggaatg gatcggccac atcaccaaca gcggaacac cacctacaac 240
 cccagcctga agtcccggat cagcatcagc cgggacacca gcaagaacca gttctccctg 300
 aagctgtcca gcgtgacccc tgccgatacc gccgtgtact actgtgcca gggcgccctc 360
 gattactggg gccagggaac cctcgtgacc gtgtctagcg gaggcggagg atctggcggc 420
 ggaggaagtg gcggaggggg atctgatatc cagatgaccc agagccccag cagcctgtct 480

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gccagcgtgg gcgacagagt gaccatcacc tgtagagcca gccaggacat cggcaactac      540
ctgagctggg tccagcagaa agtgggcaag tccccagac ggatgatcta cggcgccatc      600
aagctggccg tgggctgtgc aagcagattc agcggcagca gaagcggcag cgactacacc      660
ctgaccatca gctccctgca gcccaggagc ttccgcatct actactgcct gcagtacatc      720
cagttccctc tgaccttcgg cagcggcacc aagctggaaa tcaagagaac cgggggaggg      780
ggttcagaag tgcagctggg ggaatccggg gggggcctgg tgcagcctgg ggggagcctg      840
agactgagtt gtgccgcctc tggggtgaca tttaactact atggcatgtc ttggatccgc      900
caggcacctg gaaagggcct ggagtgggtg gccagcatca ctaattccgg cgggcgaatc      960
tactatcccg acagcgtcaa gggcagggtc acaatttccc gcgagaacac acagaaaact     1020
ctgtacctgc agatgaatag cctgagagcc gaagatacag ctgtgtacta ttgcactctg     1080
gacggcaggg atgggtgggt cgcctattgg gggcagggaa ccctggtgac agtcagctcc     1140
ggaggaggag gatctggcgg aggaggcagt gggggaggcg ggtcaaactt tatgctgacc     1200
cagccccaca gtgtgtcaga gagccctggc aagactgtca ccatctcttg taaaaggaac     1260
accggaataa ttggcagtaa ctacgtgaat tggatcagc agcatgaagg gtctagtcca     1320
accacaatca tctaccgga cgataagaga cccgacgggg tgtccgatcg attctccgga     1380
tctatcgacc ggtcaagcaa gagtgcttca ctgaccatta gcaatctgaa aacagaggac     1440
gaagcagatt acttttgcca gtcctattcc tctggcttca tctttggagg cgggactaaa     1500
ctgaccgtgc tgggcgcggc cgcaggtgca ggtggtgatt acaaagatga tgacgataaa     1560
ggtgcagcgg cgcataacca tcatcaccac                                     1590

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<210> SEQ ID NO: 90
<211> 511
<212> PRT
<213> Secuencia artificial

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<220>
<223> AXC-0001 AA

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<400> 90

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Gly Glu Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser
1           5           10          15

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Gln	Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Tyr	Ser	Ile	Thr	Ser	
			20							25				30		
Asn	Tyr	Trp	Gly	Trp	Ile	Arg	Lys	Phe	Pro	Gly	Asn	Lys	Met	Glu	Trp	
			35							40				45		
Ile	Gly	His	Ile	Thr	Asn	Ser	Gly	Asn	Thr	Thr	Tyr	Asn	Pro	Ser	Leu	
			50										60			
Lys	Ser	Arg	Ile	Ser	Ile	Ser	Arg	Asp	Thr	Ser	Lys	Asn	Gln	Phe	Ser	
65							70							75		
Leu	Lys	Leu	Ser	Ser	Val	Thr	Pro	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
						85							90			
Ala	Lys	Gly	Ala	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	
						100							105			
Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	
						115							120			
Ser	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	
						130							135			
Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Gly	Asn	
145							150							155		
Tyr	Leu	Ser	Trp	Phe	Gln	Gln	Lys	Val	Gly	Lys	Ser	Pro	Arg	Arg	Met	
						165							170			
Ile	Tyr	Gly	Ala	Ile	Lys	Leu	Ala	Val	Gly	Val	Pro	Ser	Arg	Phe	Ser	
						180							185			
Gly	Ser	Arg	Ser	Gly	Ser	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	
						195							200			
Pro	Glu	Asp	Phe	Ala	Ile	Tyr	Tyr	Cys	Leu	Gln	Tyr	Ile	Gln	Phe	Pro	
						210							215			
Leu	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Thr	Gly	Gly	
						225							230			
Gly	Gly	Ser	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	
						245							250			
Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Val	Thr	Phe	
						260							265			
Asn	Tyr	Tyr	Gly	Met	Ser	Trp	Ile	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
						275							280			

Glu Trp Val Ala Ser Ile Thr Asn Ser Gly Gly Arg Ile Tyr Tyr Pro
 290 295 300

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys
 305 310 315 320

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 325 330 335

Tyr Tyr Cys Thr Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly
 340 345 350

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
 355 360 365

Gly Gly Ser Gly Gly Gly Gly Ser Asn Phe Met Leu Thr Gln Pro His
 370 375 380

Ser Val Ser Glu Ser Pro Gly Lys Thr Val Thr Ile Ser Cys Lys Arg
 385 390 395 400

Asn Thr Gly Asn Ile Gly Ser Asn Tyr Val Asn Trp Tyr Gln Gln His
 405 410 415

Glu Gly Ser Ser Pro Thr Thr Ile Ile Tyr Arg Asp Asp Lys Arg Pro
 420 425 430

Asp Gly Val Ser Asp Arg Phe Ser Gly Ser Ile Asp Arg Ser Ser Lys
 435 440 445

Ser Ala Ser Leu Thr Ile Ser Asn Leu Lys Thr Glu Asp Glu Ala Asp
 450 455 460

Tyr Phe Cys Gln Ser Tyr Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr
 465 470 475 480

Lys Leu Thr Val Leu Gly Ala Ala Ala Gly Ala Gly Gly Asp Tyr Lys
 485 490 495

Asp Asp Asp Asp Lys Gly Ala Ala Ala His His His His His His
 500 505 510

<210> SEQ ID NO: 91

<211> 1584

<212> ADN

<213> Secuencia artificial

<220>

<223> AXC-0002 ORF

<400> 91

atgaaacacc tgtggttctt cctcctgctg gtggcagctc ccagatgggt gctgagcgga

gaagtgcagc tgcaggaatc tggccctggc ctctgtgaagc ctagccagac cctgagcctg	120
acctgtaccg tgtccggcta cagcatcacc agcaactact ggggctggat cagaaagttc	180
cccggcaaca agatggaatg gatcggccac atcaccaaca gcggaacac cacctacaac	240
cccagcctga agtcccggat cagcatcagc cgggacacca gcaagaacca gttctccctg	300
aagctgtcca gcgtgacccc tgccgatacc gccgtgtact actgtgcca gggcgccctc	360
gattactggg gccagggaac cctcgtgacc gtgtctagcg gaggcggagg atctggcggc	420
ggaggaagtg gcggaggggg atctgatatc cagatgacct agagccccag cagcctgtct	480
gccagcgtgg gcgacagagt gaccatcacc tgtagagcca gccaggacat cggcaactac	540
ctgagctggg tccagcagaa agtgggcaag tccccagac ggatgatcta cggcgccatc	600
aagctggccg tgggcgtgcc aagcagattc agcggcagca gaagcggcag cgactacacc	660
ctgaccatca gtcctctgca gcccgaggac ttcgccatct actactgcct gcagtacatc	720
cagttccctc tgaccttcgg cagcggcacc aagctggaaa tcaagagaac cgggggaggc	780
ggttcagaag tgcagctggg ggaatccggg gggggcctgg tgcagcctgg ggggagcctg	840
agactgagtt gtgccgcctc tggggtgaca tttaactact atggcatgtc ttggatccgc	900
caggcacctg gaaagggcct ggagtgggtg gccagcatca ctaattccgg cgggcgaatc	960
tactatcccg acagcgtcaa gggcagggtc acaatttccc gcgagaacac acagaaaact	1020
ctgtacctgc agatgaatag cctgagagcc gaagatacag ctgtgtacta ttgcactctg	1080
gacggcaggg atgggtgggt cgcctattgg gggcaggga ccctggtgac agtcagctcc	1140
ggaggaggag gatctggcgg aggaggcagt gggggaggcg ggtcaaactt tatgctcact	1200
cagccgtcct ctgtttctgg cgtacctggc caacgggtga ccattagctg tacgggtaat	1260
accgggaata tcgggtctaa ctacgtgaac tggatatcagc agcttcagg gacagctccc	1320
aagttgctga tctatcgca cgacaaaaga ccctcagggg tccctgaccg atttagtggc	1380
agcaaaagcg gtacttccgc ttccctggcg ataaccggct ttcaggccga agatgaggca	1440
gactactatt gccagtcata ttccagcggc ttcatcttcg gaggcggaac taagctgaca	1500
gtgttgggcg cggccgcagg tgcaggtggg gattacaaag atgatgacga taaaggtgca	1560
gcggcgcatc accatcatca ccac	1584

<210> SEQ ID NO: 92
 <211> 509
 <212> PRT
 <213> Secuencia artificial

<220>

<223> AXC-0002 AA

<400> 92

Gly Glu Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser
 1 5 10 15

Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser
 20 25 30

Asn Tyr Trp Gly Trp Ile Arg Lys Phe Pro Gly Asn Lys Met Glu Trp
 35 40 45

Ile Gly His Ile Thr Asn Ser Gly Asn Thr Thr Tyr Asn Pro Ser Leu
 50 55 60

Lys Ser Arg Ile Ser Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
 65 70 75 80

Leu Lys Leu Ser Ser Val Thr Pro Ala Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
 100 105 110

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 115 120 125

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 130 135 140

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Asn
 145 150 155 160

Tyr Leu Ser Trp Phe Gln Gln Lys Val Gly Lys Ser Pro Arg Arg Met
 165 170 175

Ile Tyr Gly Ala Ile Lys Leu Ala Val Gly Val Pro Ser Arg Phe Ser
 180 185 190

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

Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Leu Gln Tyr Ile Gln Phe Pro
 210 215 220

Leu	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Thr	Gly	Gly	
225					230					235					240	
Gly	Gly	Ser	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	
				245					250					255		
Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Val	Thr	Phe	
			260					265					270			
Asn	Tyr	Tyr	Gly	Met	Ser	Trp	Ile	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
	275						280					285				
Glu	Trp	Val	Ala	Ser	Ile	Thr	Asn	Ser	Gly	Gly	Arg	Ile	Tyr	Tyr	Pro	
	290					295					300					
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Glu	Asn	Thr	Gln	Lys	
305					310					315					320	
Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	
				325					330					335		
Tyr	Tyr	Cys	Thr	Leu	Asp	Gly	Arg	Asp	Gly	Trp	Val	Ala	Tyr	Trp	Gly	
			340					345					350			
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	
		355					360					365				
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asn	Phe	Met	Leu	Thr	Gln	Pro	Ser	
	370					375					380					
Ser	Val	Ser	Gly	Val	Pro	Gly	Gln	Arg	Val	Thr	Ile	Ser	Cys	Thr	Gly	
385					390					395					400	
Asn	Thr	Gly	Asn	Ile	Gly	Ser	Asn	Tyr	Val	Asn	Trp	Tyr	Gln	Gln	Leu	
			405						410					415		
Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Arg	Asp	Asp	Lys	Arg	Pro	
			420					425					430			
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Lys	Ser	Gly	Thr	Ser	Ala	
		435					440					445				
Ser	Leu	Ala	Ile	Thr	Gly	Phe	Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	
	450					455					460					
Cys	Gln	Ser	Tyr	Ser	Ser	Gly	Phe	Ile	Phe	Gly	Gly	Gly	Thr	Lys	Leu	
465					470					475					480	
Thr	Val	Leu	Gly	Ala	Ala	Ala	Gly	Ala	Gly	Gly	Asp	Tyr	Lys	Asp	Asp	
				485					490					495		

Asp Asp Lys Gly Ala Ala Ala His His His His His His
 500 505

<210> SEQ ID NO: 93

<211> 1620

<212> ADN

<213> Secuencia artificial

<220>

<223> MGC-0001 ORF

<400> 93

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caggtgcagc tgggtgcagtc tgggggagggc ttggtccagc ctggaggggtc cctgagactc	120
tcctgtgcag cctctggatt caccttcagt gactacgaca tggactgggt ccgccaggct	180
ccagggaagg ggctggagtg ggtggcagtt atatcatctg atgaaaacac taaatactac	240
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat	300
ctgcaaatac acagcctgag agccgaggac acggctgtgt attactgtgc aacctatacc	360
agcacctggg atgccgttga ctctctggggc cagggaaccc tggtcaccgt ctctctcagg	420
ggaggcggtt caggcgaggg tggcagcggc ggtggcgggg gtgatgttgt gatgactcag	480
tctccactct ccctgcccgt cacccttggg gagccggcct ccatctcctg cagggtctagt	540
cagagcctcc tgcataagaa cggaaagaac tatttggtat ggtacctgca gaagccaggg	600
cagtctccac agctcctgat ctatttggtt tctaatacgg cctccggggg ccctgacagg	660
ttcagtggca gtggatcagg cacagatatt aactgaaga tcagcagagt ggaggctgag	720
gatgttgagg tttattactg catgcaaact cttcaaacc cctacacttt tggccagggg	780
accaaggtgg aaatcaaacg tgggggagggc ggttcagaag tgcagctggg ggaatccggg	840
gggggcctgg tgcagcctgg ggggagcctg agactgagtt gtgccgcctc tggggtgaca	900
tttaactact atggcatgtc ttggatccgc caggcacctg gaaagggcct ggagtgggtg	960
gccagcatca ctaattccgg cgggcgaatc tactatcccg acagcgtcaa gggcaggttc	1020
acaatttccc gcgagaacac acagaaaact ctgtacctgc agatgaatag cctgagagcc	1080
gaagatacag ctgtgtacta ttgcactctg gacggcaggg atgggtgggt cgcctattgg	1140
gggcagggaa ccctggtgac agtcagctcc ggaggaggag gatctggcgg aggaggcagt	1200

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gggggaggcg ggtcaaactt tatgctgacc cagccccaca gtgtgtcaga gagccctggc      1260
aagactgtca ccattctcttg taaaaggaac accggaaata ttggcagtaa ctacgtgaat      1320
tggatatcagc agcatgaagg gtctagtcca accacaatca tctaccggga cgataagaga      1380
cccgacgggg tgtccgatcg attctccgga tctatcgacc ggtcaagcaa gagtgcttca      1440
ctgaccatta gcaatctgaa aacagaggac gaagcagatt acttttgcca gtcctattcc      1500
tctggcttca tctttggagg cgggactaaa ctgaccgtgc tgggcgcggc cgcaggtgca      1560
ggtggtgatt acaaagatga tgacgataaa ggtgcagcgg cgcataacca tcatcaccac      1620

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<210> SEQ ID NO: 94

<211> 521

<212> PRT

<213> Secuencia artificial

<220>

<223> MGC-0001 AA

<400> 94

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Gly Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly
1              5              10              15

```

```

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp
              20              25              30

```

```

Tyr Asp Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
              35              40              45

```

```

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

```

```

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
65              70              75              80

```

```

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

```

```

Cys Ala Thr Tyr Thr Ser Thr Trp Tyr Ala Val Asp Ser Trp Gly Gln
              100             105             110

```

```

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
              115             120             125

```

```

Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro Leu
              130             135             140

```

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

Ser Asn Tyr Val Asn Trp Tyr Gln Gln His Glu Gly Ser Ser Pro Thr
 420 425 430

Thr Ile Ile Tyr Arg Asp Asp Lys Arg Pro Asp Gly Val Ser Asp Arg
 435 440 445

Phe Ser Gly Ser Ile Asp Arg Ser Ser Lys Ser Ala Ser Leu Thr Ile
 450 455 460

Ser Asn Leu Lys Thr Glu Asp Glu Ala Asp Tyr Phe Cys Gln Ser Tyr
 465 470 475 480

Ser Ser Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
 485 490 495

Ala Ala Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly
 500 505 510

Ala Ala Ala His His His His His His
 515 520

<210> SEQ ID NO: 95

<211> 1614

<212> ADN

<213> Secuencia artificial

<220>

<223> MGC-0002 ORF

<400> 95

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caggtgcagc tgggtgcagtc tgggggaggc ttggtccagc ctggagggtc cctgagactc	120
tcctgtgcag cctctggatt caccttcagt gactacgaca tggactgggt ccgccaggct	180
ccaggaagg ggctggagtg ggtggcagtt atatcatctg atgaaaacac taaatactac	240
gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat	300
ctgcaaatac acagcctgag agccgaggac acggctgtgt attactgtgc aacctatacc	360
agcacctggg atgccgttga ctctggggc caggaaccc tggtcaccgt ctctcaggt	420
ggaggcggtt caggcgagg tggcagcggc ggtggcgga gtgatgttg gatgactcag	480
tctccactct ccctgccgt caccctgga gagccggcct ccatctctg caggtctagt	540
cagagcctcc tgcataagaa cggaaagaac tatttggtt ggtacctgca gaagccagg	600
cagtctccac agctcctgat ctatttgggt tctaatacgg cctccggggg ccctgacagg	660

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ttcagtggca gtggatcagg cacagatddd acactgaaga tcagcagagt ggaggctgag      720
gatgttgggg tttattactg catgcaaact cttcaaacc cctacacttt tggccagggg      780
accaaggtgg aaatcaaacg tgggggagggc gggttcagaag tgcagctggg ggaatccggg      840
ggggggcctgg tgcagcctgg ggggagcctg agactgagtt gtgccgcctc tggggtgaca      900
tttaactact atggcatgtc ttggatccgc caggcacctg gaaagggcct ggagtgggtg      960
gccagcatca ctaattccgg cgggcgaatc tactatcccg acagcgtcaa gggcaggttc     1020
acaatttccc gcgagaacac acagaaaact ctgtacctgc agatgaatag cctgagagcc     1080
gaagatacag ctgtgtacta ttgcactctg gacggcaggg atgggtgggt cgcctattgg     1140
gggcagggaa ccctggtgac agtcagctcc ggaggaggag gatctggcgg aggaggcagt     1200
gggggagggc ggtcaaactt tatgctcact cagccgtcct ctgtttctgg cgtacctggc     1260
caacgggtga ccattagctg tacgggtaat accgggaata tcgggtctaa ctacgtgaac     1320
tggtatcagc agcttccagg gacagctccc aagttgctga tctatcgca cgacaaaaga     1380
ccctcagggg tccctgaccg atttagtggc agcaaaagcg gtacttccgc ttccctggcg     1440
ataaccggct ttcaggccga agatgaggca gactactatt gccagtcata ttccagcggc     1500
ttcatcttcg gaggcggaac taagctgaca gtgttggggc cggccgcagg tgcaggtggg     1560
gattacaaag atgatgacga taaaggtgca gcggcgcac accatcatca ccac           1614

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<210> SEQ ID NO: 96
<211> 519
<212> PRT
<213> Secuencia artificial

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<220>
<223> MGC-0002 AA

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<400> 96

```

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Gly Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly
1              5              10              15

```

```

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp
20              25              30

```

```

Tyr Asp Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
35              40              45

```

Val	Ala	Val	Ile	Ser	Ser	Asp	Glu	Asn	Thr	Lys	Tyr	Tyr	Ala	Asp	Ser	50	55	60
Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	65	70	75
Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	85	90	95
Cys	Ala	Thr	Tyr	Thr	Ser	Thr	Trp	Tyr	Ala	Val	Asp	Ser	Trp	Gly	Gln	100	105	110
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	115	120	125
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Val	Val	Met	Thr	Gln	Ser	Pro	Leu	130	135	140
Ser	Leu	Pro	Val	Thr	Pro	Gly	Glu	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	145	150	155
Ser	Gln	Ser	Leu	Leu	His	Ser	Asn	Gly	Lys	Asn	Tyr	Leu	Asp	Trp	Tyr	165	170	175
Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Leu	Gly	Ser	180	185	190
Asn	Arg	Ala	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	195	200	205
Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	210	215	220
Val	Tyr	Tyr	Cys	Met	Gln	Thr	Leu	Gln	Thr	Pro	Tyr	Thr	Phe	Gly	Gln	225	230	235
Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Gly	Gly	Gly	Gly	Ser	Glu	Val	Gln	245	250	255
Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	260	265	270
Leu	Ser	Cys	Ala	Ala	Ser	Gly	Val	Thr	Phe	Asn	Tyr	Tyr	Gly	Met	Ser	275	280	285
Trp	Ile	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Ser	Ile	290	295	300
Thr	Asn	Ser	Gly	Gly	Arg	Ile	Tyr	Tyr	Pro	Asp	Ser	Val	Lys	Gly	Arg	305	310	315

Phe Thr Ile Ser Arg Glu Asn Thr Gln Lys Thr Leu Tyr Leu Gln Met
 325 330 335
 Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Leu Asp
 340 345 350
 Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
 355 360 365
 Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
 370 375 380
 Gly Ser Asn Phe Met Leu Thr Gln Pro Ser Ser Val Ser Gly Val Pro
 385 390 395 400
 Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Asn Thr Gly Asn Ile Gly
 405 410 415
 Ser Asn Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys
 420 425 430
 Leu Leu Ile Tyr Arg Asp Asp Lys Arg Pro Ser Gly Val Pro Asp Arg
 435 440 445
 Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly
 450 455 460
 Phe Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Ser Ser
 465 470 475 480
 Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala
 485 490 495
 Ala Gly Ala Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys Gly Ala Ala
 500 505 510
 Ala His His His His His His
 515

<210> SEQ ID NO: 97

<211> 10

<212> PRT

<213> *Homo sapiens*

<400> 97

Ile Leu Phe Gly Ile Ser Leu Arg Glu Val
 1 5 10

<210> SEQ ID NO: 98

<211> 8

<212> PRT

<213> Secuencia artificial

<220>

<223> CDRH2 de variantes

<220>

<221> Xaa

<222> (3)..(3)

<223> el primer Xaa es cualquier aminoácido de origen natural

<220>

<221> Xaa

<222> (4)..(4)

<223> el segundo Xaa es cualquier aminoácido de origen natural

<400> 98

Ile Thr Xaa Xaa Gly Gly Arg Ile

1

5

<210> SEQ ID NO: 99

<211> 3

<212> PRT

<213> Secuencia artificial

<220>

<223> CDRL2 de variantes

<220>

<221> X

<222> (2)..(2)

<223> Xaa es cualquier aminoácido de origen natural

<400> 99

Arg Xaa Asp

1

<210> SEQ ID NO: 100

<211> 118

<212> PRT

<213> Secuencia artificial

<220>

<223> VH de variantes de C3E-7034

<220>

<221> MISC_FEATURE

<222> (53)..(53)

<223> el primer Xaa es cualquier aminoácido de origen natural

<220>

<221> MISC_FEATURE
 <222> (54)..(54)
 <223> el segundo Xaa es cualquier aminoácido de origen natural

<400> 100

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1           5           10           15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Val Thr Phe Asn Tyr Tyr
          20           25           30

Gly Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35           40           45

Ala Ser Ile Thr Xaa Xaa Gly Gly Arg Ile Tyr Tyr Pro Asp Ser Val
          50           55           60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
          85           90           95

Thr Leu Asp Gly Arg Asp Gly Trp Val Ala Tyr Trp Gly Gln Gly Thr
          100          105          110

Leu Val Thr Val Ser Ser
          115

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<210> SEQ ID NO: 101
 <211> 109
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> VL de variantes de C3E-7034

<220>
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 <222> (52)..(52)
 <223> Xaa es cualquier aminoácido de origen natural

<400> 101

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Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1           5           10           15

Thr Val Thr Ile Ser Cys Lys Arg Asn Thr Gly Asn Ile Gly Ser Asn
          20           25           30

```

Tyr Val Asn Trp Tyr Gln Gln His Glu Gly Ser Ser Pro Thr Thr Ile
 35 40 45

Ile Tyr Arg Xaa Asp Lys Arg Pro Asp Gly Val Ser Asp Arg Phe Ser
 50 55 60

Gly Ser Ile Asp Arg Ser Ser Lys Ser Ala Ser Leu Thr Ile Ser Asn
 65 70 75 80

Leu Lys Thr Glu Asp Glu Ala Asp Tyr Phe Cys Gln Ser Tyr Ser Ser
 85 90 95

Gly Phe Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 100 105

<210> SEQ ID NO: 102

<211> 107

<212> PRT

<213> Secuencia artificial

<220>

<223> VL de variantes de C3E-7035

<220>

<221> MISC_FEATURE

<222> (52)..(52)

<223> Xaa es cualquier aminoácido de origen natural

<400> 102

Gln Ala Val Leu Thr Gln Pro Ser Ser Val Ser Gly Val Pro Gly Gln
 1 5 10 15

Arg Val Thr Ile Ser Cys Lys Arg Asn Thr Gly Asn Ile Gly Ser Asn
 20 25 30

Tyr Val Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
 35 40 45

Ile Tyr Arg Xaa Asp Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Phe Gln
 65 70 75 80

Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Ser Ser Gly Phe
 85 90 95

Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 100 105

<210> SEQ ID NO: 103

<211> 107
 <212> PRT
 <213> Secuencia artificial

<220>
 <223> VL de variantes C3E-7036

<220>
 <221> MISC_FEATURE
 <222> (52)..(52)
 <223> Xaa es cualquier aminoácido de origen natural

<400> 103

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

Arg	Val	Thr	Ile	Ser	Cys	Thr	Gly	Asn	Thr	Gly	Asn	Ile	Gly	Ser	Asn
			20					25					30		

Tyr	Val	Asn	Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu
		35					40					45			

Ile	Tyr	Arg	Xaa	Asp	Lys	Arg	Pro	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser
	50					55					60				

Gly	Ser	Lys	Ser	Gly	Thr	Ser	Ala	Ser	Leu	Ala	Ile	Thr	Gly	Phe	Gln
65					70					75					80

Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ser	Tyr	Ser	Ser	Gly	Phe
				85					90					95	

Ile	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu
		100					105			