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<110> Dow Agrosiences, LLP
 Narva, Ken
 Worden, Sarah
 Frey, Meghan
 Rangasamy, Murugesan
 Veeramani, Balaji
 Gandra, Premchand
 Lo, Wendy
 Fishilevich, Elane
 Geng, Chaoxian
 Vilcinskas, Andreas
 Knorr, Eileen

<120> Moléculas de ácido nucleico de ARN polimerasa II-215 para el control de plagas de insectos

<130> 2971-P12622.1US (76743)

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<151> 2015-03-13

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Cys Val Ile Val Ala Gly Glu Asp Arg Leu Ser Lys Gln Ala Asn
 1010 1015 1020

Glu Asn Ala Thr Leu Leu Phe Gln Cys Leu Val Arg Ser Thr Leu
 1025 1030 1035

Cys Thr	Lys Cys Val Ser	Glu	Glu Phe Arg Leu Ser	Thr Glu Ala
1040		1045		1050
Phe Glu	Trp Leu Ile Gly	Glu	Ile Glu Thr Arg Phe	Gln Gln Ala
1055		1060		1065
Gln Ala	Asn Pro Gly Glu Met	Val Gly Ala Leu Ala	Ala Gln Ser	
1070		1075		1080
Leu Gly	Glu Pro Ala Thr Gln	Met Thr Leu Asn Thr	Phe His Phe	
1085		1090		1095
Ala Gly	Val Ser Ser Lys Asn	Val Thr Leu Gly Val	Pro Arg Leu	
1100		1105		1110
Lys Glu	Ile Ile Asn Ile Ser	Lys Lys Pro Lys Ala	Pro Ser Leu	
1115		1120		1125
Thr Val	Phe Leu Thr Gly Ala	Ala Ala Arg Asp Ala	Glu Lys Ala	
1130		1135		1140
Lys Asn	Val Leu Cys Arg Leu	Glu His Thr Thr Leu	Arg Lys Val	
1145		1150		1155
Thr Ala	Asn Thr Ala Ile Tyr	Tyr Asp Pro Asp Pro	Gln Asn Thr	
1160		1165		1170
Val Ile	Pro Glu Asp Gln Glu	Phe Val Asn Val Tyr	Tyr Glu Met	
1175		1180		1185
Pro Asp	Phe Asp Pro Thr Arg	Ile Ser Pro Trp Leu	Leu Arg Ile	
1190		1195		1200
Glu Leu	Asp Arg Lys Arg Met	Thr Asp Lys Lys Leu	Thr Met Glu	
1205		1210		1215
Gln Ile	Ala Glu Lys Ile Asn	Ala Gly Phe Gly Asp	Asp Leu Asn	
1220		1225		1230
Cys Ile	Phe Asn Asp Asp Asn	Ala Glu Lys Leu Val	Leu Arg Ile	
1235		1240		1245
Arg Ile	Met Asn Ser Asp Asp	Gly Lys Phe Gly Glu	Gly Ala Asp	
1250		1255		1260
Glu Asp	Val Asp Lys Met Asp	Asp Asp Met Phe Leu	Arg Cys Ile	
1265		1270		1275
Glu Ala	Asn Met Leu Ser Asp	Met Thr Leu Gln Gly	Ile Glu Ala	
1280		1285		1290

Ile Ser Lys Val Tyr Met His Leu Pro Gln Thr Asp Ser Lys Lys
 1295 1300 1305

Arg Ile Val Ile Thr Glu Thr Gly Glu Phe Lys Ala Ile Ala Glu
 1310 1315 1320

Trp Leu Leu Glu Thr Asp Gly Thr Ser Met Met Lys Val Leu Ser
 1325 1330 1335

Glu Arg Asp Val Asp Pro Val Arg Thr Phe Ser Asn Asp Ile Cys
 1340 1345 1350

Glu Ile Phe Ser Val Leu Gly Ile Glu Ala Val Arg Lys Ser Val
 1355 1360 1365

Glu Lys Glu Met Asn Ala Val Leu Ser Phe Tyr Gly Leu Tyr Val
 1370 1375 1380

Asn Tyr Arg His Leu Ala Leu Leu Cys Asp Val Met Thr Ala Lys
 1385 1390 1395

Gly His Leu Met Ala Ile Thr Arg His Gly Ile Asn Arg Gln Asp
 1400 1405 1410

Thr Gly Ala Leu Met Arg Cys Ser Phe Glu Glu Thr Val Asp Val
 1415 1420 1425

Leu Met Asp Ala Ala Ser His Ala Glu Val Asp Pro Met Arg Gly
 1430 1435 1440

Val Ser Glu Asn Ile Ile Leu Gly Gln Leu Pro Arg Met Gly Thr
 1445 1450 1455

Gly Cys Phe Asp Leu Leu Leu Asp Ala Glu Lys Cys Lys Met Gly
 1460 1465 1470

Ile Ala Ile Pro Gln Ala His Ser Ser Asp Leu Met Ala Ser Gly
 1475 1480 1485

Met Phe Phe Gly Leu Ala Ala Thr Pro Ser Ser Met Ser Pro Gly
 1490 1495 1500

Gly Ala Met Thr Pro Trp Asn Gln Ala Ala Thr Pro Tyr Val Gly
 1505 1510 1515

Ser Ile Trp Ser Pro Gln Asn Leu Met Gly Ser Gly Met Thr Pro
 1520 1525 1530

Gly Gly Ala Ala Phe Ser Pro Ser Ala Ala Ser Asp Ala Ser Gly
 1535 1540 1545

Met Ser Pro Ala Tyr Gly Gly Trp Ser Pro Thr Pro Gln Ser Pro

1550		1555		1560
Ala Met Ser Pro Tyr Met	Ala Ser Pro His Gly Gln	Ser Pro Ser		
1565	1570	1575		
Tyr Ser Pro Ser Ser Pro	Ala Phe Gln Pro Thr Ser	Pro Ser Met		
1580	1585	1590		
Thr Pro Thr Ser Pro Gly	Tyr Ser Pro Ser Ser Pro	Gly Tyr Ser		
1595	1600	1605		
Pro Thr Ser Leu Asn Tyr	Ser Pro Thr Ser Pro Ser	Tyr Ser Pro		
1610	1615	1620		
Thr Ser Gln Ser Tyr Ser	Pro Thr Ser Pro Ser Tyr	Ser Pro Thr		
1625	1630	1635		
Ser Pro Asn Tyr Ser Pro	Thr Ser Pro Ser Tyr Ser	Pro Thr Ser		
1640	1645	1650		
Pro Asn Tyr Ser Pro Thr	Ser Pro Asn Tyr Ser Pro	Thr Ser Pro		
1655	1660	1665		
Ser Tyr Pro Ser Thr Ser	Pro Gly Tyr Ser Pro Thr	Ser Arg Ser		
1670	1675	1680		
Tyr Ser Pro Thr Ser Pro	Ser Tyr Ser Gly Thr Ser	Pro Ser Tyr		
1685	1690	1695		
Ser Pro Thr Ser Pro Ser	Tyr Ser Pro Thr Ser Pro	Ser Tyr Ser		
1700	1705	1710		
Pro Ser Ser Pro Asn Tyr	Ser Pro Thr Ser Pro Asn	Tyr Ser Pro		
1715	1720	1725		
Thr Ser Pro Asn Tyr Ser	Pro Ser Ser Pro Arg Tyr	Thr Pro Gly		
1730	1735	1740		
Ser Pro Ser Phe Ser Pro	Ser Ser Asn Ser Tyr Ser	Pro Thr Ser		
1745	1750	1755		
Pro Gln Tyr Ser Pro Thr	Ser Pro Ser Tyr Ser Pro	Ser Ser Pro		
1760	1765	1770		
Lys Tyr Ser Pro Thr Ser	Pro Asn Tyr Ser Pro Thr	Ser Pro Ser		
1775	1780	1785		
Phe Ser Gly Gly Ser Pro	Gln Tyr Ser Pro Thr Ser	Pro Lys Tyr		
1790	1795	1800		
Ser Pro Thr Ser Pro Asn	Tyr Thr Leu Ser Ser Pro	Gln His Thr		
1805	1810	1815		

Pro Thr Gly Ser Ser Arg Tyr Ser Pro Ser Thr Ser Ser Tyr Ser
1820 1825 1830

Pro Asn Ser Pro Asn Tyr Ser Pro Thr Ser Pro Gln Tyr Ser Ile
1835 1840 1845

His Ser Thr Lys Tyr Ser Pro Ala Ser Pro Thr Phe Thr Pro Thr
1850 1855 1860

Ser Pro Ser Phe Ser Pro Ala Ser Pro Ala Tyr Ser Pro Gln Pro
1865 1870 1875

Met Tyr Ser Pro Ser Ser Pro Asn Tyr Ser Pro Thr Ser Pro Ser
1880 1885 1890

Gln Asp Thr Asp
1895

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<212> ADN
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gaaaccgttg aaattctcat ggacgctgcc atgttctctg aaggagaccc attgactggg 120
gtgtctgaaa acgtgatgct tggccaattg gtcgcgctcg gtactgggtt gatggacctt 180
gtgttggtatg cgaagaaatt ggcaaacgcc atcgagtacg aagcatctga aatccagcaa 240
gtgatgagag gtctggacaa cgagtggaga agtcagacc atggacctgg aactocaatc 300
tcgactccat tcgcatcgac tccaggtttc acggcttctt ctcttttcag ccctgggtgg 360
gggtgcgttct cgctgcagc tgggtgcgtt tcgccaatgg cgagcccagc ctgcctggc 420
ttcatgtcgt ctccagggtt cagtgtcgt tctccagcgc acagcccagc gtctccgttg 480
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<210> 6
<211> 196
<212> PRT
<213> *Diabrotica virgifera*

<400> 6

Ile Thr Arg His Gly Ile Asn Arg Asp Asp Ser Gly Pro Leu Val Arg
1 5 10 15

Cys Ser Phe Glu Glu Thr Val Glu Ile Leu Met Asp Ala Ala Met Phe
20 25 30

Ser Glu Gly Asp Pro Leu Thr Gly Val Ser Glu Asn Val Met Leu Gly

35 40 45
 Gln Leu Ala Pro Leu Gly Thr Gly Leu Met Asp Leu Val Leu Asp Ala
 50 55 60

 Lys Lys Leu Ala Asn Ala Ile Glu Tyr Glu Ala Ser Glu Ile Gln Gln
 65 70 75 80

 Val Met Arg Gly Leu Asp Asn Glu Trp Arg Ser Pro Asp His Gly Pro
 85 90 95

 Gly Thr Pro Ile Ser Thr Pro Phe Ala Ser Thr Pro Gly Phe Thr Ala
 100 105 110

 Ser Ser Pro Phe Ser Pro Gly Gly Gly Ala Phe Ser Pro Ala Ala Gly
 115 120 125

 Ala Phe Ser Pro Met Ala Ser Pro Ala Ser Pro Gly Phe Met Ser Ser
 130 135 140

 Pro Gly Phe Ser Ala Ala Ser Pro Ala His Ser Pro Ala Ser Pro Leu
 145 150 155 160

 Ser Pro Thr Ser Pro Ala Tyr Ser Pro Met Ser Pro Ala Tyr Ser Pro
 165 170 175

 Thr Ser Pro Ala Tyr Ser Pro Thr Ser Pro Ala Tyr Ser Pro Thr Ser
 180 185 190

 Pro Ala Tyr Ser
 195

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 <211> 155
 <212> ADN
 <213> *Diabrotica virgifera*

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 gaaaaatgca agtatggcat cgaaatacag agcac 155

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 <211> 118
 <212> ADN
 <213> *Diabrotica virgifera*

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 ggctgcttcg atcttttgct ggacgccgaa aaatgtaaaa tgggaattgc catacctc 118

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<212> ADN
 <213> Diabrotica virgifera
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 ggtttgatgg accttggtt ggatgcgaag aaattggcaa acgccatcga g 111

<210> 10
 <211> 24
 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Secuencia del promtor T7

<400> 10
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<210> 11
 <211> 503
 <212> ADN
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<220>
 <223> Secuencia codificante de YFP parcial

<400> 11
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 ggagggcaat gtggatggcc acaccttcag catccgcggc aagggtacg gcgatgccag 120
 cgtgggcaag gtggatgcc agttcatctg caccaccgac gatgtgccg tgccctggag 180
 caccctggtg accaccctga cctacggcgc ccagtgttc gccaaatcag gcccagagct 240
 gaaggatttc tacaagagct gcatgccga tggctacgtg caggagcgca ccatcacctt 300
 cgagggcgat ggcaatttca agaccgcgc cgaggtgacc ttcgagaatg gcagcgtgta 360
 caatcgctg aagctgaatg gccagggctt caagaaggat ggccacgtgc tgggcaagaa 420
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<210> 12
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<220>
 <223> Cebador Dvv-rpII-215-1_For

<400> 12
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<210> 13
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<220>
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<400> 13
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<210> 14
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<220>
<223> Cebador Dvv-rpII-215-2_For

<400> 14
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<210> 15
<211> 48
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<213> Secuencia artificial

<220>
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<400> 15
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<210> 16
<211> 44
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<400> 16
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<210> 17
<211> 46
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<220>
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<400> 17
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<210> 18
<211> 46
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<210> 19
<211> 48
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<223> Cebador Dvv-rpII-215-2_v1_Rev

<400> 19

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<210> 20

<211> 705

<212> ADN

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aaggttgatg cacagttcat ctgcacaact ggtgatgttc ctgtgccttg gagcacactt 180
gtcaccactc tcacctatgg agcacagtgc tttgccaagt atggtccaga gttgaaggac 240
ttctacaagt cctgtatgcc agatggctat gtgcaagagc gcacaatcac ctttgaaggga 300
gatggcaact tcaagactag ggctgaagtc acctttgaga atgggtctgt ctacaatagg 360
gtcaaaactca atggtcaagg cttcaagaaa gatggtcattg tgttgggaaa gaacttggag 420
ttcaacttca ctccctactg cctctacatc tggggtgacc aagccaacca cgggtctcaag 480
tcagccttca agatctgtca tgagattact ggcagcaaag gcgacttcat agtggctgac 540
cacaccaga tgaacactcc cattgggtgga ggtccagttc atgttccaga gtatcatcac 600
atgtcttacc atgtgaaaact ttccaaagat gtgacagacc acagagacaa catgtccttg 660
aaagaaaactg tcagagctgt tgactgtcgc aagacctacc tttga 705

<210> 21

<211> 218

<212> ADN

<213> Diabrotica virgifera

<400> 21

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ttataagaat ttcccaggcc tatgaaggat tgtaccaacg mtcattggaa tctgatatca 180
aaggagatac ctcaggaaca ttaaaaaaga attattag 218

<210> 22

<211> 424

<212> ADN

<213> Diabrotica virgifera

<220>

<221> misc_feature

<222> (393)..(395)

<223> n e s a , c , g , o t

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 gggcatccca ttgaaaaagc cattgaaaac gagttttcag gaaatgctaa acaagccatg 180
 ttacacctta tccagagcgt aagagatcaa gttgcatatt tggtaaccag gctgcatgat 240
 tcaatggcag gcgtcggtag tgacgataga actttaatca gaattgttgt ttcgagatct 300
 gaaatcgatc tagaggaaat caaacaatgc tatgaagaaa tctacagtaa aaccttggct 360
 gataggatag cggtatgacac atctggcgac tannnaaaag ccttatttagc cgttggttgg 420
 taag 424

<210> 23
 <211> 397
 <212> ADN
 <213> *Diabrotica virgifera*

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 tcaatgccct tcaacgcaaa caccagaact tctccaaga cctacaaaca ctccaatcga 180
 acgtccaaca aatccaagaa gaatcagcta aacttcaagc tagctatgcc ggtgatagag 240
 ctaaagaaat caccaacagg gagcaggaag tggtagcagc ctgggcagcc ttgcagatcg 300
 cttgcgatca gagacacgga aaattgagcg atactggtga tctattcaaa ttctttaact 360
 tggtagcaac gttgatgcag tggatggagc aatggac 397

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 <212> ADN
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<400> 24
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 tttaggaaag gaattgttga gccgtaatca ctatgctagt gctgatatta aggataaatt 180
 ggtcgcgttg acgaatcaaa ggaatgctgt actacagagg tgggaagaaa gatgggagaa 240
 cttgcaactc atcctcgagg tataccaatt cgccagagat gcggccgctg ccgaagcatg 300
 gttgatcgca caagaacctt acttgatgag ccaagaacta ggacacacca ttgacgacgt 360
 tgaaaacttg ataaagaaac acgaagcgtt cgaaaaatcg gcagcggcgc aagaagagag 420
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 <212> ADN
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gcctttcttc caaaatatca agaacctcga caagtttggt tggagagttt agatacgata 180
gacgacaaaa aattgggtat tcttgagctg catcctgatg tttttgctac taatccaaga 240
atagatatta tacatcaaaa tgttagatgg caaagtttat atagatatgt aagctatgct 300
catacaaagt caagatttga agtgagaggt 330

<210> 26
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<213> Diabrotica virgifera

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gacccaaatc tccaaccctt catttttaca tgattccatt ctacaccgt ttgctgggtt 180
tgactagcgc actttcagta aaatttgccc aagatgactt gcacgttggt gatagtctag 240
atctgccaac tgacgaacaa agttatatag aagagctggt caaaagccgc ttttgggggt 300
ccttcttggt ttattttag 320

<210> 27
<211> 47
<212> ADN
<213> Secuencia artificial

<220>
<223> Cebador YFP-F_T7
<400> 27
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<210> 28
<211> 23
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<213> Secuencia artificial

<220>
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<400> 28
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<210> 29
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<220>
<223> Cebador YFP-F
<400> 29
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<210> 30
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<223> Cebador YFP-R_T7

<400> 30

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<210> 31

<211> 46

<212> ADN

<213> Secuencia artificial

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<223> Cebador Ann-F1_T7

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<210> 32

<211> 29

<212> ADN

<213> Secuencia artificial

<220>

<223> Cebador Ann-R1

<400> 32

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<210> 33

<211> 22

<212> ADN

<213> Secuencia artificial

<220>

<223> Cebador Ann-F1

<400> 33

gctccaacag tgggttcctta tc 22

<210> 34

<211> 53

<212> ADN

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<220>

<223> Cebador Ann-R1_T7

<400> 34

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<210> 35

<211> 48

<212> ADN

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<220>

<223> Cebador Ann-F2_T7

<400> 35

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<210> 36
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<220>
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<400> 36
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<210> 37
 <211> 24
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<220>
 <223> Cebador Ann-F2

<400> 37
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<210> 38
 <211> 48
 <212> ADN
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<220>
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<400> 38
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<210> 39
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<220>
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<400> 39
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<210> 40
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<220>
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<400> 40
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<210> 41
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 <212> ADN
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<220>
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<400> 41

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<210> 42

<211> 46

<212> ADN

<213> Secuencia artificial

<220>

<223> Cebador Betasp2-R1_T7

<400> 42

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<210> 43

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<223> Cebador Betasp2-F2_T7

<400> 43

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<210> 44

<211> 22

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<213> Secuencia artificial

<220>

<223> Cebador Betasp2-R2

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<210> 45

<211> 22

<212> ADN

<213> Secuencia artificial

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<211> 46

<212> ADN

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<210> 47

<211> 51

<212> ADN

<213> Secuencia artificial

<220>

<223> Cebador L4-F1_T7

<400> 47

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<210> 48

<211> 26

<212> ADN

<213> Secuencia artificial

<220>

<223> Cebador L4-R1

<400> 48

acctctcact tcaaattcttg actttg 26

<210> 49

<211> 27

<212> ADN

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<400> 49

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<211> 50

<212> ADN

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<220>

<223> Cebador L4-R1_T7

<400> 50

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<210> 51

<211> 50

<212> ADN

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<223> Cebador L4-F2_T7

<400> 51

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<210> 52

<211> 25

<212> ADN

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<220>

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<400> 52

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<210> 53

<211> 26

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<223> Cebador L4-F2

<400> 53

caaagtcaag atttgaagtg agaggt 26

<210> 54

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<211> 1885

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<213> Euschistus heros

<400> 78

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

Val Leu Ala Glu Leu Ser Lys Asp Thr Glu Tyr Gly Lys Glu Leu Ala
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Gly Val Ser Pro Thr Gly His Ile Leu Asn Pro Gln Glu Val Leu Arg
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Leu Leu Glu Ala Ile Pro Ser Gln Asp Ile Pro Leu Leu Val Met Asn
 225 230 235 240

Tyr Asn Leu Ser Lys Pro Ala Asp Leu Ile Leu Thr Arg Ile Pro Val
 245 250 255

Pro Pro Leu Ser Ile Arg Pro Ser Val Ile Ser Asp Leu Lys Ser Gly
 260 265 270

Thr Asn Glu Asp Asp Leu Thr Met Lys Leu Ser Glu Ile Val Phe Ile
 275 280 285

Asn Asp Val Ile Met Lys His Lys Leu Ser Gly Ala Lys Ala Gln Met
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Ile Ala Glu Asp Trp Glu Phe Leu Gln Leu His Cys Ala Leu Tyr Ile
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Asn Ser Glu Thr Ser Gly Ile Pro Ile Asn Met Gln Pro Lys Lys Ser
325 330 335

Ser Arg Gly Leu Val Gln Arg Leu Lys Gly Lys His Gly Arg Phe Arg
340 345 350

Gly Asn Leu Ser Gly Lys Arg Val Asp Phe Ser Ala Arg Thr Val Ile
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Ser Pro Asp Pro Asn Leu Arg Ile Glu Glu Val Gly Val Pro Ile His
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Val Ala Lys Ile Leu Thr Phe Pro Glu Arg Val Gln Pro Ala Asn Lys
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Glu Leu Leu Arg Arg Leu Val Cys Asn Gly Pro Asp Val His Pro Gly
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Tyr Gly Asn Arg Ala Lys Ile Ala Gln Glu Leu Lys Glu Gly Asp Ile
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Val Glu Arg His Leu Arg Asp Gly Asp Ile Val Leu Phe Asn Arg Gln
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Glu Asn Arg Thr Phe Arg Phe Asn Glu Cys Ala Cys Thr Pro Tyr Asn
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Ala Asp Phe Asp Gly Asp Glu Met Asn Leu His Val Pro Gln Ser Met
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Glu Thr Arg Ala Glu Val Glu Asn Leu His Val Thr Pro Arg Gln Ile
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Ile Thr Pro Gln Ser Asn Lys Pro Val Met Gly Ile Val Gln Asp Thr
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Leu Thr Ala Val Arg Lys Met Thr Lys Arg Asp Val Phe Leu Glu Lys
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Glu Gln Met Met Asn Ile Leu Met His Leu Pro Gly Trp Asn Gly Arg
565 570 575

Met Pro Ile Pro Ala Ile Leu Lys Pro Lys Pro Leu Trp Thr Gly Lys
 580 585 590

Gln Val Phe Ser Leu Ile Ile Pro Gly Glu Val Asn Met Ile Arg Thr
 595 600 605

His Ser Thr His Pro Asp Asp Glu Asp Asn Gly Pro Tyr Lys Trp Ile
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Ser Pro Gly Asp Thr Lys Val Met Val Glu Ala Gly Lys Leu Val Met
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Asp Lys Thr Gly Gly Ser Ala Lys Lys Ser Leu Thr Glu Tyr Asn Asn
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<213> *Euschistus heros*

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Asn Met Asp Glu Asn Ala Ser Asn Arg Lys Pro Gly His Gly Gly Cys
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Thr Leu Gly Ser Gly Gly Lys Ala Asn Ile Phe Tyr Val Leu Leu Cys
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Asp Trp Gly Glu Glu Ala Ala Thr Thr Ala Met Trp Arg Leu Ser Arg
 660 665 670

Met Thr Ser Ala Tyr Leu Met Asn Arg Gly Phe Ser Ile Gly Ile Gly
 675 680 685

Asp Val Thr Pro Ser Pro Arg Leu Leu His Leu Lys Gln Glu Leu Leu
 690 695 700

Asn Ala Gly Tyr Thr Lys Cys Asn Glu Phe Ile Gln Lys Gln Ala Asp
 705 710 715 720

Gly Lys Leu Gln Cys Gln Pro Gly Cys Ser Ala Asp Glu Thr Leu Glu
 725 730 735

Ala Val Ile Leu Lys Glu Leu Ser Val Ile Arg Asp Arg Ala Gly Lys
 740 745 750

Ala Cys Leu Asn Glu Leu Gly Ser Gln Asn Ser Pro Leu Ile Met Ala
 755 760 765

Leu Ala Gly Ser Lys Gly Ser Phe Ile Asn Ile Ser Gln Met Ile Ala
 770 775 780

Cys Val Gly Gln Gln Ala Ile Ser Gly Lys Arg Val Pro Asn Gly Phe
 785 790 795 800

Glu Asp Arg Ala Leu Pro His Tyr Glu Arg His Ser Lys Ile Pro Ala
 805 810 815

Ala Lys Gly Phe Val Glu Asn Ser Phe Phe Ser Gly Leu Thr Pro Thr
 820 825 830

Glu Phe Phe Phe His Thr Met Gly Gly Arg Glu Gly Leu Val Asp Thr
 835 840 845

Ala Val Lys Thr Ala Glu Thr Gly Tyr Met Gln Arg Arg Leu Val Lys
 850 855 860

Ser Leu Glu Asp Leu Cys Leu His Tyr Asp Met Thr Val Arg Asn Ser
 865 870 875 880

Thr Gly Asp Val Ile Gln Phe Val Tyr Gly Gly Asp Gly Leu Asp Pro
 885 890 895

Thr Tyr Met Glu Gly Asn Gly Cys Pro Val Glu Leu Lys Arg Val Trp
 900 905 910

Asp Gly Val Arg Ala Asn Tyr Pro Phe Gln Gln Glu Lys Pro Leu Ser
 915 920 925

Tyr Asp Asp Val Ile Glu Gly Ser Asp Val Leu Leu Asp Ser Ser Glu

930 935 940
 Phe Ser Cys Cys Ser His Glu Phe Lys Glu Gln Leu Arg Ser Phe Val
 945 950 955 960
 Lys Asp Gln Ala Lys Lys Cys Leu Glu Ile Gln Thr Gly Trp Glu Lys
 965 970 975
 Lys Ser Pro Leu Ile Ser Glu Leu Glu Arg Val Thr Leu Ser Gln Leu
 980 985 990
 Ile His Phe Phe Gln Thr Cys Arg Glu Lys Tyr Leu Asn Ala Lys Ile
 995 1000 1005
 Glu Pro Gly Thr Ala Val Gly Ala Leu Ala Ala Gln Ser Ile Gly
 1010 1015 1020
 Glu Pro Gly Thr Gln Met Thr Leu Lys Thr Phe His Phe Ala Gly
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 Val Ala Ser Met Asn Ile Thr Gln Gly Val Pro Arg Ile Lys Glu
 1040 1045 1050
 Ile Ile Asn Ala Ser Lys Asn Ile Ser Thr Pro Ile Ile Thr Ala
 1055 1060 1065
 Tyr Leu Glu Asn Asp Thr Asp Pro Glu Phe Ala Arg Gln Val Lys
 1070 1075 1080
 Gly Arg Ile Glu Lys Thr Thr Leu Gly Glu Val Thr Glu Tyr Ile
 1085 1090 1095
 Glu Glu Val Tyr Val Pro Thr Asp Cys Phe Leu Ile Ile Lys Leu
 1100 1105 1110
 Asp Val Glu Arg Ile Arg Leu Leu Lys Leu Glu Val Asn Ala Asp
 1115 1120 1125
 Ser Ile Lys Tyr Ser Ile Cys Thr Ser Lys Leu Lys Ile Lys Asn
 1130 1135 1140
 Leu Gln Val Leu Val Gln Thr Ser Ser Val Leu Thr Val Asn Thr
 1145 1150 1155
 Gln Ala Gly Lys Asp Thr Leu Asp Gly Ser Leu Arg Tyr Leu Lys
 1160 1165 1170
 Glu Asn Leu Leu Lys Val Val Ile Lys Gly Val Pro Asn Val Asn
 1175 1180 1185
 Arg Ala Val Ile His Glu Glu Glu Asp Ala Gly Val Lys Arg Tyr
 1190 1195 1200

Lys Leu Leu Val Glu Gly Asp Asn Leu Arg Asp Val Met Ala Thr
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Arg Gly Ile Lys Gly Thr Lys Cys Thr Ser Asn Asn Thr Tyr Gln
1220 1225 1230

Val Phe Ser Thr Leu Gly Ile Glu Ala Ala Arg Ser Thr Ile Met
1235 1240 1245

Ser Glu Ile Lys Leu Val Met Glu Asn His Gly Met Ser Ile Asp
1250 1255 1260

His Arg His Pro Met Leu Val Ala Asp Leu Met Thr Cys Arg Gly
1265 1270 1275

Glu Val Leu Gly Ile Thr Arg Gln Gly Leu Ala Lys Met Lys Glu
1280 1285 1290

Ser Val Leu Asn Leu Ala Ser Phe Glu Lys Thr Ala Asp His Leu
1295 1300 1305

Phe Asp Ala Ala Tyr Tyr Gly Gln Thr Asp Ala Ile Thr Gly Val
1310 1315 1320

Ser Glu Ser Ile Ile Met Gly Ile Pro Met Gln Ile Gly Thr Gly
1325 1330 1335

Leu Phe Lys Leu Leu His Arg Tyr Pro Phe Phe Ile Leu Phe Leu
1340 1345 1350

Ile Phe Arg Tyr Phe Ser Val Val Gly Gly Leu Ile Met Lys Arg
1355 1360 1365

Gln Cys Val Val Val Ser Met Asn Ile Ala Thr Ile Arg Ser Cys
1370 1375 1380

Tyr Ser Glu Val Ser Ser Thr Tyr Tyr Ile Leu Pro Ile Phe
1385 1390 1395

<210> 81

<211> 1140

<212> ADN

<213> Euschistus heros

<400> 81

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cccgtctcaa ggggaaggaa gggcgagtca gggggaatct catggggaag agagtagact 240

tcagtgccag ggcggtgata acagcagacg ccaacatctc ccttgaggaa gtgggagtcc 300

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<210> 82

<211> 379

<212> PRT

<213> Euschistus heros

<400> 82

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 35 40 45

Gln Lys Ser Gly Arg Pro Leu Lys Ser Ile Ser Ala Arg Leu Lys Gly
 50 55 60

Lys Glu Gly Arg Val Arg Gly Asn Leu Met Gly Lys Arg Val Asp Phe
 65 70 75 80

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

Val Gly Val Pro Val Glu Val Ala Lys Ile His Thr Phe Pro Glu Lys
 100 105 110

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

Pro Asn Glu Tyr Pro Gly Ala Asn Tyr Val Ile Arg Thr Asp Gly Gln
 130 135 140

Arg Ile Asp Leu Asn Phe Asn Arg Gly Asp Ile Lys Leu Glu Glu Gly
 145 150 155 160

Tyr Val Val Glu Arg His Met Gln Asp Gly Asp Ile Val Leu Phe Asn
 165 170 175

Arg Gln Pro Ser Leu His Lys Met Ser Met Met Gly His Lys Val Arg
 180 185 190

Val Met Ser Gly Lys Thr Phe Arg Leu Asn Leu Ser Val Thr Ser Pro
 195 200 205

Tyr Asn Ala Asp Phe Asp Gly Asp Glu Met Asn Leu His Met Pro Gln
 210 215 220

Ser Tyr Asn Ser Ile Ala Glu Leu Glu Glu Ile Cys Met Val Pro Lys
 225 230 235 240

Gln Ile Leu Gly Pro Gln Ser Asn Lys Pro Val Met Gly Ile Val Gln
 245 250 255

Asp Thr Leu Thr Gly Leu Arg Phe Phe Thr Met Arg Asp Ala Phe Phe
 260 265 270

Asp Arg Gly Glu Met Met Gln Ile Leu Tyr Ser Ile Asp Leu Asp Lys
 275 280 285

Tyr Asn Asp Ile Gly Leu Asp Thr Val Thr Lys Glu Gly Lys Lys Leu
 290 295 300

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

Ala Ile Glu Lys Pro Lys Gln Leu Trp Thr Gly Lys Gln Ile Leu Ser
 325 330 335

Phe Ile Phe Pro Asn Val Phe Tyr Gln Ala Ser Ser Asn Glu Ser Leu
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 355 360 365

Gly Glu Ile Met Ser Gly Ile Ile Asp Lys Arg
 370 375

<210> 83

<211> 490

<212> ADN

<213> Euschistus heros

<400> 83
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<210> 84
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 <212> ADN
 <213> Euschistus heros

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<210> 85
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 <212> ADN
 <213> Euschistus heros

<400> 85
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<213> Secuencia artificial

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<400> 86

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<210> 87

<211> 54

<212> ADN

<213> Secuencia artificial

<220>

<223> Cebador BSB_rpII-215-1_Rev

<400> 87

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<210> 88

<211> 48

<212> ADN

<213> Secuencia artificial

<220>

<223> Cebador BSB_rpII-215-2_For

<400> 88

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<210> 89

<211> 49

<212> ADN

<213> Secuencia artificial

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<400> 89

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<212> ADN

<213> Secuencia artificial

<220>

<223> Cebador BSB_rpII-215-3_For

<400> 90

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<210> 91

<211> 48

<212> ADN

<213> Secuencia artificial

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<223> Cebador BSB_rpII-215-3_Rev

<400> 91

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<210> 92
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 <212> ADN
 <213> Secuencia artificial

<220>
 <223> Hebra sentido de ARNdh de YFP

<400> 92
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<210> 93
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 <212> ADN
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<220>
 <223> Cebador YFPv2-F

<400> 93
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<210> 94
 <211> 46
 <212> ADN
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<400> 94
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<210> 95
 <211> 1259
 <212> ARN
 <213> Diabrotica virgifera

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<210> 96

<211> 6927

<212> ARN

<213> *Diabrotica virgifera*

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Leu Gly Gly Leu Met Asp Pro Arg Gln Gly Val Ile Asp Arg His Ser
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Arg Cys Gln Thr Cys Ala Gly Asn Met Thr Glu Cys Pro Gly His Phe
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Lys Thr Ile Lys Ile Leu Arg Cys Val Cys Phe Phe Cys Ser Lys Met
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 Asp Asp Leu Thr His Lys Leu Ala Asp Ile Ile Lys Ala Asn Asn Glu
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 Leu Gln Arg Asn Glu Ala Ala Gly Thr Ala Ala His Ile Ile Leu Glu
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 Asn Ile Lys Met Leu Gln Phe His Val Ala Thr Leu Val Asp Asn Asp
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 Met Pro Gly Met Pro Arg Ala Met Gln Lys Ser Gly Lys Pro Leu Lys
 325 330 335
 Ala Ile Lys Ala Arg Leu Lys Gly Lys Glu Gly Arg Ile Arg Gly Asn
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 Leu Met Gly Lys Arg Val Asp Phe Ser Ala Arg Thr Val Ile Thr Pro
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 Asp Pro Asn Leu Arg Ile Asp Gln Val Gly Val Pro Arg Ser Ile Ala
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 Gln Asn Met Thr Phe Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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 Xaa Xaa Xaa Xaa Xaa Asn Gly Asp Arg Ile Asp Leu Arg Phe His Pro
 420 425 430
 Lys Pro Ser Asp Leu His Leu Gln Cys Gly Tyr Lys Val Glu Arg His
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 Ile Arg Asp Gly Asp Leu Val Ile Phe Asn Arg Gln Pro Thr Leu His
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Lys Met Ser Met Met Gly His Arg Val Lys Val Leu Pro Trp Ser Thr
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Phe Arg Met Asn Leu Ser Cys Thr Ser Pro Tyr Asn Ala Asp Phe Asp
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Gly Asp Glu Met Asn Leu His Val Pro Gln Ser Met Glu Thr Arg Ala
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Glu Val Glu Asn Leu His Ile Thr Pro Arg Gln Ile Ile Thr Pro Gln
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Ala Asn Gln Pro Val Met Gly Ile Val Gln Asp Thr Leu Thr Ala Val
530 535 540

Arg Lys Met Thr Lys Arg Asp Val Phe Ile Glu Lys Glu Gln Met Met
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Asn Ile Leu Met Phe Leu Pro Ile Trp Asp Gly Lys Met Pro Arg Pro
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Ala Ile Leu Lys Pro Lys Pro Leu Trp Thr Gly Lys Gln Ile Phe Ser
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Leu Ile Ile Pro Gly Asn Val Asn Met Ile Arg Thr His Ser Thr His
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Pro Asp Asp Glu Asp Asp Gly Pro Tyr Arg Trp Ile Ser Pro Gly Asp
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Thr Lys Val Met Val Glu His Gly Glu Leu Ile Met Gly Ile Leu Cys
625 630 635 640

Lys Lys Ser Leu Gly Thr Ser Pro Gly Ser Leu Leu His Ile Cys Met
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Leu Glu Leu Gly His Glu Val Cys Gly Arg Phe Tyr Gly Asn Ile Gln
660 665 670

Thr Val Ile Asn Asn Trp Leu Leu Leu Glu Gly His Ser Ile Gly Ile
675 680 685

Gly Asp Thr Ile Ala Asp Pro Gln Thr Tyr Leu Glu Ile Gln Lys Ala
690 695 700

Ile His Lys Ala Lys Glu Asp Val Ile Glu Val Ile Gln Lys Ala His
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Asn Met Glu Leu Glu Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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Ser Glu	Glu Phe Arg Leu	Ser	Thr Glu Ala Phe	Glu	Trp Leu Ile
1055		1060		1065	
Gly Glu	Ile Glu Thr Arg	Phe	Gln Gln Ala Gln	Ala	Asn Pro Gly
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Glu Met	Val Gly Ala Leu	Ala	Ala Gln Ser Leu	Gly	Glu Pro Ala
1085		1090		1095	
Thr Gln	Met Thr Leu Asn	Thr	Phe His Phe Ala	Gly	Val Ser Ser
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Lys Asn	Val Thr Leu Gly	Val	Pro Arg Leu Lys	Glu	Ile Ile Asn
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Arg Leu	Glu His Thr Thr	Leu	Arg Lys Val Thr	Ala	Asn Thr Ala
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Ile Tyr	Tyr Asp Pro Asp	Pro	Gln Asn Thr Val	Ile	Pro Glu Asp
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Gln Glu	Phe Val Asn Val	Tyr	Tyr Glu Met Pro	Asp	Phe Asp Pro
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Thr Arg	Ile Ser Pro Trp	Leu	Leu Arg Ile Glu	Leu	Asp Arg Lys
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Arg Met	Thr Asp Lys Lys	Leu	Thr Met Glu Gln	Ile	Ala Glu Lys
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Ile Asn	Ala Gly Phe Gly	Asp	Asp Leu Asn Cys	Ile	Phe Asn Asp
1235		1240		1245	
Asp Asn	Ala Glu Lys Leu	Val	Leu Arg Ile Arg	Ile	Met Asp Ser
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Asp Asp	Gly Lys Phe Gly	Glu	Gly Ala Asp Glu	Asp	Val Asp Lys

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Ser Asp Met Thr Leu Gln Gly Ile Glu Ala Ile Ser Lys Val Tyr				
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Met His Leu Pro Gln Thr Asp Ser Lys Lys Arg Ile Val Ile Thr				
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Asp Ala Gly Glu Phe Lys Ala Ile Ala Glu Trp Leu Leu Glu Thr				
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Asp Gly Thr Ser Met Met Lys Val Leu Ser Glu Arg Asp Val Asp				
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Pro Val Arg Thr Phe Ser Asn Asp Ile Cys Glu Ile Phe Ser Val				
1355		1360		1365
Leu Gly Ile Glu Ala Val Arg Lys Ser Val Glu Lys Glu Met Asn				
1370		1375		1380
Ala Val Leu Ser Phe Tyr Gly Leu Tyr Val Asn Tyr Arg His Leu				
1385		1390		1395
Ala Leu Leu Cys Asp Val Met Thr Ala Lys Gly His Leu Met Ala				
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Ile Thr Arg His Gly Ile Asn Arg Gln Asp Thr Gly Ala Leu Met				
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Arg Cys Ser Phe Glu Glu Thr Val Asp Val Leu Leu Asp Ala Ala				
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Ser His Ala Glu Val Asp Pro Met Arg Gly Val Ser Glu Asn Ile				
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Ile Met Gly Gln Leu Pro Arg Met Gly Thr Gly Cys Phe Asp Leu				
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Leu Leu Asp Ala Glu Lys Cys Lys Met Gly Ile Ala Ile Pro Gln				
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Ala His Gly Ala Asp Ile Met Ser Ser Gly Met Phe Phe Gly Ser				
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Ala Ala Thr Pro Ser Ser Met Ser Pro Gly Gly Ala Met Thr Pro				
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Trp Asn Gln Ala Ala Thr Pro Tyr Met Gly Asn Ala Trp Ser Pro				
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His Asn Leu Met Gly Ser Gly Met Thr Pro Gly Gly Pro Ala Phe
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Ser Pro Ser Ala Ala Ser Asp Ala Ser Gly Met Ser Pro Gly Tyr
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Gly Ala Trp Ser Pro Thr Pro Asn Ser Pro Ala Met Ser Pro Tyr
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Met Ser Ser Pro Arg Gly Gln Ser Pro Ser Tyr Ser Pro Ser Ser
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Pro Ser Phe Gln Pro Thr Ser Pro Ser Ile Thr Pro Thr Ser Pro
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Gly Tyr Ser Pro Ser Ser Pro Gly Tyr Ser Pro Thr Ser Pro Asn
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Tyr Ser Pro Thr Ser Pro Ser Tyr Ser Pro Thr Ser Pro Ser Tyr
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Leu Gly Gly Leu Met Asp Pro Arg Gln Gly Val Ile Asp Arg His Ser
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Arg Cys Gln Thr Cys Ala Gly Asn Met Thr Glu Cys Pro Gly His Phe
65 70 75 80

Gly His Ile Glu Leu Ala Lys Pro Val Phe His Val Gly Phe Val Thr
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Lys Thr Ile Lys Ile Leu Arg Cys Val Cys Phe Phe Cys Ser Lys Met
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Leu Val Ser Pro Asn Asn Pro Lys Ile Lys Glu Val Val Met Lys Ser
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Lys Gly Gln Pro Arg Lys Arg Leu Ala Phe Val Tyr Asp Leu Cys Lys
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Gly Lys Asn Ile Cys Glu Gly Gly Asp Glu Met Asp Val Gly
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Lys Ala Asn Asn Glu Leu Gln Arg Asn Glu Ala Ala Gly Thr Ala Ala
 20 25 30

His Ile Ile Leu Glu Asn Ile Lys Met Leu Gln Phe His Val Ala Thr
 35 40 45

Leu Val Asp Asn Asp Met Pro Gly Met Pro Arg Ala Met Gln Lys Ser
 50 55 60

Gly Lys Pro Leu Lys Ala Ile Lys Ala Arg Leu Lys Gly Lys Glu Gly
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Arg Ile Arg Gly Asn Leu Met Gly Lys Arg Val Asp Phe Ser Ala Arg
 85 90 95

Thr Val Ile Thr Pro Asp Pro Asn Leu Arg Ile Asp Gln Val Gly Val
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Pro Arg Ser Ile Ala Gln Asn Met Thr Phe Pro
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Asn Gly Asp Arg Ile Asp Leu Arg Phe His Pro Lys Pro Ser Asp Leu
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His Leu Gln Cys Gly Tyr Lys Val Glu Arg His Ile Arg Asp Gly Asp
 20 25 30

Leu Val Ile Phe Asn Arg Gln Pro Thr Leu His Lys Met Ser Met Met
 35 40 45

Gly His Arg Val Lys Val Leu Pro Trp Ser Thr Phe Arg Met Asn Leu
50 55 60

Ser Cys Thr Ser Pro Tyr Asn Ala Asp Phe Asp Gly Asp Glu Met Asn
65 70 75 80

Leu His Val Pro Gln Ser Met Glu Thr Arg Ala Glu Val Glu Asn Leu
85 90 95

His Ile Thr Pro Arg Gln Ile Ile Thr Pro Gln Ala Asn Gln Pro Val
100 105 110

Met Gly Ile Val Gln Asp Thr Leu Thr Ala Val Arg Lys Met Thr Lys
115 120 125

Arg Asp Val Phe Ile Glu Lys Glu Gln Met Met Asn Ile Leu Met Phe
130 135 140

Leu Pro Ile Trp Asp Gly Lys Met Pro Arg Pro Ala Ile Leu Lys Pro
145 150 155 160

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

Asn Val Asn Met Ile Arg Thr His Ser Thr His Pro Asp Asp Glu Asp
180 185 190

Asp Gly Pro Tyr Arg Trp Ile Ser Pro Gly Asp Thr Lys Val Met Val
195 200 205

Glu His Gly Glu Leu Ile Met Gly Ile Leu Cys Lys Lys Ser Leu Gly
210 215 220

Thr Ser Pro Gly Ser Leu Leu His Ile Cys Met Leu Glu Leu Gly His
225 230 235 240

Glu Val Cys Gly Arg Phe Tyr Gly Asn Ile Gln Thr Val Ile Asn Asn
245 250 255

Trp Leu Leu Leu Glu Gly His Ser Ile Gly Ile Gly Asp Thr Ile Ala
260 265 270

Asp Pro Gln Thr Tyr Leu Glu Ile Gln Lys Ala Ile His Lys Ala Lys
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Glu Asp Val Ile Glu Val Ile Gln Lys Ala His Asn Met Glu Leu Glu
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Pro
305

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Leu Val Arg Ser Thr Leu Cys Thr Lys Cys Val Ser Glu Glu Phe Arg
 35 40 45

Leu Ser Thr Glu Ala Phe Glu Trp Leu Ile Gly Glu Ile Glu Thr Arg
 50 55 60

Phe Gln Gln Ala Gln Ala Asn Pro Gly Glu Met Val Gly Ala Leu Ala
 65 70 75 80

Ala Gln Ser Leu Gly Glu Pro Ala Thr Gln Met Thr Leu Asn Thr Phe
 85 90 95

His Phe Ala Gly Val Ser Ser Lys Asn Val Thr Leu Gly Val Pro Arg
 100 105 110

Leu Lys Glu Ile Ile Asn Ile Ser Lys Lys Pro Lys Ala Pro Ser Leu
 115 120 125

Thr Val Phe Leu Thr Gly Ala Ala Ala Arg Asp Ala Glu Lys Ala Lys
 130 135 140

Asn Val Leu Cys Arg Leu Glu His Thr Thr Leu Arg Lys Val Thr Ala
 145 150 155 160

Asn Thr Ala Ile Tyr Tyr Asp Pro Asp Pro Gln Asn Thr Val Ile Pro
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Glu Asp Gln Glu Phe Val Asn Val Tyr Tyr Glu Met Pro Asp Phe Asp
 180 185 190

Pro Thr Arg Ile Ser Pro Trp Leu Leu Arg Ile Glu Leu Asp Arg Lys
 195 200 205

Arg Met Thr Asp Lys Lys Leu Thr Met Glu Gln Ile Ala Glu Lys Ile
 210 215 220

Asn Ala Gly Phe Gly Asp Asp Leu Asn Cys Ile Phe Asn Asp Asp Asn
 225 230 235 240

Ala Glu Lys Leu Val Leu Arg Ile Arg Ile Met Asp Ser Asp Asp Gly
 245 250 255

Lys Phe Gly Glu Gly Ala Asp Glu Asp Val Asp Lys Met Asp Asp Asp
260 265 270

Met Phe Leu Arg Cys Ile Glu Ala Asn Met Leu Ser Asp Met Thr Leu
275 280 285

Gln Gly Ile Glu Ala Ile Ser Lys Val Tyr Met His Leu Pro Gln Thr
290 295 300

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

Ile Ala Glu Trp Leu Leu Glu Thr Asp Gly Thr Ser Met Met Lys Val
325 330 335

Leu Ser Glu Arg Asp Val Asp Pro Val Arg Thr Phe Ser Asn Asp Ile
340 345 350

Cys Glu Ile Phe Ser Val Leu Gly Ile Glu Ala Val Arg Lys Ser Val
355 360 365

Glu Lys Glu Met Asn Ala Val Leu Ser Phe Tyr Gly Leu Tyr Val Asn
370 375 380

Tyr Arg His Leu Ala Leu Leu Cys Asp Val Met Thr Ala Lys Gly His
385 390 395 400

Leu Met Ala Ile Thr Arg His Gly Ile Asn Arg Gln Asp Thr Gly Ala
405 410 415

Leu Met Arg Cys Ser Phe Glu Glu Thr Val Asp Val Leu Leu Asp Ala
420 425 430

Ala Ser His Ala Glu Val Asp Pro Met Arg Gly Val Ser Glu Asn Ile
435 440 445

Ile Met Gly Gln Leu Pro Arg Met Gly Thr Gly Cys Phe Asp Leu Leu
450 455 460

Leu Asp Ala Glu Lys Cys Lys Met Gly Ile Ala Ile Pro Gln Ala His
465 470 475 480

Gly Ala Asp Ile Met Ser Ser Gly Met Phe Phe Gly Ser Ala Ala Thr
485 490 495

Pro Ser Ser Met Ser Pro Gly Gly Ala Met Thr Pro Trp Asn Gln Ala
500 505 510

Ala Thr Pro Tyr Met Gly Asn Ala Trp Ser Pro His Asn Leu Met Gly
515 520 525

Ser Gly Met Thr Pro Gly Gly Pro Ala Phe Ser Pro Ser Ala Ala Ser
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Asp Ala Ser Gly Met Ser Pro Gly Tyr Gly Ala Trp Ser Pro Thr Pro
 545 550 555 560

Asn Ser Pro Ala Met Ser Pro Tyr Met Ser Ser Pro Arg Gly Gln Ser
 565 570 575

Pro Ser Tyr Ser Pro Ser Ser Pro Ser Phe Gln Pro Thr Ser Pro Ser
 580 585 590

Ile Thr Pro Thr Ser Pro Gly Tyr Ser Pro Ser Ser Pro Gly Tyr Ser
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Pro Thr Ser Pro Asn Tyr Ser Pro Thr Ser Pro Ser Tyr Ser Pro Thr
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 gacgacaugu uuuuacggug uaucgaggcc aacaugcuga gcgacaugac uuacagggu 3900

aucgaagcca uuuccaaagu guacaugcau uugccgcaga cagacuccaa gaaaaggau 3960
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 accaguauga ugaagguucu aucugaaaga gacguggauc ccguaagaac guucuccaac 4080
 gauaucugcg agaauuucuc cguacucggc aucgaggccg uacguaaauc gguggagaaa 4140
 gaaaugaacg ccguguuguc guucuauggu cucuacguua acuaccguca cuuggcuuug 4200
 cuuugcgacg ugaugacggc caaaggucan cucauggccu ucacgcguca cgguaucac 4260
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 aagaugggua uagccauccc ccaagcucan ggagccgaca uaaugucauc gggcauguuc 4500
 uucggcucgg cggccacucc gagcagcaug agccccggag gagccaugac uccuggaac 4560
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 ccuggcuauug gagcgugguc uccuacgcc aacucgccc caaugucucc uuacaugagu 4740
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 ccucuauc cuccacuuc ccuggauc ucgccagcu cccagguua cucaccaacg 4860
 agccccauu acagcccaac cucaccaagc uauucuccaa caaguccgag uuauucgcu 4920
 acgucgcan nnnnnnnnnn nnnnnnnnnn nnnnnnnnn nnnnn 4965

<210> 119
 <211> 476
 <212> ARN
 <213> Meligethes aeneus

<400> 119
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 cucaguccgg augaaaucg gcguauguca gucacagagg gcggcauccg cuuuccagag 120
 acaauggagg cgggccgccc caaaugggg ggccuauug acccgagaca aggggucauc 180
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 auuuuaagau gcgucugcuu uuucgagc aaaauguuag uuaguccaaa uauccaaaa 360
 auaaaagagg uggucaugaa auccaaaggu cagccgagga aaagguuggc uuuguuuac 420
 gaucucugca aagguaaaaa uauuugcgag gguggggaug aauggaugu aggaaa 476

<210> 120
 <211> 371
 <212> ARN
 <213> Meligethes aeneus

<400> 120
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 gaguugcaaa ggaacgaggc ggccgguacg gcugcgaca ucauccugga aaacauaaag 120

augcugcagu uucacguggc aaccucgguc gacaacgaca ugccgggcgau gccaaagagcc 180
 augcagaagu cggggaagcc ccuaaaagcg auaaaggcuc gguuaaaagg uaaggagggc 240
 aggauucgug guaaccuuau ggguaagcgu guggauuuuu ccgcgcgguac cguaaucacg 300
 cccgauccca aucugcgauu cgaucagguc gggguuccga gguccaucgc gcagaacaug 360
 acguucccug a 371

<210> 121
 <211> 917
 <212> ARN
 <213> *Meligethes aeneus*

<400> 121
 aauggugaca gaauagauuu gagguuccau cccaaaccgu cagauuugca uuucacagugu 60
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 acccuccaca agaugaguau gaugggggcac agggucaaaug ugcugcccug guccacuuuc 180
 aggauaauu uguccguuac ucccccuac aacgccgauu ucgacggcga cgaaaugaac 240
 uugcacguuc cgcaaaguau ggaaacaaga gccgaagugg aaaaccugca cauaaccccg 300
 aggcaauua ucacgccga agccaauca cccgucaugg guaucgugca agauacucuu 360
 accgcgguaga gaaagaugac gaaaaggac guuuucaucg agaaggaaca gaugaugaac 420
 auacucaugu ucuugccgau uugggacggg aaaaugccca gaccggccau ccugaaacc 480
 aaacccucuc ggacgggaaa gcaaaauuuc ucgcugauua ucccgggaaa uguaaauug 540
 auccguacgc acucgacgca ucccgacgac gaggacgacg guccguaccg guggaucucc 600
 cccggcgaca ccaaggucan gguggagcac ggcgaguuga ucauggggau ccucugcaaa 660
 aaauccucg guacuuccc cgguucucuc cuccacauu gcauguugga gcuggggcac 720
 gaggugugcg gcagguucua cgguuacac cagaccguga ucaacaauug gcugcuccuc 780
 gaaggucaca gcaucggauu cggagacacg aucgccgauc cucagaccua cuuggagau 840
 caaaaggcca uccacaaagc caaagaggau gucauagagg ucauccagaa ggcucacaac 900
 auggagcugg aaccac 917

<210> 122
 <211> 1899
 <212> ARN
 <213> *Meligethes aeneus*

<400> 122
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 aagugcguuu cggaggaguu caggcugagc accgaagccu ucgaauuguu gaucggagaa 180
 aucgagacga gauuccagca ggcucaggcg aaucggcg agauggugg cgcuuggcc 240
 gcgcaguccc uuggagaacc cgccacucag augacacuca acacuucca uuugcugga 300
 guguccuca aaaacguaac ccucggugug ccgcgucuaa aggaaucan caacaucucc 360

aagaagccua aagcgccuuc ccuaccguc uucuaaccg gggcugcagc cagggaugcg 420
gaaaaggcca aaaacgugcu cugucgcuug gaacauacca cguugagaaa agaacggca 480
aacaccgcca uuacuacga ucccgaacca cagaauaccg uuauuccgga ggauaggaa 540
uucguuaug uuacuaua aaugcccgau uucgauccga ccaggauuc gccauggcu 600
cuucguauug aauggauag aaaacguug acggacaaaa aaugacuau ggaacagau 660
gcggaaaaa ucaacgccg cuucggugac gauuugaau guauuuuaa ugacgacaac 720
gccgagaaac uggugcugcg gauucguau auggacagcg acgacguua auucggcgaa 780
ggggccgagc aagacgugga uaaaaggac gacgacagu uuuuacggug uaucgaggcc 840
aacaugcuga gcgacaugac uuacagggg aucgaagcca uuuccaaagu guacaugcau 900
uugccgcaga cagacuccaa gaaaaggau guuaaacug acgcgggcga guuuaaagcc 960
auugcggaau ggcucugga aacugacgu accaguaa ugaagguucu aucugaaaga 1020
gacguggauc ccguaagaac guucuccaac gauaucugcg agauuuucuc cguacucggc 1080
aucgaggccg uacguaaauc gguggagaaa gaaaugaacg ccguguuguc guucucggu 1140
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cucauggcca ucacgcguca cguaucaac agacaggaca ccgugcucu caugagaugc 1260
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uccgcagccu ccgaugcuuc uggaugugc ccuggcuau gagcgugguc uccuacgcca 1680
aacucgccc caaugucucc uuacaugagu ucuccucgcg ggcaaagucc aucauacagu 1740
cccugagcc ccuauucca accaaccucc ccucuauc cuccacuuc ccuggauac 1800
ucgccagcu cccagguua cucaccaac agccccaau acagcccaac cucaccaagc 1860
uuuuccaa caaguccgag uuauucgcu acgucgcca 1899

<210> 123

<211> 376

<212> ARN

<213> *Meligethes aeneus*

<400> 123

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aaucggcg agggccgac gaagacgug aaaaaugga cgacgacau uuuuacggu 120
guaucgagg caacaugcug agcgauga cuuacaggg uaucgaagcc auuuccaaag 180
uguacaugca uuugccgag acagacucca agaaaaggau cguauaacu gacgcgggcg 240
aguuaaagc cauugcgga uggcuacug aaacugacg uaccaguaug augaagguuc 300

uaucugaaag agacguggau cccguaagaa cguucuccaa cgauaucugc gagauuuucu 360
ccguacucgg caucga 376

<210> 124
<211> 409
<212> ADN
<213> Secuencia artificial

<220>
<223> ADN que codifica ARNdh de rpII215 v1 de Meliethes

<400> 124
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ggctgcttcg atcttttgcg ggacgccgaa aaatgtaaaa tgggaattgc catacctcga 120
agctagtacc agtcatcacg ctggagcgca catataggcc ctccatcaga aagtcattgt 180
gtatatctct cataggggaa gagctgcttg cgtatttccc ttccgtagtc agagtcatca 240
atcagctgca ccgtgtcgta aagcgggacg ttcgcaagct cgtccgcggt agaggtatgg 300
caattcccat ttacatttt tcggcgctcca gaaaagatc gaagcagcct gtgcccattc 360
ttggtagttg accgaggata atgttttcag atactcctct cattgggtc 409

<210> 125
<211> 24
<212> ADN
<213> Secuencia artificial

<220>
<223> Conjunto PRB 1 de sondas RPII215-2v1

<400> 125
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<210> 126
<211> 173
<212> ADN
<213> Secuencia artificial

<220>
<223> polinucleótido de bucle de ARNdh

<400> 126
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gtgtatatct ctcataggga acgagctgct tgcgtatttc ccttccgtag tcagagtcatt 120
caatcagctg caccgtgtcg taaagcggga cgttcgcaag ctgcgccggt gta 173

<210> 127
<211> 409
<212> ARN
<213> Secuencia artificial

<220>
<223> ARNdh de rpII215 v1

<400> 127
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ggcugcuucg aucuuuugcu ggacgccgaa aaauguaaaa uggaauuugc cauaccucga 120

agcuaguacc agucaucacg cuggagcgca cauauaggcc cuccaucaga aagucauugu 180
guauaucucu cauaggggaac gagcugcuug cguauuuucc uuccguaguc agagucauca 240
aucagcugca ccgugucgua aagcgggacg uucgcaagcu cguccgcggu agagguaugg 300
caauucccau uuuaacauuu ucggcgucca gcaaaagauc gaagcagccu gugcccauuc 360
uugguaguug accgaggaua auguuuucag auacuccucu cauuggguc 409

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