

LISTA DE SECUENCIAS

<110> Bayer CropScience LP
Bayer CropScience NV

<120> Evento de Élite EE-GM4 de soja

<130> APA16-6015 WO

<160> 30

<170> PatentIn versión 3.5

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aggggaaagc taggatactt tattgggttat ataattcagt gtgcaaaaag atattgacaa 180
atactacttt gttaagtta gacccctttt tagaaaagta ggcccaggcg ctctatcata 240
gctataaacc tattcagcac aatgggctcg agggcgatcg ctacgggaac tcgagaagga 300
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atggaatccg aggaggtttc cggatattac cctttgttga aaagtctcaa ttgccctttg 180
gtcttctgag actgtatctt tgatatTTTT ggagtagaca agtgtgtcgt gctccaccag 240
ttatcacatc aatccatatt taaagttaaa acaaataatt ctaaaaaaaaa ttgattgggtt 300
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1 5 10 15
gct att cca gtt tct aac gtg aac tcc ctt act gat acc gtg ggt gat 96
Ala Ile Pro Val Ser Asn Val Asn Ser Leu Thr Asp Thr Val Gly Asp
20 25 30

ctt aag aag gct tgg gaa gag ttc caa aag acc gga tct ttc tct ctt Leu Lys Lys Ala Trp Glu Glu Phe Gln Lys Thr Gly Ser Phe Ser Leu 35 40 45	144
act gct ctc caa cag gga ttc tct gct tct caa ggt gga acc ttc aac Thr Ala Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly Thr Phe Asn 50 55 60	192
tac ctt acc ctt ctc cag tct gga att tct ctt gct gga tcc ttc gtt Tyr Leu Thr Leu Leu Gln Ser Gly Ile Ser Leu Ala Gly Ser Phe Val 65 70 75 80	240
cca ggt gga act ttc gtg gct cca atc atc aac atg gtg att gga tgg Pro Gly Gly Thr Phe Val Ala Pro Ile Ile Asn Met Val Ile Gly Trp 85 90 95	288
ctt tgg cca cac aag aac aag aac gct gat acc gag aac ctc att aac Leu Trp Pro His Lys Asn Lys Asn Ala Asp Thr Glu Asn Leu Ile Asn 100 105 110	336
ctc atc gat tcc gag att cag aag cag ctt aac aag gct ctt ctc gat Leu Ile Asp Ser Glu Ile Gln Lys Gln Leu Asn Lys Ala Leu Leu Asp 115 120 125	384
gct gat agg aac gag tgg tcc tct tac ctt gag tcc atc ttc gat tcc Ala Asp Arg Asn Glu Trp Ser Ser Tyr Leu Glu Ser Ile Phe Asp Ser 130 135 140	432
tcc aac aac ctc aac ggt gct att gtg gat gct cag tgg agt gga act Ser Asn Asn Leu Asn Gly Ala Ile Val Asp Ala Gln Trp Ser Gly Thr 145 150 155 160	480
gtt aac act acc aac agg acc ctt aga aac cca acc gag tcc gat tac Val Asn Thr Thr Asn Arg Thr Leu Arg Asn Pro Thr Glu Ser Asp Tyr 165 170 175	528
acc aac gtt gtg acc aac ttc att gct gct gat ggc gat att gcc aac Thr Asn Val Val Thr Asn Phe Ile Ala Ala Asp Gly Asp Ile Ala Asn 180 185 190	576
aac gag aac cac atc atg aac gga aac ttc gat gtt gct gct gct cca Asn Glu Asn His Ile Met Asn Gly Asn Phe Asp Val Ala Ala Ala Pro 195 200 205	624
tac ttc gtt att gga gct acc gct aga ttc gct gct atg caa tcc tac Tyr Phe Val Ile Gly Ala Thr Ala Arg Phe Ala Ala Met Gln Ser Tyr 210 215 220	672
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Ile	Lys	Phe	Cys	Asn	Ala	Trp	Ile	Asp	Lys	Val	Gly	Leu	Ser	Asp	Ala		
225					230					235					240		
caa	ctt	act	acc	cag	aag	gct	aac	ctt	gat	agg	acc	aag	cag	aac	atg		768
Gln	Leu	Thr	Thr	Gln	Lys	Ala	Asn	Leu	Asp	Arg	Thr	Lys	Gln	Asn	Met		
				245					250					255			
agg	aac	gct	atc	ctt	aac	tac	acc	cag	cag	ggt	atg	aag	gtg	ttc	aag		816
Arg	Asn	Ala	Ile	Leu	Asn	Tyr	Thr	Gln	Gln	Val	Met	Lys	Val	Phe	Lys		
			260					265					270				
gac	tcc	aag	aac	atg	cca	acc	att	ggc	acc	aac	aag	ttc	tct	gtg	gac		864
Asp	Ser	Lys	Asn	Met	Pro	Thr	Ile	Gly	Thr	Asn	Lys	Phe	Ser	Val	Asp		
		275					280					285					
acc	tac	aac	gtg	tac	atc	aag	ggc	atg	acc	ttg	aac	gtg	ctc	gat	att		912
Thr	Tyr	Asn	Val	Tyr	Ile	Lys	Gly	Met	Thr	Leu	Asn	Val	Leu	Asp	Ile		
	290					295					300						
gtg	gct	att	tgg	cca	tcc	ctt	tac	cca	gat	gat	tac	acc	tct	cag	act		960
Val	Ala	Ile	Trp	Pro	Ser	Leu	Tyr	Pro	Asp	Asp	Tyr	Thr	Ser	Gln	Thr		
305					310				315					320			
gct	ctt	gag	caa	act	agg	gtg	acc	ttc	tct	aac	atg	gtg	ggc	caa	gaa		1008
Ala	Leu	Glu	Gln	Thr	Arg	Val	Thr	Phe	Ser	Asn	Met	Val	Gly	Gln	Glu		
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gaa	ggc	act	gac	gga	tct	ctc	agg	atc	tac	aac	acc	ttc	gac	tca	ttc		1056
Glu	Gly	Thr	Asp	Gly	Ser	Leu	Arg	Ile	Tyr	Asn	Thr	Phe	Asp	Ser	Phe		
			340					345					350				
tct	tac	cag	cac	tcc	cca	atc	cca	aac	aac	aac	gtg	aac	ctc	atc	tcc		1104
Ser	Tyr	Gln	His	Ser	Pro	Ile	Pro	Asn	Asn	Asn	Val	Asn	Leu	Ile	Ser		
		355					360					365					
tac	tac	aac	gac	gag	ctt	cag	aac	ctt	gag	ctt	gga	gtt	tac	acc	cca		1152
Tyr	Tyr	Asn	Asp	Glu	Leu	Gln	Asn	Leu	Glu	Leu	Gly	Val	Tyr	Thr	Pro		
	370					375					380						
cca	aag	aag	gga	tct	gga	tac	tct	tac	cca	tac	ggc	ttc	gtg	ctt	aac		1200
Pro	Lys	Lys	Gly	Ser	Gly	Tyr	Ser	Tyr	Pro	Tyr	Gly	Phe	Val	Leu	Asn		
385					390					395				400			
tac	gcc	aac	tcc	aag	tac	aag	tac	ggc	gat	tct	aac	gat	cca	gag	tct		1248
Tyr	Ala	Asn	Ser	Lys	Tyr	Lys	Tyr	Gly	Asp	Ser	Asn	Asp	Pro	Glu	Ser		
				405					410					415			
ctt	gga	gga	ctt	tct	acc	ctt	tcc	gct	cca	att	caa	cag	gtt	aac	gct		1296
Leu	Gly	Gly	Leu	Ser	Thr	Leu	Ser	Ala	Pro	Ile	Gln	Gln	Val	Asn	Ala		
			420					425					430				

gct acc cag aac tct aag tac ctc gat ggc gag att ctt aac gga att Ala Thr Gln Asn Ser Lys Tyr Leu Asp Gly Glu Ile Leu Asn Gly Ile 435 440 445	1344
gga gct tcc ctt cca gga tat tgc act act gga tgc tct cca act gaa Gly Ala Ser Leu Pro Gly Tyr Cys Thr Thr Gly Cys Ser Pro Thr Glu 450 455 460	1392
cca cca ttc tct tgc act tct acc gct aac gga tac aag gct tct tgc Pro Pro Phe Ser Cys Thr Ser Thr Ala Asn Gly Tyr Lys Ala Ser Cys 465 470 475 480	1440
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ctc gtg tcc tac gat ctc aac cca aag aac gtg ttc gga gag ctt gat Leu Val Ser Tyr Asp Leu Asn Pro Lys Asn Val Phe Gly Glu Leu Asp 515 520 525	1584
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tcc ctt att tct tct tcc aac ctc acc ctt tac tct acc acc gac atg Ser Leu Ile Ser Ser Ser Asn Leu Thr Leu Tyr Ser Thr Thr Asp Met 610 615 620	1872
aac aac acc ctt cca ctt aac gtg tac gtg att gga gag aac gga aac	1920

Asn 625	Asn	Thr	Leu	Pro	Leu 630	Asn	Val	Tyr	Val	Ile 635	Gly	Glu	Asn	Gly	Asn 640	
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Tyr	Thr	Leu	Gln	Asp	Leu	Tyr	Asn	Thr	Thr	Asn	Val	Leu	Ser	Thr	Gly	
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gat	att	acc	ctc	caa	atc	acc	ggc	gga	gat	cag	aag	att	ttc	atc	gac	2016
Asp	Ile	Thr	Leu	Gln	Ile	Thr	Gly	Gly	Asp	Gln	Lys	Ile	Phe	Ile	Asp	
			660					665					670			
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Arg	Ile	Glu	Phe	Val	Pro	Thr	Met	Pro	Val	Pro	Gly	Asn	Thr	Asn	Asn	
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Asn	Asn	Gly	Asn	Asn	Asn	Gly	Asn	Asn	Asn	Pro	Pro	His	His	Val	Cys	
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gct	att	gct	gga	act	cag	cag	tct	tgt	tct	gga	cca	cca	aag	ttc	gag	2160
Ala	Ile	Ala	Gly	Thr	Gln	Gln	Ser	Cys	Ser	Gly	Pro	Pro	Lys	Phe	Glu	
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caa	gtg	tcc	gat	ctt	gag	aag	att	acc	acc	cag	gtg	tac	atg	ctt	ttc	2208
Gln	Val	Ser	Asp	Leu	Glu	Lys	Ile	Thr	Thr	Gln	Val	Tyr	Met	Leu	Phe	
				725					730					735		
aag	tcc	tcc	cca	tac	gaa	gaa	ctt	gct	ctt	gag	gtg	tcc	tct	tac	cag	2256
Lys	Ser	Ser	Pro	Tyr	Glu	Glu	Leu	Ala	Leu	Glu	Val	Ser	Ser	Tyr	Gln	
			740					745					750			
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Ile	Ser	Gln	Val	Ala	Leu	Lys	Val	Met	Ala	Leu	Ser	Asp	Glu	Leu	Phe	
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tgc	gaa	gag	aag	aac	gtg	ctt	agg	aag	ctt	gtg	aac	aag	gcc	aag	caa	2352
Cys	Glu	Glu	Lys	Asn	Val	Leu	Arg	Lys	Leu	Val	Asn	Lys	Ala	Lys	Gln	
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Leu	Leu	Glu	Ala	Ser	Asn	Leu	Leu	Val	Gly	Gly	Asn	Phe	Glu	Thr	Thr	
785					790				795					800		
cag	aac	tgg	gtg	ttg	gga	act	aac	gcc	tac	atc	aac	tac	gat	tcc	ttc	2448
Gln	Asn	Trp	Val	Leu	Gly	Thr	Asn	Ala	Tyr	Ile	Asn	Tyr	Asp	Ser	Phe	
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ctc	ttc	aac	ggc	aac	tac	ctt	tct	ctt	cag	cca	gct	tct	gga	ttc	ttc	2496
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acc agg tac aag gtg tca gga ttc att gga cag tct aac cag gtg gag	2592
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850 855 860	
ctt atc att tcc aga tac ggc aaa gag atc gac aag atc ctc aac gtt	2640
Leu Ile Ile Ser Arg Tyr Gly Lys Glu Ile Asp Lys Ile Leu Asn Val	
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cca tat gct gga cca ctt cca att acc gct gat gct tcc att act tgc	2688
Pro Tyr Ala Gly Pro Leu Pro Ile Thr Ala Asp Ala Ser Ile Thr Cys	
885 890 895	
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Cys Ala Pro Glu Ile Gly Gln Cys Asp Gly Glu Gln Ser Asp Ser His	
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Phe Phe Asn Tyr Ser Ile Asp Val Gly Ala Leu His Pro Glu Leu Asn	
915 920 925	
cca gga att gag atc gga ctc aag atc gtt cag tcc aac ggt tac atc	2832
Pro Gly Ile Glu Ile Gly Leu Lys Ile Val Gln Ser Asn Gly Tyr Ile	
930 935 940	
acc att tcc aac ctc gag atc att gag gaa agg cca ctt acc gag atg	2880
Thr Ile Ser Asn Leu Glu Ile Ile Glu Glu Arg Pro Leu Thr Glu Met	
945 950 955 960	
gaa atc cag gct gtg aat agg aag aac cag aag tgg gag agg gaa aag	2928
Glu Ile Gln Ala Val Asn Arg Lys Asn Gln Lys Trp Glu Arg Glu Lys	
965 970 975	
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Leu Leu Glu Cys Ala Ser Ile Ser Glu Leu Leu Gln Pro Ile Ile Asn	
980 985 990	
cag att gac tcc ctc ttc aag gat gga aac tgg tac aac gat atc ctt	3024
Gln Ile Asp Ser Leu Phe Lys Asp Gly Asn Trp Tyr Asn Asp Ile Leu	
995 1000 1005	
cca cat gtg acc tac cag gac ctc aag aac att atc atc cca gag	3069
Pro His Val Thr Tyr Gln Asp Leu Lys Asn Ile Ile Ile Pro Glu	
1010 1015 1020	
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Tyr	His	Glu	Ile	Glu	Gln	Lys	Met	Lys	Glu	Ala	Leu	Lys	Tyr	Ala		
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Phe	Thr	Gln	Leu	Asp	Glu	Lys	Asn	Leu	Ile	His	Asn	Gly	His	Phe		
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gat	gct	tct	gct	tcc	cag	tcc	att	aac	atc	ctc	gag	ttc	gat	gag		3339
Asp	Ala	Ser	Ala	Ser	Gln	Ser	Ile	Asn	Ile	Leu	Glu	Phe	Asp	Glu		
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gat	aag	gct	tac	aag	ctt	agg	gtt	tac	gct	caa	gga	tct	gga	act		3384
Asp	Lys	Ala	Tyr	Lys	Leu	Arg	Val	Tyr	Ala	Gln	Gly	Ser	Gly	Thr		
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atc	cag	ttc	gga	aac	tgc	gaa	gat	gag	gcc	att	cag	ttc	aac	acc		3429
Ile	Gln	Phe	Gly	Asn	Cys	Glu	Asp	Glu	Ala	Ile	Gln	Phe	Asn	Thr		
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aac	agc	ttc	atc	tac	caa	gag	aag	atc	gtg	tac	ttc	gat	acc	cca		3474
Asn	Ser	Phe	Ile	Tyr	Gln	Glu	Lys	Ile	Val	Tyr	Phe	Asp	Thr	Pro		
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Ser	Val	Asn	Leu	His	Ile	Gln	Ser	Glu	Gly	Ser	Glu	Phe	Ile	Val		
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35 40 45

Thr Ala Leu Gln Gln Gly Phe Ser Ala Ser Gln Gly Gly Thr Phe Asn
50 55 60

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

Pro Gly Gly Thr Phe Val Ala Pro Ile Ile Asn Met Val Ile Gly Trp
85 90 95

Leu Trp Pro His Lys Asn Lys Asn Ala Asp Thr Glu Asn Leu Ile Asn
100 105 110

Leu Ile Asp Ser Glu Ile Gln Lys Gln Leu Asn Lys Ala Leu Leu Asp
115 120 125

Ala Asp Arg Asn Glu Trp Ser Ser Tyr Leu Glu Ser Ile Phe Asp Ser
130 135 140

Ser Asn Asn Leu Asn Gly Ala Ile Val Asp Ala Gln Trp Ser Gly Thr
145 150 155 160

Val Asn Thr Thr Asn Arg Thr Leu Arg Asn Pro Thr Glu Ser Asp Tyr
165 170 175

Thr Asn Val Val Thr Asn Phe Ile Ala Ala Asp Gly Asp Ile Ala Asn
180 185 190

Asn Glu Asn His Ile Met Asn Gly Asn Phe Asp Val Ala Ala Ala Pro
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Tyr Phe Val Ile Gly Ala Thr Ala Arg Phe Ala Ala Met Gln Ser Tyr
210 215 220

Ile Lys Phe Cys Asn Ala Trp Ile Asp Lys Val Gly Leu Ser Asp Ala
225 230 235 240

Gln Leu Thr Thr Gln Lys Ala Asn Leu Asp Arg Thr Lys Gln Asn Met
245 250 255

Arg Asn Ala Ile Leu Asn Tyr Thr Gln Gln Val Met Lys Val Phe Lys
260 265 270

Asp Ser Lys Asn Met Pro Thr Ile Gly Thr Asn Lys Phe Ser Val Asp
275 280 285

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

Val Ala Ile Trp Pro Ser Leu Tyr Pro Asp Asp Tyr Thr Ser Gln Thr
305 310 315 320

Ala Leu Glu Gln Thr Arg Val Thr Phe Ser Asn Met Val Gly Gln Glu
325 330 335

Glu Gly Thr Asp Gly Ser Leu Arg Ile Tyr Asn Thr Phe Asp Ser Phe
340 345 350

Ser Tyr Gln His Ser Pro Ile Pro Asn Asn Asn Val Asn Leu Ile Ser
355 360 365

Tyr Tyr Asn Asp Glu Leu Gln Asn Leu Glu Leu Gly Val Tyr Thr Pro
370 375 380

Pro Lys Lys Gly Ser Gly Tyr Ser Tyr Pro Tyr Gly Phe Val Leu Asn
385 390 395 400

Tyr Ala Asn Ser Lys Tyr Lys Tyr Gly Asp Ser Asn Asp Pro Glu Ser
405 410 415

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

Ala Thr Gln Asn Ser Lys Tyr Leu Asp Gly Glu Ile Leu Asn Gly Ile
435 440 445

Gly Ala Ser Leu Pro Gly Tyr Cys Thr Thr Gly Cys Ser Pro Thr Glu
450 455 460

Pro Pro Phe Ser Cys Thr Ser Thr Ala Asn Gly Tyr Lys Ala Ser Cys
465 470 475 480

Asn Pro Ser Asp Thr Asn Gln Lys Ile Asn Ala Leu Tyr Pro Phe Thr
485 490 495

Gln Ala Asn Val Lys Gly Asn Thr Gly Lys Leu Gly Val Leu Ala Ser
500 505 510

Leu Val Ser Tyr Asp Leu Asn Pro Lys Asn Val Phe Gly Glu Leu Asp
515 520 525

Ser Asp Thr Asn Asn Val Ile Leu Lys Gly Ile Pro Ala Glu Lys Gly
530 535 540

Tyr Phe Pro Asn Asn Ala Arg Pro Thr Val Val Lys Glu Trp Ile Asn
545 550 555 560

Gly Ala Ser Ala Val Pro Leu Asp Ser Gly Asn Thr Leu Phe Met Thr
565 570 575

Ala Thr Asn Leu Thr Ala Thr Gln Tyr Arg Ile Arg Ile Arg Tyr Ala
580 585 590

Asn Pro Asn Ser Asn Thr Gln Ile Gly Val Arg Ile Thr Gln Asn Gly
595 600 605

Ser Leu Ile Ser Ser Ser Asn Leu Thr Leu Tyr Ser Thr Thr Asp Met
610 615 620

Asn Asn Thr Leu Pro Leu Asn Val Tyr Val Ile Gly Glu Asn Gly Asn
625 630 635 640

Tyr Thr Leu Gln Asp Leu Tyr Asn Thr Thr Asn Val Leu Ser Thr Gly
645 650 655

Asp Ile Thr Leu Gln Ile Thr Gly Gly Asp Gln Lys Ile Phe Ile Asp
660 665 670

Arg Ile Glu Phe Val Pro Thr Met Pro Val Pro Gly Asn Thr Asn Asn
675 680 685

Asn Asn Gly Asn Asn Asn Gly Asn Asn Asn Pro Pro His His Val Cys
690 695 700

Ala Ile Ala Gly Thr Gln Gln Ser Cys Ser Gly Pro Pro Lys Phe Glu
705 710 715 720

Gln Val Ser Asp Leu Glu Lys Ile Thr Thr Gln Val Tyr Met Leu Phe
725 730 735

Lys Ser Ser Pro Tyr Glu Glu Leu Ala Leu Glu Val Ser Ser Tyr Gln
740 745 750

Ile Ser Gln Val Ala Leu Lys Val Met Ala Leu Ser Asp Glu Leu Phe
755 760 765

Cys Glu Glu Lys Asn Val Leu Arg Lys Leu Val Asn Lys Ala Lys Gln
770 775 780

Leu Leu Glu Ala Ser Asn Leu Leu Val Gly Gly Asn Phe Glu Thr Thr
785 790 795 800

Gln Asn Trp Val Leu Gly Thr Asn Ala Tyr Ile Asn Tyr Asp Ser Phe
805 810 815

Leu Phe Asn Gly Asn Tyr Leu Ser Leu Gln Pro Ala Ser Gly Phe Phe
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Thr Ser Tyr Ala Tyr Gln Lys Ile Asp Glu Ser Thr Leu Lys Pro Tyr
835 840 845

Thr Arg Tyr Lys Val Ser Gly Phe Ile Gly Gln Ser Asn Gln Val Glu
850 855 860

Leu Ile Ile Ser Arg Tyr Gly Lys Glu Ile Asp Lys Ile Leu Asn Val
865 870 875 880

Pro Tyr Ala Gly Pro Leu Pro Ile Thr Ala Asp Ala Ser Ile Thr Cys
885 890 895

Cys Ala Pro Glu Ile Gly Gln Cys Asp Gly Glu Gln Ser Asp Ser His
900 905 910

Phe Phe Asn Tyr Ser Ile Asp Val Gly Ala Leu His Pro Glu Leu Asn
915 920 925

Pro Gly Ile Glu Ile Gly Leu Lys Ile Val Gln Ser Asn Gly Tyr Ile
930 935 940

Thr Ile Ser Asn Leu Glu Ile Ile Glu Glu Arg Pro Leu Thr Glu Met
945 950 955 960

Glu Ile Gln Ala Val Asn Arg Lys Asn Gln Lys Trp Glu Arg Glu Lys
965 970 975

Leu Leu Glu Cys Ala Ser Ile Ser Glu Leu Leu Gln Pro Ile Ile Asn
980 985 990

Gln Ile Asp Ser Leu Phe Lys Asp Gly Asn Trp Tyr Asn Asp Ile Leu
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Pro His Val Thr Tyr Gln Asp Leu Lys Asn Ile Ile Ile Pro Glu
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Leu Pro Lys Leu Lys His Trp Phe Ile Glu Asn Leu Pro Gly Glu
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Tyr His Glu Ile Glu Gln Lys Met Lys Glu Ala Leu Lys Tyr Ala
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Phe Thr Gln Leu Asp Glu Lys Asn Leu Ile His Asn Gly His Phe
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Thr Thr Asn Leu Ile Asp Trp Gln Val Glu Gly Asp Ala Gln Met
1070 1075 1080

Lys Val Leu Glu Asn Asp Ala Leu Ala Leu Gln Leu Phe Asn Trp
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Asp Ala Ser Ala Ser Gln Ser Ile Asn Ile Leu Glu Phe Asp Glu
1100 1105 1110

Asp Lys Ala Tyr Lys Leu Arg Val Tyr Ala Gln Gly Ser Gly Thr
1115 1120 1125

Ile Gln Phe Gly Asn Cys Glu Asp Glu Ala Ile Gln Phe Asn Thr
1130 1135 1140

Asn Ser Phe Ile Tyr Gln Glu Lys Ile Val Tyr Phe Asp Thr Pro
1145 1150 1155

Ser Val Asn Leu His Ile Gln Ser Glu Gly Ser Glu Phe Ile Val
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att gag ttt gct tct cct act cct gga act ctt gaa cct atc ttc gaa 96
Ile Glu Phe Ala Ser Pro Thr Pro Gly Thr Leu Glu Pro Ile Phe Glu
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ata atg ggt ttt aca aag gtc gct acc cac agg tct aag aac gtt cat 144
Ile Met Gly Phe Thr Lys Val Ala Thr His Arg Ser Lys Asn Val His
35 40 45

ctg tac aga caa gga gag ata aat cta atc ctg aac aat gag cca aac 192
Leu Tyr Arg Gln Gly Glu Ile Asn Leu Ile Leu Asn Asn Glu Pro Asn
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agc att gct tcc tac ttt gcc gct gaa cat ggt cca tca gtg tgt gga 240
Ser Ile Ala Ser Tyr Phe Ala Ala Glu His Gly Pro Ser Val Cys Gly
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atg gcc ttt agg gtt aaa gat agc cag aag gca tat aat cgt gct ttg 288
Met Ala Phe Arg Val Lys Asp Ser Gln Lys Ala Tyr Asn Arg Ala Leu
85 90 95

gaa ctg gga gcc caa cca att cac att gat act ggg cca atg gaa ctt 336
Glu Leu Gly Ala Gln Pro Ile His Ile Asp Thr Gly Pro Met Glu Leu
100 105 110

aac ctt cca gcc ata aag gga att gga ggt gct cct ttg tat ctt att 384
Asn Leu Pro Ala Ile Lys Gly Ile Gly Gly Ala Pro Leu Tyr Leu Ile
115 120 125

gac cgc ttc gga gag ggc tct tcc att tac gat atc gac ttc gtt tac Asp Arg Phe Gly Glu Gly Ser Ser Ile Tyr Asp Ile Asp Phe Val Tyr 130 135 140	432
ttg gaa ggt gtc gaa cgc aat cca gtt gga gct ggt ttg aaa gtg atc Leu Glu Gly Val Glu Arg Asn Pro Val Gly Ala Gly Leu Lys Val Ile 145 150 155 160	480
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aac ttc tat gag aaa ctc ttc aac ttt aga gag gca agg tat ttc gac Asn Phe Tyr Glu Lys Leu Phe Asn Phe Arg Glu Ala Arg Tyr Phe Asp 180 185 190	576
att aag gga gaa tac aca ggt cta act tct aaa gct atg tca gca cca Ile Lys Gly Glu Tyr Thr Gly Leu Thr Ser Lys Ala Met Ser Ala Pro 195 200 205	624
gac gga atg att agg att cct ctt aat gag gaa agt tct aag ggt gct Asp Gly Met Ile Arg Ile Pro Leu Asn Glu Glu Ser Ser Lys Gly Ala 210 215 220	672
gga caa atc gaa gag ttc ctt atg cag ttt aac ggt gag gga atc caa Gly Gln Ile Glu Glu Phe Leu Met Gln Phe Asn Gly Glu Gly Ile Gln 225 230 235 240	720
cac gtt gct ttt ttg aca gac gat ctt gtc aag act tgg gat gct ctg His Val Ala Phe Leu Thr Asp Asp Leu Val Lys Thr Trp Asp Ala Leu 245 250 255	768
aag aaa att gga atg agg ttt atg act gca cct ccc gat acc tat tac Lys Lys Ile Gly Met Arg Phe Met Thr Ala Pro Pro Asp Thr Tyr Tyr 260 265 270	816
gaa atg ctc gaa gga cga ctt cca gat cac ggt gaa ccc gtt gac cag Glu Met Leu Glu Gly Arg Leu Pro Asp His Gly Glu Pro Val Asp Gln 275 280 285	864
ctc caa gct aga ggt ata cta ctt gat gga agt tct gtg gaa gga gat Leu Gln Ala Arg Gly Ile Leu Leu Asp Gly Ser Ser Val Glu Gly Asp 290 295 300	912
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ttc ttt gag ttt att cag cgt aaa gga gat gac ggc ttt ggc cca tgg Phe Phe Glu Phe Ile Gln Arg Lys Gly Asp Asp Gly Phe Gly Pro Trp	1008

325	330	335	
aac ttt gcg caa ctt ttc gaa agt att gag cgt gac caa gtt cgt aga			1056
Asn Phe Ala Gln Leu Phe Glu Ser Ile Glu Arg Asp Gln Val Arg Arg			
340	345	350	
ggt gtt ctt act gct gat tga			1077
Gly Val Leu Thr Ala Asp			
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 <213> Secuencia artificial

<220>
 <223> Constructo sintético

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			20					25					30		

Ile	Met	Gly	Phe	Thr	Lys	Val	Ala	Thr	His	Arg	Ser	Lys	Asn	Val	His
		35					40					45			

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

Ser	Ile	Ala	Ser	Tyr	Phe	Ala	Ala	Glu	His	Gly	Pro	Ser	Val	Cys	Gly
65					70					75				80	

Met	Ala	Phe	Arg	Val	Lys	Asp	Ser	Gln	Lys	Ala	Tyr	Asn	Arg	Ala	Leu
				85					90					95	

Glu	Leu	Gly	Ala	Gln	Pro	Ile	His	Ile	Asp	Thr	Gly	Pro	Met	Glu	Leu
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Asn	Leu	Pro	Ala	Ile	Lys	Gly	Ile	Gly	Gly	Ala	Pro	Leu	Tyr	Leu	Ile
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115

120

125

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

Asp His Leu Thr His Asn Val Tyr Arg Gly Arg Met Val Tyr Trp Ala
 165 170 175

Asn Phe Tyr Glu Lys Leu Phe Asn Phe Arg Glu Ala Arg Tyr Phe Asp
 180 185 190

Ile Lys Gly Glu Tyr Thr Gly Leu Thr Ser Lys Ala Met Ser Ala Pro
 195 200 205

Asp Gly Met Ile Arg Ile Pro Leu Asn Glu Glu Ser Ser Lys Gly Ala
 210 215 220

Gly Gln Ile Glu Glu Phe Leu Met Gln Phe Asn Gly Glu Gly Ile Gln
 225 230 235 240

His Val Ala Phe Leu Thr Asp Asp Leu Val Lys Thr Trp Asp Ala Leu
 245 250 255

Lys Lys Ile Gly Met Arg Phe Met Thr Ala Pro Pro Asp Thr Tyr Tyr
 260 265 270

Glu Met Leu Glu Gly Arg Leu Pro Asp His Gly Glu Pro Val Asp Gln
 275 280 285

Leu Gln Ala Arg Gly Ile Leu Leu Asp Gly Ser Ser Val Glu Gly Asp
 290 295 300

Lys Arg Leu Leu Leu Gln Ile Phe Ser Glu Thr Leu Met Gly Pro Val
 305 310 315 320

Phe Phe Glu Phe Ile Gln Arg Lys Gly Asp Asp Gly Phe Gly Pro Trp
325 330 335

Asn Phe Ala Gln Leu Phe Glu Ser Ile Glu Arg Asp Gln Val Arg Arg
340 345 350

Gly Val Leu Thr Ala Asp
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<210> 11
<211> 8068
<212> ADN
<213> Secuencia artificial

<220>
<223> Plásmido transformador pSZ8832 - secuencia entre bordes T-DNA

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<223> Polylinker

<220>
<221> característica_misc
<222> (131)..(400)
<223> Región no traducida 3' del transcrito 35S (sentido contrario a las agujas del reloj)

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<222> (401)..(411)
<223> Polylinker

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<222> (412)..(3969)
<223> Secuencia de codificación cry14Ab-1.b (sentido contrario a las agujas del reloj)

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<221> característica_misc
<222> (3970)..(5276)
<223> Promotor ubiquitin-10 (sentido contrario a las agujas del reloj)

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<221> característica_misc
<222> (5382)..(5576)
<223> Región no traducida 3' del transcrito 35S (sentido contrario a las agujas del reloj)

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<223> Polylinker

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<222> (5589)..(6665)
<223> Secuencia de codificación hppdPf-4Pa (sentido contrario a las agujas del reloj)

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<222> (6666)..(7037)
<223> Peptídico de tránsito optimizado TPotpY-1Pf (sentido contrario a las agujas del reloj)

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<221> característica_misc
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<223> Polylinker

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<222> (7059)..(7185)
<223> Secuencia líder de ARN genómico del Virus del Grabado del Tabaco (sentido contrario a las agujas del reloj)

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<221> característica_misc
<222> (7186)..(7191)
<223> Secuencia polylinker

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<221> característica_misc
<222> (7192)..(7941)
<223> Región promotora doblemente potenciada del transcrito CaMV 35S (sentido contrario a las agujas del reloj)

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caatgcaacc tgttgctgtg ctatggctct agtgcaaact cgtgattatg ctatagccac	240
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gatatgtcaa caaacatgta agtctatgac tctgagataa gcttataggg ggaatctgag	420
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