

SEQUENCE LISTING

<110> Nomad Bioscience GmbH

<120> Process of Providing Plants with Abiotic Stress Resistance

<130> PCT-16524

<160> 31

<170> PatentIn version 3.3

<210> 1

<211> 204

<212> DNA

<213> artificial

<220>

<223> complete CDS of codon-optimised CspB gene

<400> 1

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<210> 2

<211> 67

<212> PRT

<213> Bacillus subtilis

<400> 2

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Phe Ile Glu Val Glu Gly Gln Asp Asp Val Phe Val His Phe Ser Ala
              20              25              30

Ile Gln Gly Glu Gly Phe Lys Thr Leu Glu Glu Gly Gln Ala Val Ser
              35              40              45

Phe Glu Ile Val Glu Gly Asn Arg Gly Pro Gln Ala Ala Asn Val Thr
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Lys Glu Ala
65
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<210> 3

<211> 213

<212> DNA

<213> artificial

<220>

<223> complete cds of E. coli cspA gene, optimised

<400> 3

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 ggttacaaat ctctggacga aggtcagaaa gtgtccttca ccatcgaaag cggcgctaaa 180
 ggcccggcag ctggtaacgt aaccagcctg taa 213

<210> 4
 <211> 70
 <212> PRT
 <213> Escherichia coli
 <400> 4

Met Ser Gly Lys Met Thr Gly Ile Val Lys Trp Phe Asn Ala Asp Lys
 1 5 10 15

Gly Phe Gly Phe Ile Thr Pro Asp Asp Gly Ser Lys Asp Val Phe Val
 20 25 30

His Phe Ser Ala Ile Gln Asn Asp Gly Tyr Lys Ser Leu Asp Glu Gly
 35 40 45

Gln Lys Val Ser Phe Thr Ile Glu Ser Gly Ala Lys Gly Pro Ala Ala
 50 55 60

Gly Asn Val Thr Ser Leu
 65 70

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 <211> 423
 <212> DNA
 <213> Arabidopsis thaliana

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 cctaattgga agattggaaa agatgctaag gatacagttc aggaatgcgt ctctgagttc 180
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<210> 6
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 <212> PRT
 <213> Arabidopsis thaliana

<400> 6
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 1 5 10 15

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

Arg Ile Met Lys Lys Ala Leu Pro Pro Asn Gly Lys Ile Gly Lys Asp
35 40 45

Ala Lys Asp Thr Val Gln Glu Cys Val Ser Glu Phe Ile Ser Phe Ile
50 55 60

Thr Ser Glu Ala Ser Asp Lys Cys Gln Lys Glu Lys Arg Lys Thr Val
65 70 75 80

Asn Gly Asp Asp Leu Leu Trp Ala Met Ala Thr Leu Gly Phe Glu Asp
85 90 95

Tyr Leu Glu Pro Leu Lys Ile Tyr Leu Ala Arg Tyr Arg Glu Leu Glu
100 105 110

Gly Asp Asn Lys Gly Ser Gly Lys Ser Gly Asp Gly Ser Asn Arg Asp
115 120 125

Ala Gly Gly Gly Val Ser Gly Glu Glu Met Pro Ser Trp
130 135 140

<210> 7
<211> 1323
<212> DNA
<213> artificial

<220>
<223> Complete CDS of Brassica napus cultivar Hua shuang No. 5
transcription factor LAS, splice sites removed

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<210> 8
<211> 441
<212> PRT
<213> brassica napus

<400> 8

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Glu Asn Pro Pro Pro Pro Pro Pro Leu Cys Leu Ala Ser Ser Ser Ala
          20           25           30

Ala Thr Ser Ala Ala His His Leu Arg Arg Leu Leu Phe Thr Ala Ala
          35           40           45

Asp Phe Ile Ser Gln Ser Asn Val Ser Ala Ala Gln Asn Ile Leu Ser
          50           55           60

Ile Leu Ser Ser Asn Ser Ser Pro Tyr Gly Asp Ser Thr Glu Arg Leu
65           70           75           80

Val His Leu Phe Thr Lys Ala Leu Ser Val Arg Ile Gly Leu Ser Glu
          85           90           95

Asn Thr Ala Thr Trp Thr Ala Asn Glu Met Ala Ser Ser Ser Thr Val
          100          105          110

Phe Thr Ser Ser Val Cys Lys Glu Gln Phe Leu Phe Arg Thr Lys Asn
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Asn Asn Asn Ser Asp Leu Glu Ser Cys Tyr Tyr Leu Trp Leu Asn Gln
          130          135          140

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Leu Thr Pro Phe Ile Arg Phe Ser His Leu Thr Ala Asn Gln Ala Ile
 145 150 155 160

Leu Asp Ala Thr Glu Thr Asn Asn Gly Asn Gly Ala Leu His Ile Leu
 165 170 175

Asp Leu Asp Ile Ser Gln Gly Leu Gln Trp Pro Pro Leu Met Gln Ala
 180 185 190

Leu Ala Glu Arg Ser Ser Ser Asn Pro Ser Ser Thr Pro Pro Pro Ser
 195 200 205

Leu Arg Ile Thr Gly Cys Gly Arg Asp Val Thr Val Leu Asn Arg Thr
 210 215 220

Gly Asp Arg Leu Thr Arg Phe Ala Asn Ser Leu Gly Leu Gln Phe Gln
 225 230 235 240

Phe His Thr Leu Val Ile Ala Glu Glu Asp Leu Ala Gly Leu Leu Leu
 245 250 255

Gln Ile Arg Leu Leu Ala Leu Ser Ala Val Gln Gly Glu Ser Ile Ala
 260 265 270

Val Asn Cys Val His Phe Leu His Arg Phe Phe Asn Asp Asp Gly Asp
 275 280 285

Met Ile Gly His Phe Leu Ser Ala Ile Lys Ser Leu Asn Pro Arg Ile
 290 295 300

Val Thr Met Ala Glu Arg Glu Ala Asn His Gly Asp Pro Ser Phe Leu
 305 310 315 320

Thr Arg Phe Ser Glu Ala Leu Asp His Phe Met Ala Ile Phe Asp Ser
 325 330 335

Leu Glu Ala Thr Leu Pro Pro Asn Ser Lys Glu Arg Leu Thr Leu Glu
 340 345 350

Gln Arg Trp Phe Gly Met Glu Ile Leu Asp Val Val Ala Ala Glu Ala
 355 360 365

Ala Glu Arg Lys Gln Arg His Arg Arg Phe Glu Val Trp Glu Glu Met
 370 375 380

Met Lys Arg His Gly Phe Ala Asn Val Pro Ile Gly Ser Phe Ala Phe
 385 390 395 400

Ser Gln Ala Lys Leu Leu Leu Arg Leu His Tyr Pro Ser Glu Gly Tyr
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Asn Leu Gln Phe Leu Asn Asp Ser Leu Phe Leu Gly Trp Lys Asn Arg
 420 425 430

Leu Leu Phe Ser Val Ser Ser Trp Lys
 435 440

<210> 9
 <211> 1029
 <212> DNA
 <213> artificial

<220>
 <223> complete CDS of GmRD22, C843G silent mutation

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 gccatcactg atatccttta ccccgattgg gtggaagaga aaagtacctc agtgaatggt 180
 ggaggcaagg gcgtaaactg gcatgcagga aaaggaggag gtggcaccaa tgtcaacggt 240
 ggtggaaaag gatcaggcgg aggcgtgaac gtgcatgcag gtcacaaggg aaagccagtg 300
 catgtttctg ttgggtcaaa gtctccattc aattacatct acgcttcaac ggagactcaa 360
 ttacacgatg accccaactg cgcactcttc ttcttggaag aggacttgca tcccgggaaca 420
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 gttcccaag 1029

<210> 10
 <211> 343
 <212> PRT
 <213> soybean

<400> 10

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Val Ala Ile His Ala Ala Leu Pro Pro Glu Val Tyr Trp Lys Ser Val

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Leu	Pro	Thr	Thr	Pro	Met	Pro	Lys	Ala	Ile	Thr	Asp	Ile	Leu	Tyr	Pro
		35					40					45			
Asp	Trp	Val	Glu	Glu	Lys	Ser	Thr	Ser	Val	Asn	Val	Gly	Gly	Lys	Gly
	50					55					60				
Val	Asn	Val	His	Ala	Gly	Lys	Gly	Gly	Gly	Gly	Thr	Asn	Val	Asn	Val
65					70					75					80
Gly	Gly	Lys	Gly	Ser	Gly	Gly	Gly	Val	Asn	Val	His	Ala	Gly	His	Lys
				85					90					95	
Gly	Lys	Pro	Val	His	Val	Ser	Val	Gly	Ser	Lys	Ser	Pro	Phe	Asn	Tyr
			100					105					110		
Ile	Tyr	Ala	Ser	Thr	Glu	Thr	Gln	Leu	His	Asp	Asp	Pro	Asn	Val	Ala
		115					120					125			
Leu	Phe	Phe	Leu	Glu	Lys	Asp	Leu	His	Pro	Gly	Thr	Lys	Leu	Asn	Leu
	130					135					140				
His	Phe	Thr	Thr	Ser	Ser	Asn	Ile	Gln	Ala	Thr	Phe	Leu	Pro	Arg	Gln
145					150					155					160
Val	Ala	Asp	Ser	Ile	Pro	Phe	Ser	Ser	Ser	Lys	Val	Glu	Val	Val	Phe
				165					170					175	
Asn	Lys	Phe	Ser	Val	Lys	Pro	Gly	Ser	Glu	Glu	Ala	Gln	Ile	Met	Lys
			180					185					190		
Asn	Thr	Leu	Ser	Glu	Cys	Glu	Glu	Gly	Gly	Ile	Lys	Gly	Glu	Glu	Lys
		195					200					205			
Tyr	Cys	Ala	Thr	Ser	Leu	Glu	Ser	Met	Ile	Asp	Phe	Ser	Thr	Ser	Lys
	210					215					220				
Leu	Gly	Lys	Asn	Val	Glu	Val	Val	Ser	Thr	Glu	Val	Val	Glu	Asp	Lys
225					230					235					240
Glu	Thr	Gly	Leu	Gln	Lys	Tyr	Thr	Val	Ala	Pro	Gly	Val	Asn	Lys	Leu
				245					250					255	
Ser	Gly	Asp	Lys	Ala	Val	Val	Cys	His	Lys	Gln	Asn	Tyr	Pro	Tyr	Ala
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Val	Phe	Tyr	Cys	His	Lys	Thr	Glu	Thr	Thr	Arg	Ala	Tyr	Ser	Val	Pro
		275					280					285			

Leu Glu Gly Ala Asn Gly Val Arg Val Lys Ala Val Ala Val Cys His
 290 295 300

Thr His Thr Ser Glu Trp Asn Pro Lys His Leu Ala Phe Gln Val Leu
 305 310 315 320

Lys Val Lys Pro Gly Thr Val Pro Val Cys His Phe Leu Pro Glu Asp
 325 330 335

His Val Val Trp Val Pro Lys
 340

<210> 11
 <211> 855
 <212> DNA
 <213> Brassica rapa

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 gagatcctca gtatctacca gaatgctatt tccatggttag acgacaagaa ggtccttaaa 180
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<210> 12
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 <212> PRT
 <213> brassica rapa

<400> 12

Met Ala Met Glu Glu Lys Leu Val Ile Asn Glu Leu Glu Gln Gly Arg
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 20 25 30

Glu Ser Ser Lys Asn Leu Ile Ser Glu Ile Leu Ser Ile Tyr Gln Asn
35 40 45

Ala Ile Ser Met Leu Asp Asp Lys Lys Val Leu Lys Arg Ser Arg Glu
50 55 60

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

Glu Lys Lys Thr Glu Lys Val Ser Phe Phe Val Gly Ala Gly Gln Glu
85 90 95

Lys Gly Ser Ile Asp Asp Gly Tyr Cys Trp Arg Lys Tyr Gly Gln Lys
100 105 110

Glu Ile His Gly Ser Ile Asn Pro Arg Gly Tyr Phe Arg Cys Thr His
115 120 125

Arg Phe Thr Gln Asn Cys Leu Ala Val Lys Gln Val Gln Lys Ser Asp
130 135 140

Arg Asp Pro Ser Ile Phe Glu Val Lys Tyr Val Gly Ser His Thr Cys
145 150 155 160

Asn Asn Thr Thr Thr Ser Pro Lys Thr Pro Asn Phe Ser Ile Ser Met
165 170 175

Phe Gln Gln Glu Asp Ile Lys Pro Thr Lys Thr Glu Glu Ala Met Met
180 185 190

Ser Leu Glu Asp Leu Glu Ser Thr Lys Asn Ile Phe Arg Thr Phe Ser
195 200 205

Phe Ser Asn Tyr Glu Ile Glu Asn Ala Gly Gly Gly Trp Lys Gly Asn
210 215 220

Leu Phe His Glu Asp Gln Leu Ser Pro Ala Ala Thr Thr Ser Gly Ser
225 230 235 240

Gly Ile Thr Ser Glu Val Ala Thr Ala Pro Ala Ser Val Glu Asn Ser
245 250 255

Glu Thr Ala Asp Ser Tyr Phe Ser Ser Leu Asp Asn Ile Ile Asp Phe
260 265 270

Gly Pro Asp Trp Leu Leu Ser Cys Asp Val Leu Asn Trp
275 280 285

<210> 13
<211> 939

<212> DNA
<213> artificial

<220>
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<213> artificial

<220>
<223> HaHB1-Helianthus annuus HD-Zip subfamily I transcription factor; splice sites removed G561A, G750A

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20 25 30

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35 40 45

Leu Gly Lys Arg Ser Met Ser Ser Tyr Ser Gly Leu Asn Asn Asn Asn
50 55 60

Met Asp Gly Cys Asp Gln Glu Gly Asn Met Asn Gly Glu Asp Glu Leu
65 70 75 80

Ser Asp Asp Gly Ser Gln Leu Leu Ala Gly Glu Lys Lys Arg Arg Leu
85 90 95

Asn Met Glu Gln Val Lys Thr Leu Glu Arg Asn Phe Glu Leu Gly Asn
100 105 110

Lys Leu Glu Pro Glu Arg Lys Met Gln Leu Ala Arg Ala Leu Gly Leu
115 120 125

Gln Pro Arg Gln Ile Ala Ile Trp Phe Gln Asn Arg Arg Ala Arg Trp
130 135 140

Lys Thr Lys Gln Leu Glu Lys Asp Tyr Asp Ala Leu Lys Arg Gln Phe
145 150 155 160

Glu Ala Val Lys Ala Glu Asn Asp Ser Leu Gln Ser Gln Asn His Lys
165 170 175

Leu His Ala Glu Ile Met Ala Leu Lys Asn Arg Glu Pro Ala Glu Leu
180 185 190

Ile Asn Leu Asn Ile Lys Glu Thr Glu Gly Ser Cys Ser Asn Arg Ser
195 200 205

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

Asp Ser Pro Leu Ser Ser His His Gln His Gln His Gln Pro Ile Pro
225 230 235 240

Asn Leu Phe Pro Ser Ser Asn Ile Asp Arg Pro Asn Ser Asn Asn Ile
245 250 255

Val Ala His Gln Leu Phe His Asn Ser Ser Ser Arg Pro Ala Asp His
260 265 270

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

Cys Phe Ser Thr Met Phe Val Gly Met Asp Asp Gln Ser Gly Phe Trp
290 295 300

Pro Trp Leu Glu Gln Pro Gln Phe Asn
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<210> 15
<211> 1734

<212> DNA

<213> *Nicotiana tabacum*

<400> 15

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<210> 16

<211> 578

<212> PRT

<213> *Nicotiana tabacum*

<400> 16

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

Leu Glu Leu Ser Ser Ser Arg Ser Val Met Ala Ala Lys Thr Arg His
20 25 30

Phe Lys Trp Asp Val Glu Tyr Ile His Trp Ser Pro Asp Gly Glu Glu
35 40 45

Ser Val Val Met Gly Ile Asn Gly Gln Phe Pro Gly Pro Thr Ile Arg
50 55 60

Ala Lys Ala Gly Asp Thr Val Ala Val His Leu Thr Asn Lys Leu His
65 70 75 80

Thr Glu Gly Val Val Ile His Trp His Gly Ile Arg Gln Ile Gly Thr
85 90 95

Pro Trp Ala Asp Gly Thr Ala Ala Ile Ser Gln Cys Ala Ile Asn Pro
100 105 110

Gly Glu Thr Phe Leu Tyr Arg Phe Lys Val Asp Lys Ala Gly Thr Tyr
115 120 125

Phe Tyr His Gly His Tyr Gly Met Gln Arg Ser Ala Gly Leu Tyr Gly
130 135 140

Ser Leu Ile Val Glu Val Gly Glu Gly Glu Lys Glu Pro Phe His Tyr
145 150 155 160

Asp Gly Glu Phe Asn Leu Leu Leu Ser Asp Trp Trp His Lys Gly Ser
165 170 175

His Glu Gln Glu Val Asp Leu Ser Ser Asn Pro Leu Arg Trp Ile Gly
180 185 190

Glu Pro Gln Thr Leu Leu Leu Asn Gly Arg Gly Gln Tyr Asn Cys Ser
195 200 205

Leu Ala Ala Arg Phe Ser Lys Pro Pro Leu Pro Gln Cys Lys Leu Arg
210 215 220

Gly Gly Glu Gln Tyr Ala Pro Gln Ile Leu Arg Val Arg Pro Asn Lys
225 230 235 240

Ile Tyr Arg Leu Arg Val Ala Ser Thr Thr Ala Leu Gly Ser Leu Ser
245 250 255

Leu Ala Ile Gly Gly His Lys Met Val Val Val Glu Ala Asp Gly Asn
 260 265 270

Tyr Val Gln Pro Phe Ser Val Gln Asp Met Asp Ile Tyr Ser Gly Glu
 275 280 285

Ser Tyr Ser Val Leu Phe Lys Thr Asp Gln Asp Pro Thr Lys Asn Tyr
 290 295 300

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

Leu Thr Leu Leu Asn Tyr Leu Pro Asn Ser Ala Ser Lys Phe Pro Thr
 325 330 335

Leu Pro Pro Pro Ile Ala Pro Leu Trp Asn Asp Tyr Asn His Ser Lys
 340 345 350

Ser Phe Ser Asn Lys Ile Phe Ala Leu Met Gly Ser Pro Lys Pro Pro
 355 360 365

Pro Gln Asn His Arg Arg Ile Ile Leu Leu Asn Thr Gln Asn Lys Ile
 370 375 380

Asp Gly Tyr Thr Lys Trp Ala Ile Asn Asn Val Ser Leu Val Leu Pro
 385 390 395 400

Thr Gln Leu Tyr Leu Gly Ser Ile Arg Tyr Gly Ile Asn Ala Phe Asp
 405 410 415

Thr Lys Pro Pro Pro Asp Asn Phe Pro Lys Asp Tyr Asp Val Leu Lys
 420 425 430

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

Lys Phe Asn Thr Thr Ile Asp Ile Ile Leu Gln Asn Ala Asn Ala Leu
 450 455 460

Ala Lys Asp Val Ser Glu Ile His Pro Trp His Leu His Gly His Asp
 465 470 475 480

Phe Trp Val Leu Gly Tyr Gly Glu Gly Lys Phe Ser Glu Lys Asp Val
 485 490 495

Lys Lys Phe Asn Leu Lys Asn Pro Pro Leu Arg Asn Thr Ala Val Ile
 500 505 510

Phe Pro Phe Gly Trp Thr Ala Leu Arg Phe Val Thr Asp Asn Pro Gly
 515 520 525

Val Trp Ala Phe His Cys His Ile Glu Pro His Leu His Met Gly Met
 530 535 540

Gly Val Ile Phe Ala Glu Gly Val His Leu Val Lys Lys Ile Pro Lys
 545 550 555 560

Glu Ala Leu Ala Cys Gly Leu Thr Gly Lys Met Leu Met Ser Asn Lys
 565 570 575

His Asn

<210> 17
 <211> 2310
 <212> DNA
 <213> artificial

<220>
 <223> CDS of AVP1_ARATH with E229D mutation; splices sites removed:
 A261G, C2004G, A2190T

<400> 17
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 gtgattggta tcgccttttc gcttttccaa tggtagcttg tatctcgcgt gaaactcacc 120
 tctgacctcg gcgcctcgtc ttccgggtgga gctaacaatg ggaagaatgg atacgggtgat 180
 tatctaactc aggaagagga aggtgttaat gaccagagtg ttgtcgctaa gtgcgctgag 240
 attcagactg ctattttccga ggggtgcaact tcatttctat tcacggagta caaatatggt 300
 ggtgtcttca tgattttctt tgctgctggt atctttgttt tcctcggctc tgttgagggg 360
 ttcagcactg ataacaagcc ttgtacttac gacaccacca gaacctgcaa gcctgcattg 420
 gctactgcag ctttcagtac cattgctttc gtgcttggtg ctgttacctc tgttctatct 480
 ggtttccttg ggatgaagat tgctacatac gctaattgcta ggaccacttt ggagggcgagg 540
 aaaggtggtg gaaaggcggt cattgttgca ttcaggtctg gtgctgtgat gggtttcctt 600
 cttgcagcga gtggtctatt ggtgctttac attactatca atgtgttcaa gatctattac 660
 ggagatgact ggggaaggct ttttgacgct attactgggt atggtcttgg tgggtcttcc 720
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 gacctgtcgt gtaaaattga gaggaatatt ccagaggatg atccaagaaa cccagctgtc 840
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 ggatcatatg ctgaagcatc atgcgctgct cttgttggtg cctcgatctc atctttcgga 960
 atcaaccacg acttactgct catgtgctac ccattgctca tcagttcaat gggaatcttg 1020
 gtttggttga tcacaactct ctttgccact gacttctttg agattaagct tgtcaaggag 1080
 attgaaccag cattgaagaa ccagctcatt atctcaactg ttattatgac tgttggtatt 1140
 gctattgtgt catgggttgg cttaccgacc tcctttacca tcttcaactt tggaacacaa 1200

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aaagtgtgtca agaactggca gctattcctt tgtgtttgtg ttggtctttg ggctggactc 1260
attattgggtt tcgtcactga gtactacact agtaacgcct acagccctgt gcaagatggt 1320
gcagattcat gcagaactgg tgcagctacc aatgttatct tcggccttgc tcttggttac 1380
aaatccgtca ttattccaat ctttgctatt gctatcagta tattcgttag cttcagcttt 1440
gctgctatgt atgggtgttg tgttgcgtct cttgggtatgc tcagtaccat tgccactggg 1500
ttggcaattg atgcttatgg tcccatcagt gacaatgctg gtgggtattgc tgaaatggct 1560
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attgggctcc ttgttggtgc catgcttcct tactggttct ctgccatgac aatgaagagt 1800
gtgggaagtg cagctcttaa gatgggtgaa gaagttcgca ggcagttcaa caccatccct 1860
ggacttatgg aaggaaccgc aaaaccagac tacgccacat gtgtcaagat ctccaccgat 1920
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aaggcagctg tgattggaga cacaattggg gaccatttga aggatacttc aggaccttca 2220
ttgaacatcc tcatcaagct catggtgtgt gagtctcttg tctttgctcc cttcttcgcc 2280
actcacggtg gtatcctttt caagtacttc 2310

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<210> 18
<211> 770
<212> PRT
<213> artificial

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<220>
<223> AVP1_ARATH of A. thaliana, with E229D mutation; splices sites
      removed: A261G, C2004G, A2190T

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<400> 18

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Met Val Ala Pro Ala Leu Leu Pro Glu Leu Trp Thr Glu Ile Leu Val
1           5           10           15

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

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Val Val Ser Arg Val Lys Leu Thr Ser Asp Leu Gly Ala Ser Ser Ser
          35           40           45

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Gly Gly Ala Asn Asn Gly Lys Asn Gly Tyr Gly Asp Tyr Leu Ile Glu
50           55           60

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Glu Glu Glu Gly Val Asn Asp Gln Ser Val Val Ala Lys Cys Ala Glu

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65		70		75		80
Ile Gln Thr Ala	Ile Ser Glu Gly Ala	Thr Ser Phe Leu Phe	Thr Glu			
	85	90	95			
Tyr Lys Tyr Val Gly Val Phe Met Ile Phe Phe Ala Ala Val Ile Phe						
	100	105	110			
Val Phe Leu Gly Ser Val Glu Gly Phe Ser Thr Asp Asn Lys Pro Cys						
	115	120	125			
Thr Tyr Asp Thr Thr Arg Thr Cys Lys Pro Ala Leu Ala Thr Ala Ala						
	130	135	140			
Phe Ser Thr Ile Ala Phe Val Leu Gly Ala Val Thr Ser Val Leu Ser						
	145	150	155			160
Gly Phe Leu Gly Met Lys Ile Ala Thr Tyr Ala Asn Ala Arg Thr Thr						
	165	170	175			
Leu Glu Ala Arg Lys Gly Val Gly Lys Ala Phe Ile Val Ala Phe Arg						
	180	185	190			
Ser Gly Ala Val Met Gly Phe Leu Leu Ala Ala Ser Gly Leu Leu Val						
	195	200	205			
Leu Tyr Ile Thr Ile Asn Val Phe Lys Ile Tyr Tyr Gly Asp Asp Trp						
	210	215	220			
Glu Gly Leu Phe Asp Ala Ile Thr Gly Tyr Gly Leu Gly Gly Ser Ser						
	225	230	235			240
Met Ala Leu Phe Gly Arg Val Gly Gly Gly Ile Tyr Thr Lys Ala Ala						
	245	250	255			
Asp Val Gly Ala Asp Leu Val Gly Lys Ile Glu Arg Asn Ile Pro Glu						
	260	265	270			
Asp Asp Pro Arg Asn Pro Ala Val Ile Ala Asp Asn Val Gly Asp Asn						
	275	280	285			
Val Gly Asp Ile Ala Gly Met Gly Ser Asp Leu Phe Gly Ser Tyr Ala						
	290	295	300			
Glu Ala Ser Cys Ala Ala Leu Val Val Ala Ser Ile Ser Ser Phe Gly						
	305	310	315			320
Ile Asn His Asp Phe Thr Ala Met Cys Tyr Pro Leu Leu Ile Ser Ser						
	325	330	335			

Met Gly Ile Leu Val Cys Leu Ile Thr Thr Leu Phe Ala Thr Asp Phe
 340 345 350

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

Leu Ile Ile Ser Thr Val Ile Met Thr Val Gly Ile Ala Ile Val Ser
 370 375 380

Trp Val Gly Leu Pro Thr Ser Phe Thr Ile Phe Asn Phe Gly Thr Gln
 385 390 395 400

Lys Val Val Lys Asn Trp Gln Leu Phe Leu Cys Val Cys Val Gly Leu
 405 410 415

Trp Ala Gly Leu Ile Ile Gly Phe Val Thr Glu Tyr Tyr Thr Ser Asn
 420 425 430

Ala Tyr Ser Pro Val Gln Asp Val Ala Asp Ser Cys Arg Thr Gly Ala
 435 440 445

Ala Thr Asn Val Ile Phe Gly Leu Ala Leu Gly Tyr Lys Ser Val Ile
 450 455 460

Ile Pro Ile Phe Ala Ile Ala Ile Ser Ile Phe Val Ser Phe Ser Phe
 465 470 475 480

Ala Ala Met Tyr Gly Val Ala Val Ala Ala Leu Gly Met Leu Ser Thr
 485 490 495

Ile Ala Thr Gly Leu Ala Ile Asp Ala Tyr Gly Pro Ile Ser Asp Asn
 500 505 510

Ala Gly Gly Ile Ala Glu Met Ala Gly Met Ser His Arg Ile Arg Glu
 515 520 525

Arg Thr Asp Ala Leu Asp Ala Ala Gly Asn Thr Thr Ala Ala Ile Gly
 530 535 540

Lys Gly Phe Ala Ile Gly Ser Ala Ala Leu Val Ser Leu Ala Leu Phe
 545 550 555 560

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

Pro Lys Val Ile Ile Gly Leu Leu Val Gly Ala Met Leu Pro Tyr Trp
 580 585 590

Phe Ser Ala Met Thr Met Lys Ser Val Gly Ser Ala Ala Leu Lys Met
 595 600 605

Val Glu Glu Val Arg Arg Gln Phe Asn Thr Ile Pro Gly Leu Met Glu
610 615 620

Gly Thr Ala Lys Pro Asp Tyr Ala Thr Cys Val Lys Ile Ser Thr Asp
625 630 635 640

Ala Ser Ile Lys Glu Met Ile Pro Pro Gly Cys Leu Val Met Leu Thr
645 650 655

Pro Leu Ile Val Gly Phe Phe Phe Gly Val Glu Thr Leu Ser Gly Val
660 665 670

Leu Ala Gly Ser Leu Val Ser Gly Val Gln Ile Ala Ile Ser Ala Ser
675 680 685

Asn Thr Gly Gly Ala Trp Asp Asn Ala Lys Lys Tyr Ile Glu Ala Gly
690 695 700

Val Ser Glu His Ala Lys Ser Leu Gly Pro Lys Gly Ser Glu Pro His
705 710 715 720

Lys Ala Ala Val Ile Gly Asp Thr Ile Gly Asp Pro Leu Lys Asp Thr
725 730 735

Ser Gly Pro Ser Leu Asn Ile Leu Ile Lys Leu Met Ala Val Glu Ser
740 745 750

Leu Val Phe Ala Pro Phe Phe Ala Thr His Gly Gly Ile Leu Phe Lys
755 760 765

Tyr Phe
770

<210> 19
<211> 945
<212> DNA
<213> artificial

<220>
<223> SNAC1 - Oryza sativa, Complete CDS, codon optimized

<400> 19
atgggaatga gacgagaacg agacgcagaa gccgagctta atctgccacc tggctttcgt 60
tttcatccga ctgatgatga actagtggaa cactaccttt gcagaaaagc agctgggtcaa 120
aggctcccag ttcctatcat agctgaggtt gatctctata aatttgaccc ctgggatctt 180
ccggaaaggg cattgtttgg ggctcgtgaa tggtaactttt tcacccacag cgataggaag 240
tacccaaacg gatctcgtcc aaacagggcc gctggaaaacg gttattggaa agcgactgga 300
gctgacaagc cagtagctcc tagggggaga acgctcggtta ttaaaaaggc tctagttttc 360
tacgctggaa aagccccaag aggcgttaag actgactgga ttatgcatga atatagactg 420

gctgatgctg gaagagctgc tgcgggggct aagaaaggta gtttgagatt agacgattgg 480
 gtcctctgtc ggctatataa caagaagaac gagtgggaga agatgcaaca ggggaaagag 540
 gttaaggagg aagcctcgga tatgggtgact tcccagtcgc atagccacac ccactcttgg 600
 ggagaaaccc gcacaccaga gtctgagatc gttgataacg acccctttcc ggaattggat 660
 tctttccctg cttttcaacc tgcacctcca cctgcaactg caatgatggt cccgaagaaa 720
 gaatcaatgg acgacgcaac agcagcagct gctgctgccg cgacaatccc taggaataat 780
 tcaagccttt tcgtagatct ttcctacgac gatattcagg ggatgtatag cggcttagac 840
 atgttgccctc ccggcgacga cttctattcc tcattgttcg caagtccccg tgtcaaagga 900
 acaacacctc gagcaggtgc tggaatggga atgggtgcctt tttaa 945

<210> 20
 <211> 314
 <212> PRT
 <213> Oryza sativa

<400> 20

Met Gly Met Arg Arg Glu Arg Asp Ala Glu Ala Glu Leu Asn Leu Pro
 1 5 10 15

Pro Gly Phe Arg Phe His Pro Thr Asp Asp Glu Leu Val Glu His Tyr
 20 25 30

Leu Cys Arg Lys Ala Ala Gly Gln Arg Leu Pro Val Pro Ile Ile Ala
 35 40 45

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

Leu Phe Gly Ala Arg Glu Trp Tyr Phe Phe Thr Pro Arg Asp Arg Lys
 65 70 75 80

Tyr Pro Asn Gly Ser Arg Pro Asn Arg Ala Ala Gly Asn Gly Tyr Trp
 85 90 95

Lys Ala Thr Gly Ala Asp Lys Pro Val Ala Pro Arg Gly Arg Thr Leu
 100 105 110

Gly Ile Lys Lys Ala Leu Val Phe Tyr Ala Gly Lys Ala Pro Arg Gly
 115 120 125

Val Lys Thr Asp Trp Ile Met His Glu Tyr Arg Leu Ala Asp Ala Gly
 130 135 140

Arg Ala Ala Ala Gly Ala Lys Lys Gly Ser Leu Arg Leu Asp Asp Trp
 145 150 155 160

Val Leu Cys Arg Leu Tyr Asn Lys Lys Asn Glu Trp Glu Lys Met Gln
 165 170 175
 Gln Gly Lys Glu Val Lys Glu Glu Ala Ser Asp Met Val Thr Ser Gln
 180 185 190
 Ser His Ser His Thr His Ser Trp Gly Glu Thr Arg Thr Pro Glu Ser
 195 200 205
 Glu Ile Val Asp Asn Asp Pro Phe Pro Glu Leu Asp Ser Phe Pro Ala
 210 215 220
 Phe Gln Pro Ala Pro Pro Pro Ala Thr Ala Met Met Val Pro Lys Lys
 225 230 235 240
 Glu Ser Met Asp Asp Ala Thr Ala Ala Ala Ala Ala Ala Thr Ile
 245 250 255
 Pro Arg Asn Asn Ser Ser Leu Phe Val Asp Leu Ser Tyr Asp Asp Ile
 260 265 270
 Gln Gly Met Tyr Ser Gly Leu Asp Met Leu Pro Pro Gly Asp Asp Phe
 275 280 285
 Tyr Ser Ser Leu Phe Ala Ser Pro Arg Val Lys Gly Thr Thr Pro Arg
 290 295 300
 Ala Gly Ala Gly Met Gly Met Val Pro Phe
 305 310

<210> 21
 <211> 720
 <212> DNA
 <213> artificial

<220>
 <223> IPT isopentenyl transferase IPT (E88G)

<400> 21
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 cttgcccagc agactgggct tccagtcctt tcgctcgatc gggccaatg ttgtcctcag 120
 ctgtcaaccg gaagcggacg accaacagtg gaagaactga aaggaacgag ccgtctatac 180
 cttgatgatc ggcctctggt gaagggtatc atcgagcca agcaagctca tgaaaggctg 240
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 attcgccacg agtttagcaga cgaggagacc ttcattgaacg tggccaaggc cagagttaag 420
 cagatgttac gccctgctgc aggcctttct attatccaag agttgggtga tctttggaaa 480
 gagcctcggc tgaggcccat actgaaagag atcgatggat atcgatatgc catgttggtt 540

gctagccaga accagatcac atccgatatg ctattgcagc ttgacgcaga tatggaggat 600
aagttgattc atgggatcgc tcaggagtat ctcatccatg cacgccgaca agaacagaaa 660
ttccctcgag ttaacgcagc cgcttacgac ggattcgaag gtcatccatt cggaatgtat 720

<210> 22
<211> 240
<212> PRT
<213> artificial

<220>
<223> IPT isopentenyl transferase IPT (E88G)

<400> 22

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

Asp Arg Val Gln Cys Cys Pro Gln Leu Ser Thr Gly Ser Gly Arg Pro
35 40 45

Thr Val Glu Glu Leu Lys Gly Thr Ser Arg Leu Tyr Leu Asp Asp Arg
50 55 60

Pro Leu Val Lys Gly Ile Ile Ala Ala Lys Gln Ala His Glu Arg Leu
65 70 75 80

Met Gly Glu Val Tyr Asn Tyr Glu Ala His Gly Gly Leu Ile Leu Glu
85 90 95

Gly Gly Ser Ile Ser Leu Leu Lys Cys Met Ala Gln Ser Ser Tyr Trp
100 105 110

Ser Ala Asp Phe Arg Trp His Ile Ile Arg His Glu Leu Ala His Glu
115 120 125

Glu Thr Phe Met Asn Val Ala Lys Ala Arg Val Lys Gln Met Leu Arg
130 135 140

Pro Ala Ser Gly Leu Ser Ile Ile Gln Glu Leu Val Asp Leu Trp Lys
145 150 155 160

Glu Pro Arg Leu Arg Arg Ile Leu Lys Glu Ile Asp Gly Tyr Arg Tyr
165 170 175

Ala Met Leu Phe Val Ser Gln Asn Gln Ile Thr Ser Asp Met Leu Leu
180 185 190

Gln Leu Asp Ala Asp Met Glu Asp Lys Leu Ile His Gly Ile Ala Gln
195 200 205

Glu Tyr Leu Ile His Ala Arg Arg Gln Glu Gln Lys Phe Pro Arg Val
 210 215 220

Asn Ala Ala Ala Tyr Asp Gly Phe Glu Gly His Pro Phe Gly Met Tyr
 225 230 235 240

<210> 23
 <211> 513
 <212> DNA
 <213> Tomato

<400> 23
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 accggtgaga aagggtgttg aaagatgggg aagcctttgc actacaaggg ctcaaccttc 180
 caccgtgtga tcccagggtt catgtgtcaa ggaggtgatt tcaccgccgg aaacgggacc 240
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 ggccctggaa tcctctccat ggctaagtct ggacctggaa ccaacgggtc tcagtttttc 360
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 gaaggcatgg atgtgattaa gaaggcagag gctgttggat ctagctctgg aagggtgctcc 480
 aagcctgtgg ttattgctga ctgcggtcaa ctc 513

<210> 24
 <211> 171
 <212> PRT
 <213> Tomato

<400> 24

Met Ala Asn Pro Lys Val Phe Phe Asp Leu Thr Ile Gly Gly Ala Pro
 1 5 10 15

Ala Gly Arg Val Val Met Glu Leu Phe Ala Asp Thr Thr Pro Lys Thr
 20 25 30

Ala Glu Asn Phe Arg Ala Leu Cys Thr Gly Glu Lys Gly Val Gly Lys
 35 40 45

Met Gly Lys Pro Leu His Tyr Lys Gly Ser Thr Phe His Arg Val Ile
 50 55 60

Pro Gly Phe Met Cys Gln Gly Gly Asp Phe Thr Ala Gly Asn Gly Thr
 65 70 75 80

Gly Gly Glu Ser Ile Tyr Gly Ala Lys Phe Asn Asp Glu Asn Phe Val
 85 90 95

Lys Lys His Thr Gly Pro Gly Ile Leu Ser Met Ala Asn Ala Gly Pro

100

105

110

Gly Thr Asn Gly Ser Gln Phe Phe Ile Cys Thr Ala Lys Thr Glu Trp
 115 120 125

Leu Asn Gly Lys His Val Val Phe Gly Gln Val Val Glu Gly Met Asp
 130 135 140

Val Ile Lys Lys Ala Glu Ala Val Gly Ser Ser Ser Gly Arg Cys Ser
 145 150 155 160

Lys Pro Val Val Ile Ala Asp Cys Gly Gln Leu
 165 170

<210> 25

<211> 4780

<212> DNA

<213> artificial

<220>

<223> nucleotide sequence of T-DNA o fpNMD2492

<400> 25

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cactgatagt ttaaaactgaa ggcgggaaac gacaatctga tctaagctag gcatggaatt      180
ccaatccac aaaaatctga gcttaacagc acagttgctc ctctcagagc agaatcgggt      240
attcaacacc ctcatatcaa ctactacgtt gtgtataacg gtccacatgc cggatatatac      300
gatgactggg gttgtacaaa ggcggcaaca aacggcgttc ccggagttgc acacaagaaa      360
tttgccacta ttacagaggc aagagcagca gctgacgcgt acacaacaag tcagcaaaca      420
gacaggttga acttcatccc caaaggagaa gctcaactca agcccaagag ctttgctaag      480
gccctaaca gcccaccaa gcaaaaagcc cactggctca cgctaggaac caaaaggccc      540
agcagtgatc cagcccaaaa agagatctcc tttgccccgg agattacaat ggacgatttc      600
ctctatcttt acgatctagg aaggaagttc gaaggtgaag gtgacgacac tatgttcacc      660
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aagaacacag agaaagacat atttctcaag atcagaagta ctattccagt atggacgatt      900
caaggcttgc ttcataaacc aaggcaagta atagagattg gagtctctaa aaaggtagtt      960
cctactgaat ctaaggccat gcatggagtc taagattcaa atcgaggatc taacagaact     1020
cgccgtgaag actggcgaac agttcataca gagtctttta cgactcaatg acaagaagaa     1080
aatcttcgtc aacatgggtg agcacgacac tctggtctac tccaaaaatg tcaaagatac     1140
agtctcagaa gaccaaaggg ctattgagac ttttcaacaa aggataatct cgggaaacct     1200

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tggctcctac aaatgccatc attgcgataa aggaaaggct atcattcaag atctctctgc	1320
cgacagtggc cccaaagatg gacccccacc cagcaggagc atcgtggaaa aagaagacgt	1380
tccaaccacg tcttcaaagc aagtggattg atgtgacatc tccactgacg taagggatga	1440
cgcacaatcc cactatcctt cgcaagaccc ttctctata taaggaagtt catttcattt	1500
ggagaggaca cgctcgagta taagagctca tttttacaac aattaccaac aacaacaaac	1560
aacaacaaac attacaatta catttacaat tatcgatacc atgggagacc attaagttgg	1620
taatttgagg tctcttaagg atcctctaga gtcaagcaga tcgttcaaac atttggaat	1680
aaagtttctt aagattgaat cctggtgccc gtcttgccg gattatcata taatttctgt	1740
tgaattacgt taagcatgta ataattaaca tgtaatgcat gacgttattt atgagatggg	1800
tttttatgat tagagtcccg caattataca tttaatacgc gatagaaaac aaaatatagc	1860
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