

06-03-2012 listage séquences_ST25
SEQUENCE LISTING

<110> Institut National de la Recherche Agronomique
Vilmorin & Cie

<120> Cucurbitacées androïques, procédés d'obtention et utilisations de
ces cucurbitacées androïques

<130> INR-B-0008-PCT1

<150> FR1200149
<151> 2012-01-16

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<170> PatentIn version 3.5

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attgg	2225

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 <212> DNA
 <213> Cucumis melo

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atccaaatgg gtcttgccga aaacagggtg tggtatgact tcttgatga gtggatggag	180
aacaatccag atgcttttagg attgagaaaa aatggagtgt ctttgtttag agaattggct	240
ctatttcaag actaccatgg cttgccggct tttaaaaagg cggttggtga atcaatggaa	300

06-03-2012 listage séquences_ST25

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 cccactcctt actatccagg gtttgacagg gacttaaaat ggcgtacaga agttcaaata 480
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 <213> Cucumis melo

<400> 12

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Pro Thr Gln Asn Pro Ser Gly Ile Ile Gln Met Gly Leu Ala Glu Asn
 35 40 45

Arg Val Cys Tyr Asp Phe Leu Asp Glu Trp Met Glu Asn Asn Pro Asp
 50 55 60

Ala Leu Gly Leu Arg Lys Asn Gly Val Ser Leu Phe Arg Glu Leu Ala
 65 70 75 80

Leu Phe Gln Asp Tyr His Gly Leu Pro Ala Phe Lys Lys Ala Leu Val
 85 90 95

06-03-2012 listage séquences_ST25

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 Lys Leu Val Leu Thr Ala Gly Ala Thr Ala Ala Asn Glu Ile Leu Ile
 115 120 125
 Ser Cys Leu Ala Asp Pro Gly Glu Ala Phe Leu Val Pro Thr Pro Tyr
 130 135 140
 Tyr Pro Gly Phe Asp Arg Asp Leu Lys Trp Arg Thr Glu Val Gln Ile
 145 150 155 160
 Ile Pro Ile His Cys Ser Ser Ser Asn Ser Phe Gln Ile Thr Glu Ala
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 Ala Met Glu Glu Ala Met Glu Gln Ala Gln Thr Leu Asn Leu Arg Val
 180 185 190
 Lys Gly Ile Met Ile Thr Asn Pro Ser Asn Pro Leu Gly Thr Thr Leu
 195 200 205
 Ser Gln Lys Glu Ile Asn Ser Val Val Asp Phe Ala Ile Ala Asn Ala
 210 215 220
 Ile His Ile Val Ser Asp Glu Ile Tyr Ser Ala Thr Val Phe Glu His
 225 230 235 240
 Pro Lys Phe Arg Thr Val Met Asp Pro Asn Leu Gln Lys Phe Pro Ile
 245 250 255
 Trp Asp Arg Ile His Leu Val Tyr Ser Leu Ser Lys Asp Leu Gly Leu
 260 265 270
 Pro Gly Phe Arg Val Gly Met Ile Tyr Ser Asn Asp Leu Ala Val Val
 275 280 285
 Asp Ala Ala Thr Lys Met Ser Ser Phe Cys Leu Val Ser Ser Gln Thr
 290 295 300
 Gln Tyr Phe Val Ser Gln Ile Val Gly Asp Glu Lys Phe Arg Gly Asn
 305 310 315 320
 Tyr Met Gln Glu Met Lys Arg Arg Ile Arg Lys Arg Arg Leu Met Leu
 325 330 335
 Glu Ser Ser Leu Arg Gln Gly Gly Val Arg Cys Leu Lys Gly Asn Ala
 340 345 350
 Gly Leu Phe Cys Trp Val Asp Met Arg His Leu Leu Lys Tyr Pro Ser
 355 360 365

06-03-2012 listage séquences_ST25

Phe Glu Glu Glu Met Glu Ile Trp Lys Thr Ile Leu Tyr Glu Val Gly
370 375 380

Ile Asn Ile Ser Pro Gly Ser Ser Phe His Cys Ser Glu Pro Gly Trp
385 390 395 400

Phe Arg Met Cys Phe Ala Asn Met Glu Glu His Thr Phe Lys Val Ala
405 410 415

Met His Arg Leu Lys Thr Phe Leu Asn Ser Thr Ser Pro Leu Asn Ala
420 425 430

Tyr Glu Leu Ser Pro Thr Asn Ile
435 440

<210> 13
<211> 2225
<212> DNA
<213> Cucumis melo

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tggcaagagt acgagaagaa cccttatcac cctactcaaa acccctccgg gattatccaa 240
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gcaagcccaa acattgaatt tacgagtcaa agggattatg attacgaacc catccaaccc 1260

06-03-2012 listage séquences_ST25

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attgg						2225

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 <212> DNA
 <213> Cucumis melo

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tccaacccat	taggcaccac attgagccag aaagagatta actcgggtggg ggatttcgct 660
atagccaatg	caatccacat cgtgagcgat gagatatatt ccgccacagt ttttgagcac 720
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06-03-2012 listage séquences_ST25

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<210> 15
<211> 440
<212> PRT
<213> Cucumis melo

<400> 15

Met Ala Met Leu Ser Thr Lys Ala Gly His Asp Ser His Gly Gln Asn
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20 25 30

Pro Thr Gln Asn Pro Ser Gly Ile Ile Gln Met Gly Phe Ala Glu Asn
35 40 45

Arg Val Cys Tyr Asp Phe Leu Asp Glu Trp Met Glu Asn Asn Pro Asp
50 55 60

Ala Leu Gly Leu Arg Lys Asn Gly Val Ser Leu Phe Arg Glu Leu Ala
65 70 75 80

Leu Phe Gln Asp Tyr His Gly Leu Pro Ala Phe Lys Lys Ala Leu Val
85 90 95

Glu Ser Met Glu Glu Ile Arg Gly Asn Lys Met Lys Phe Glu Met Asn
100 105 110

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

Ser Cys Leu Ala Asp Pro Gly Glu Ala Phe Leu Val Pro Thr Pro Tyr
130 135 140

Tyr Pro Gly Phe Asp Arg Asp Leu Lys Trp Arg Thr Glu Val Gln Ile
145 150 155 160

06-03-2012 listage séquences_ST25

Ile Pro Ile His Cys Ser Ser Ser Asn Ser Phe Gln Ile Thr Glu Ala
165 170 175

Ala Met Glu Glu Ala Met Glu Gln Ala Gln Thr Leu Asn Leu Arg Val
180 185 190

Lys Gly Ile Met Ile Thr Asn Pro Ser Asn Pro Leu Gly Thr Thr Leu
195 200 205

Ser Gln Lys Glu Ile Asn Ser Val Val Asp Phe Ala Ile Ala Asn Ala
210 215 220

Ile His Ile Val Ser Asp Glu Ile Tyr Ser Ala Thr Val Phe Glu His
225 230 235 240

Pro Lys Phe Arg Thr Val Met Asp Pro Asn Leu Gln Lys Phe Pro Ile
245 250 255

Trp Asp Arg Ile His Leu Val Tyr Ser Leu Ser Lys Asp Leu Gly Leu
260 265 270

Pro Gly Phe Arg Val Gly Met Ile Tyr Ser Asn Asp Leu Ala Val Val
275 280 285

Asp Ala Ala Thr Lys Met Ser Ser Phe Cys Leu Val Ser Ser Gln Thr
290 295 300

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

Tyr Met Gln Glu Met Lys Arg Arg Ile Arg Lys Arg Arg Leu Met Leu
325 330 335

Glu Ser Ser Leu Arg Gln Gly Gly Val Arg Cys Leu Lys Gly Asn Ala
340 345 350

Gly Leu Phe Cys Trp Val Asp Met Arg His Leu Leu Lys Tyr Pro Ser
355 360 365

Phe Glu Glu Glu Met Glu Ile Trp Lys Thr Ile Leu Tyr Glu Val Gly
370 375 380

Ile Asn Ile Ser Pro Gly Ser Ser Phe His Cys Ser Glu Pro Gly Trp
385 390 395 400

Phe Arg Met Cys Phe Ala Asn Met Glu Glu His Thr Phe Lys Val Ala
405 410 415

Met His Arg Leu Lys Thr Phe Leu Asn Ser Thr Ser Pro Leu Asn Ala
420 425 430

06-03-2012 listage séquences_ST25

Tyr Glu Leu Ser Pro Thr Asn Ile
435 440

<210> 16
<211> 2225
<212> DNA
<213> Cucumis melo

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06-03-2012 listage séquences_ST25

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 <212> DNA
 <213> Cucumis melo

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06-03-2012 listage séquences_ST25

taa

1323

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 <212> PRT
 <213> Cucumis melo

<400> 18

Met Ala Met Leu Ser Thr Lys Ala Gly His Asp Ser His Gly Gln Asn
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Ser Ser Tyr Phe Phe Gly Trp Gln Glu Tyr Glu Lys Asn Pro Tyr His
 20 25 30

Pro Thr Gln Asn Pro Ser Gly Ile Ile Gln Met Gly Leu Ala Glu Asn
 35 40 45

Arg Val Cys Tyr Asp Phe Leu Asp Glu Trp Met Glu Asn Asn Pro Asp
 50 55 60

Ala Leu Gly Leu Arg Lys Asn Gly Val Ser Leu Phe Arg Glu Leu Ala
 65 70 75 80

Leu Phe Gln Asp Tyr His Gly Leu Pro Ala Phe Lys Lys Ala Leu Val
 85 90 95

Glu Ser Met Glu Glu Ile Arg Gly Asn Lys Met Lys Phe Glu Met Asn
 100 105 110

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

Ser Cys Leu Ala Asp Pro Gly Glu Ala Phe Leu Val Pro Thr Pro Tyr
 130 135 140

Tyr Pro Gly Phe Asp Arg Asp Leu Lys Trp Arg Thr Glu Val Gln Ile
 145 150 155 160

Ile Pro Ile His Cys Ser Ser Ser Asn Ser Phe Gln Ile Thr Glu Ala
 165 170 175

Ala Met Glu Glu Ala Met Glu Gln Ala Gln Thr Leu Asn Leu Arg Val
 180 185 190

Lys Gly Ile Met Ile Thr Asn Pro Ser Asn Pro Leu Gly Thr Thr Leu
 195 200 205

Ser Gln Lys Glu Ile Asn Ser Val Val Asp Phe Ala Ile Ala Asn Ala
 210 215 220

Ile His Ile Val Ser Asp Glu Ile Tyr Ser Ala Thr Val Phe Glu His
 Pge p

06-03-2012 listage séquences_ST25

225 230 235 240

Pro Lys Phe Arg Thr Val Met Asp Pro Asn Leu Gln Lys Phe Pro Ile
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Trp Asp Arg Ile His Leu Val Tyr Ser Leu Ser Lys Asp Leu Gly Leu
260 265 270

Pro Gly Phe Arg Val Gly Met Ile Tyr Ser Asn Asp Leu Ala Val Val
275 280 285

Asp Ala Ala Thr Lys Met Phe Ser Phe Cys Leu Val Ser Ser Gln Thr
290 295 300

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

Tyr Met Gln Glu Met Lys Arg Arg Ile Arg Lys Arg Arg Leu Met Leu
325 330 335

Glu Ser Ser Leu Arg Gln Gly Gly Val Arg Cys Leu Lys Gly Asn Ala
340 345 350

Gly Leu Phe Cys Trp Val Asp Met Arg His Leu Leu Lys Tyr Pro Ser
355 360 365

Phe Glu Glu Glu Met Glu Ile Trp Lys Thr Ile Leu Tyr Glu Val Gly
370 375 380

Ile Asn Ile Ser Pro Gly Ser Ser Phe His Cys Ser Glu Pro Gly Trp
385 390 395 400

Phe Arg Met Cys Phe Ala Asn Met Glu Glu His Thr Phe Lys Val Ala
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Tyr Glu Leu Ser Pro Thr Asn Ile
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<212> DNA
<213> Citrullus lanatus

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Lys Val Cys Pro Asp Leu Leu Asp Glu Trp Met Glu Asn Asn Pro Asp
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Ser Cys Leu Ala Asp Pro Gly Glu Ala Phe Leu Val Pro Thr Pro Tyr
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Tyr Pro Gly Phe Asp Arg Asp Leu Lys Trp Arg Thr Glu Val Gln Ile
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Ile Pro Ile His Cys Ser Ser Ser Asn Ser Phe Gln Ile Thr Glu Ala
165 170 175

Ala Met Glu Glu Ala Met Glu Gln Ala Gln Thr Leu Asn Leu Arg Val
180 185 190

Lys Gly Ile Met Ile Thr Asn Pro Ser Asn Pro Leu Gly Thr Thr Leu
195 200 205

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210 215 220

Ile His Ile Val Ser Asp Glu Ile Tyr Ser Ala Thr Val Phe Glu His
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Pro Lys Phe Arg Thr Val Met Asp Pro Asn Leu Gln Lys Phe Pro Ile
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Trp Asp Arg Ile His Leu Val Tyr Ser Leu Ser Lys Asp Leu Gly Leu
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Asp Ala Ala Thr Lys Met Ser Ser Phe Cys Leu Val Ser Ser Gln Thr
290 295 300

Gln Tyr Phe Val Ser Gln Ile Val Gly Asp Glu Lys Phe Arg Gly Asn
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Tyr Met Gln Glu Met Lys Arg Arg Ile Arg Lys Arg Arg Leu Met Leu
325 330 335

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Glu Ser Ser Leu Arg Gln Gly Gly Val Arg Cys Leu Lys Gly Asn Ala
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Gly Leu Phe Cys Trp Val Asp Met Arg His Leu Leu Lys Tyr Pro Ser
355 360 365

Phe Glu Glu Glu Met Glu Ile Trp Lys Thr Ile Leu Tyr Glu Val Gly
370 375 380

Ile Asn Ile Ser Pro Gly Ser Ser Phe His Cys Ser Glu Pro Gly Trp
385 390 395 400

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

Ile His Ile Val Ser Asp Glu Ile Tyr Ser Ala Thr Val Phe Glu His
225 230 235 240

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

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Phe Glu Glu Glu Met Glu Ile Trp Lys Thr Ile Leu Tyr Glu Val Gly
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Ile Asn Ile Ser Pro Gly Ser Ser Phe His Cys Ser Glu Pro Gly Trp
385 390 395 400

Phe Arg Met Cys Phe Ala Asn Met Glu Glu His Thr Phe Lys Glu Ala
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cgacagggcg gtgttagatg tttgaaaggg aatgcagggt tgttttggtt ggtggatatg	1080
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<210> 27
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 <212> PRT
 <213> Lagenaria siceraria

<220>

06-03-2012 listage séquences_ST25

<221> misc_feature

<222> (58)..(58)

<223> Xaa can be any naturally occurring amino acid

<400> 27

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Ser Ser Tyr Phe Phe Gly Leu Gln Glu Tyr Glu Lys Asp Pro Tyr His
20 25 30

Pro Ile Gln Asn Pro Ser Gly Ile Ile Gln Met Gly Leu Ala Glu Asn
35 40 45

Lys Val Cys Pro Asp Leu Leu Asp Glu Xaa Met Glu Asn Asn Pro Asp
50 55 60

Ala Leu Gly Leu Arg Arg Asn Gly Val Ser Glu Phe Arg Glu Leu Ala
65 70 75 80

Leu Phe Gln Asp Tyr His Gly Leu Pro Ala Phe Lys Lys Ala Leu Val
85 90 95

Glu Ser Met Glu Glu Ile Arg Gly Asn Lys Met Lys Phe Glu Met Asn
100 105 110

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

Ser Cys Leu Ala Asp Pro Gly Glu Ala Phe Leu Val Pro Thr Pro Tyr
130 135 140

Tyr Pro Gly Phe Asp Arg Asp Leu Lys Trp Arg Thr Glu Val Gln Ile
145 150 155 160

Ile Pro Ile His Cys Ser Ser Ser Asn Ser Phe Gln Ile Thr Glu Ala
165 170 175

Ala Met Glu Glu Ala Met Glu Gln Ala Gln Thr Leu Asn Leu Arg Val
180 185 190

Lys Gly Ile Met Ile Thr Asn Pro Ser Asn Pro Leu Gly Thr Thr Leu
195 200 205

Ser Gln Lys Glu Ile Asn Ser Val Val Asp Phe Ala Ile Ala Asn Ala
210 215 220

Ile His Ile Val Ser Asp Glu Ile Tyr Ser Ala Thr Val Phe Glu His
225 230 235 240

Pro Lys Phe Arg Thr Val Met Asp Pro Asn Leu Gln Lys Phe Pro Ile
245 250 255

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Trp Asp Arg Ile His Leu Val Tyr Ser Leu Ser Lys Asp Leu Gly Leu
260 265 270

Pro Gly Phe Arg Val Gly Met Ile Tyr Ser Asn Asp Leu Ala Val Val
275 280 285

Asp Ala Ala Thr Lys Met Ser Ser Phe Cys Leu Val Ser Ser Gln Thr
290 295 300

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

Tyr Met Gln Glu Met Lys Arg Arg Ile Arg Lys Arg Arg Leu Met Leu
325 330 335

Glu Ser Ser Leu Arg Gln Gly Gly Val Arg Cys Leu Lys Gly Asn Ala
340 345 350

Gly Leu Phe Cys Trp Val Asp Met Arg His Leu Leu Lys Tyr Pro Ser
355 360 365

Phe Glu Glu Glu Met Glu Ile Trp Lys Thr Ile Leu Tyr Glu Val Gly
370 375 380

Ile Asn Ile Ser Pro Gly Ser Ser Phe His Cys Ser Glu Pro Gly Trp
385 390 395 400

Phe Arg Met Cys Phe Ala Asn Met Glu Glu His Thr Phe Lys Glu Ala
405 410 415

Met His Arg Leu Lys Ala Phe Leu Asn Ser Thr Ser Ser Leu Asn Gly
420 425 430

His Glu Leu Ser Pro Thr Asn Val
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<210> 28

<211> 1961

<212> DNA

<213> Momordica charantia

<400> 28

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gccatgattc tcatggacaa aattcttcct acttctttgg attgcaagag tatgagaagg 180

acccttatca ccctattcaa aaccctcgg gaattataca aatgggtctt gccgaaaaca 240

aggtaattct tgaatgtaat taagttggac tacaaccatt attgttcctt ttgtagttta 300

actacacatg gtcgaatcat ttgttatcaa atgacattgt agtcggttga aatatattga 360

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gtaattaagt aagaaaaaga tgtaaacgcg gatgcatcaa agtaaaacca aataaaaata	420
tgttacgtag caattaatth atttaatgaa ttttgtaagg tttagttaac ggthttctttt	480
atatatgctt gttatgatca cgatgattat ggattatgga ttatggthttt ggaggtagaa	540
aatttgattg taacatgtga tatttaaath ggthtttgca gtatgtcctg accttttgga	600
tgagtggatg gagaacaath cagatgcttt gggattgaga agaaatggag tgtctgagtt	660
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cctacaacct tagthttatt cataaagggc tcttcaaath ttctthttctt tctthttattt	780
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aactgctgcc aatgaaathc tcatactthg tcttgccgat cccggtgaag cgttcctcgt	960
tcccactcct tactatccag ggtaaataaa ttcaataact ttccaatata taaatcttct	1020
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ttgacagggg cttaaaathg cgtacagaag ttcaataath tccaatccat tgttcgagtt	1140
caaacagctt ccaaatcaca gaagcggcga tgg	1200
tgaatthacg agtcaaaggg attatgatha cga	1260
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ccccggctc atctththcat tgctctgaac ctggttggtt cagaatgtgc thtgctaata	1860
tggaggagca cactthcaag gaggccatgc atcgtcttaa ggcctthctc aactctacct	1920
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3/3

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 <211> 1323
 <212> DNA
 <213> Momordica charentia

<400> 29	
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atacaaatgg gtcttgccga aaacaaggta tgcctgacc thttggatga gtggatggag	180
aacaathccag atgctthggg attgagaaga aatggagthg ctgagththg agaathagct	240

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ctattttcaag actatcatgg cttgccagct tttaaaaagg tgttggttga atcaatggaa 300
gaaatacgag gaaacaaaat gaaatttgag atgaacaaac tggtgctaac cgctggtgca 360
actgctgcca atgaaatcct catatcttgt cttgccgatc ccggtgaagc gttcctcgtt 420
cccactcctt actatccagg gtttgacagg gacttaaaat ggcgtacaga agttcaaata 480
attccaatcc attgttcgag ttcaaacagc ttccaaatca cagaagcggc gatggaggaa 540
gccatggagc aagcccaaac attgaattta cgagtcaaag ggattatgat tacgaaccca 600
tccaacccat taggcaccac attgagccag aaagagatta actcgggtggt ggatttcgct 660
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ccaaagtttc gaactgtcat ggacccgaac ctacaaaaat tccaatttg ggaccgaatc 780
cacttggtgt acagcttgtc caaagatctg ggcctacccg gggtccgcgt gggcatgatt 840
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tctttctcaa cacagtattt tgtgtcgcaa attgtagggg atgaaaaatt tcgaggcaat 960
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aggcatcttt tgaagtaccc gagtttcgaa gaggaaatgg agatttgga gacgattttg 1140
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ttcagaatgt gctttgctaa tatggaggag cacactttca aggaggccat gcacgtctt 1260
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<210> 30
<211> 440
<212> PRT
<213> Momordica charantia

<400> -30

Met Ala Ser Leu Ser Ser Lys Ala Ser His Asp Ser His Gly Gln Asn
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Ser Ser Tyr Phe Phe Gly Leu Gln Glu Tyr Glu Lys Asp Pro Tyr His
20 25 30

Pro Ile Gln Asn Pro Ser Gly Ile Ile Gln Met Gly Leu Ala Glu Asn
35 40 45

Lys Val Cys Pro Asp Leu Leu Asp Glu Trp Met Glu Asn Asn Pro Asp
50 55 60

Ala Leu Gly Leu Arg Arg Asn Gly Val Ser Glu Phe Arg Glu Leu Ala
65 70 75 80

Leu Phe Gln Asp Tyr His Gly Leu Pro Ala Phe Lys Lys Val Leu Val
Pge p

Glu Ser Met Glu Glu Ile Arg Gly Asn Lys Met Lys Phe Glu Met Asn
100 105 110

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

Ser Cys Leu Ala Asp Pro Gly Glu Ala Phe Leu Val Pro Thr Pro Tyr
130 135 140

Tyr Pro Gly Phe Asp Arg Asp Leu Lys Trp Arg Thr Glu Val Gln Ile
145 150 155 160

Ile Pro Ile His Cys Ser Ser Ser Asn Ser Phe Gln Ile Thr Glu Ala
165 170 175

Ala Met Glu Glu Ala Met Glu Gln Ala Gln Thr Leu Asn Leu Arg Val
180 185 190

Lys Gly Ile Met Ile Thr Asn Pro Ser Asn Pro Leu Gly Thr Thr Leu
195 200 205

Ser Gln Lys Glu Ile Asn Ser Val Val Asp Phe Ala Ile Ala Asn Ala
210 215 220

Ile His Ile Val Ser Asp Glu Ile Tyr Ser Ala Thr Val Phe Glu His
225 230 235 240

Pro Lys Phe Arg Thr Val Met Asp Pro Asn Leu Gln Lys Phe Pro Ile
245 250 255

Trp Asp Arg Ile His Leu Val Tyr Ser Leu Ser Lys Asp Leu Gly Leu
260 265 270

Pro Gly Phe Arg Val Gly Met Ile Tyr Ser Asn Asp Leu Ala Val Val
275 280 285

Asp Ala Ala Thr Lys Met Ser Ser Phe Cys Leu Val Ser Ser Gln Thr
290 295 300

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

Tyr Met Gln Glu Met Lys Arg Arg Ile Arg Lys Arg Arg Leu Met Leu
325 330 335

Glu Ser Ser Leu Arg Gln Gly Gly Val Arg Cys Leu Lys Gly Asn Ala
340 345 350

Gly Leu Phe Cys Trp Val Asp Met Arg His Leu Leu Lys Tyr Pro Ser

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355

360

365

Phe Glu Glu Glu Met Glu Ile Trp Lys Thr Ile Leu Tyr Glu Val Gly
370 375 380

Ile Asn Ile Ser Pro Gly Ser Ser Phe His Cys Ser Glu Pro Gly Trp
385 390 395 400

Phe Arg Met Cys Phe Ala Asn Met Glu Glu His Thr Phe Lys Glu Ala
405 410 415

Met His Arg Leu Lys Ala Phe Leu Asn Ser Thr Ser Ser Leu Asn Gly
420 425 430

His Glu Leu Ser Pro Thr Asn Val
435 440

<210> 31
<211> 1869
<212> DNA
<213> Cucurbita pepo

<220>
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<222> (763)..(765)
<223> n = a, t, g or c

<220>
<221> misc_feature
<222> (798)..(799)
<223> n = a, t, g or c

<220>
<221> misc_feature
<222> (801)..(1068)
<223> n = a, t, g or c

<220>
<221> misc_feature
<222> (1604)..(1605)
<223> n = a, t, g or c

<220>
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<222> (1704)..(1869)
<223> n = a, t, g or c

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tgatggcatc cttgtcttct aaagctagcc atgatttctca tggacaaaat tcttcctact 180
tctttggatt gcaagagtat gagaaggacc cttatcaccc tattcaaaac ccctcgggaa 240
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aaccattatt gttccttttg tagtttaact acacatgggc gaatcatttg ttatcaaatg 360
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cttgccagct	tttaaaaagg	tacctagcct	acaaccctag	ttnnntcata	aagggctctt		780
caaatttctt	tcttttttnc	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		840
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		900
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		960
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn		1020
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 <211> 1245
 <212> DNA
 <213> Cucurbita pepo

<220>
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 <222> (280)..(534)
 <223> n = a, t, g or c

<220>
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 <222> (995)..(996)
 <223> n = a, t, g or c

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<220>
<221> misc_feature
<222> (1094)..(1245)
<223> n = a, t, g or c

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aacaatccag atgctttggg attgagaaga aatggagtgt ctgagttag agaattagct      240
ctatttcaag actatcatgg ctgcccagct tttaaaaagn nnnnnnnnnn nnnnnnnnnn      300
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tcaaattctg ggggacgaga aattccgaag gaattacatg gaggaacga agagacggat     1080
ccggaagagg aaagnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     1140
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     1200
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<210> 33
<211> 558
<212> PRT
<213> Cucurbita pepo

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<220>
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<222> (94)..(372)
<223> X = G, P, A, V, L, I, M, C, F, Y, W, H, K, R, Q, N, E, D, S or T

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<220>
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<222> (526)..(526)
<223> X = G, P, A, V, L, I, M, C, F, Y, W, H, K, R, Q, N, E, D, S or T

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<400> 33

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Met Ala Ser Leu Ser Ser Lys Ala Ser His Asp Ser His Gly Gln Asn

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			20					25					30				
Pro	Ile	Gln	Asn	Pro	Ser	Gly	Ile	Ile	Gln	Met	Gly	Leu	Ala	Glu	Asn		
		35					40					45					
Lys	Val	Cys	Pro	Asp	Leu	Leu	Asp	Glu	Trp	Met	Glu	Asn	Asn	Pro	Asp		
	50					55					60						
Ala	Leu	Gly	Leu	Arg	Arg	Asn	Gly	Val	Ser	Glu	Phe	Arg	Glu	Leu	Ala		
65					70					75					80		
Leu	Phe	Gln	Asp	Tyr	His	Gly	Leu	Pro	Ala	Phe	Lys	Lys	Xaa	Xaa	Xaa		
				85					90					95			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
			100					105					110				
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		115					120					125					
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	130					135					140						
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				165				170							175		
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			180				185						190				
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		195					200					205					
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	210					215					220						
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
225					230					235						240	
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				245				250						255			
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			260					265					270				
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275

280

285

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 305 310 315 320

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 325 330 335

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 340 345 350

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 355 360 365

Xaa Xaa Xaa Xaa Phe Asp Arg Asp Leu Lys Trp Arg Thr His Val Gln
 370 375 380

Ile Ile Pro Ile His Cys Trp Ser Ser Asn Gly Phe Arg Ile Thr Ala
 385 390 395 400

Ala Ala Met Glu Glu Ala Met Glu Arg Ala Glu Lys Leu Asn Leu Arg
 405 410 415

Val Lys Gly Val Leu Ile Thr Asn Pro Ser Asn Pro Leu Gly Thr Thr
 420 425 430

Met Ser Arg Asn Glu Leu Asn Leu Val Val Asp Phe Ala Lys Ala Lys
 435 440 445

Gly Ile His Ile Val Ser Asp Glu Ile Tyr Ser Ala Thr Val Tyr Glu
 450 455 460

Thr Pro Lys Phe Arg Thr Ile Met Asp Asp Ser Leu Lys Lys Ser Ser
 465 470 475 480

Ile Trp Asp Arg Ile His Val Val Tyr Ser Leu Ser Lys Asp Leu Gly
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