

PhoenixTemp21163.tmp.txt
SEQUENCE LISTING

<110> Shirley, Amber

<120> TRANSGENIC PLANTS WITH INCREASED STRESS TOLERANCE AND YIELD

<130> PF57972

<160> 45

<170> PatentIn version 3.4

<210> 1

<211> 615

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)..(615)

<223> methionine sulfoxide reductase family protein (BN51364980)

<400> 1

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Cys	Arg	Ser	Leu	Thr	Lys	Pro	Arg	Asn	Leu	Asn	Leu	Ser	Val	Leu	Leu	
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cgg	tgt	tcc	atg	ggt	tcc	ttt	aac	tct	tct	cag	aaa	tca	gac	aac	gtc	192
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Gln	Glu	Ala	Ala	Lys	Ser	Asp	Phe	Ala	Ser	Ile	Ser	Glu	Gly	Glu	Trp	
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aag	aaa	cgg	cta	aca	cca	gaa	cag	tat	tac	atc	acc	aga	cag	aag	gga	288
Lys	Lys	Arg	Leu	Thr	Pro	Glu	Gln	Tyr	Tyr	Ile	Thr	Arg	Gln	Lys	Gly	
			85					90						95		

aca	gag	aga	gct	ttc	act	ggt	gag	tat	tgg	aat	aca	aag	acc	cca	gga	336
Thr	Glu	Arg	Ala	Phe	Thr	Gly	Glu	Tyr	Trp	Asn	Thr	Lys	Thr	Pro	Gly	
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gta	tac	aaa	tgt	atc	tgt	tgc	gac	acg	cca	ctg	ttt	gac	tca	tca	aca	384
Val	Tyr	Lys	Cys	Ile	Cys	Cys	Asp	Thr	Pro	Leu	Phe	Asp	Ser	Ser	Thr	
		115					120					125				

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

aac	aat	gtg	aag	tca	aag	ctg	gac	ctc	tct	atc	atc	ttc	atg	cct	aga	480
Asn	Asn	Val	Lys	Ser	Lys	Leu	Asp	Leu	Ser	Ile	Ile	Phe	Met	Pro	Arg	
145					150					155					160	

caa	gaa	ggt	atc	tgt	gct	ggt	tgt	aac	gcc	cat	ctt	ggt	cat	gtc	ttc	528
Gln	Glu	Val	Ile	Cys	Ala	Val	Cys	Asn	Ala	His	Leu	Gly	His	Val	Phe	
				165					170					175		

gat	gac	ggt	cca	cga	cca	acc	gga	aaa	cga	tat	tgc	ctc	aac	agt	gct	576
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Asp Asp Gly Pro Arg Pro Thr Gly Lys Arg Tyr Cys Leu Asn Ser Ala
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615

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<212> PRT
<213> Brassica napus

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20 25 30

Cys Arg Ser Leu Thr Lys Pro Arg Asn Leu Asn Leu Ser Val Leu Leu
35 40 45

Arg Cys Ser Met Gly Ser Phe Asn Ser Ser Gln Lys Ser Asp Asn Val
50 55 60

Gln Glu Ala Ala Lys Ser Asp Phe Ala Ser Ile Ser Glu Gly Glu Trp
65 70 75 80

Lys Lys Arg Leu Thr Pro Glu Gln Tyr Tyr Ile Thr Arg Gln Lys Gly
85 90 95

Thr Glu Arg Ala Phe Thr Gly Glu Tyr Trp Asn Thr Lys Thr Pro Gly
100 105 110

Val Tyr Lys Cys Ile Cys Cys Asp Thr Pro Leu Phe Asp Ser Ser Thr
115 120 125

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

Asn Asn Val Lys Ser Lys Leu Asp Leu Ser Ile Ile Phe Met Pro Arg
145 150 155 160

Gln Glu Val Ile Cys Ala Val Cys Asn Ala His Leu Gly His Val Phe
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180 185 190

Ala Leu Lys Leu Glu Ser Leu Glu Arg Thr Arg Glu
195 200

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<212> DNA
<213> Oryza sativa

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<222> (1)..(615)
<223> methionine sulfoxide reductase family protein (OS34096188)

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tcc tcc aaa tcc aaa ccc att ttc tca act ctt ctt cgt tct tct cct      96
Ser Ser Lys Ser Lys Pro Ile Phe Ser Thr Leu Leu Arg Ser Ser Pro
      20      25      30

tcc acc att ttc ccc cca aag tcc gtt act ccc acc act ctt ttc gtt      144
Ser Thr Ile Phe Pro Pro Lys Ser Val Thr Pro Thr Thr Leu Phe Val
      35      40      45

tct gcc acc ccc ttc ttc act ctc cat ccc aag ctt ggt ttt cgt ggt      192
Ser Ala Thr Pro Phe Phe Thr Leu His Pro Lys Leu Gly Phe Arg Gly
      50      55      60

ggg att gtg gcc atg gcc gca cct ggc tct ctc cgc aaa tcc gag gaa      240
Gly Ile Val Ala Met Ala Ala Pro Gly Ser Leu Arg Lys Ser Glu Glu
      65      70      75      80

gag tgg cgc gca att ctc tcc cct gaa cag ttt cgg atc ctc agg caa      288
Glu Trp Arg Ala Ile Leu Ser Pro Glu Gln Phe Arg Ile Leu Arg Gln
      85      90      95

aag ggc acc gag ttc cct gga aca gga gag tat gac aag ttc tat gaa      336
Lys Gly Thr Glu Phe Pro Gly Thr Gly Glu Tyr Asp Lys Phe Tyr Glu
      100      105      110

gag gga gtt tac aac tgt gct ggt tgt ggg act cca ctc tac agg tcc      384
Glu Gly Val Tyr Asn Cys Ala Gly Cys Gly Thr Pro Leu Tyr Arg Ser
      115      120      125

ata aca aaa ttc aat tct ggt tgt ggc tgg cca gcc ttc tat gag ggg      432
Ile Thr Lys Phe Asn Ser Gly Cys Gly Trp Pro Ala Phe Tyr Glu Gly
      130      135      140

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Ile Pro Gly Ala Ile Asn Arg Asn Pro Asp Pro Asp Gly Met Arg Thr
      145      150      155      160

gaa ata acg tgt gct gct tgt ggg gga cat cta ggt cac gtc ttt aaa      528
Glu Ile Thr Cys Ala Ala Cys Gly Gly His Leu Gly His Val Phe Lys
      165      170      175

gga gaa gga ttt cca aca ccc act aac gaa cgc cat tgt gtc aat agc      576
Gly Glu Gly Phe Pro Thr Pro Thr Asn Asn Glu Arg His Cys Val Asn Ser
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att tcg ctg aaa ttt gcg cca gcc aat tct tat tct taa      615
Ile Ser Leu Lys Phe Ala Pro Ala Asn Ser Tyr Ser
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<210> 4
<211> 204
<212> PRT
<213> Oryza sativa

<400> 4

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20 25 30

Ser Thr Ile Phe Pro Pro Lys Ser Val Thr Pro Thr Thr Leu Phe Val
35 40 45

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

Gly Ile Val Ala Met Ala Ala Pro Gly Ser Leu Arg Lys Ser Glu Glu
65 70 75 80

Glu Trp Arg Ala Ile Leu Ser Pro Glu Gln Phe Arg Ile Leu Arg Gln
85 90 95

Lys Gly Thr Glu Phe Pro Gly Thr Gly Glu Tyr Asp Lys Phe Tyr Glu
100 105 110

Glu Gly Val Tyr Asn Cys Ala Gly Cys Gly Thr Pro Leu Tyr Arg Ser
115 120 125

Ile Thr Lys Phe Asn Ser Gly Cys Gly Trp Pro Ala Phe Tyr Glu Gly
130 135 140

Ile Pro Gly Ala Ile Asn Arg Asn Pro Asp Pro Asp Gly Met Arg Thr
145 150 155 160

Glu Ile Thr Cys Ala Ala Cys Gly Gly His Leu Gly His Val Phe Lys
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Ile Ser Leu Lys Phe Ala Pro Ala Asn Ser Tyr Ser
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<210> 5
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<212> DNA
<213> Oryza sativa

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<222> (1)..(645)
<223> methionine sulfoxide reductase family protein (OS32583643)

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48

PhoenixTemp21163.tmp.txt

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Pro	Leu	Ala	Pro	Cys	Cys	Gly	Val	Ala	Trp	Ser	Arg	Ala	Ser	Tyr	Arg	
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Arg	Ala	Ser	Val	Arg	Ala	Met	Gly	Ala	Ala	Ser	Ser	Ser	Ser	Ser	Ser	
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tcg	tcg	tcg	tct	ccg	tcg	ccg	cag	ggt	caa	gcc	caa	gcc	caa	gcc	caa	240
Ser	Ser	Ser	Ser	Pro	Ser	Pro	Gln	Gly	Gln	Ala	Gln	Ala	Gln	Ala	Gln	
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ggt	aaa	ccg	aac	tac	agt	aca	tct	ctg	act	gat	gag	gag	tgg	agg	aag	288
Gly	Lys	Pro	Asn	Tyr	Ser	Thr	Ser	Leu	Thr	Asp	Glu	Glu	Trp	Arg	Lys	
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cgc	ctg	aca	aaa	gat	cag	tat	tac	att	act	cgg	cag	aag	ggc	aca	gaa	336
Arg	Leu	Thr	Lys	Asp	Gln	Tyr	Tyr	Ile	Thr	Arg	Gln	Lys	Gly	Thr	Glu	
			100					105					110			
aga	gca	ttt	act	ggg	gaa	tac	tgg	aac	acc	aaa	acc	ccg	ggc	atc	tac	384
Arg	Ala	Phe	Thr	Gly	Glu	Tyr	Trp	Asn	Thr	Lys	Thr	Pro	Gly	Ile	Tyr	
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cat	tgt	gtc	tgc	tgt	gac	acc	cct	ctt	ttt	gag	tca	tcg	acc	aaa	ttt	432
His	Cys	Val	Cys	Cys	Asp	Thr	Pro	Leu	Phe	Glu	Ser	Ser	Thr	Lys	Phe	
	130					135					140					
gat	agt	ggt	act	ggg	tgg	ccg	tca	tat	tat	caa	ccc	att	gga	gat	aat	480
Asp	Ser	Gly	Thr	Gly	Trp	Pro	Ser	Tyr	Tyr	Gln	Pro	Ile	Gly	Asp	Asn	
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gta	aag	tgc	aag	ctt	gat	atg	tcc	atc	ata	ttc	atg	cct	cgg	act	gag	528
Val	Lys	Cys	Lys	Leu	Asp	Met	Ser	Ile	Ile	Phe	Met	Pro	Arg	Thr	Glu	
				165					170					175		
gtg	ctg	tgt	gct	gtc	tgt	gac	gct	cat	ctg	ggg	cac	gtg	ttt	gat	gat	576
Val	Leu	Cys	Ala	Val	Cys	Asp	Ala	His	Leu	Gly	His	Val	Phe	Asp	Asp	
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ggg	cca	cga	cca	aca	ggg	aaa	aga	tac	tgt	atc	aat	agc	gca	tct	ctc	624
Gly	Pro	Arg	Pro	Thr	Gly	Lys	Arg	Tyr	Cys	Ile	Asn	Ser	Ala	Ser	Leu	
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Lys	Leu	Lys	Lys	Thr	Gln											
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<210> 6
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 <213> Oryza sativa

<400> 6

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Ser Ser Ser Ser Pro Ser Pro Gln Gly Gln Ala Gln Ala Gln Ala Gln
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Gly Lys Pro Asn Tyr Ser Thr Ser Leu Thr Asp Glu Glu Trp Arg Lys
85 90 95
Arg Leu Thr Lys Asp Gln Tyr Tyr Ile Thr Arg Gln Lys Gly Thr Glu
100 105 110
Arg Ala Phe Thr Gly Glu Tyr Trp Asn Thr Lys Thr Pro Gly Ile Tyr
115 120 125
His Cys Val Cys Cys Asp Thr Pro Leu Phe Glu Ser Ser Thr Lys Phe
130 135 140
Asp Ser Gly Thr Gly Trp Pro Ser Tyr Tyr Gln Pro Ile Gly Asp Asn
145 150 155 160
Val Lys Cys Lys Leu Asp Met Ser Ile Ile Phe Met Pro Arg Thr Glu
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<211> 609
<212> DNA
<213> Glycine max

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<222> (1)..(609)
<223> methionine sulfoxide reductase family protein (GM53626178)

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Ala Ser Ile Ser Pro Thr Lys Cys Val Thr Pro Thr Thr Leu Phe Val

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ggg att gtg gcc atg gcc gcc gct ggc tcg ctc cgc aaa tca gag gaa	240		
Gly Ile Val Ala Met Ala Ala Ala Gly Ser Leu Arg Lys Ser Glu Glu			
65 70 75 80			
gag tgg cgc gca gtt ctc tcc cct gaa cag ttt cgt att ctc agg caa	288		
Glu Trp Arg Ala Val Leu Ser Pro Glu Gln Phe Arg Ile Leu Arg Gln			
85 90 95			
aag ggc acc gag ttc cct gga aca gga gag tat gac aag ttc ttt gat	336		
Lys Gly Thr Glu Phe Pro Gly Thr Gly Glu Tyr Asp Lys Phe Phe Asp			
100 105 110			
gag gga gtt tac aac tgt gct ggt tgt ggg aca cct ctc tac agg tcc	384		
Glu Gly Val Tyr Asn Cys Ala Gly Cys Gly Thr Pro Leu Tyr Arg Ser			
115 120 125			
tta aca aaa ttc aat tct ggt tgt ggc tgg cca gcc ttc tat gag ggg	432		
Leu Thr Lys Phe Asn Ser Gly Cys Gly Trp Pro Ala Phe Tyr Glu Gly			
130 135 140			
att cct gga gcc ata aat cgc aat ccg gac cct gat ggg atg agg aca	480		
Ile Pro Gly Ala Ile Asn Arg Asn Pro Asp Pro Asp Gly Met Arg Thr			
145 150 155 160			
gaa ata acg tgt gct gct tgt ggg gga cat cta ggt cac gtc ttt aaa	528		
Glu Ile Thr Cys Ala Ala Cys Gly Gly His Leu Gly His Val Phe Lys			
165 170 175			
gga gaa gga ttt cca acg ccc act aac gaa cgc cat tgt gtc aat agc	576		
Gly Glu Gly Phe Pro Thr Pro Thr Asn Glu Arg His Cys Val Asn Ser			
180 185 190			
att tca ctg aaa ttt gcg cca gcc aat tct taa	609		
Ile Ser Leu Lys Phe Ala Pro Ala Asn Ser			
195 200			

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 <211> 202
 <212> PRT
 <213> Glycine max

<400> 8

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35 40 45
Ser Ala Thr Pro Phe Phe Thr Ala Ser Pro Lys Arg Gly Phe Arg Gly
50 55 60
Gly Ile Val Ala Met Ala Ala Ala Gly Ser Leu Arg Lys Ser Glu Glu
65 70 75 80

PhoenixTemp21163.tmp.txt

Glu Trp Arg Ala Val₈₅ Leu Ser Pro Glu Gln₉₀ Phe Arg Ile Leu Arg Gln₉₅
 Lys Gly Thr Glu₁₀₀ Phe Pro Gly Thr Gly₁₀₅ Glu Tyr Asp Lys Phe₁₁₀ Phe Asp
 Glu Gly Val₁₁₅ Tyr Asn Cys Ala Gly₁₂₀ Cys Gly Thr Pro Leu₁₂₅ Tyr Arg Ser
 Leu Thr₁₃₀ Lys Phe Asn Ser Gly₁₃₅ Cys Gly Trp Pro Ala₁₄₀ Phe Tyr Glu Gly
 Ile Pro Gly Ala Ile Asn₁₅₀ Arg Asn Pro Asp Pro₁₅₅ Asp Gly Met Arg Thr₁₆₀
 Glu Ile Thr Cys Ala₁₆₅ Ala Cys Gly Gly His₁₇₀ Leu Gly His Val Phe₁₇₅ Lys
 Gly Glu Gly Phe₁₈₀ Pro Thr Pro Thr Asn₁₈₅ Glu Arg His Cys Val₁₉₀ Asn Ser
 Ile Ser Leu₁₉₅ Lys Phe Ala Pro Ala₂₀₀ Asn Ser

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 <213> Triticum aestivum

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 <223> methionine sulfoxide reductase family protein (TA6540264)

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 Pro Ser Leu Leu Leu Ala Arg Ser Ser Ser Ala Ala Thr Ala Ala Ala
 20 25 30
 tcg tcc gcc cgc ccc gcc tcc ctc tcc ctc tcg tgc tcg cgg tcg cgg 144
 Ser Ser Ala Arg Pro Ala Ser Leu Ser Leu Ser Cys Ser Arg Ser Arg
 35 40 45
 gcg cgg gcc tac tgc cca gcc gga cga cgg ttg ccg ggc gcc gtg gtg 192
 Ala Arg Ala Tyr Cys Pro Ala Gly Arg Arg Leu Pro Gly Ala Val Val
 50 55 60
 gct atg tcg tcg gcg gcg ccc acg ccg ggg ccc gtg cag aag tcg gag 240
 Ala Met Ser Ser Ala Ala Pro Thr Pro Gly Pro Val Gln Lys Ser Glu
 65 70 75 80
 gag gag tgg gag gcc gtc ctc acg ccg gag cag ttc cgc atc ctc cgc 288
 Glu Glu Trp Glu Ala Val Leu Thr Pro Glu Gln Phe Arg Ile Leu Arg
 85 90 95

PhoenixTemp21163.tmp.txt

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 Arg Lys Gly Thr 100 Glu Tyr Pro Gly Thr 105 Lys Phe Phe
 agt gag ggt att tac gga tgt gct ggc tgt gga acc ccc ttg tac aaa 384
 Ser Glu Gly Ile Tyr Gly Cys Ala 120 Gly Cys Gly Thr Pro 125 Leu Tyr Lys
 tca tct acg aag ttc aac tca ggg tgt ggt tgg cca gca ttc tat gaa 432
 Ser Ser Thr Lys Phe Asn Ser 135 Gly Cys Gly Trp Pro 140 Ala Phe Tyr Glu
 gga ttt cct gga gcc ata aaa cgg acg gcg gat cct gat ggg agg cga 480
 Gly Phe Pro Gly Ala Ile 150 Arg Thr Ala Asp 155 Pro Asp Gly Arg Arg 160
 att gag atc aca tgt gct gct tgt gaa gga cat ctg ggg cat gtg ttc 528
 Ile Glu Ile Thr Cys 165 Ala Ala Cys Glu Gly 170 His Leu Gly His Val Phe 175
 aaa ggg gag ggg ttc aac acg ccg act gat gag cga cac tgc gtc aac 576
 Lys Gly Glu Gly 180 Phe Asn Thr Pro Thr 185 Asp Glu Arg His Cys Val Asn 190
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<210> 10
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 <212> PRT
 <213> Triticum aestivum

<400> 10

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 Ser Ser Ala Arg Pro Ala Ser Leu Ser Leu Ser Cys Ser Arg Ser Arg
 35 40 45
 Ala Arg Ala Tyr Cys Pro Ala Gly Arg Arg Leu Pro Gly Ala Val Val
 50 55 60
 Ala Met Ser Ser Ala Ala Pro Thr Pro Gly Pro Val Gln Lys Ser Glu
 65 70 75 80
 Glu Glu Trp Glu Ala Val Leu Thr Pro Glu Gln Phe Arg Ile Leu Arg
 85 90 95
 Arg Lys Gly Thr Glu Tyr Pro Gly Thr Gly Glu Tyr Asp Lys Phe Phe
 100 105 110
 Ser Glu Gly Ile Tyr Gly Cys Ala Gly Cys Gly Thr Pro Leu Tyr Lys
 115 120 125
 Ser Ser Thr Lys Phe Asn Ser Gly Cys Gly Trp Pro Ala Phe Tyr Glu

130

135

140

Gly Phe Pro Gly Ala Ile Lys Arg Thr Ala Asp Pro Asp Gly Arg Arg
 145 150 155 160

Ile Glu Ile Thr Cys Ala Ala Cys Glu Gly His Leu Gly His Val Phe
 165 170 175

Lys Gly Glu Gly Phe Asn Thr Pro Thr Asp Glu Arg His Cys Val Asn
 180 185 190

Ser Ile Ser Leu Lys Phe Val Pro Ala Ser Glu Glu Ala Ser
 195 200 205

<210> 11

<211> 933

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)..(933)

<223> homeodomain leucine zipper protein (BN45206322)

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 1 5 10 15

tta tgt ccc act act tcc aca gat cag ccg aat cca aga aga tgc ggg 96
 Leu Cys Pro Thr Thr Ser Thr Asp Gln Pro Asn Pro Arg Arg Cys Gly
 20 25 30

aga gaa ttt cag tcg atg ctc gaa ggt tac gag gag gaa gaa gaa gaa 144
 Arg Glu Phe Gln Ser Met Leu Glu Gly Tyr Glu Glu Glu Glu Glu Glu
 35 40 45

gcc ata acc gag gaa aga gga caa acc ggt tta gcc gag aag aag aga 192
 Ala Ile Thr Glu Glu Arg Gly Gln Thr Gly Leu Ala Glu Lys Lys Arg
 50 55 60

cgg tta aac att aac caa gtt aaa gcc ttg gag aaa aat ttc gag tta 240
 Arg Leu Asn Ile Asn Gln Val Lys Ala Leu Glu Lys Asn Phe Glu Leu
 65 70 75 80

gag aac aag ctt gag cct gag agg aaa gtg aag tta gct caa gaa ctt 288
 Glu Asn Lys Leu Glu Pro Glu Arg Lys Val Lys Leu Ala Gln Glu Leu
 85 90 95

ggt ctc caa cct cgt caa gta gct gtt tgg ttt cag aac cgc cgt gcg 336
 Gly Leu Gln Pro Arg Gln Val Ala Val Trp Phe Gln Asn Arg Arg Ala
 100 105 110

cgg tgg aag aca aaa cag ctt gag aaa gat tac ggt gtt ctc aaa acg 384
 Arg Trp Lys Thr Lys Gln Leu Glu Lys Asp Tyr Gly Val Leu Lys Thr
 115 120 125

caa tac gat tct ctc cgc cat aac ttt gat tcc ctc cgc cgt gaa aat 432
 Gln Tyr Asp Ser Leu Arg His Asn Phe Asp Ser Leu Arg Arg Glu Asn
 130 135 140

gaa tct ctt ctt caa gag atc ggt aaa cta aaa gct aag ctt aac gga 480
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PhoenixTemp21163.tmp.txt

145		150		155		160										
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atg Met	gag Glu	agt Ser	gat Asp 180	gtt Val	tcc Ser	gtc Val	aag Lys	gaa Glu 185	gaa Glu	gaa Glu	gtt Val	tcg Ser	ttg Leu 190	ccg Pro	gag Glu	576
cag Gln	atc Ile	aca Thr 195	gag Glu	ccg Pro	ccg Pro	tct Ser	tct Ser 200	cct Pro	ccg Pro	cag Gln	ctt Leu	cta Leu 205	gag Glu	cat His	tcc Ser	624
gac Asp	agt Ser 210	ttc Phe	aat Asn	tac Tyr	cgg Arg	agt Ser 215	ttc Phe	acc Thr	gac Asp	ctc Leu	cgc Arg 220	gac Asp	ctt Leu	ctt Leu	ccg Pro	672
tta Leu 225	aag Lys	gcc Ala	gcg Ala	gct Ala	tcc Ser 230	tcc Ser	gtc Val	gcc Ala	gcc Ala	gct Ala 235	gga Gly	tcg Ser	tcg Ser	gac Asp	agt Ser 240	720
agc Ser	gat Asp	tcg Ser	agc Ser	gcc Ala 245	gtg Val	ttg Leu	aac Asn	gag Glu	gaa Glu 250	agt Ser	agc Ser	tct Ser	aac Asn	gtt Val 255	acg Thr	768
gcg Ala	gct Ala	ccg Pro	gcg Ala 260	acg Thr	gtt Val	ccc Pro	ggc Gly	ggc Gly 265	agt Ser	ttc Phe	ttg Leu	cag Gln	ttt Phe 270	gtg Val	aaa Lys	816
atg Met	gag Glu	cag Gln 275	acg Thr	gag Glu	gat Asp	cac His	gac Asp 280	gac Asp	ttt Phe	ctg Leu	agt Ser	gga Gly 285	gaa Glu	gaa Glu	gcg Ala	864
tgc Cys	ggg Gly 290	ttt Phe	ttc Phe	tcc Ser	gat Asp	gaa Glu 295	cag Gln	cca Pro	ccg Pro	tct Ser	ctg Leu 300	cac His	tgg Trp	tat Tyr	tcc Ser	912
acc Thr 305	gtt Val	gat Asp	cag Gln	tgg Trp	aac Asn 310	tga										933

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 <213> Brassica napus

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

PhoenixTemp21163.tmp.txt

Glu Asn Lys Leu Glu Pro Glu Arg Lys Val Lys Leu Ala Gln Glu Leu
85 90 95

Gly Leu Gln Pro Arg Gln Val Ala Val Trp Phe Gln Asn Arg Arg Ala
100 105 110

Arg Trp Lys Thr Lys Gln Leu Glu Lys Asp Tyr Gly Val Leu Lys Thr
115 120 125

Gln Tyr Asp Ser Leu Arg His Asn Phe Asp Ser Leu Arg Arg Glu Asn
130 135 140

Glu Ser Leu Leu Gln Glu Ile Gly Lys Leu Lys Ala Lys Leu Asn Gly
145 150 155 160

Glu Glu Glu Gly Asp Asp Val Asp Glu Glu Glu Asn Asn Leu Ala Thr
165 170 175

Met Glu Ser Asp Val Ser Val Lys Glu Glu Glu Val Ser Leu Pro Glu
180 185 190

Gln Ile Thr Glu Pro Pro Ser Ser Pro Pro Gln Leu Leu Glu His Ser
195 200 205

Asp Ser Phe Asn Tyr Arg Ser Phe Thr Asp Leu Arg Asp Leu Leu Pro
210 215 220

Leu Lys Ala Ala Ala Ser Ser Val Ala Ala Ala Gly Ser Ser Asp Ser
225 230 235 240

Ser Asp Ser Ser Ala Val Leu Asn Glu Glu Ser Ser Ser Asn Val Thr
245 250 255

Ala Ala Pro Ala Thr Val Pro Gly Gly Ser Phe Leu Gln Phe Val Lys
260 265 270

Met Glu Gln Thr Glu Asp His Asp Asp Phe Leu Ser Gly Glu Glu Ala
275 280 285

Cys Gly Phe Phe Ser Asp Glu Gln Pro Pro Ser Leu His Trp Tyr Ser
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Thr Val Asp Gln Trp Asn
305 310

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<212> DNA
<213> Glycine max

<220>
<221> CDS

PhoenixTemp21163.tmp.txt

<222> (1)..(996)

<223> homeodomain leucine zipper protein (GM48923793)

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acc caa caa ccc tct tct caa cct ctc gat tct tct ctc ttc ctc tct	96
Thr Gln Gln Pro Ser Ser Gln Pro Leu Asp Ser Ser Leu Phe Leu Ser	
20 25 30	
gca cct tcc tct gct cct ttc ctc ggt tgc aga tcc atg atg agt ttt	144
Ala Pro Ser Ser Ala Pro Phe Leu Gly Ser Arg Ser Met Met Ser Phe	
35 40 45	
gat gga gaa gga ggg aag ggg tgt aac ggc tcc ttc ttc cgc gcg ttt	192
Asp Gly Glu Gly Gly Lys Gly Cys Asn Gly Ser Phe Phe Arg Ala Phe	
50 55 60	
gac atg gac gac aat ggg gat gag tgc atg gac gag tac ttt cat caa	240
Asp Met Asp Asp Asn Gly Asp Glu Cys Met Asp Glu Tyr Phe His Gln	
65 70 75 80	
ccc gag aag aag cga cgt ctc tct gcg agc cag gtt cag ttt cta gag	288
Pro Glu Lys Lys Arg Arg Leu Ser Ala Ser Gln Val Gln Phe Leu Glu	
85 90 95	
aag agc ttc gag gag gag aac aag ctt gaa ccc gag aga aag acc aaa	336
Lys Ser Phe Glu Glu Glu Asn Lys Leu Glu Pro Glu Arg Lys Thr Lys	
100 105 110	
cta gcc aaa gac ctt ggt ttg cag cca cgg caa gtt gct att tgg ttc	384
Leu Ala Lys Asp Leu Gly Leu Gln Pro Arg Gln Val Ala Ile Trp Phe	
115 120 125	
cag aac cgt aga gct cgg tgg aag aac aaa cag ctg gag aag gat tac	432
Gln Asn Arg Arg Ala Arg Trp Lys Asn Lys Gln Leu Glu Lys Asp Tyr	
130 135 140	
gag act ctg cat gca agt ttt gag agt ctc aag tcc aac tat gac tgt	480
Glu Thr Leu His Ala Ser Phe Glu Ser Leu Lys Ser Asn Tyr Asp Cys	
145 150 155 160	
ctt ctc aag gag aaa gac aag tta aaa gct gag gtg gcg agc ctc act	528
Leu Leu Lys Glu Lys Asp Lys Leu Lys Ala Glu Val Ala Ser Leu Thr	
165 170 175	
gag aag gtg ctt gca aga ggg aaa caa gag ggg cac atg aag cag gct	576
Glu Lys Val Leu Ala Arg Gly Lys Gln Glu Gly His Met Lys Gln Ala	
180 185 190	
gaa agt gaa agt gaa gaa aca aaa gga tta ttg cat ttg cag gaa cag	624
Glu Ser Glu Ser Glu Glu Thr Lys Gly Leu Leu His Leu Gln Glu Gln	
195 200 205	
gaa cca ccc cag agg ctt tta ctg caa tca gtt tgc gag gga gaa gga	672
Glu Pro Pro Gln Arg Leu Leu Leu Gln Ser Val Ser Glu Gly Glu Gly	
210 215 220	
tcc aaa gtc tct tct gtc gtt ggg ggt tgt aaa cag gaa gat atc agt	720
Ser Lys Val Ser Ser Val Val Gly Gly Cys Lys Gln Glu Asp Ile Ser	
225 230 235 240	
tca gca agg agt gac att ttg gat tca gat agt cca cat tac acc gat	768
Ser Ala Arg Ser Asp Ile Leu Asp Ser Asp Ser Pro His Tyr Thr Asp	
245 250 255	
gga gtt cac tct gcg ctg cta gag cat ggt gat tct tct tat gtg ttt	816

PhoenixTemp21163.tmp.txt

Gly	Val	His	Ser	Ala	Leu	Leu	Glu	His	Gly	Asp	Ser	Ser	Tyr	Val	Phe		
			260					265					270				
gag	cct	gat	caa	tca	gat	atg	tca	caa	gat	gaa	gaa	gat	aac	ctc	agc		864
Glu	Pro	Asp	Gln	Ser	Asp	Met	Ser	Gln	Asp	Glu	Glu	Asp	Asn	Leu	Ser		
		275					280					285					
aag	agt	ctc	tac	cct	tcg	tac	ctc	ttt	ccc	aaa	ctt	gaa	gaa	gat	gtg		912
Lys	Ser	Leu	Tyr	Pro	Ser	Tyr	Leu	Phe	Pro	Lys	Leu	Glu	Glu	Asp	Val		
	290					295					300						
gat	tac	tcc	gac	cca	cct	gaa	agt	tct	tgt	aat	ttt	gga	ttt	cct	gag		960
Asp	Tyr	Ser	Asp	Pro	Pro	Glu	Ser	Ser	Cys	Asn	Phe	Gly	Phe	Pro	Glu		
305					310					315					320		
gaa	gat	cat	gtc	ctt	tgg	acc	tgg	gct	tac	tac	taa						996
Glu	Asp	His	Val	Leu	Trp	Thr	Trp	Ala	Tyr	Tyr							
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 <213> Glycine max

<400> 14

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

Glu Lys Val Leu Ala Arg Gly Lys Gln Glu Gly His Met Lys Gln Ala
 180 185 190
 Glu Ser Glu Ser Glu Glu Thr Lys Gly Leu Leu His Leu Gln Glu Gln
 195 200 205
 Glu Pro Pro Gln Arg Leu Leu Leu Gln Ser Val Ser Glu Gly Glu Gly
 210 215 220
 Ser Lys Val Ser Ser Val Val Gly Gly Cys Lys Gln Glu Asp Ile Ser
 225 230 235 240
 Ser Ala Arg Ser Asp Ile Leu Asp Ser Asp Ser Pro His Tyr Thr Asp
 245 250 255
 Gly Val His Ser Ala Leu Leu Glu His Gly Asp Ser Ser Tyr Val Phe
 260 265 270
 Glu Pro Asp Gln Ser Asp Met Ser Gln Asp Glu Glu Asp Asn Leu Ser
 275 280 285
 Lys Ser Leu Tyr Pro Ser Tyr Leu Phe Pro Lys Leu Glu Glu Asp Val
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 305 310 315 320
 Glu Asp His Val Leu Trp Thr Trp Ala Tyr Tyr
 325 330

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 <211> 1023
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> CDS
 <222> (1)..(1023)
 <223> homeodomain leucine zipper protein (TA55969932)

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1 5 10 15	
cag atg ctc ttc atg gac tgc ggc gcg ggc ggc atc gcc ggc gcg gcc	96
Gln Met Leu Phe Met Asp Cys Gly Ala Gly Gly Ile Ala Gly Ala Ala	
20 25 30	
ggc atg ttc cat cga ggg gtg aga ccg gtc ctc ggc ggc atg gaa gaa	144
Gly Met Phe His Arg Gly Val Arg Pro Val Leu Gly Gly Met Glu Glu	
35 40 45	
ggg cgc ggc gtg aag cgg ccc ttc ttc acc tcg ccg gat gac atg ctg	192
Gly Arg Gly Val Lys Arg Pro Phe Phe Thr Ser Pro Asp Asp Met Leu	
50 55 60	

PhoenixTemp21163.tmp.txt

gag Glu 65	gag Glu	gag Glu	tac Tyr	tac Tyr	gac Asp 70	gag Glu	cag Gln	ctc Leu	ccg Pro	gag Glu 75	aag Lys	aag Lys	cgg Arg	cgc Arg	ctc Leu 80	240
acg Thr	ccg Pro	gag Glu	cag Gln	gtc Val 85	cac His	ctg Leu	ctg Leu	gag Glu	agg Arg 90	agc Ser	ttc Phe	gag Glu	gag Glu	gag Glu 95	aac Asn	288
aag Lys	ctg Leu	gag Glu	ccg Pro 100	gag Glu	agg Arg	aag Lys	acg Thr	gag Glu 105	ctg Leu	gcc Ala	cgc Arg	aag Lys	ctc Leu 110	ggg Gly	ctg Leu	336
cag Gln	cca Pro	cgg Arg 115	cag Gln	gtg Val	gcc Ala	gtc Val	tgg Trp 120	ttc Phe	cag Gln	aac Asn	cgc Arg	cgc Arg 125	gcc Ala	cgg Arg	tgg Trp	384
aag Lys	aca Thr 130	aag Lys	acg Thr	ctg Leu	gag Glu	cgc Arg 135	gac Asp	ttc Phe	gac Asp	cgc Arg	ctc Leu 140	aag Lys	gcg Ala	tcc Ser	ttc Phe	432
gac Asp 145	gcc Ala	ctc Leu	cgc Arg	gcc Ala	gac Asp 150	cac His	gac Asp	gcg Ala	ctc Leu	ctc Leu 155	cag Gln	gac Asp	aac Asn	cac His	cgg Arg 160	480
ctc Leu	cgg Arg	tca Ser	cag Gln	gtg Val 165	gta Val	acg Thr	ttg Leu	acc Thr	gag Glu 170	aag Lys	atg Met	caa Gln	gat Asp	aag Lys 175	gag Glu	528
gcg Ala	ccg Pro	gaa Glu	ggc Gly 180	agc Ser	ttc Phe	ggt Gly	gca Ala	gcc Ala 185	gcc Ala	gac Asp	gcc Ala	tcg Ser	gag Glu 190	ccg Pro	gag Glu	576
cag Gln	gcg Ala 195	gcg Ala	gag Glu	gag Ala	aag Lys	gct Ala 200	tcc Ser	ttg Leu	gcc Ala	gac Asp	gcc Ala 205	gag Glu	gag Glu	cag Gln	624	
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aag Lys 225	gac Asp	gag Glu	gag Glu	agg Arg	ctg Leu 230	agc Ser	ccg Pro	ggg Gly	agc Ser	ggc Gly 235	ggg Gly	agc Ser	gag Ala	gtg Val	ctg Leu 240	720
gac Asp	gag Ala	agg Arg	gac Asp	gag Ala 245	ctg Leu	ctc Leu	ggg Gly	agc Ser	gga Gly 250	tgc Cys	ggc Gly	ctc Leu	gcc Ala	ggc Gly 255	gtg Val	768
gtg Val	gac Asp	agc Ser	agc Ser 260	gtg Val	gac Asp	tcg Ser	tac Tyr	tgc Cys 265	ttc Phe	ccg Pro	ggg Gly	ggc Gly	gcc Ala 270	ggc Gly	ggc Gly	816
gac Asp	gag Glu	tac Tyr 275	cac His	gag Glu	tgc Cys	gtg Val	gtg Val 280	ggc Gly	ccc Pro	gtg Val	gag Ala	ggc Gly 285	ggc Gly	atc Ile	cag Gln	864
tcg Ser	gag Glu 290	gag Glu	gac Asp	gac Asp	ggc Gly	gag Ala 295	ggc Gly	agc Ser	gac Asp	gag Glu	ggc Gly 300	tgc Cys	agc Ser	tac Tyr	tac Tyr	912
ccc Pro 305	gac Asp	gac Asp	gcc Ala	gcc Ala	gtc Val 310	ttc Phe	ttc Phe	gcc Ala	gcc Ala	gag Ala 315	caa Gln	ggg Gly	cac His	ggc Gly	cac His 320	960
cat His	cgc Arg	acg Thr	gac Asp	gac Asp 325	gac Asp	gat Asp	cag Gln	cag Gln	gac Asp 330	gac Asp	ggc Gly	cag Gln	atc Ile	agc Ser 335	tac Tyr	1008

tgg atg tgg aac tag
 Trp Met Trp Asn
 340

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 <211> 340
 <212> PRT
 <213> Triticum aestivum

<400> 16

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 20 25 30

Gly Met Phe His Arg Gly Val Arg Pro Val Leu Gly Gly Met Glu Glu
 35 40 45

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

Glu Glu Glu Tyr Tyr Asp Glu Gln Leu Pro Glu Lys Lys Arg Arg Leu
 65 70 75 80

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

Lys Leu Glu Pro Glu Arg Lys Thr Glu Leu Ala Arg Lys Leu Gly Leu
 100 105 110

Gln Pro Arg Gln Val Ala Val Trp Phe Gln Asn Arg Arg Ala Arg Trp
 115 120 125

Lys Thr Lys Thr Leu Glu Arg Asp Phe Asp Arg Leu Lys Ala Ser Phe
 130 135 140

Asp Ala Leu Arg Ala Asp His Asp Ala Leu Leu Gln Asp Asn His Arg
 145 150 155 160

Leu Arg Ser Gln Val Val Thr Leu Thr Glu Lys Met Gln Asp Lys Glu
 165 170 175

Ala Pro Glu Gly Ser Phe Gly Ala Ala Ala Asp Ala Ser Glu Pro Glu
 180 185 190

Gln Ala Ala Ala Glu Ala Lys Ala Ser Leu Ala Asp Ala Glu Glu Gln
 195 200 205

Ala Ala Ala Ala Glu Ala Phe Glu Val Val Gln Gln Gln Leu His Val
 210 215 220

Lys Asp Glu Glu Arg Leu Ser Pro Gly Ser Gly Gly Ser Ala Val Leu
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PhoenixTemp21163.tmp.txt

225 230 235 240

Asp Ala Arg Asp Ala Leu Leu Gly Ser Gly Cys Gly Leu Ala Gly Val
245 250 255

Val Asp Ser Ser Val Asp Ser Tyr Cys Phe Pro Gly Gly Ala Gly Gly
260 265 270

Asp Glu Tyr His Glu Cys Val Val Gly Pro Val Ala Gly Gly Ile Gln
275 280 285

Ser Glu Glu Asp Asp Gly Ala Gly Ser Asp Glu Gly Cys Ser Tyr Tyr
290 295 300

Pro Asp Asp Ala Ala Val Phe Phe Ala Ala Ala Gln Gly His Gly His
305 310 315 320

His Arg Thr Asp Asp Asp Asp Gln Gln Asp Asp Gly Gln Ile Ser Tyr
325 330 335

Trp Met Trp Asn
340

<210>	17
<211>	534
<212>	DNA
<213>	Brassica napus

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<223> zinc finger protein containing an A20 domain and an AN1 domain
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cta tgc atc aac aac tgc ggt ttc ttc gga agc gct gcc aca atg aac 96
Leu Cys Ile Asn Asn Cys Gly Phe Phe Gly Ser Ala Ala Thr Met Asn
20 25 30

atg	tgt	tcc	aag	tgt	cac	aag	gct	atc	ctg	ttt	caa	cag	gaa	cag	ggg	144
Met	Cys	Ser	Lys	Cys	His	Lys	Ala	Ile	Leu	Phe	Gln	Gln	Glu	Gln	Gly	
		35					40					45				

gct agg ttt gca tct gca gtg tct ggt ggt aca tca tca tcc agc aac 192
Ala Arg Phe Ala Ser Ala Val Ser Gly Gly Thr Ser Ser Ser Ser Asn
50 55 60

atc tta aag gaa acc ttt gct gct acc gcg ctg gtt gat gct gaa acc 240
Ile Leu Lys Glu Thr Phe Ala Ala Thr Ala Leu Val Asp Ala Glu Thr
65 70 75 80

aaa tcc gtt gag ccg gtg gct gtc tct gta cag cca tct tct gtc caa 288
Lys Ser Val Glu Pro Val Ala Val Ser Val Gln Pro Ser Ser Val Gln
85 90 95

ggt gcc gca gag gta gta gct cca gaa gcc gct gca gca aaa cta aag 336
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PhoenixTemp21163.tmp.txt

Val Ala Ala Glu Val Val Ala Pro Glu Ala Ala Ala Ala Lys Leu Lys
 100 105 110
 gaa gga cca agc cga tgt gct act tgc aat aaa cgg gtt ggt ctg act 384
 Glu Gly Pro Ser Arg Cys Ala Thr Cys Asn Lys Arg Val Gly Leu Thr
 115 120 125
 gga ttc aaa tgt cgc tgt ggt gac ctc ttc tgc ggg acg cac cgt tat 432
 Gly Phe Lys Cys Arg Cys Gly Asp Leu Phe Cys Gly Thr His Arg Tyr
 130 135 140
 gca gac ata cac aac tgc tcc ttc aat tac cat gcc gct gcg caa gaa 480
 Ala Asp Ile His Asn Cys Ser Phe Asn Tyr His Ala Ala Ala Gln Glu
 145 150 155 160
 gct ata gct aaa gca aac ccg gtt gtg aag gca gag aag ctt gac aaa 528
 Ala Ile Ala Lys Ala Asn Pro Val Val Lys Ala Glu Lys Leu Asp Lys
 165 170 175
 atc tga 534
 Ile

<210> 18
 <211> 177
 <212> PRT
 <213> Brassica napus

<400> 18

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

Ala Ile Ala Lys Ala Asn Pro Val Val Lys Ala Glu Lys Leu Asp Lys
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Ile

<210> 19
 <211> 564
 <212> DNA
 <213> Brassica napus

<220>
 <221> CDS
 <222> (1)..(564)
 <223> zinc finger protein containing an A20 domain and an AN1 domain
 (BN51359456)

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 1 5 10 15
 gct aac aac tgc ggc ttc ctc ggc agc tcc gcc acc atg aat cta tgc 96
 Ala Asn Asn Cys Gly Phe Leu Gly Ser Ser Ala Thr Met Asn Leu Cys
 20 25 30
 tcc aac tgc tac ggc gat ctc tgc ctt aag caa cag caa gct tcc atg 144
 Ser Asn Cys Tyr Gly Asp Leu Cys Leu Lys Gln Gln Ala Ser Met
 35 40 45
 aaa tcc acc gtc gaa tcc tct ctc tcc gcc gta tct cct ccg tcg tca 192
 Lys Ser Thr Val Glu Ser Ser Leu Ser Ala Val Ser Pro Pro Ser Ser
 50 55 60
 gag atc ggc tct atg caa tcc acc gtt gaa tcc tct ctc tcc gac gta 240
 Glu Ile Gly Ser Met Gln Ser Thr Val Glu Ser Ser Leu Ser Asp Val
 65 70 75 80
 tct cct cca tca ccg gag acc att tcc atc tcc tct cca atg atc cag 288
 Ser Pro Pro Ser Pro Glu Thr Ile Ser Ile Ser Ser Pro Met Ile Gln
 85 90 95
 cct ctc gtt cga aac cca tca gct gaa ttg gag gta acg gcg acg aag 336
 Pro Leu Val Arg Asn Pro Ser Ala Glu Leu Glu Val Thr Ala Thr Lys
 100 105 110
 acg gtg act ccg ccg ccg gag cag cag cag aaa cgg ccg aat cgg tgc 384
 Thr Val Thr Pro Pro Pro Glu Gln Gln Gln Lys Arg Pro Asn Arg Cys
 115 120 125
 acg acg tgt agg aaa cgg gtc ggg ttg acc ggg ttc aag tgc cgg tgc 432
 Thr Thr Cys Arg Lys Arg Val Gly Leu Thr Gly Phe Lys Cys Arg Cys
 130 135 140
 ggg acg act ttt tgc ggg gct cac agg tac ccg gag gtc cat gga tgc 480
 Gly Thr Thr Phe Cys Gly Ala His Arg Tyr Pro Glu Val His Gly Cys
 145 150 155 160
 acc ttc gat ttc aaa tgc gcc ggt cgc gaa gag atc gcc aag gcg aac 528
 Thr Phe Asp Phe Lys Ser Ala Gly Arg Glu Glu Ile Ala Lys Ala Asn
 165 170 175
 cca ctc gtc aaa gcg gcg aag ctt cag aag att tga 564
 Pro Leu Val Lys Ala Ala Lys Leu Gln Lys Ile

180

<210> 20
<211> 187
<212> PRT
<213> Brassica napus

<400> 20

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20 25 30

Ser Asn Cys Tyr Gly Asp Leu Cys Leu Lys Gln Gln Gln Ala Ser Met
35 40 45

Lys Ser Thr Val Glu Ser Ser Leu Ser Ala Val Ser Pro Pro Ser Ser
50 55 60

Glu Ile Gly Ser Met Gln Ser Thr Val Glu Ser Ser Leu Ser Asp Val
65 70 75 80

Ser Pro Pro Ser Pro Glu Thr Ile Ser Ile Ser Ser Pro Met Ile Gln
85 90 95

Pro Leu Val Arg Asn Pro Ser Ala Glu Leu Glu Val Thr Ala Thr Lys
100 105 110

Thr Val Thr Pro Pro Pro Glu Gln Gln Gln Lys Arg Pro Asn Arg Cys
115 120 125

Thr Thr Cys Arg Lys Arg Val Gly Leu Thr Gly Phe Lys Cys Arg Cys
130 135 140

Gly Thr Thr Phe Cys Gly Ala His Arg Tyr Pro Glu Val His Gly Cys
145 150 155 160

Thr Phe Asp Phe Lys Ser Ala Gly Arg Glu Glu Ile Ala Lys Ala Asn
165 170 175

Pro Leu Val Lys Ala Ala Lys Leu Gln Lys Ile
180 185

<210> 21
<211> 465
<212> DNA
<213> Hordeum vulgare

<220>
<221> CDS
<222> (1)..(465)
<223> zinc finger protein containing an A20 domain and an AN1 domain
(HV62552639)

PhoenixTemp21163.tmp.txt

<400> 21
 atg gcc cag gag agt tgt gat ctc aac aag gac gag gcc gag atc ctg 48
 Met Ala Gln Glu Ser Cys Asp Leu Asn Lys Asp Glu Ala Glu Ile Leu
 1 5 10 15

aag cca tcc tcc tcc aca cct tcg cct cct tcg cca gcc aca cca cca 96
 Lys Pro Ser Ser Ser Thr Pro Ser Pro Ser Pro Ala Thr Pro Pro
 20 25 30

cca cca acc gct caa ata cca gaa cca caa cct cca cac tca cca cca 144
 Pro Pro Thr Ala Gln Ile Pro Glu Pro Gln Pro Pro His Ser Pro Pro
 35 40 45

caa cca ccg gca gct caa ttc ttg tcc agg ccc tgc gag gtt gtt ccc 192
 Gln Pro Pro Ala Ala Gln Phe Leu Ser Arg Pro Cys Glu Val Val Pro
 50 55 60

ata gag act tcc aaa aag agg aaa cat gct gat gcg gtg tca atg gcc 240
 Ile Glu Thr Ser Lys Lys Arg Lys His Ala Asp Ala Val Ser Met Ala
 65 70 75 80

att gtg gtt gag cca ttg tcg tct gtg ctg ttc gtt aac cgt tgc aac 288
 Ile Val Val Glu Pro Leu Ser Ser Val Leu Phe Val Asn Arg Cys Asn
 85 90 95

gtg tgc cgc aag aga gtt ggt ttg acc ggg ttc cgt tgc cgg tgt gag 336
 Val Cys Arg Lys Arg Val Gly Leu Thr Gly Phe Arg Cys Arg Cys Glu
 100 105 110

aag ctc ttt tgt ccg cgc cac cgg cat tca gaa agc cac gac tgc tca 384
 Lys Leu Phe Cys Pro Arg His Arg His Ser Glu Ser His Asp Cys Ser
 115 120 125

ttt gat tat aaa act gtg ggt cgg gag gag att gcc cgg gca aac cct 432
 Phe Asp Tyr Lys Thr Val Gly Arg Glu Glu Ile Ala Arg Ala Asn Pro
 130 135 140

ctg atc agg gct gcc aag atc att agg ata tga 465
 Leu Ile Arg Ala Ala Lys Ile Ile Arg Ile
 145 150

<210> 22
 <211> 154
 <212> PRT
 <213> Hordeum vulgare

<400> 22
 Met Ala Gln Glu Ser Cys Asp Leu Asn Lys Asp Glu Ala Glu Ile Leu
 1 5 10 15

Lys Pro Ser Ser Ser Thr Pro Ser Pro Ser Pro Ala Thr Pro Pro
 20 25 30

Pro Pro Thr Ala Gln Ile Pro Glu Pro Gln Pro Pro His Ser Pro Pro
 35 40 45

Gln Pro Pro Ala Ala Gln Phe Leu Ser Arg Pro Cys Glu Val Val Pro
 50 55 60

Ile Glu Thr Ser Lys Lys Arg Lys His Ala Asp Ala Val Ser Met Ala
 65 70 75 80

PhoenixTemp21163.tmp.txt

Ile Val Val Glu Pro Leu Ser Ser Val Leu Phe Val Asn Arg Cys Asn
85 90 95

Val Cys Arg Lys Arg Val Gly Leu Thr Gly Phe Arg Cys Arg Cys Glu
100 105 110

Lys Leu Phe Cys Pro Arg His Arg His Ser Glu Ser His Asp Cys Ser
115 120 125

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

Leu Ile Arg Ala Ala Lys Ile Ile Arg Ile
145 150

<210> 23
<211> 516
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (1)..(516)
<223> zinc finger protein containing an A20 domain and an AN1 domain
(ZM61995511)

<400> 23
atg gaa cac aag gag gcg ggc tgc cag cag ccg gag ggc cca atc cta 48
Met Glu His Lys Glu Ala Gly Cys Gln Gln Pro Glu Gly Pro Ile Leu
1 5 10 15

tgc atc aat aac tgc ggc ttc ttc ggc agt gct gcg acg atg aac atg 96
Cys Ile Asn Asn Cys Gly Phe Phe Gly Ser Ala Ala Thr Met Asn Met
20 25 30

tgc tcc aag tgc cac aag gag atg ata acg aag cag gag cag gcc cag 144
Cys Ser Lys Cys His Lys Glu Met Ile Thr Lys Gln Glu Gln Ala Gln
35 40 45

ctg gct gcc tcc ccc atc gat agc att gtc aat ggc ggt gac ggc ggg 192
Leu Ala Ala Ser Pro Ile Asp Ser Ile Val Asn Gly Gly Asp Gly Gly
50 55 60

aaa gga cct gta att gct gca tct gta aat gtg gca gtt cct caa gtt 240
Lys Gly Pro Val Ile Ala Ala Ser Val Asn Val Ala Val Pro Gln Val
65 70 75 80

gag cag aag act att gtt gtg cag ccc atg ctt gta gct gaa acc agc 288
Glu Gln Lys Thr Ile Val Val Gln Pro Met Leu Val Ala Glu Thr Ser
85 90 95

gag gct gct gct gta atc ccc aag gcc aag gaa ggc cca gac cgg tgc 336
Glu Ala Ala Ala Val Ile Pro Lys Ala Lys Glu Gly Pro Asp Arg Cys
100 105 110

gcg gcc tgc agg aag cgt gtt ggg ctg acg gga ttt agc tgc cga tgc 384
Ala Ala Cys Arg Lys Arg Val Gly Leu Thr Gly Phe Ser Cys Arg Cys
115 120 125

ggg aac atg tac tgt tgc gtg cac cgc tac tcc gac aaa cat gac tgt 432
Gly Asn Met Tyr Cys Ser Val His Arg Tyr Ser Asp Lys His Asp Cys
130 135 140

PhoenixTemp21163.tmp.txt

cag ttc gac tat cgg act gca gca agg gac gcg att gcc aag gcc aat 480
Gln Phe Asp Tyr Arg Thr Ala Ala Arg Asp Ala Ile Ala Lys Ala Asn
145 150 155 160

cct gtg gtg agg gcg gag aag ctc gac aag atc tga 516
Pro Val Val Arg Ala Glu Lys Leu Asp Lys Ile
165 170

<210> 24
<211> 171
<212> PRT
<213> Zea mays

<400> 24

Met Glu His Lys Glu Ala Gly Cys Gln Gln Pro Glu Gly Pro Ile Leu
1 5 10 15

Cys Ile Asn Asn Cys Gly Phe Phe Gly Ser Ala Ala Thr Met Asn Met
20 25 30

Cys Ser Lys Cys His Lys Glu Met Ile Thr Lys Gln Glu Gln Ala Gln
35 40 45

Leu Ala Ala Ser Pro Ile Asp Ser Ile Val Asn Gly Gly Asp Gly Gly
50 55 60

Lys Gly Pro Val Ile Ala Ala Ser Val Asn Val Ala Val Pro Gln Val
65 70 75 80

Glu Gln Lys Thr Ile Val Val Gln Pro Met Leu Val Ala Glu Thr Ser
85 90 95

Glu Ala Ala Ala Val Ile Pro Lys Ala Lys Glu Gly Pro Asp Arg Cys
100 105 110

Ala Ala Cys Arg Lys Arg Val Gly Leu Thr Gly Phe Ser Cys Arg Cys
115 120 125

Gly Asn Met Tyr Cys Ser Val His Arg Tyr Ser Asp Lys His Asp Cys
130 135 140

Gln Phe Asp Tyr Arg Thr Ala Ala Arg Asp Ala Ile Ala Lys Ala Asn
145 150 155 160

Pro Val Val Arg Ala Glu Lys Leu Asp Lys Ile
165 170

<210> 25
<211> 720
<212> DNA
<213> Linum usitatissimum

<220>
<221> CDS

PhoenixTemp21163.tmp.txt

<222> (1)..(720)

<223> zinc finger protein containing an A20 domain and an AN1 domain
(LU61567101)

<400> 25

atg	gct	cct	tca	cct	tgc	gtc	cac	ggc	tgc	acg	gcc	aat	tgc	ccc	cgc	48
Met	Ala	Pro	Ser	Pro	Cys	Val	His	Gly	Cys	Thr	Ala	Asn	Cys	Pro	Arg	
1				5					10					15		

tgc	cac	tct	tac	gga	cac	ccc	atc	ttc	ggg	aac	tca	gat	ctc	gcc	gct	96
Cys	His	Ser	Tyr	Gly	His	Pro	Ile	Phe	Gly	Asn	Ser	Asp	Leu	Ala	Ala	
			20					25					30			

ggc	ggc	agc	gat	acg	tcc	acg	tgc	gtg	ttt	gga	aaa	gta	gga	tcc	gtc	144
Gly	Gly	Ser	Asp	Thr	Ser	Thr	Ser	Val	Phe	Gly	Lys	Val	Gly	Ser	Val	
		35					40					45				

gtg	att	cag	tgc	cct	gcg	aag	aat	cac	gcg	ttc	ggc	caa	gct	tgt	ggc	192
Val	Ile	Gln	Ser	Pro	Ala	Lys	Asn	His	Ala	Phe	Gly	Gln	Ala	Cys	Gly	
	50					55					60					

ccg	gtt	ttt	ccc	tgc	agc	tcc	tcc	cct	ttc	cgc	cgc	atc	aag	ttc	ggc	240
Pro	Val	Phe	Pro	Ser	Ser	Ser	Ser	Pro	Phe	Arg	Arg	Ile	Lys	Phe	Gly	
65					70					75					80	

ccc	aaa	gat	ggc	gag	ggg	aaa	gga	ccg	ctg	aag	ccg	atc	gag	aag	cag	288
Pro	Lys	Asp	Gly	Glu	Gly	Lys	Gly	Pro	Leu	Lys	Pro	Ile	Glu	Lys	Gln	
				85					90					95		

ccg	tgc	aag	aag	cgt	ccg	ttc	tgc	ttc	tct	ccc	gac	gag	acg	att	gac	336
Pro	Ser	Lys	Lys	Arg	Pro	Phe	Cys	Phe	Ser	Pro	Asp	Glu	Thr	Ile	Asp	
			100					105					110			

gcg	acg	gtt	cct	ccg	tcc	acc	aaa	ccg	ttc	ggt	tgc	ttc	cgt	tcc	gtc	384
Ala	Thr	Val	Pro	Pro	Ser	Thr	Lys	Pro	Phe	Gly	Ser	Phe	Arg	Ser	Val	
		115					120					125				

tgt	gtc	acg	gac	gcc	gac	gag	gcc	agg	ttg	aag	gcg	aac	cgc	gag	ttc	432
Cys	Val	Thr	Asp	Ala	Asp	Glu	Ala	Arg	Leu	Lys	Ala	Asn	Arg	Glu	Phe	
	130					135					140					

ttc	gct	ccg	gta	tcc	cgc	aaa	cgt	ggc	ttc	gat	ccg	act	gac	atg	acc	480
Phe	Ala	Pro	Val	Ser	Arg	Lys	Arg	Gly	Phe	Asp	Pro	Thr	Asp	Met	Thr	
145					150					155					160	

ttc	ggt	aac	gcc	gcc	gcc	gct	gcg	gct	aat	gcg	agg	gag	gaa	gcg	aag	528
Phe	Gly	Asn	Ala	Ala	Ala	Ala	Ala	Ala	Asn	Ala	Arg	Glu	Glu	Ala	Lys	
			165						170					175		

aag	tgg	tgc	ggc	agt	tgc	aag	aag	cgc	gtg	ggg	ctg	tta	ggg	ttc	aag	576
Lys	Trp	Cys	Gly	Ser	Cys	Lys	Lys	Arg	Val	Gly	Leu	Leu	Gly	Phe	Lys	
			180					185					190			

tgc	agg	tgt	acg	aag	ttc	ttc	tgt	ggg	aag	cat	cgg	tat	cct	gag	gag	624
Cys	Arg	Cys	Thr	Lys	Phe	Phe	Cys	Gly	Lys	His	Arg	Tyr	Pro	Glu	Glu	
		195					200					205				

cat	ggt	tgt	acg	ttc	gat	cat	gtg	gcg	ttc	ggg	agg	cgg	att	atc	gag	672
His	Gly	Cys	Thr	Phe	Asp	His	Val	Ala	Phe	Gly	Arg	Arg	Ile	Ile	Glu	
	210					215					220					

aaa	cag	aat	cct	gtt	ctc	gag	acc	gac	aag	ctg	gtg	gac	aga	atc	tga	720
Lys	Gln	Asn	Pro	Val	Leu	Glu	Thr	Asp	Lys	Leu	Val	Asp	Arg	Ile		
225					230					235						

<210> 26

<211> 239

<212> PRT

<213> Linum usitatissimum

<400> 26

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

<210> 27

<211> 510

<212> DNA

<213> Linum usitatissimum

PhoenixTemp21163.tmp.txt

<220>
 <221> CDS
 <222> (1)..(510)
 <223> zinc finger protein containing an A20 domain and an AN1 domain
 (LU61893412)

<400> 27

atg gac cat gac gag gca ggc tgc cag gct cct tcc gat cat cct att	48
Met Asp His Asp Glu Ala Gly Cys Gln Ala Pro Ser Asp His Pro Ile	
1 5 10 15	
ctg tgc gtt aac aat tgc ggc ttc ttc gga agt gct gcc acc atg aac	96
Leu Cys Val Asn Asn Cys Gly Phe Phe Gly Ser Ala Ala Thr Met Asn	
20 25 30	
atg tgc tca aag tgc cac aag gat acg atg cta aac caa gag caa tcc	144
Met Cys Ser Lys Cys His Lys Asp Thr Met Leu Asn Gln Glu Gln Ser	
35 40 45	
aag ctt gct gct tca tcg gca gca agt atc ctc aac gga tcg tcg atg	192
Lys Leu Ala Ala Ser Ser Ala Ala Ser Ile Leu Asn Gly Ser Ser Met	
50 55 60	
agc ctc gga agg gaa ctc gtt att gct gct aag acc aat tcg gta gaa	240
Ser Leu Gly Arg Glu Leu Val Ile Ala Ala Lys Thr Asn Ser Val Glu	
65 70 75 80	
ccc aag acc atc tcc gtc caa cca tct tct gct tca agt gct gaa gag	288
Pro Lys Thr Ile Ser Val Gln Pro Ser Ser Ala Ser Ser Ala Glu Glu	
85 90 95	
agt atc gaa atg aag ctg cca aaa gaa ggg ccc agt agg tgc aac act	336
Ser Ile Glu Met Lys Leu Pro Lys Glu Gly Pro Ser Arg Cys Asn Thr	
100 105 110	
tgc aac aaa cgt gtc ggt ttg acc gga ttc aaa tgt cgg tgc gag aac	384
Cys Asn Lys Arg Val Gly Leu Thr Gly Phe Lys Cys Arg Cys Glu Asn	
115 120 125	
atg ttc tgc gca aac cat cgc tac tcg gac aag cac aat tgc ccc ttt	432
Met Phe Cys Ala Asn His Arg Tyr Ser Asp Lys His Asn Cys Pro Phe	
130 135 140	
gat tac cgc act gct ggc cgt gaa gct atc tca aag gcc aat cct ttg	480
Asp Tyr Arg Thr Ala Gly Arg Glu Ala Ile Ser Lys Ala Asn Pro Leu	
145 150 155 160	
gtg aag gcg gag aag ctc gac aaa atc tga	510
Val Lys Ala Glu Lys Leu Asp Lys Ile	
165	

<210> 28
 <211> 169
 <212> PRT
 <213> Linum usitatissimum

<400> 28

Met Asp His Asp Glu Ala Gly Cys Gln Ala Pro Ser Asp His Pro Ile
1 5 10 15
Leu Cys Val Asn Asn Cys Gly Phe Phe Gly Ser Ala Ala Thr Met Asn
20 25 30
Met Cys Ser Lys Cys His Lys Asp Thr Met Leu Asn Gln Glu Gln Ser

35

Lys Leu Ala Ala Ser Ser Ala Ala Ser Ile Leu Asn Gly Ser Ser Met
50 55 60
Ser Leu Gly Arg Glu Leu Val Ile Ala Ala Lys Thr Asn Ser Val Glu
65 70 75 80
Pro Lys Thr Ile Ser Val Gln Pro Ser Ser Ala Ser Ser Ala Glu Glu
85 90 95
Ser Ile Glu Met Lys Leu Pro Lys Glu Gly Pro Ser Arg Cys Asn Thr
100 105 110
Cys Asn Lys Arg Val Gly Leu Thr Gly Phe Lys Cys Arg Cys Glu Asn
115 120 125
Met Phe Cys Ala Asn His Arg Tyr Ser Asp Lys His Asn Cys Pro Phe
130 135 140
Asp Tyr Arg Thr Ala Gly Arg Glu Ala Ile Ser Lys Ala Asn Pro Leu
145 150 155 160
Val Lys Ala Glu Lys Leu Asp Lys Ile
165

<210> 29
<211> 495
<212> DNA
<213> Oryza sativa

<220>
<221> CDS
<222> (1)..(495)
<223> zinc finger protein containing an A20 domain and an AN1 domain
(OS39781852)

<400> 29
atg gcg cag cgc gac aag aag gat cag gag ccg acg gag ctc agg gcg 48
Met Ala Gln Arg Asp Lys Lys Asp Gln Glu Pro Thr Glu Leu Arg Ala
1 5 10 15
ccg gag atc acg ctg tgc gcc aac agc tgc gga ttc ccg ggc aac ccg 96
Pro Glu Ile Thr Leu Cys Ala Asn Ser Cys Gly Phe Pro Gly Asn Pro
20 25 30
gcc acg cag aac ctc tgc cag aac tgc ttc ttg gcg gcc acg gcg tcc 144
Ala Thr Gln Asn Leu Cys Gln Asn Cys Phe Leu Ala Ala Thr Ala Ser
35 40 45
acc tcg tcg ccg tct tct ttg tgc tca ccg gtg ctc gac aag cag ccg 192
Thr Ser Ser Pro Ser Ser Leu Ser Ser Pro Val Leu Asp Lys Gln Pro
50 55 60
ccg agg ccg gcg gcg ccg ctg gtt gag cct cag gct cct ctc cca ccg 240
Pro Arg Pro Ala Ala Pro Leu Val Glu Pro Gln Ala Pro Leu Pro Pro
65 70 75 80
cct gtg gag gag atg gcc tcc gcg ctc gcg acg gcg ccg gcg ccg gtc 288

PhoenixTemp21163.tmp.txt

Pro Val Glu Glu Met Ala Ser Ala Leu Ala Thr Ala Pro Ala Pro Val
85 90 95

gcc aag acg tcg gcg gtg aac cgg tgc tcc agg tgc cgg aag cgt gtc 336
Ala Lys Thr Ser Ala Val Asn Arg Cys Ser Arg Cys Arg Lys Arg Val
100 105 110

ggc ctc acc ggg ttc cgg tgc cgg tgc ggc cac ctg ttc tgc ggc gag 384
Gly Leu Thr Gly Phe Arg Cys Arg Cys Gly His Leu Phe Cys Gly Glu
115 120 125

cac cgg tac tcc gac cgc cac ggc tgc agc tac gac tac aag tcg gcg 432
His Arg Tyr Ser Asp Arg His Gly Cys Ser Tyr Asp Tyr Lys Ser Ala
130 135 140

gcg agg gac gcc atc gcc agg gac aac ccg gtg gtg cgc gcg gcc aag 480
Ala Arg Asp Ala Ile Ala Arg Asp Asn Pro Val Val Arg Ala Ala Lys
145 150 155 160

atc gtt agg ttc tga 495
Ile Val Arg Phe

<210> 30
<211> 164
<212> PRT
<213> Oryza sativa

<400> 30

Met Ala Gln Arg Asp Lys Lys Asp Gln Glu Pro Thr Glu Leu Arg Ala
1 5 10 15

Pro Glu Ile Thr Leu Cys Ala Asn Ser Cys Gly Phe Pro Gly Asn Pro
20 25 30

Ala Thr Gln Asn Leu Cys Gln Asn Cys Phe Leu Ala Ala Thr Ala Ser
35 40 45

Thr Ser Ser Pro Ser Ser Leu Ser Ser Pro Val Leu Asp Lys Gln Pro
50 55 60

Pro Arg Pro Ala Ala Pro Leu Val Glu Pro Gln Ala Pro Leu Pro Pro
65 70 75 80

Pro Val Glu Glu Met Ala Ser Ala Leu Ala Thr Ala Pro Ala Pro Val
85 90 95

Ala Lys Thr Ser Ala Val Asn Arg Cys Ser Arg Cys Arg Lys Arg Val
100 105 110

Gly Leu Thr Gly Phe Arg Cys Arg Cys Gly His Leu Phe Cys Gly Glu
115 120 125

His Arg Tyr Ser Asp Arg His Gly Cys Ser Tyr Asp Tyr Lys Ser Ala
130 135 140

Ala Arg Asp Ala Ile Ala Arg Asp Asn Pro Val Val Arg Ala Ala Lys
145 150 155 160

Ile Val Arg Phe

<210> 31
 <211> 495
 <212> DNA
 <213> Oryza sativa

<220>
 <221> CDS
 <222> (1)..(495)
 <223> zinc finger protein containing an A20 domain and an AN1 domain
 (OS34701560)

<400> 31
 atg gcc gaa gaa cac cga tgc caa gct ccc gaa ggt cac aga ctc tgc 48
 Met Ala Glu Glu His Arg Cys Gln Ala Pro Glu Gly His Arg Leu Cys
 1 5 10 15
 tcc aac aac tgc ggt ttc ttt ggt agc ccc gcc acc atg aat ctc tgt 96
 Ser Asn Asn Cys Gly Phe Phe Gly Ser Pro Ala Thr Met Asn Leu Cys
 20 25 30
 tcc aaa tgc tac aga gac atc cgt ttg aag gaa gaa gaa caa gcc aaa 144
 Ser Lys Cys Tyr Arg Asp Ile Arg Leu Lys Glu Glu Glu Gln Ala Lys
 35 40 45
 acc aaa tcc aca atc gaa acc gct ctt tca gga tct tcc tcc gcc acc 192
 Thr Lys Ser Thr Ile Glu Thr Ala Leu Ser Gly Ser Ser Ser Ala Thr
 50 55 60
 gtc acc gca acc gcc gtc gtt gcc tcc tcc gtg gaa tcc cct tcg gcg 240
 Val Thr Ala Thr Ala Val Val Ala Ser Ser Val Glu Ser Pro Ser Ala
 65 70 75 80
 ccg gtt gaa tcc ctc cct caa cca ccg gtg ctg att tcg ccg gat ata 288
 Pro Val Glu Ser Leu Pro Gln Pro Pro Val Leu Ile Ser Pro Asp Ile
 85 90 95
 gcc gca ccg gtt cag gcg aac ccg tgc ggc gcg tgt agg aag cgc gtg 336
 Ala Ala Pro Val Gln Ala Asn Arg Cys Gly Ala Cys Arg Lys Arg Val
 100 105 110
 ggg ttg aca ggg ttc aag tgc agg tgc gga aca acg ttt tgt ggg agc 384
 Gly Leu Thr Gly Phe Lys Cys Arg Cys Gly Thr Thr Phe Cys Gly Ser
 115 120 125
 cac agg tac ccc gag aaa cac gcg tgt ggc ttc gat ttc aag gcg gtg 432
 His Arg Tyr Pro Glu Lys His Ala Cys Gly Phe Asp Phe Lys Ala Val
 130 135 140
 ggg aga gag gag ata gca cgg gcg aat ccc gtg atc aaa ggc gag aag 480
 Gly Arg Glu Glu Ile Ala Arg Ala Asn Pro Val Ile Lys Gly Glu Lys
 145 150 155 160
 cta cgg agg att taa 495
 Leu Arg Arg Ile

<210> 32
 <211> 164
 <212> PRT
 <213> Oryza sativa

<400> 32

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

<210> 33

<211> 513

<212> DNA

<213> Oryza sativa

<220>

<221> CDS

<222> (1)..(513)

<223> zinc finger protein containing an A20 domain and an AN1 domain
 (OS36821256)

<400> 33

atg gcg cag agg gag aag aag gtg gag gag ccg acg gag ctg agg gcg
 Met Ala Gln Arg Glu Lys Lys Val Glu Glu Pro Thr Glu Leu Arg Ala
 1 5 10 15 48
 ccg gag atg acg ctc tgc gcc aac agc tgc ggg ttc ccg ggc aac ccg
 Pro Glu Met Thr Leu Cys Ala Asn Ser Cys Gly Phe Pro Gly Asn Pro
 20 25 30 96
 gcg acc aac aac ctc tgc cag aac tgc ttc ttg gct gcc tcg gcg tct
 Ala Thr Asn Asn Leu Cys Gln Asn Cys Phe Leu Ala Ala Ser Ala Ser
 144

PhoenixTemp21163.tmp.txt

35	40	45	
tct tct tct tct tcc gcc gct gcc tcg ccg tcg acg acg tcg ttg ccg			192
Ser Ser Ser Ser Ser Ala Ala Ala Ser Pro Ser Thr Thr Ser Leu Pro			
50	55	60	
gtg ttt ccg gtg gtg gag aag ccg agg cag gcc gta cag tcg tcg gcg			240
Val Phe Pro Val Val Glu Lys Pro Arg Gln Ala Val Gln Ser Ser Ala			
65	70	75	80
gcg gcg gcg gtg gcg ctg gtg gtt gag cgg ccg acg gcg ggg ccg gtg			288
Ala Ala Ala Val Ala Leu Val Val Glu Arg Pro Thr Ala Gly Pro Val			
85	90	95	
gag tcg tcg tcg aag gcg tcg agg tcg tcg tcg gtc aac cga tgc cac			336
Glu Ser Ser Ser Lys Ala Ser Arg Ser Ser Ser Val Asn Arg Cys His			
100	105	110	
agc tgc cgg agg cgg gtg ggc ctg acc ggg ttc cgg tgc cgc tgc ggc			384
Ser Cys Arg Arg Arg Val Gly Leu Thr Thr Gly Phe Arg Cys Arg Cys Gly			
115	120	125	
gag ctc tac tgc ggc gcg cac cgg tac tcc gac cgc cac gac tgc agc			432
Glu Leu Tyr Cys Gly Ala His Arg Tyr Ser Asp Arg His Asp Cys Ser			
130	135	140	
ttc gac tac aag tcg gcg gcg agg gac gcc atc gcc agg gag aac ccc			480
Phe Asp Tyr Lys Ser Ala Ala Arg Asp Ala Ile Ala Arg Glu Asn Pro			
145	150	155	160
gtc gtc cgc gcc gcc aag atc gtt agg ttc taa			513
Val Val Arg Ala Ala Lys Ile Val Arg Phe			
165	170		

<210> 34
 <211> 170
 <212> PRT
 <213> Oryza sativa

<400> 34

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

PhoenixTemp21163.tmp.txt

Ser Cys Arg Arg Arg Val Gly Leu Thr Gly Phe Arg Cys Arg Cys Gly
115 120 125

Glu Leu Tyr Cys Gly Ala His Arg Tyr Ser Asp Arg His Asp Cys Ser
130 135 140

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

Val Val Arg Ala Ala Lys Ile Val Arg Phe
165 170

<210> 35
<211> 486
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (1)..(486)
<223> zinc finger protein containing an A20 domain and an AN1 domain
(GM51659494)

<400> 35
atg gct cag aaa acc gag aaa gaa gaa acc gac ttc aaa gtt ccg gaa 48
Met Ala Gln Lys Thr Glu Lys Glu Glu Thr Asp Phe Lys Val Pro Glu
1 5 10 15
acg att acg ctt tgc gtc aac aac tgc ggc gtc acc gga aac cct gcc 96
Thr Ile Thr Leu Cys Val Asn Asn Cys Gly Val Thr Gly Asn Pro Ala
20 25 30
acg aat aac atg tgc cag aag tgc ttc act gcc tct acc gcc acc act 144
Thr Asn Asn Met Cys Gln Lys Cys Phe Thr Ala Ser Thr Ala Thr Thr
35 40 45
tcc ggc gcc gga ggt gcc gga ata gct tct ccg gcg acc aga tcc gcc 192
Ser Gly Ala Gly Gly Ala Gly Ile Ala Ser Pro Ala Thr Arg Ser Gly
50 55 60
gtc tcc gcg cgt cct cag aag aga tct ttt cct gaa gag ccc tcg ccg 240
Val Ser Ala Arg Pro Gln Lys Arg Ser Phe Pro Glu Glu Pro Ser Pro
65 70 75 80
gtg gcg gat cct cct tct tcg gac cag acg acg ccg tcg gag gcg aag 288
Val Ala Asp Pro Pro Ser Ser Asp Gln Thr Thr Pro Ser Glu Ala Lys
85 90 95
cgc gtg gtc aac cgc tgc tcc gga tgc cgg cgg aag gtc gga ctc acc 336
Arg Val Val Asn Arg Cys Ser Gly Cys Arg Arg Lys Val Gly Leu Thr
100 105 110
gga ttc cgg tgc cgg tgc ggc gag ctc ttc tgc gcc gag cac cgg tac 384
Gly Phe Arg Cys Arg Cys Gly Glu Leu Phe Cys Ala Glu His Arg Tyr
115 120 125
tcc gac cgc cac gac tgc agc tat gac tac aaa gcc gcc gga aga gaa 432
Ser Asp Arg His Asp Cys Ser Tyr Asp Tyr Lys Ala Ala Gly Arg Glu
130 135 140
gcc atc gcg agg gag aat ccg gtg atc aga gct gcg aag atc gtc aaa 480
Ala Ile Ala Arg Glu Asn Pro Val Ile Arg Ala Lys Lys Ile Val Lys
145 150 155 160

gtc tga
Val

<210> 36
<211> 161
<212> PRT
<213> Glycine max

<400> 36

Met Ala Gln Lys Thr Glu Lys Glu Glu Thr Asp Phe Lys Val Pro Glu
1 5 10 15

Thr Ile Thr Leu Cys Val Asn Asn Cys Gly Val Thr Gly Asn Pro Ala
20 25 30

Thr Asn Asn Met Cys Gln Lys Cys Phe Thr Ala Ser Thr Ala Thr Thr
35 40 45

Ser Gly Ala Gly Gly Ala Gly Ile Ala Ser Pro Ala Thr Arg Ser Gly
50 55 60

Val Ser Ala Arg Pro Gln Lys Arg Ser Phe Pro Glu Glu Pro Ser Pro
65 70 75 80

Val Ala Asp Pro Pro Ser Ser Asp Gln Thr Thr Pro Ser Glu Ala Lys
85 90 95

Arg Val Val Asn Arg Cys Ser Gly Cys Arg Arg Lys Val Gly Leu Thr
100 105 110

Gly Phe Arg Cys Arg Cys Gly Glu Leu Phe Cys Ala Glu His Arg Tyr
115 120 125

Ser Asp Arg His Asp Cys Ser Tyr Asp Tyr Lys Ala Ala Gly Arg Glu
130 135 140

Ala Ile Ala Arg Glu Asn Pro Val Ile Arg Ala Ala Lys Ile Val Lys
145 150 155 160

Val

<210> 37
<211> 519
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (1)..(519)
<223> zinc finger protein containing an A20 domain and an AN1 domain
(GM49780101)

PhoenixTemp21163.tmp.txt

<400> 37
 atg gag cct cat gat gag act gga tgc cag gct cct gaa cgc ccc att 48
 Met Glu Pro His Asp Glu Thr Gly Cys Gln Ala Pro Glu Arg Pro Ile
 1 5 10 15

ctt tgc att aat aat tgt ggc ttc ttt gga aga gca gct acc atg aac 96
 Leu Cys Ile Asn Asn Cys Gly Phe Phe Gly Arg Ala Ala Thr Met Asn
 20 25 30

atg tgt tcc aag tgt tac aag gac atg ctg ttg aag cag gag cag gac 144
 Met Cys Ser Lys Cys Tyr Lys Asp Met Leu Leu Lys Gln Glu Gln Asp
 35 40 45

aaa ttt gca gca tca tcc gtt gaa aac att gtg aat ggc agt tcc aat 192
 Lys Phe Ala Ala Ser Ser Val Glu Asn Ile Val Asn Gly Ser Ser Asn
 50 55 60

ggc aat gga aag cag gct gtg gct act ggt gct gtt gct gta caa gtt 240
 Gly Asn Gly Lys Gln Ala Val Ala Thr Gly Ala Val Ala Val Gln Val
 65 70 75 80

gaa gct gtg gag gtc aag att gtc tgt gct cag agt tct gtg gat tcg 288
 Glu Ala Val Glu Val Lys Ile Val Cys Ala Gln Ser Ser Val Asp Ser
 85 90 95

tcc tcc ggt gat agt ttg gag atg aaa gcc aag act ggt ccc agt aga 336
 Ser Ser Gly Asp Ser Leu Glu Met Lys Ala Lys Thr Gly Pro Ser Arg
 100 105 110

tgt gct aca tgc cgg aaa cgt gtt ggt tta act ggt ttc agc tgc aaa 384
 Cys Ala Thr Cys Arg Lys Arg Val Gly Leu Thr Gly Phe Ser Cys Lys
 115 120 125

tgt ggc aac ctc ttc tgt gca atg cat cgc tat tct gat aaa cat gat 432
 Cys Gly Asn Leu Phe Cys Ala Met His Arg Tyr Ser Asp Lys His Asp
 130 135 140

tgc cct ttt gat tat agg act gtt ggt cag gat gcc ata gct aaa gcc 480
 Cys Pro Phe Asp Tyr Arg Thr Val Gly Gln Asp Ala Ile Ala Lys Ala
 145 150 155 160

aac ccc ata att aag gca gat aag ctc gac aaa atc tag 519
 Asn Pro Ile Ile Lys Ala Asp Lys Leu Asp Lys Ile
 165 170

<210> 38
 <211> 172
 <212> PRT
 <213> Glycine max

<400> 38
 Met Glu Pro His Asp Glu Thr Gly Cys Gln Ala Pro Glu Arg Pro Ile
 1 5 10 15

Leu Cys Ile Asn Asn Cys Gly Phe Phe Gly Arg Ala Ala Thr Met Asn
 20 25 30

Met Cys Ser Lys Cys Tyr Lys Asp Met Leu Leu Lys Gln Glu Gln Asp
 35 40 45

Lys Phe Ala Ala Ser Ser Val Glu Asn Ile Val Asn Gly Ser Ser Asn
 50 55 60

Gly Asn Gly Lys Gln Ala Val Ala Thr Gly Ala Val Ala Val Gln Val
65 70 75 80

Glu Ala Val Glu Val Lys Ile Val Cys Ala Gln Ser Ser Val Asp Ser
85 90 95

Ser Ser Gly Asp Ser Leu Glu Met Lys Ala Lys Thr Gly Pro Ser Arg
100 105 110

Cys Ala Thr Cys Arg Lys Arg Val Gly Leu Thr Gly Phe Ser Cys Lys
115 120 125

Cys Gly Asn Leu Phe Cys Ala Met His Arg Tyr Ser Asp Lys His Asp
130 135 140

Cys Pro Phe Asp Tyr Arg Thr Val Gly Gln Asp Ala Ile Ala Lys Ala
145 150 155 160

Asn Pro Ile Ile Lys Ala Asp Lys Leu Asp Lys Ile
165 170

<210> 39
<211> 525
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (1)..(525)
<223> zinc finger protein containing an A20 domain and an AN1 domain
(GM59637305)

<400> 39
atg gac cat gac aag act ggg tgc caa gct cct cct gaa ggt cct ata 48
Met Asp His Asp Lys Thr Gly Cys Gln Ala Pro Pro Glu Gly Pro Ile
1 5 10 15
ttg tgc atc aac aac tgt ggg ttt ttt gga agt gca gct acc atg aac 96
Leu Cys Ile Asn Asn Cys Gly Phe Phe Gly Ser Ala Ala Thr Met Asn
20 25 30
atg tgt tct aaa tgc cac aaa gac ata ttg ctg aaa cag gag cag gcc 144
Met Cys Ser Lys Cys His Lys Asp Ile Leu Leu Lys Glu Glu Ala
35 40 45
aag ctt gca gca tca tcc att ggg aat att atg aat ggg tca tca agc 192
Lys Leu Ala Ala Ser Ser Ile Gly Asn Ile Met Asn Gly Ser Ser Ser
50 55 60
agc act gaa aag gaa cct gtt gtt gct gct gct gct aat att gat atc 240
Ser Thr Glu Lys Glu Pro Val Val Ala Ala Ala Asn Ile Asp Ile
65 70 75 80
cca gtt att cca gta gag cct aaa act gtc tct gtg caa cct tta ttt 288
Pro Val Ile Pro Val Glu Pro Lys Thr Val Ser Val Gln Pro Leu Phe
85 90 95
ggg tca ggt cca gag ggg agt gtt gag gca aag ccg aag gat gga cca 336
Gly Ser Gly Pro Glu Gly Ser Val Glu Ala Lys Pro Lys Asp Gly Pro
100 105 110

PhoenixTemp21163.tmp.txt

aaa cgt tgc agc agc tgc aac aag cga gtt ggt ttg aca ggg ttt aat 384
 Lys Arg Cys Ser Ser Cys Asn Lys Arg Val Gly Leu Thr Gly Phe Asn
 115 120 125

tgt cga tgt ggt gac ctt ttt ttg tgc tgt aca tcg cta ctc gac aag 432
 Cys Arg Cys Gly Asp Leu Phe Leu Cys Cys Thr Ser Leu Leu Asp Lys
 130 135 140

cat aat tgc cca ttt gat tac cgc act gcc gct caa gat gct ata gct 480
 His Asn Cys Pro Phe Asp Tyr Arg Thr Ala Ala Gln Asp Ala Ile Ala
 145 150 155 160

aaa gca aac cca gtt gtc aag gct gaa aag ctt gat aag atc taa 525
 Lys Ala Asn Pro Val Val Lys Ala Glu Lys Leu Asp Lys Ile

<210> 40
 <211> 174
 <212> PRT
 <213> Glycine max
 <400> 40

Met Asp His Asp Lys Thr Gly Cys Gln Ala Pro Pro Glu Gly Pro Ile
 1 5 10 15

Leu Cys Ile Asn Asn Cys Gly Phe Phe Gly Ser Ala Ala Thr Met Asn
 20 25 30

Met Cys Ser Lys Cys His Lys Asp Ile Leu Leu Lys Gln Glu Gln Ala
 35 40 45

Lys Leu Ala Ala Ser Ser Ile Gly Asn Ile Met Asn Gly Ser Ser Ser
 50 55 60

Ser Thr Glu Lys Glu Pro Val Val Ala Ala Ala Ala Asn Ile Asp Ile
 65 70 75 80

Pro Val Ile Pro Val Glu Pro Lys Thr Val Ser Val Gln Pro Leu Phe
 85 90 95

Gly Ser Gly Pro Glu Gly Ser Val Glu Ala Lys Pro Lys Asp Gly Pro
 100 105 110

Lys Arg Cys Ser Ser Cys Asn Lys Arg Val Gly Leu Thr Gly Phe Asn
 115 120 125

Cys Arg Cys Gly Asp Leu Phe Leu Cys Cys Thr Ser Leu Leu Asp Lys
 130 135 140

His Asn Cys Pro Phe Asp Tyr Arg Thr Ala Ala Gln Asp Ala Ile Ala
 145 150 155 160

Lys Ala Asn Pro Val Val Lys Ala Glu Lys Leu Asp Lys Ile
 165 170

<210> 41

<211> 498
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> CDS
 <222> (1)..(498)
 <223> zinc finger protein containing an A20 domain and an AN1 domain
 (TA55974113)

<400> 41
 atg gcg cag cgg gat cac aag cag gag gag ccc acg gag ctg cgg gcg 48
 Met Ala Gln Arg Asp His Lys Gln Glu Glu Pro Thr Glu Leu Arg Ala
 1 5 10 15
 ccg gag atc acg ctc tgc gcc aac agc tgc ggc ttc ccg ggc aac ccg 96
 Pro Glu Ile Thr Leu Cys Ala Asn Ser Cys Gly Phe Pro Gly Asn Pro
 20 25 30
 gcc acg cag aac ctc tgc cag aac tgc ttc ttg gcc ggc ccg gcg tcc 144
 Ala Thr Gln Asn Leu Cys Gln Asn Cys Phe Leu Ala Gly Pro Ala Ser
 35 40 45
 acg tcg ccg tct tcc tcc tcc tcc tcc tct tct ctg ccg ggc gtg 192
 Thr Ser Pro Ser Ser Ser Ser Ser Ser Ser Ser Leu Pro Gly Val
 50 55 60
 tcc gcg ccg acc ccc gtc atc gac agg ccg agg ccg gcg ccg ttg gag 240
 Ser Ala Pro Thr Pro Val Ile Asp Arg Pro Arg Pro Ala Pro Leu Glu
 65 70 75 80
 gcg gag ctg gca cgc ccc gcc gtc gac ctt gct ccg gcg acg gag gcg 288
 Ala Glu Leu Ala Arg Pro Ala Val Asp Leu Ala Pro Ala Thr Glu Ala
 85 90 95
 aag ccg gcg agg acg tcg gtg aac ccg tgc tcc agc tgc ccg aag cgc 336
 Lys Pro Ala Arg Thr Ser Val Asn Arg Cys Ser Ser Cys Arg Lys Arg
 100 105 110
 gtg ggg ctg acg ggg ttc ccg tgc ccg tgc ggc gac atg ttc tgc ggc 384
 Val Gly Leu Thr Gly Phe Arg Cys Arg Cys Gly Asp Met Phe Cys Gly
 115 120 125
 gag cac cgg tac tcg gac ccg cac ggg tgc agc tac gac tac aag gcc 432
 Glu His Arg Tyr Ser Asp Arg His Gly Cys Ser Tyr Asp Tyr Lys Ala
 130 135 140
 gcc gcc agg gac gcc atc gcc agg gac aac ccc gtc gtg cgc gcc gcc 480
 Ala Ala Arg Asp Ala Ile Ala Arg Asp Asn Pro Val Val Arg Ala Ala
 145 150 155 160
 aag atc gtc agg ttc tga 498
 Lys Ile Val Arg Phe
 165

<210> 42
 <211> 165
 <212> PRT
 <213> Triticum aestivum

<400> 42
 Met Ala Gln Arg Asp His Lys Gln Glu Glu Pro Thr Glu Leu Arg Ala
 1 5 10 15
 Pro Glu Ile Thr Leu Cys Ala Asn Ser Cys Gly Phe Pro Gly Asn Pro

20

25

30

Ala Thr Gln Asn Leu Cys Gln Asn Cys Phe Leu Ala Gly Pro Ala Ser
 35 40 45

Thr Ser Pro Ser Ser Ser Ser Ser Ser Ser Ser Ser Leu Pro Gly Val
 50 55 60

Ser Ala Pro Thr Pro Val Ile Asp Arg Pro Arg Pro Ala Pro Leu Glu
 65 70 75 80

Ala Glu Leu Ala Arg Pro Ala Val Asp Leu Ala Pro Ala Thr Glu Ala
 85 90 95

Lys Pro Ala Arg Thr Ser Val Asn Arg Cys Ser Ser Cys Arg Lys Arg
 100 105 110

Val Gly Leu Thr Gly Phe Arg Cys Arg Cys Gly Asp Met Phe Cys Gly
 115 120 125

Glu His Arg Tyr Ser Asp Arg His Gly Cys Ser Tyr Asp Tyr Lys Ala
 130 135 140

Ala Ala Arg Asp Ala Ile Ala Arg Asp Asn Pro Val Val Arg Ala Ala
 145 150 155 160

Lys Ile Val Arg Phe
 165

<210> 43
 <211> 207
 <212> PRT
 <213> Physcomitrella patens

<220>
 <221> MISC_FEATURE
 <222> (1)..(207)
 <223> methionine sulfoxide reductase family protein (EST65)

<400> 43

Met Val Ala Glu Ser Val Leu Val Cys Arg Ser Ser Val Val Gly Ala
 1 5 10 15

Gly Leu Gln Ser Phe Val Gly Glu Gly Ala Lys Arg Glu Ser Ala Gly
 20 25 30

Pro Gly Arg Ser Val Phe Leu Gly Ala Gln Val Gln Lys Met Gly Ala
 35 40 45

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

Ser Gly Asp Val Ser Glu Gln Thr Asp Tyr Lys Thr Phe Ser Asp Glu
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65					70					75					80
Glu	Trp	Lys	Lys	Arg ₈₅	Leu	Ser	Gln	Gln	Gln ₉₀	Phe	Tyr	Val	Ala	Arg ₉₅	Lys
Lys	Gly	Thr	Glu ₁₀₀	Arg	Pro	Phe	Thr	Gly ₁₀₅	Glu	Tyr	Trp	Asn	Thr ₁₁₀	Lys	Thr
Ala	Gly	Thr ₁₁₅	Tyr	Leu	Cys	Val	Cys ₁₂₀	Cys	Lys	Thr	Pro	Leu ₁₂₅	Phe	Ser	Ser
Lys	Thr ₁₃₀	Lys	Phe	Asp	Ser	Gly ₁₃₅	Thr	Gly	Trp	Pro	Ser ₁₄₀	Tyr	Tyr	Asp	Thr
Ile ₁₄₅	Gly	Asp	Asn	Val	Lys ₁₅₀	Ser	His	Met	Asp	Trp ₁₅₅	Ser	Ile	Pro	Phe	Met ₁₆₀
Pro	Arg	Thr	Glu	Val ₁₆₅	Val	Cys	Ala	Val	Cys ₁₇₀	Asp	Ala	His	Leu	Gly ₁₇₅	His
Val	Phe	Asp	Asp ₁₈₀	Gly	Pro	Arg	Pro	Thr ₁₈₅	Gly	Lys	Arg	Tyr	Cys ₁₉₀	Ile	Asn
Ser	Ala	Ala ₁₉₅	Ile	Asp	Leu	Lys	Ala ₂₀₀	Glu	Lys	Gln	Glu	Glu ₂₀₅	Arg	Asn	

<210> 44
<211> 339
<212> PRT
<213> Physcomitrella patens

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<220>
<221> MISC_FEATURE
<222> (1)..(339)
<223> homeodomain leucine zipper protein (EST12)
<400> 44
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Met Val Val Pro Ser Leu Pro Ala Phe Gly Gly Gln Asn Ala Met Leu
1 5 10 15

Arg Arg Asn Ile Asp Asn Asn Thr Asp Thr Leu Ile Ser Leu Leu Gln
20 25 30

Gly Ser Cys Ser Pro Arg Val Ser Met Gln Gln Val Pro Arg Ser Ser
35 40 45

Glu Ser Leu Glu Asn Met Met Gly Ala Cys Gly Gln Lys Leu Pro Tyr
50 55 60

Phe Ser Ser Phe Asp Gly Pro Ser Val Glu Glu Gln Glu Asp Val Asp
65 70 75 80

Glu Gly Ile Asp Glu Phe Ala His His Val Glu Lys Lys Arg Arg Leu

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

<210> 45
 <211> 188

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<212> PRT
<213> Physcomitrella patens

<220>
<221> MISC_FEATURE
<222> (1)..(188)
<223> zinc finger protein containing an A20 domain and an AN1 domain
      (EST307)

<400> 45
Met Ala Thr Glu Arg Val Ser Gln Glu Thr Thr Ser Gln Ala Pro Glu
1          5          10
Gly Pro Val Met Cys Lys Asn Leu Cys Gly Phe Phe Gly Ser Gln Ala
20         25         30
Thr Met Gly Leu Cys Ser Lys Cys Tyr Arg Glu Thr Val Met Gln Ala
35         40         45
Lys Met Thr Ala Leu Ala Glu Gln Ala Thr Gln Ala Ala Gln Ala Thr
50         55         60
Ser Ala Thr Ala Ala Ala Val Gln Pro Pro Ala Pro Val His Glu Thr
65         70         75         80
Lys Leu Thr Cys Glu Val Glu Arg Thr Met Ile Val Pro His Gln Ser
85         90         95
Ser Ser Tyr Gln Gln Asp Leu Val Thr Pro Ala Ala Ala Ala Pro Gln
100        105        110
Ala Val Lys Ser Ser Ile Ala Ala Pro Ser Arg Pro Glu Pro Asn Arg
115        120        125
Cys Gly Ser Cys Arg Lys Arg Val Gly Leu Thr Gly Phe Lys Cys Arg
130        135        140
Cys Gly Asn Leu Tyr Cys Ala Leu His Arg Tyr Ser Asp Lys His Thr
145        150        155        160
Cys Thr Tyr Asp Tyr Lys Ala Ala Gly Gln Glu Ala Ile Ala Lys Ala
165        170        175
Asn Pro Leu Val Val Ala Glu Lys Val Val Lys Phe
180        185

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