

SEQUENCE LISTING

<110> BASF Plant Science GmbH

<120> Plants having increased seed yield-related traits and a method for making the same

<130> PF59353

<160> 59

<170> PatentIn version 3.3

<210> 1

<211> 948

<212> DNA

<213> Arabidopsis thaliana

<400> 1

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<212> PRT

<213> Arabidopsis thaliana

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Gly Leu Thr Ile Tyr Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly		190
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Ser Val Val Gly Pro Leu Met Ala Ala Gly Pro Val Met Leu Ile Ala		205
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Gly Gln Leu Gly Gly Gly Gly Ser Pro Leu Ser Ser Gly Ala Gly Gly		255
	260	265
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 <213> Arabidopsis thaliana

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gccgttgagg tggtaaccg tagaccaaga ggtagaccac caggatccaa aaacaaaccc	240
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 <213> Arabidopsis thaliana

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Leu Leu Thr Lys Gly Asp Leu Gly Ile Ala Met Asn Gln Ser Gln Asp	25
	30
	35
Asn Asp Gln Asp Glu Glu Asp Asp Pro Arg Glu Gly Ala Val Glu Val	40
	45

50		55		60
Val Asn Arg Arg Pro Arg Gly Arg Pro Pro Gly Ser Lys Asn Lys Pro				
65		70		80
Lys Ala Pro Ile Phe Val Thr Arg Asp Ser Pro Asn Ala Leu Arg Ser				
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His Val Leu Glu Ile Ser Asp Gly Ser Asp Val Ala Asp Thr Ile Ala				
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His Phe Ser Arg Arg Arg Gln Arg Gly Val Cys Val Leu Ser Gly Thr				
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Gly Ser Val Ala Asn Val Thr Leu Arg Gln Ala Ala Ala Pro Gly Gly				
	130		135	140
Val Val Ser Leu Gln Gly Arg Phe Glu Ile Leu Ser Leu Thr Gly Ala				
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Phe Leu Pro Gly Pro Ser Pro Pro Gly Ser Thr Gly Leu Thr Val Tyr				
	165		170	175
Leu Ala Gly Val Gln Gly Gln Val Val Gly Gly Ser Val Val Gly Pro				
	180		185	190
Leu Leu Ala Ile Gly Ser Val Met Val Ile Ala Ala Thr Phe Ser Asn				
	195		200	205
Ala Thr Tyr Glu Arg Leu Pro Met Glu Glu Glu Glu Asp Gly Gly Gly				
	210		215	220
Ser Arg Gln Ile His Gly Gly Gly Asp Ser Pro Pro Arg Ile Gly Ser				
225		230		235
Asn Leu Pro Asp Leu Ser Gly Met Ala Gly Pro Gly Tyr Asn Met Pro				
	245		250	255
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<210> 5
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 <212> DNA
 <213> Aquilegia formosa x Aquilegia pubescens

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<210> 6
 <211> 288
 <212> PRT
 <213> Aquilegia formosa x Aquilegia pubescens

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	210				215						220						
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		260						265				270					
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<210> 7
 <211> 948
 <212> DNA
 <213> Brassica napus

<400> 7

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<210> 8
 <211> 315
 <212> PRT
 <213> Brassica napus

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 35 40 45
 His Gln Glu Val Asn Thr Asn Asn Asn Glu Asp Asp Arg Asp Asn
 50 55 60
 Leu Ser Gly Asp Asp His Glu Pro Arg Glu Gly Ala Val Glu Ala Pro
 65 70 75 80
 Thr Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys Asn Lys Pro Lys
 85 90 95
 Pro Pro Ile Phe Val Thr Arg Asp Ser Pro Asn Ala Leu Lys Ser His
 100 105 110
 Val Met Glu Ile Ala Ser Gly Thr Asp Val Ile Glu Thr Leu Ala Thr
 115 120 125
 Phe Ala Arg Arg Arg Gln Arg Gly Ile Cys Ile Leu Ser Gly Asn Gly
 130 135 140
 Thr Val Ala Asn Val Thr Leu Arg Gln Pro Ser Val Ala Pro Val Ala
 145 150 155 160
 Ala Ala Pro Gly Gly Ala Ala Val Leu Ala Leu Gln Gly Arg Phe Glu
 165 170 175
 Ile Leu Ser Leu Thr Gly Ser Phe Leu Pro Gly Pro Ala Pro Pro Gly
 180 185 190
 Ser Thr Gly Leu Thr Ile Tyr Leu Ala Gly Gly Gln Gly Gln Val Val
 195 200 205
 Gly Gly Ser Val Val Gly Pro Leu Met Ala Ala Gly Pro Val Met Leu
 210 215 220
 Ile Ala Ala Thr Phe Ser Asn Ala Thr Tyr Glu Arg Leu Pro Leu Asp
 225 230 235 240
 Glu Glu Glu Ala Ala Glu Arg Gly Gly Gly Gly Ser Asp Gly Gly Val
 245 250 255
 Val Pro Gly Gln Leu Gly Gly Val Gly Ser Pro Leu Ser Ser Gly Gly
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<210> 9
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 <212> DNA
 <213> Brassica rapa

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<213> Brassica rapa

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35          40          45
His Gln Glu Val Asn Thr Asn Asn Asn Asn Glu Asp Asp Arg Asp Asn
50          55          60
Leu Ser Gly Asp Asp His Glu Pro Arg Glu Gly Ala Val Glu Ala Pro
65          70          75          80
Thr Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys Asn Lys Pro Lys
85          90          95
Pro Pro Ile Phe Val Thr Arg Asp Ser Pro Asn Ala Leu Lys Ser His
100         105         110
Val Met Glu Ile Ala Ser Gly Thr Asp Val Ile Glu Thr Leu Ala Thr
115         120         125
Phe Ala Arg Arg Arg Gln Arg Gly Ile Cys Ile Leu Ser Gly Asn Gly
130         135         140
Thr Val Ala Asn Val Thr Leu Arg Gln Pro Ser Val Ala Pro Val Ala
145         150         155         160
Ala Ala Pro Gly Gly Ala Ala Val Leu Ala Leu Gln Gly Arg Phe Glu
165         170         175
Ile Leu Ser Leu Thr Gly Ser Phe Leu Pro Gly Pro Ala Pro Pro Gly
180         185         190
Ser Thr Gly Leu Thr Ile Tyr Leu Ala Gly Gly Gln Gly Gln Val Val
195         200         205
Gly Gly Ser Val Val Gly Pro Leu Met Ala Ala Gly Pro Val Met Leu
210         215         220
Ile Ala Ala Thr Phe Ser Asn Ala Thr Tyr Glu Arg Leu Pro Leu Asp
225         230         235         240
Glu Glu Glu Ala Ala Glu Arg Gly Gly Gly Gly Ser Asp Gly Gly Val
245         250         255
Val Pro Gly Gln Leu Gly Gly Val Gly Ser Pro Leu Ser Ser Gly Gly
260         265         270
Gly Gly Gly His Gly Asn Gln Gly Leu Pro Ala Tyr Asn Met Pro Gly
275         280         285
Asn Leu Ala Ser Asn Gly Gly Gly Gly Gly Gln Met Ser Gly Gln Glu
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Ala Tyr Gly Trp Ala Gln Ala Arg Ser Gly Phe
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 <212> DNA
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 acgcgccgcc ctagggggacg tccaccgggc tccagaaaca agccgaaacc gccgatattc 240
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 taa 843

<210> 12
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 <212> PRT
 <213> Glycine max

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

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<210> 13
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 <212> DNA
 <213> *Gossypium hirsutum*

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 accgtgtact tagctggtgg tcaaggacaa gttgttgagg gaagtgttgt cggctcactt 540
 atagcagcag ggcctgttat ggtcattgca gcaacttttt ccaacgcaac ttatgaaaga 600
 ctgccttttag aagatgaaga agaagttgta agcgccggtc acggtggacc gatgcaaggc 660
 ggagcaaacg attcaccgcc ggaaattggg agtagcggag gcggcggttc acacacaggt 720
 ctgcctgatc catcttcact tccaatatac aatttgccct ctaatttact ctcaaattgga 780
 gggcaactag ggcattgaacc ctatgggttg acacatggga gaccacccta ttaa 834

<210> 14
 <211> 277
 <212> PRT
 <213> *Gossypium hirsutum*

<400> 14
 Met Asp Pro Ala Gly Asn Ser Pro Ala Leu Asn Lys Arg Asp Leu Glu
 1 5 10 15
 Ile Ser Met Asn Asp Ala Asn Lys Ser Arg Ser Asn Gly Arg Gly Asp
 20 25 30
 Asp Asp Asp Glu Asp Arg Asp Thr Gly Asp Glu Pro Lys Glu Gly Ala
 35 40 45
 Val Glu Val Gly Asn Arg Arg Pro Arg Gly Arg Pro Pro Gly Ser Lys
 50 55 60
 Asn Lys Pro Lys Pro Pro Ile Phe Val Thr Arg Asp Ser Pro Asn Ala
 65 70 75 80
 Leu Arg Ser His Val Met Glu Val Ala Ser Gly Thr Asp Val Ala Glu
 85 90 95
 Ser Ile Ala Gln Phe Ala Arg Arg Arg Gln Arg Gly Val Cys Leu Leu
 100 105 110
 Ser Gly Ser Gly Ser Val Ala Asn Val Thr Leu Arg Gln Pro Ala Ala
 115 120 125
 Pro Gly Ala Val Val Ala Leu His Gly Arg Phe Glu Ile Leu Ser Leu
 130 135 140
 Thr Gly Ala Phe Leu Pro Gly Pro Ala Pro Pro Gly Ser Thr Gly Leu
 145 150 155 160
 Thr Val Tyr Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly Ser Val
 165 170 175
 Val Gly Ser Leu Ile Ala Ala Gly Pro Val Met Val Ile Ala Ala Thr
 180 185 190
 Phe Ser Asn Ala Thr Tyr Glu Arg Leu Pro Leu Glu Asp Glu Glu Glu
 195 200 205

Val	Val	Ser	Ala	Gly	His	Gly	Gly	Pro	Met	Gln	Gly	Gly	Ala	Asn	Asp
	210					215					220				
Ser	Pro	Pro	Glu	Ile	Gly	Ser	Ser	Gly	Gly	Gly	Gly	Ser	His	Thr	Gly
225					230					235					240
Leu	Pro	Asp	Pro	Ser	Ser	Leu	Pro	Ile	Tyr	Asn	Leu	Pro	Pro	Asn	Leu
				245					250					255	
Leu	Ser	Asn	Gly	Gly	Gln	Leu	Gly	His	Glu	Pro	Tyr	Gly	Trp	Thr	His
			260					265					270		
Gly	Arg	Pro	Pro	Tyr											
	275														

<210> 15
 <211> 813
 <212> DNA
 <213> Lactuca sativa

<400> 15
 atgtctaacc gatggtggac cggccaggtc aacgtggcag gcgtagaaac atcatctcag 60
 gcgatcaaga aaccagatct gggatatctca atgaatgata ccaccacagg aagtgaagaa 120
 gatgaaagag acaacaacag cgatgatcca agagaagggtg caattgaccc ttctaaccgt 180
 aggccacgag gccgacctcc gggatccaaa aacaaaccaa agccaccgat tttcgtcacc 240
 agagacagcc ctaacgccct ccgcagccac gtcattggagg tagcgagtgg tacagatatc 300
 gcagaaagta tagctcaatt cagccgaaaa cgacaacgcg gtgtgtgtgt gatgagtgtc 360
 agcggcacag tcatgaatgt aaccctaaga caaccttcgg cacctggctc agtcatggct 420
 ctacaaggcc ggttcgagat tttatcccta accggtgcct tcttaccggg tccttctcct 480
 cctggatcca ccgggctcac tatatatatta gctggtggcc agggccagggt tgtgggagggt 540
 agcgtgggtg gatcattggt ggcattcagga ccagtgtggt ttatagcagc cacgttctcc 600
 aacgccacat atgaaagact cccggttgag gaagaggagg aagcagatac cgtgacacct 660
 gggctaggtg gtggtggatc accaccgcaa ctcggaatgg gtgatcagaa tccgatggca 720
 ggggtataata tgcagccgaa tttgatcccg aatggtggtg gacagatgaa ccatgaagct 780
 tttgcttttg ctcattggccg gccacgtac tag 813

<210> 16
 <211> 270
 <212> PRT
 <213> Lactuca sativa

<400> 16
 Met Ser Asn Arg Trp Trp Thr Gly Gln Val Asn Val Ala Gly Val Glu
 1 5 10 15
 Thr Ser Ser Gln Ala Ile Lys Lys Pro Asp Leu Gly Ile Ser Met Asn
 20 25 30
 Asp Thr Thr Thr Gly Ser Glu Glu Asp Glu Arg Asp Asn Asn Ser Asp
 35 40 45
 Asp Pro Arg Glu Gly Ala Ile Asp Pro Ser Asn Arg Arg Pro Arg Gly
 50 55 60
 Arg Pro Pro Gly Ser Lys Asn Lys Pro Lys Pro Pro Ile Phe Val Thr
 65 70 75 80
 Arg Asp Ser Pro Asn Ala Leu Arg Ser His Val Met Glu Val Ala Ser
 85 90 95
 Gly Thr Asp Ile Ala Glu Ser Ile Ala Gln Phe Ser Arg Lys Arg Gln
 100 105 110
 Arg Gly Val Cys Val Met Ser Ala Ser Gly Thr Val Met Asn Val Thr
 115 120 125
 Leu Arg Gln Pro Ser Ala Pro Gly Ser Val Met Ala Leu Gln Gly Arg
 130 135 140
 Phe Glu Ile Leu Ser Leu Thr Gly Ala Phe Leu Pro Gly Pro Ser Pro
 145 150 155 160
 Pro Gly Ser Thr Gly Leu Thr Ile Tyr Leu Ala Gly Gly Gln Gly Gln

				165					170					175			
Val	Val	Gly	Gly	Ser	Val	Val	Gly	Ser	Leu	Val	Ala	Ser	Gly	Pro	Val		
			180					185					190				
Met	Val	Ile	Ala	Ala	Thr	Phe	Ser	Asn	Ala	Thr	Tyr	Glu	Arg	Leu	Pro		
		195					200					205					
Val	Glu	Glu	Glu	Glu	Glu	Ala	Asp	Thr	Val	Thr	Pro	Gly	Leu	Gly	Gly		
	210					215					220						
Gly	Gly	Ser	Pro	Pro	Gln	Leu	Gly	Met	Gly	Asp	Gln	Asn	Pro	Met	Ala		
225					230					235					240		
Gly	Tyr	Asn	Met	Gln	Pro	Asn	Leu	Ile	Pro	Asn	Gly	Gly	Gly	Gln	Met		
				245					250					255			
Asn	His	Glu	Ala	Phe	Ala	Leu	Ala	His	Gly	Arg	Pro	Thr	Tyr				
		260						265					270				

<210> 17
 <211> 882
 <212> DNA
 <213> Lotus japonicus

<400> 17
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 tcacctggct tgagcaaacg tcacacggac cttgtgatca atgaaaacag cagcgggtgg 120
 aatagagatg aagatgaaga tgataacagg gaagatgagc caaaagaagg tgcagttgag 180
 gttggaactc ggagaccaag gggaagacca ccgggatcca agaacaagcc aagaccaccc 240
 atctttgtaa caagggacag cccaaacgcc ctgaggagtc atgttatgga ggttgacagga 300
 ggagctgatg tcgcagaaaag cgtggcccag tttgcgagga ggccgccagcg tggggtttgt 360
 gtgatgagcg ggagtggctc tgtggcaaac gttaccctga gacaacctgc ggctccgggt 420
 gctgtttag cactccatgg caggtttgag atcttatccc taactggggc gttcctacct 480
 ggccctgctc ctccaggatc cactggtcta acagtgtatc tttctggagg acagggtcag 540
 gtagtgggag ggagtgtggt ggggtctcta gttgcagcag gaccagttat ggtcattgct 600
 gcaacttttg ctaatgcaac atatgagagg ttgccacttg atgatgatga tgagggacct 660
 agtggggccg ctacggcggc aagcggagga ggaagtggat cgtctcctcc acctggaatt 720
 ggaattggca gtggtggggg tcatcaactg caggctggac tggttccaga tccatcatcc 780
 atgccgttgt ataattctgcc accaaatctg ttgtccaatg gaggaggagg acaagtgggg 840
 catgatgctc ttgcttgggc tcatggaaga acaccttact ga 882

<210> 18
 <211> 293
 <212> PRT
 <213> Lotus japonicus

<400> 18
 Met Ala Asn Pro Trp Trp Thr Ser Gln Gly Gly Phe Ser Gly Val Asp
 1 5 10 15
 Pro Gly Thr His Ser Pro Gly Leu Ser Lys Arg His Thr Asp Leu Val
 20 25 30
 Ile Asn Glu Asn Ser Ser Gly Gly Asn Arg Asp Glu Asp Glu Asp Asp
 35 40 45
 Asn Arg Glu Asp Glu Pro Lys Glu Gly Ala Val Glu Val Gly Thr Arg
 50 55 60
 Arg Pro Arg Gly Arg Pro Pro Gly Ser Lys Asn Lys Pro Arg Pro Pro
 65 70 75 80
 Ile Phe Val Thr Arg Asp Ser Pro Asn Ala Leu Arg Ser His Val Met
 85 90 95
 Glu Val Ala Gly Gly Ala Asp Val Ala Glu Ser Val Ala Gln Phe Ala
 100 105 110
 Arg Arg Arg Gln Arg Gly Val Cys Val Met Ser Gly Ser Gly Ser Val
 115 120 125
 Ala Asn Val Thr Leu Arg Gln Pro Ala Ala Pro Gly Ala Val Val Ala

130		135		140
Leu His Gly Arg Phe Glu Ile Leu Ser Leu Thr Gly Ala Phe Leu Pro				
145		150		155
Gly Pro Ala Pro Pro Gly Ser Thr Gly Leu Thr Val Tyr Leu Ser Gly				160
		165		170
Gly Gln Gly Gln Val Val Gly Gly Ser Val Val Gly Ser Leu Val Ala				175
		180		185
Ala Gly Pro Val Met Val Ile Ala Ala Thr Phe Ala Asn Ala Thr Tyr				190
		195		200
Glu Arg Leu Pro Leu Asp Asp Asp Glu Gly Pro Ser Gly Ala Ala				205
		210		215
Thr Ala Ala Ser Gly Gly Ser Gly Ser Ser Pro Pro Pro Gly Ile				220
225		230		235
Gly Ile Gly Ser Gly Gly His Gln Leu Gln Ala Gly Leu Val Pro				240
		245		250
Asp Pro Ser Ser Met Pro Leu Tyr Asn Leu Pro Pro Asn Leu Leu Ser				255
		260		265
Asn Gly Gly Gly Gly Gln Val Gly His Asp Ala Leu Ala Trp Ala His				270
		275		280
Gly Arg Thr Pro Tyr				285
290				

<210> 19
 <211> 708
 <212> DNA
 <213> Oryza sativa

<400> 19	
atggcgtcca aggagccaag cggcgaccac gaccacgaga tgaacgggac cagcgccggg	60
ggcggcgagc ccaaggacgg cgcggtggtg accggcgcga accggcgccc ccgcggacgg	120
ccgccgggct ccaagaacaa gcccaagccg cccatcttcg tgacgcggga cagcccgaac	180
gcgctgcgca gccacgtcat ggaggtggcc ggcggcgcgg atgtcgccga gtccatcgcg	240
cacttcgcgc ggcggcgcca gcgcggcgctc tgcgtgctca gcggggccgg caccgtgacc	300
gacgtggccc tgcgccagcc ggccgcgcgg agcgccgtgg tggcgctccg tgggcggttc	360
gagatcctgt ccctgacggg gacgttctct cgggggcggg cgccgcgggg ctccaccggg	420
ctgaccgtgt acctcgccgg cgggcagggg caggtggtgg gcggcagcgt ggtggggacg	480
ctcaccgcgg cggggccggt catggtgatc gcctccacct tcgccaacgc cacctacgag	540
aggctgccgc tggatcagga ggaggaggaa gcagcggcag gcggcatgat ggcgcgcggc	600
ccactcatgg ccggcgccgc cgatccacta cttttcggcg ggggaatgca cgacgcgggg	660
cttgctgcat ggcaccatgc ccgccctccg ccgcgcggcg cctactag	708

<210> 20
 <211> 235
 <212> PRT
 <213> Oryza sativa

<400> 20	
Met Ala Ser Lys Glu Pro Ser Gly Asp His Asp His Glu Met Asn Gly	
1	5 10 15
Thr Ser Ala Gly Gly Gly Glu Pro Lys Asp Gly Ala Val Val Thr Gly	
	20 25 30
Arg Asn Arg Arg Pro Arg Gly Arg Pro Pro Gly Ser Lys Asn Lys Pro	
	35 40 45
Lys Pro Pro Ile Phe Val Thr Arg Asp Ser Pro Asn Ala Leu Arg Ser	
	50 55 60
His Val Met Glu Val Ala Gly Gly Ala Asp Val Ala Glu Ser Ile Ala	
65	70 75 80
His Phe Ala Arg Arg Arg Gln Arg Gly Val Cys Val Leu Ser Gly Ala	
	85 90 95

Gly Thr Val Thr Asp Val Ala Leu Arg Gln Pro Ala Ala Pro Ser Ala
 100 105 110
 Val Val Ala Leu Arg Gly Arg Phe Glu Ile Leu Ser Leu Thr Gly Thr
 115 120 125
 Phe Leu Pro Gly Pro Ala Pro Pro Gly Ser Thr Gly Leu Thr Val Tyr
 130 135 140
 Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly Ser Val Val Gly Thr
 145 150 155 160
 Leu Thr Ala Ala Gly Pro Val Met Val Ile Ala Ser Thr Phe Ala Asn
 165 170 175
 Ala Thr Tyr Glu Arg Leu Pro Leu Asp Gln Glu Glu Glu Ala Ala
 180 185 190
 Ala Gly Gly Met Met Ala Pro Pro Leu Met Ala Gly Ala Ala Asp
 195 200 205
 Pro Leu Leu Phe Gly Gly Gly Met His Asp Ala Gly Leu Ala Ala Trp
 210 215 220
 His His Ala Arg Pro Pro Pro Pro Pro Pro Tyr
 225 230 235

<210> 21
 <211> 801
 <212> DNA
 <213> *Oryza sativa*

<400> 21
 atgggcttgc cggagcagcc gtccggctcg tcgggcccga aggcggagct cccggtggcc 60
 aaggagccgg aggcgagccc gacggggggc gcggcggcgg accacgccga cgagaacaac 120
 gaatccggcg gcggcgagcc gcgggagggc gccgtggtgg cggcgcccaa ccggcgcccc 180
 cgcggccgcc cgccgggctc caagaacaag ccgaagccgc ccatcttcgt gacgcgcgac 240
 agccccaacg cgctgcgcag tcacgtcatg gaggtggccg gcggcgccga cgtcgccgac 300
 gccatcgcg agttctcgcg ccgcccagcg cgcgcgctct gcgtgctcag cggcgccggg 360
 acggtcgcca acgtcgcgct gcgccagccg tcggcgcccg gcgccgtcgt cgccctgcac 420
 ggccgcttcg agatcctctc cctcaccggc accttcctcc caggcccggc gcctccgggt 480
 tccacggggc tcaccgtcta cctcgccggc ggccagggcc aggttgctcg cggcagcgtc 540
 gtgggggtcg tcatcgccgc gggcccggtc atggtgatcg cgtccacgtt cgccaacgcc 600
 acctacgagc gcctgccact ggaggaagaa gaggagggt caggcccgcc catgcccggc 660
 ggcgccgagc ccctcatggc cggcggccac ggcacgcgcg acccttcggc gctgccaatg 720
 ttcaacctgc cgccgagcaa cgggctcggc ggcgcgcgcg acggcttccc atggcgcgcg 780
 caccctgcc caccgtactg a 801

<210> 22
 <211> 266
 <212> PRT
 <213> *Oryza sativa*

<400> 22
 Met Gly Leu Pro Glu Gln Pro Ser Gly Ser Ser Gly Pro Lys Ala Glu
 1 5 10 15
 Leu Pro Val Ala Lys Glu Pro Glu Ala Ser Pro Thr Gly Gly Ala Ala
 20 25 30
 Ala Asp His Ala Asp Glu Asn Asn Glu Ser Gly Gly Gly Glu Pro Arg
 35 40 45
 Glu Gly Ala Val Val Ala Ala Pro Asn Arg Arg Pro Arg Gly Arg Pro
 50 55 60
 Pro Gly Ser Lys Asn Lys Pro Lys Pro Pro Ile Phe Val Thr Arg Asp
 65 70 75 80
 Ser Pro Asn Ala Leu Arg Ser His Val Met Glu Val Ala Gly Gly Ala
 85 90 95
 Asp Val Ala Asp Ala Ile Ala Gln Phe Ser Arg Arg Arg Gln Arg Gly

			100						105					110			
Val	Cys	Val	Leu	Ser	Gly	Ala	Gly	Thr	Val	Ala	Asn	Val	Ala	Leu	Arg		
		115					120					125					
Gln	Pro	Ser	Ala	Pro	Gly	Ala	Val	Val	Ala	Leu	His	Gly	Arg	Phe	Glu		
		130				135					140						
Ile	Leu	Ser	Leu	Thr	Gly	Thr	Phe	Leu	Pro	Gly	Pro	Ala	Pro	Pro	Gly		
145					150					155					160		
Ser	Thr	Gly	Leu	Thr	Val	Tyr	Leu	Ala	Gly	Gly	Gln	Gly	Gln	Val	Val		
				165					170					175			
Gly	Gly	Ser	Val	Val	Gly	Ser	Leu	Ile	Ala	Ala	Gly	Pro	Val	Met	Val		
			180					185					190				
Ile	Ala	Ser	Thr	Phe	Ala	Asn	Ala	Thr	Tyr	Glu	Arg	Leu	Pro	Leu	Glu		
		195					200					205					
Glu	Glu	Glu	Gly	Ser	Gly	Pro	Pro	Met	Pro	Gly	Gly	Ala	Glu	Pro			
		210			215					220							
Leu	Met	Ala	Gly	Gly	His	Gly	Ile	Ala	Asp	Pro	Ser	Ala	Leu	Pro	Met		
225					230				235						240		
Phe	Asn	Leu	Pro	Pro	Ser	Asn	Gly	Leu	Gly	Gly	Gly	Gly	Asp	Gly	Phe		
				245				250						255			
Pro	Trp	Ala	Ala	His	Pro	Cys	Pro	Pro	Tyr								
			260					265									

<210> 23
 <211> 855
 <212> DNA
 <213> Populus tremuloides

<400> 23
 atggcaaacc ggtggtggac agggcaagtg ggattgccgg ggatggacac atcaaccagt 60
 tcatcatctc caatgaaaaa gccagatcta ggtatatcca tgtccaacaa caatagagaa 120
 gccaccgaga gtggtgctgg caaagaagat gagcaagaag acgaaagaga aaatagcgac 180
 gagcctagag aaggcgctat agatatcgcc tctcgccgcc ctagaggccg tccaccaggg 240
 tccaagaaca agcctaagcc accaattttc gttactcgag acagccctaa tgcactcaag 300
 agtcatgtga tggagatagc tagtggatct gatatagctg aaaatttagc ttgttttgca 360
 aggaagagac aaagaggagt ttgtgtgctt agtggaaagt gtatggtaac caatgtaacc 420
 ctcaagcaac cttctgcctc aggtgctggt atggctctcc atggtaggtt tgagattttg 480
 tctactactg gagcgttctt gcctggacca gccccacctg gagcgacagg actaactata 540
 tatttagccg gagggcaagg acaagtggta ggaggcagt tggtaggatc actagttgca 600
 tcaggaccgg taatggttat tgctgcaaca ttttcaaata ctacttatga gagattgcca 660
 ctagaagatg aagaggaagg cagtgggtgg gcacaagggc agctcgggtg cggcaacggg 720
 agcgggtgagg gtaatggtgg gggcatgggg gatccagcaa catcaatgcc agtttatcaa 780
 ttgccaaata tggatgcctaa tggacaattg aaccatgaag gatatgggtg ggctcacggc 840
 agaccaccct attag 855

<210> 24
 <211> 284
 <212> PRT
 <213> Populus tremuloides

<400> 24
 Met Ala Asn Arg Trp Trp Thr Gly Gln Val Gly Leu Pro Gly Met Asp
 1 5 10 15
 Thr Ser Thr Ser Ser Ser Ser Pro Met Lys Lys Pro Asp Leu Gly Ile
 20 25 30
 Ser Met Ser Asn Asn Asn Arg Glu Ala Thr Glu Ser Gly Ala Gly Lys
 35 40 45
 Glu Asp Glu Gln Glu Asp Glu Arg Glu Asn Ser Asp Glu Pro Arg Glu
 50 55 60
 Gly Ala Ile Asp Ile Ala Ser Arg Arg Pro Arg Gly Arg Pro Pro Gly

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

<210> 25
 <211> 885
 <212> DNA
 <213> Solanum tuberosum

<400> 25	
atgtcaaacc	catggtggac
aggccaagta	ggtttacaag
gagttgaaac	atcatcatcc
gcggttgcg	cttctctcaa
gaagccagat	ctaggcgtat
caatgaacga	tatagtgggt
ggtagtggtg	gtcatgatga
agatagggac	catagcgacg
accctaaaga	gggtgcagtc
gaagtagcca	ctcgtcgacc
cagaggtcga	ccagctggct
caaagaacaa	acctaaacca
ccaatatattg	ttacaaggga
tagccctaac	gcacttagaa
gccacgtaat	ggaagttgct
aatggagctg	atgtggcgga
aagtatagct	caatttgcta
ggaaaagaca	aagaggtggt
tgtgttttga	gtgctactgg
aactgttact	aatgtaaccc
taagacaacc	atctgtcct
ggagctgtca	tggcattaca
cggccgggttc	gagatcttat
cgttgaccgg	agctttctta
cctggaccgg	cccctcctgg
atcaacaggg	ttgactatat
acctagcagg	aggacaagga
caagttgtgg	gaggaagtgt
agtagggtct	ttagtggctt
ccggaccagt	tatggtaatt
gcatcaactt	tttttaaatgc
aacatatgag	aggctacctt
tggaggagga	ggaagaaggc
gggtggaacgg	tggcccaagg
acaacttggt	gggtggtgat
cgccaccggg	aatgggagga
agtgggtggtg	gtggtggagg
acaacaacaa	caaggtggtg
gtggtatggg	tgatattcca
tcatcaaata	tgccagtata
taatttgcca	ccaaatttgc
taccaaatgg	tggacaaatg
aacctgaag	catttggttg
ggcacatgga	cgccttcctt
tttaa	

<210> 26
 <211> 294
 <212> PRT
 <213> Solanum tuberosum

<400> 26	
Met	Ser
Asn	Pro
Trp	Trp
Thr	Gly
Gln	Val
Gly	Leu
Gln	Gly
Val	Glu
1	5
10	15
Thr	Ser
Ser	Ser
Ala	Gly
Ser	Pro
Ser	Leu
Lys	Lys
Pro	Asp
Leu	Gly

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<210> 28
 <211> 312
 <212> PRT
 <213> *Thlaspi caerulescens*

<400> 28
 Met Ala Asn Pro Trp Trp Thr Gly Gln Val Asn Leu Ser Gly Leu Glu
 1 5 10 15
 Thr Thr Pro Pro Gly Ser Ser Gln Leu Lys Lys Ser Asp Leu His Ile
 20 25 30
 Ser Met Asn Met Ala Met Asp Ser Gly His Asn Asn His His His
 35 40 45
 Gln Glu Val Asp Asn Asn Asn Asn Asp Asp Asp Arg Asp Asn Leu
 50 55 60
 Ser Gly Asp Glu His Glu Pro Arg Glu Gly Ala Val Glu Ala Pro Thr
 65 70 75 80
 Arg Arg Pro Arg Gly Arg Pro Ala Gly Ser Lys Asn Lys Pro Lys Pro
 85 90 95
 Pro Ile Phe Val Thr Arg Asp Ser Pro Asn Ala Leu Lys Ser His Val
 100 105 110
 Met Glu Ile Ala Ser Gly Thr Asp Val Ile Glu Thr Leu Ala Thr Phe
 115 120 125
 Ala Arg Arg Arg Gln Arg Gly Ile Cys Ile Leu Ser Gly Asn Gly Thr
 130 135 140
 Val Ala Asn Val Thr Leu Arg Gln Pro Ser Ser Ala Ala Val Ala Ala
 145 150 155 160
 Ala Pro Gly Gly Ala Ala Val Leu Ala Leu Gln Gly Arg Phe Glu Ile
 165 170 175
 Leu Ser Leu Thr Gly Ser Phe Leu Pro Gly Pro Ala Pro Pro Gly Ser
 180 185 190
 Thr Gly Leu Thr Ile Tyr Leu Ala Gly Gly Gln Gly Gln Val Val Gly
 195 200 205
 Gly Ser Val Val Gly Pro Leu Met Ala Ala Gly Pro Val Met Leu Ile
 210 215 220
 Ala Ala Thr Phe Ser Asn Ala Thr Tyr Glu Arg Leu Pro Leu Glu Glu
 225 230 235 240
 Glu Glu Ala Ala Glu Arg Gly Gly Gly Gly Gly Ser Val Pro Gly Gln
 245 250 255
 Leu Gly Gly Gly Gly Ser Pro Leu Ser Ser Gly Gly Gly Gly Gly Asp
 260 265 270
 Gly Asn Gln Gly Leu Pro Val Tyr Asn Met Pro Gly Asn Leu Val Ser
 275 280 285
 Asn Gly Gly Gly Gly Gly Gly Gln Met Ser Gly Gln Glu Ala Tyr Gly
 290 295 300
 Trp Ala Gln Ala Arg Ser Gly Phe
 305 310

<210> 29
 <211> 876
 <212> DNA
 <213> *Vitis vinifera*

<400> 29
 atggcgaaacc ggtggtgggc tgggcaggtg ggtctgcaag gtgtagatac ctcacagct 60
 tcacctgcaa tgaagaaacc agatctggga atatccatga atgaaaatgg aggaagcggg 120
 agcggaggcg gaggagagga agaagaggaa aaagaaaaca gtgatgagcc cagagagggt 180
 gcaattgagg tggctacgcg caggcctagg ggccggccgc ctggctccaa gaacaagcca 240
 aaacctccga tttttgtgac aaggacagc cctaacgctc tgcgcagcca cgttatggag 300
 gtggcacaacg gctccgacat cacagaaagc atagcccaat tcgcgagaag gcggcaacga 360

ggcgtctgcg	tgctcagcgc	aagtgggaca	gtcatgaacg	taacgcttcg	ccagccttct	420
gcccctggtg	gtgcagttat	ggcacttcat	ggccgattcg	aaattctttc	cttaaccggc	480
gcgttcctac	cgggaccagc	gccaccaggc	tccactggac	taaccatata	cctagcaggc	540
ggtcaagctc	aggtcgtggg	tggtagcgtg	gtgggttcac	tcatagcggc	aggtccagtt	600
atggtgattg	cagctacctt	ttcgaatgca	acctacgaga	ggctccccct	agaagacgaa	660
gaagagggcg	gcagcgcagc	acaggagcag	ctcgctggcg	gcggaggcgg	tggtgggtca	720
ccgccaggga	ttggcggcag	tggggggcag	cagcaggcag	ggatggcaga	tccttcctcc	780
atgccgggtt	ataatttgcc	accaaatttg	cttccaaatg	gtggacaact	gaaccatgat	840
gcttatgggt	gggcacatgg	gcgccagcct	tactag			876

<210> 30
 <211> 291
 <212> PRT
 <213> Vitis vinifera

<400> 30
 Met Ala Asn Arg Trp Trp Ala Gly Gln Val Gly Leu Gln Gly Val Asp
 1 5 10 15
 Thr Ser Ser Ala Ser Pro Ala Met Lys Lys Pro Asp Leu Gly Ile Ser
 20 25 30
 Met Asn Glu Asn Gly Gly Ser Gly Ser Gly Gly Gly Gly Glu Glu Glu
 35 40 45
 Glu Glu Lys Glu Asn Ser Asp Glu Pro Arg Glu Gly Ala Ile Glu Val
 50 55 60
 Ala Thr Arg Arg Pro Arg Gly Arg Pro Pro Gly Ser Lys Asn Lys Pro
 65 70 75 80
 Lys Pro Pro Ile Phe Val Thr Arg Asp Ser Pro Asn Ala Leu Arg Ser
 85 90 95
 His Val Met Glu Val Ala Asn Gly Ser Asp Ile Thr Glu Ser Ile Ala
 100 105 110
 Gln Phe Ala Arg Arg Arg Gln Arg Val Cys Val Leu Ser Ala Ser
 115 120 125
 Gly Thr Val Met Asn Val Thr Leu Arg Gln Pro Ser Ala Pro Gly Gly
 130 135 140
 Ala Val Met Ala Leu His Gly Arg Phe Glu Ile Leu Ser Leu Thr Gly
 145 150 155 160
 Ala Phe Leu Pro Gly Pro Ala Pro Pro Gly Ser Thr Gly Leu Thr Ile
 165 170 175
 Tyr Leu Ala Gly Gly Gln Ala Gln Val Val Gly Gly Ser Val Val Gly
 180 185 190
 Ser Leu Ile Ala Ala Gly Pro Val Met Val Ile Ala Ala Thr Phe Ser
 195 200 205
 Asn Ala Thr Tyr Glu Arg Leu Pro Leu Glu Asp Glu Glu Glu Ala Gly
 210 215 220
 Ser Ala Ala Gln Glu Gln Leu Ala Gly Gly Gly Gly Gly Gly Ser
 225 230 235 240
 Pro Pro Gly Ile Gly Gly Ser Gly Gly Gln Gln Ala Gly Met Ala
 245 250 255
 Asp Pro Ser Ser Met Pro Val Tyr Asn Leu Pro Pro Asn Leu Leu Pro
 260 265 270
 Asn Gly Gly Gln Leu Asn His Asp Ala Tyr Gly Trp Ala His Gly Arg
 275 280 285
 Gln Pro Tyr
 290

<210> 31
 <211> 783
 <212> DNA
 <213> Vitis vinifera

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<400> 31
atggaccccg cagctgtttc gccgatgcta aataaacgcg atcgcgagat atcaatcaac 60
gataaccccg gcacaggaga cgatgaagaa gagaaagaca acgaaggcga gcccacggag 120
ggtgcagtag aagtcggcac tcgtagacca agaggtcgcc cgcctggatc caaaaacaag 180
cccaaaccac ctattttcgt cacgcgcgac agcccgaacg cccttcggag ccacgtgatg 240
gaggtggccg gcggccacga cgttgccgaa agcgtcgccc agttcgcccc taggcgtcaa 300
cgaggggtct gcgtcctcag cggcagcggc tccgtagcca acgtgactct gagacagccc 360
gccgcgcctg gcgccgtggt ggcactccat ggaagattcg agattctgtc cctaacagga 420
gcattcctcc ccggacctgc ccctcccggc tccactggac tcaccgtgta cctcgccgga 480
ggtcagggcc aggttgtggg aggaagtgtg gttggatcac tggtagcggc aggcccgggtg 540
atagtgatag ccgccacttt tgcgaacgca acatacgaag gactgcctct ggaagaagaa 600
gaagaaggtg ggcaggcgcc gccgccgagt ggttcgccgc ctgcaattgg aagcagtggg 660
ggacagcatc actctggcct gccggagctg cccatataca atctgccacc gaacctactc 720
cctaacggcg gcccaattgag tcatgacccc tactcatggg ctcatgctcg gcccccttac 780
tga 783

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<210> 32
<211> 260
<212> PRT
<213> Vitis vinifera

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<400> 32
Met Asp Pro Ala Ala Val Ser Pro Met Leu Asn Lys Arg Asp Arg Glu
1 5 10 15
Ile Ser Ile Asn Asp Asn Pro Gly Thr Gly Asp Asp Glu Glu Glu Lys
20 25 30
Asp Asn Glu Gly Glu Pro Thr Gly Ala Val Glu Val Gly Thr Arg
35 40 45
Arg Pro Arg Gly Arg Pro Pro Gly Ser Lys Asn Lys Pro Lys Pro Pro
50 55 60
Ile Phe Val Thr Arg Asp Ser Pro Asn Ala Leu Arg Ser His Val Met
65 70 75 80
Glu Val Ala Gly Gly His Asp Val Ala Glu Ser Val Ala Gln Phe Ala
85 90 95
Arg Arg Arg Gln Arg Gly Val Cys Val Leu Ser Gly Ser Gly Ser Val
100 105 110
Ala Asn Val Thr Leu Arg Gln Pro Ala Ala Pro Gly Ala Val Val Ala
115 120 125
Leu His Gly Arg Phe Glu Ile Leu Ser Leu Thr Gly Ala Phe Leu Pro
130 135 140
Gly Pro Ala Pro Pro Gly Ser Thr Gly Leu Thr Val Tyr Leu Ala Gly
145 150 155 160
Gly Gln Gly Gln Val Val Gly Gly Ser Val Val Gly Ser Leu Val Ala
165 170 175
Ala Gly Pro Val Ile Val Ile Ala Ala Thr Phe Ala Asn Ala Thr Tyr
180 185 190
Glu Arg Leu Pro Leu Glu Glu Glu Gly Gly Gln Ala Pro Pro
195 200 205
Pro Ser Gly Ser Pro Pro Ala Ile Gly Ser Ser Gly Gly Gln His His
210 215 220
Ser Gly Leu Pro Glu Leu Pro Ile Tyr Asn Leu Pro Pro Asn Leu Leu
225 230 235 240
Pro Asn Gly Gly Gln Leu Ser His Asp Pro Tyr Ser Trp Ala His Ala
245 250 255
Arg Pro Pro Tyr
260

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<210> 33

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<211> 810
 <212> DNA
 <213> Zea mays

<400> 33
 atggcacctt cctccaagga cggcgccacc gccaccgagc agccgacgag cggcgacgac 60
 gaccgggaga acggcggcac gggcgagccc aaggaaggcg cgggtggtggc gggcaaccgg 120
 cgcccccgcg ggcggccgcc ggggtccaag aacaagccca agccgcccac cttcgtgacg 180
 cgcgacagcc ccaacgcgct gcgcagccac gtgatggagg tggccggcgg cgccgacgtg 240
 gccgagtcca tcgcccactt cgcgcgccgc aggcagcgcg gcgtgtgcgt gctcagcggc 300
 gcgggcaccg tcgccgacgt ggcgctccgc cagcccgcgg ctccggggcg cgtggtcgcc 360
 ctccgcggcc gcttcgagat cctctcgctc accggcacgt tcctgccggg ccccgcgccg 420
 ccgggctcca cggggctcac cgtgtacctc gcgggcggcc aggggcaggt cgtcggcggc 480
 agcgtcgctc gcacgctcac cgcggcgggg cccgtcatgg tgatggcgtc cacgttcgcc 540
 aacgccacct acgagaggct gccgctggac gacgccgacg aggagcccgc cgggcagcag 600
 gcggcgcgacg tgcctcccgg accgggcgga gggcagccta tggtaatggg cgggatggcc 660
 gaccctcag cggtgccaat gttcggcggc gccggcggtg tgccgccaag cctcatgcca 720
 gcaggggccc cagccgcctc ctccggtgcg ggctgcagc tcgggcacga ccgacttgca 780
 tgggctcatg cacggccacc gccatactag 810

<210> 34
 <211> 269
 <212> PRT
 <213> Zea mays

<400> 34
 Met Ala Pro Ser Ser Lys Asp Gly Ala Thr Ala Thr Glu Gln Pro Thr
 1 5 10 15
 Ser Gly Asp Asp Arg Glu Asn Gly Gly Thr Gly Glu Pro Lys Glu
 20 25 30
 Gly Ala Val Val Ala Gly Asn Arg Arg Pro Arg Gly Arg Pro Pro Gly
 35 40 45
 Ser Lys Asn Lys Pro Lys Pro Pro Ile Phe Val Thr Arg Asp Ser Pro
 50 55 60
 Asn Ala Leu Arg Ser His Val Met Glu Val Ala Gly Gly Ala Asp Val
 65 70 75 80
 Ala Glu Ser Ile Ala His Phe Ala Arg Arg Arg Gln Arg Gly Val Cys
 85 90 95
 Val Leu Ser Gly Ala Gly Thr Val Ala Asp Val Ala Leu Arg Gln Pro
 100 105 110
 Ala Ala Pro Gly Ala Val Val Ala Leu Arg Gly Arg Phe Glu Ile Leu
 115 120 125
 Ser Leu Thr Gly Thr Phe Leu Pro Gly Pro Ala Pro Pro Gly Ser Thr
 130 135 140
 Gly Leu Thr Val Tyr Leu Ala Gly Gly Gln Gly Gln Val Val Gly Gly
 145 150 155 160
 Ser Val Val Gly Thr Leu Thr Ala Ala Gly Pro Val Met Val Met Ala
 165 170 175
 Ser Thr Phe Ala Asn Ala Thr Tyr Glu Arg Leu Pro Leu Asp Asp Ala
 180 185 190
 Asp Glu Glu Pro Ala Gly Gln Gln Ala Ala Gln Leu Pro Pro Gly Pro
 195 200 205
 Gly Gly Gly Gln Pro Met Val Met Gly Gly Met Ala Asp Pro Ser Ala
 210 215 220
 Val Pro Met Phe Gly Gly Ala Gly Gly Val Pro Pro Ser Leu Met Pro
 225 230 235 240
 Ala Gly Ala Ala Ala Ala Ser Ser Gly Ala Gly Leu Gln Leu Gly His
 245 250 255
 Asp Arg Leu Ala Trp Ala His Ala Arg Pro Pro Pro Tyr

260

265

<210> 35
 <211> 2194
 <212> DNA
 <213> *Oryza sativa*

<400> 35
 aatccgaaaa gtttctgcac cgttttcacc ccctaactaa caatataggg aacgtgtgct 60
 aaatataaaa tgagacctta tatatgtagc gctgataact agaactatgc aagaaaaact 120
 catccaccta ctttagtggt aatcgggcta aataaaaaag agtcgctaca ctagtttcgt 180
 tttccttagt aattaagtgg gaaaatgaaa tcattattgc ttagaatata cgttcacatc 240
 tctgtcatga agttaaatta ttcgaggtag ccataattgt catcaaactc ttcttgaata 300
 aaaaaatcctt tctagctgaa ctcaatgggt aaagagagag atttttttta aaaaaataga 360
 atgaagatat tctgaacgta ttggcaaaga tttaaacata taattatata attttatagt 420
 ttgtgcattc gtcatatcgc acatcattaa ggacatgtct tactccatcc caatttttat 480
 ttagtaatta aagacaattg acttattttt attattttatc ttttttcgat tagatgcaag 540
 gtacttacgc acacactttg tgctcatgtg catgtgtgag tgcacctcct caatacacgt 600
 tcaactagca acacatctct aatatcactc gcctatttta tacatttagg tagcaatatc 660
 tgaattcaag cactccacca tcaccagacc acttttaata atatctaaaa taaaaaaat 720
 aattttacag aatagcatga aaagtatgaa acgaactatt taggtttttc acatacaaaa 780
 aaaaaaagaa ttttgctcgt gcgcgagcgc caatctccca tattgggcac acaggcaaca 840
 acagagtggc tgcccacaga acaaccaca aaaaacgatg atctaacgga ggacagcaag 900
 tccgcaacaa ccttttaaca gcaggctttg cggccaggag agaggaggag aggcaaagaa 960
 aaccaagcat cctccttctc ccattctataa attcctcccc cttttcccc tctctatata 1020
 ggaggcatcc aagccaagaa gagggagagc accaaggaca cgcgactagc agaagccgag 1080
 cgaccgcctt ctcgatccat atcttcgggt cgagttcctg gtcgatctct tccctcctcc 1140
 acctcctcct cacagggtat gtgcctccct tcggttggtc ttggatttat tgttctaggt 1200
 tgtgtagtac gggcgttgat gttaggaaag gggatctgta tctgtgatga ttctgttct 1260
 tggatttggg atagaggggt tcttgatgtt gcatgttatt ggttcggttt gattagtagt 1320
 atggttttca atcgtctgga gagctctatg gaaatgaaat ggtttaggga tcggaatcct 1380
 gcgattttgt gagtaccttt tgtttgaggt aaaatcagag caccggtgat tttgcttgg 1440
 gtaataaagt acggttggtt ggtcctcgat tctggtagt atgcttctcg atttgacgaa 1500
 gctatccttt gtttattccc tattgaacaa aaataatcca actttgaaga cgggtccggt 1560
 gatgagattg aatgattgat tcttaagcct gtccaaaatt tcgcagctgg cttgtttaga 1620
 tacagtagtc cccatcacga aattcatgga aacagttata atcctcagga acaggggatt 1680
 ccctgttctt ccgatttgct ttagtcccag aatttttttt cccaaatatc ttaaaaagtc 1740
 actttctggt tcagttcaat gaattgattg ctacaaataa tgcttttata gcgttatcct 1800
 agctgtagtt cagttaatag gtaatacccc tatagtttag tcaggagaag aacttatccg 1860
 atttctgata tccattttta attatatgaa atgaactgta gcataagcag tattcatttg 1920
 gattattttt tttattagct ctcacccctt cattattctg agctgaaagt ctggcatgaa 1980
 ctgtcctcaa ttttgttttc aaattcacat cgattatcta tgcattatcc tcttgtatct 2040
 acctgtagaa gtttcttttt ggttattcct tgactgcttg attacagaaa gaaatttatg 2100
 aagctgtaat cgggatagtt atactgcttg ttcttatgat tcatttcctt tgtgcagttc 2160
 ttggtgtagc ttgccacttt caccagcaaa gttc 2194

<210> 36
 <211> 173
 <212> PRT
 <213> Artificial sequence

<220>
 <223> conserved domain comprised in SEQ ID NO: 2

<400> 36
 Glu Pro Arg Glu Gly Ala Val Glu Ala Pro Thr Arg Arg Pro Arg Gly
 1 5 10 15
 Arg Pro Ala Gly Ser Lys Asn Lys Pro Lys Pro Pro Ile Phe Val Thr
 20 25 30

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

<210> 37
 <211> 14
 <212> PRT
 <213> Artificial sequence

<220>
 <223> AT hook

<220>
 <221> VARIANT
 <222> (8)..(8)
 <223> /replace ="Ala"

<220>
 <221> VARIANT
 <222> (11)..(11)
 <223> /replace ="Arg"

<400> 37
 Arg Arg Pro Arg Gly Arg Pro Pro Gly Ser Lys Asn Lys Pro
 1 5 10

<210> 38
 <211> 125
 <212> PRT
 <213> Artificial sequence

<220>
 <223> PPC domain (DUF296) comprised in SEQ ID NO: 2

<400> 38
 Leu Lys Ser His Val Met Glu Ile Ala Ser Gly Thr Asp Val Ile Glu
 1 5 10 15
 Thr Leu Ala Thr Phe Ala Arg Arg Arg Gln Arg Gly Ile Cys Ile Leu
 20 25 30
 Ser Gly Asn Gly Thr Val Ala Asn Val Thr Leu Arg Gln Pro Ser Thr
 35 40 45
 Ala Ala Val Ala Ala Ala Pro Gly Gly Ala Ala Val Leu Ala Leu Gln
 50 55 60
 Gly Arg Phe Glu Ile Leu Ser Leu Thr Gly Ser Phe Leu Pro Gly Pro

65		70		75		80									
Ala	Pro	Pro	Gly	Ser	Thr	Gly	Leu	Thr	Ile	Tyr	Leu	Ala	Gly	Gly	Gln
			85						90					95	
Gly	Gln	Val	Val	Gly	Gly	Ser	Val	Val	Gly	Pro	Leu	Met	Ala	Ala	Gly
			100						105					110	
Pro	Val	Met	Leu	Ile	Ala	Ala	Thr	Phe	Ser	Asn	Ala	Thr			
		115					120					125			

<210> 39
 <211> 52
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer: prm8135

<400> 39
 ggggacaagt ttgtacaaaa aagcaggctt aaacaatggc gaatccatgg tg 52

<210> 40
 <211> 50
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer: prm8136

<400> 40
 ggggaccact ttgtacaaga aagctgggtt aaaaaccatt ttaacgcacg 50

<210> 41
 <211> 948
 <212> DNA
 <213> Brassica oleracea

<400> 41
 atgcgaaaatc catggtggac aggacaagtg aatctctcca gtctcgaaac gacgccgccg 60
 agttcctctc agttaaaagac accagatctc cacatctcca tgaacatggc catggtctca 120
 ggtcataaca accaccatca tcatcaccaa gaagtcaaca ccaacaacaa caacgaagac 180
 gatagagaca acttgagcgg cgacgaccgc gagccacgtg aaggagccgt ggaagctccc 240
 acgcgccgac cacgtggacg tcctgctggt tccaagaaca aaccaaagcc accaatcttt 300
 gtcacgcgtg attctccaaa cgctctcaag agccatgtca tggagatcgc tagtgggact 360
 gatgtcatag aaaccctagc tactttcgct aggcgggcgc aacgtggcat ctgcatcttg 420
 agcggtaacg gcacggtggc taacgtcaca ctccgtcaac catcagtggc tccggttgca 480
 gctgcccctg gtggtgcggc tgtattggcg ttacaaggga ggtttgagat tctttctcta 540
 accggttctt tcttacctgg accggctcca cctggatcca ctggtttaac tatttactta 600
 gctggtggtc aaggtcaggt tggtggagga agcgtgggtg gggcattgat ggctgctggt 660
 ccggtgatgc taatcgctgc cacgttttct aatgcgactt atgagagatt acctttggat 720

gaggaagaag	cggctgaaag	aggtggcggg	ggaagcgacg	gaggagtggg	tccagggcag	780
ctcggggg	taggttcccc	gctgagtagt	ggtggcggg	gaggccacgg	gaaccaagga	840
cttcccgcat	ataatatgcc	cggaacctt	gcttctaata	gcggtggagg	aggacagatg	900
agcagccaag	aagcgtacgg	ttgggctcaa	gctaggtcag	gatttttaa		948

<210> 42

<211> 315

<212> PRT

<213> Brassica oleracea

<400> 42

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

Gly Gly Ser Val Val Gly Ala Leu Met Ala Ala Gly Pro Val Met Leu
 210 215 220
 Ile Ala Ala Thr Phe Ser Asn Ala Thr Tyr Glu Arg Leu Pro Leu Asp
 225 230 235 240
 Glu Glu Glu Ala Ala Glu Arg Gly Gly Gly Gly Ser Asp Gly Gly Val
 245 250 255
 Val Pro Gly Gln Leu Gly Gly Val Gly Ser Pro Leu Ser Ser Gly Gly
 260 265 270
 Gly Gly Gly His Gly Asn Gln Gly Leu Pro Ala Tyr Asn Met Pro Gly
 275 280 285
 Asn Leu Ala Ser Asn Gly Gly Gly Gly Gly Gln Met Ser Ser Gln Glu
 290 295 300
 Ala Tyr Gly Trp Ala Gln Ala Arg Ser Gly Phe
 305 310 315

<210> 43
 <211> 918
 <212> DNA
 <213> *Medicago truncatula*

<400> 43
 atggcgaaaca ggtggtggac cggaccggtt ggtctaggag ggatggacaa ctacagtaacc 60
 tcctctccac taggaaaacc ggatctgggt ttctccatga atcaaagtgc tgtaacagga 120
 gtgaacaaca tgaacaacaa caacaatgaa gaagaagaag atgagaaaga aaacagcgac 180
 gaacacaaag gaggtgcaat agaaacaaac acctccacgc gccgccaag aggccgtcca 240
 tcaggttcaa aaaacaaacc aaaaccacca atattcataa caagagatag ccctaacgcg 300
 ctacgaagcc atgtcatgga agtagcaaca ggaacagata tatcagatag catcgttcag 360
 tttgcaagaa aaagacagag aggtatttgc attctaagcg caagtgaac cgtcgttaac 420
 gtttctctcc ggcaacctac aggtcccgga gctgtggtag cgcttcagg gagatttgat 480
 atactctctt tgactggttc tgtgcttcct ggaccttcac cgccgggagc tactggtttg 540
 actatttatc tttctggagg acaaggacag gtggttggcg gcggagttgt tgggtcccctt 600
 gtggcggcag gaccagttat gttgatggcg gcgacatttt cgaatgctac gtatgagagg 660
 ctgccggttg aggatggtga tgatcaagaa gggcatcagg gtggtggtgg tgatgatgag 720
 tctccgacgc gtgcagcggg gatgggacag ttagcgattg gatctgttgg agaaggttct 780
 tcaattccac caggctataa caatgttggg ggtaatttgg gtgtttcaaa tggaggacaa 840
 caacaattgt tgaataatca tgaggcttat aataattctc cttgggggtca tgctagtcac 900
 ggtagaccac catactaa 918

<210> 4
 <211> 305
 <212> PRT
 <213> Medicago truncatula
 <400> 44

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Met Ala Asn Arg Trp Trp Thr Gly Pro Val Gly Leu Gly Gly Met Asp
1           5           10           15
Asn Ser Val Thr Ser Ser Pro Leu Gly Lys Pro Asp Leu Gly Phe Ser
          20           25           30
Met Asn Gln Ser Ala Val Thr Gly Val Asn Asn Met Asn Asn Asn Asn
          35           40           45
Asn Glu Glu Glu Glu Asp Glu Lys Glu Asn Ser Asp Glu His Lys Gly
          50           55           60
Gly Ala Ile Glu Thr Asn Thr Ser Thr Arg Arg Pro Arg Gly Arg Pro
65           70           75           80
Ser Gly Ser Lys Asn Lys Pro Lys Pro Pro Ile Phe Ile Thr Arg Asp
          85           90           95
Ser Pro Asn Ala Leu Arg Ser His Val Met Glu Val Ala Thr Gly Thr
          100          105          110
Asp Ile Ser Asp Ser Ile Val Gln Phe Ala Arg Lys Arg Gln Arg Gly
          115          120          125
Ile Cys Ile Leu Ser Ala Ser Gly Thr Val Val Asn Val Ser Leu Arg
          130          135          140
Gln Pro Thr Gly Pro Gly Ala Val Val Ala Leu Pro Gly Arg Phe Asp
145          150          155          160
Ile Leu Ser Leu Thr Gly Ser Val Leu Pro Gly Pro Ser Pro Pro Gly
          165          170          175
Ala Thr Gly Leu Thr Ile Tyr Leu Ser Gly Gly Gln Gly Gln Val Val
          180          185          190
Gly Gly Gly Val Val Gly Pro Leu Val Ala Ala Gly Pro Val Met Leu
          195          200          205
Met Ala Ala Thr Phe Ser Asn Ala Thr Tyr Glu Arg Leu Pro Val Glu
          210          215          220
Asp Gly Asp Asp Gln Glu Gly His Gln Gly Gly Gly Gly Asp Asp Glu
225          230          235          240
Ser Pro Thr Arg Ala Ala Gly Met Gly Gln Leu Ala Ile Gly Ser Val

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245 250 255
 Gly Glu Gly Ser Ser Ile Pro Pro Gly Tyr Asn Asn Val Gly Gly Asn
 260 265 270
 Leu Gly Val Ser Asn Gly Gly Gln Gln Gln Leu Leu Asn Asn His Glu
 275 280 285
 Ala Tyr Asn Asn Ser Pro Trp Gly His Ala Ser His Gly Arg Pro Pro
 290 295 300
 Tyr
 305

<210> 45
 <211> 632
 <212> DNA
 <213> Arabidopsis thaliana

<400> 45
 gcagttccct actctcgcgt taacgctagc atggatctcg ggccccaaat aatgatttta 60
 ttttgactga tagtgacctg ttcgttgcaa caaattgatg agcaatgctt ttttataatg 120
 ccaactttgt acaaaaaagc aggccttcaca atgtccttgct gtggaggaaa ctgcggatgt 180
 ggatctggct gcaagtgcgg caacggttgt ggaggttgca aaatgtaccc tgacttgga 240
 ttctccggcg agacaaccac aactgagact tttgtcttg gcggtgcacc ggcgatgaag 300
 aatcagtacg aggcttcagg ggagagtaac aacgctgaga acgatgcttg caagtgtgga 360
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<210> 46
 <211> 81
 <212> PRT
 <213> Arabidopsis thaliana

<400> 46
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 65 70 75 80
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<210> 47
 <211> 2194
 <212> DNA
 <213> Oryza sativa

<400> 47
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aaaaaatctt	tctagctgaa	ctcaatgggt	aaagagagag	atTTTTTTTt	aaaaaataga	360
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gtacttacgc	acacactttg	tgctcatgtg	catgtgtgag	tgcacctcct	caatacacgt	600
tcaactagca	acacatctct	aatatcactc	gcctatttta	tacatttagg	tagcaatatc	660
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 <211> 53
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer: prm03240

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<210> 49
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 <213> Artificial sequence

<220>
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<210> 50
 <211> 1566
 <212> DNA
 <213> Chlamydomonas reinhardtii

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 gccaagcccc tgaccttcac ccgtcagggtg ctagccctgt gcgccgcgcc cttcctgctg 360
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 ggcttcggcc aggaggaggg caccttcac ctgcgcacca ccattctgcc tcgcgaggag 1500
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<210> 51
 <211> 521
 <212> PRT
 <213> Chlamydomonas reinhardtii

<400> 51
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 35 40 45
 Lys Glu Gly Lys Val Leu His Pro His Leu Leu Asn Glu Asn Val Val
 50 55 60
 Lys Thr Gln Tyr Ala Val Arg Gly Glu Leu Tyr Leu Arg Ala Glu Gln
 65 70 75 80
 Leu Arg Lys Glu Gly Lys Glu Ile Ile Phe Thr Asn Val Gly Asn Pro
 85 90 95
 His Ala Leu Gly Ala Lys Pro Leu Thr Phe Thr Arg Gln Val Leu Ala
 100 105 110
 Leu Cys Ala Ala Pro Phe Leu Leu Asp His Pro Lys Val Glu Asp Met
 115 120 125
 Phe Pro Ala Asp Ala Ile Ala Arg Ala Lys Lys Ile Leu Ala Ser Phe
 130 135 140

Lys Gly Gly Val Gly Ala Tyr Thr Asp Ser Arg Gly Asn Pro Leu Val
 145 150 155 160
 Arg Glu Glu Val Ala Arg Phe Ile Glu Lys Arg Asp Gly Val Pro Ser
 165 170 175
 Asn Pro Asp His Ile Phe Leu Thr Asp Gly Ala Ser Val Ala Val Arg
 180 185 190
 Leu Cys Leu Asn Ala Met Ile Arg His Asp Arg Asp Ser Val Leu Val
 195 200 205
 Pro Ile Pro Gln Tyr Pro Leu Tyr Ser Ala Ser Ile Arg Leu Tyr Gly
 210 215 220
 Gly Thr Leu Val Gly Tyr Phe Leu Asp Glu Arg Arg Gly Trp Gly Leu
 225 230 235 240
 Ser Val Glu Glu Leu Gln Arg Ala Leu Gln Glu Ala Arg Glu Glu Gly
 245 250 255
 Lys Leu Val Arg Gly Leu Val Phe Ile Asn Pro Gly Asn Pro Thr Gly
 260 265 270
 Gln Cys Leu Ser Lys Glu Asn Leu Gln Glu Leu Ile Lys Phe Ala Tyr
 275 280 285
 Gln Glu Lys Ile Val Leu Met Ala Asp Glu Val Tyr Gln Glu Asn Val
 290 295 300
 Tyr Gln Asp Glu Arg Pro Phe Val Ser Ala Lys Lys Val Met Trp Glu
 305 310 315 320
 Met Gly Glu Pro Tyr Arg Ser His Val Glu Leu Leu Ser Phe His Thr
 325 330 335
 Val Ser Lys Gly Thr Ala Gly Glu Cys Gly Leu Arg Gly Gly Tyr Val
 340 345 350
 Glu Met Thr Asn Ile His Pro Gly Ala Ile Glu Glu Val Cys Lys Cys
 355 360 365
 Ala Ser Ile Asn Leu Ser Pro Asn Thr Met Gly Gln Ile Ala Leu Ser
 370 375 380
 Val Leu Val Asn Pro Pro Lys Pro Gly Asp Pro Ser Tyr Asp Gln Tyr
 385 390 395 400
 Thr Lys Glu Lys Ala Ser Glu Leu Val Ser Leu Arg Arg Arg Ala His
 405 410 415
 Met Val Thr Asp Gly Phe Asn Ala Leu Asp Gly Val Thr Cys Asn Phe
 420 425 430
 Thr Glu Gly Ala Met Tyr Ser Phe Pro Gln Ile Lys Leu Pro Ala Lys
 435 440 445
 Ala Leu Glu Ala Ala Lys Ala Ala Gly Lys Ala Gly Asp Val Phe Tyr
 450 455 460
 Cys Leu Lys Leu Leu Glu Ala Thr Gly Ile Ser Thr Val Pro Gly Ser
 465 470 475 480
 Gly Phe Gly Gln Glu Glu Gly Thr Phe His Leu Arg Thr Thr Ile Leu
 485 490 495
 Pro Arg Glu Glu Val Met Thr His Phe Val Glu Lys Phe Asp Lys Phe
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 His Lys Asp Phe Met Lys Gln Tyr Ser
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<210> 52
 <211> 1416
 <212> DNA
 <213> *Oryza sativa*

<400> 52
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 gagcagaagg ccaagaagcc gtcgctggtg gtgagggcgg tggcgacgcg gcgggcccgg 240

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<210> 56
 <211> 483
 <212> PRT
 <213> Oryza sativa

<400> 56

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Ile	Leu	Tyr	Cys	Asn	Ile	Gly	Asn	Pro	Gln	Ser	Leu	Gly	Gln	Lys	Pro
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65				70						75				80	
Leu	Glu	Lys	Glu	Glu	Thr	Lys	Ser	Leu	Phe	Ser	Ala	Asp	Ala	Ile	Ser
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Arg	Ala	Thr	Thr	Ile	Leu	Ala	Ser	Ile	Pro	Gly	Arg	Ala	Thr	Gly	Ala
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Tyr	Ser	His	Ser	Gln	Gly	Ile	Lys	Gly	Leu	Arg	Asp	Ala	Ile	Ala	Ala
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Ile	Arg	Asn	Glu	Lys	Asp	Gly	Ile	Leu	Cys	Pro	Ile	Pro	Gln	Tyr	Pro
			165					170					175		
Leu	Tyr	Ser	Ala	Ser	Ile	Ala	Leu	His	Gly	Gly	Ala	Leu	Val	Pro	Tyr
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Tyr	Leu	Asn	Glu	Ser	Thr	Gly	Trp	Gly	Leu	Glu	Ile	Ser	Asp	Leu	Lys
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225				230						235				240	
Asn	Gln	Arg	Asp	Ile	Val	Lys	Phe	Cys	Lys	Asn	Glu	Gly	Leu	Val	Leu
			245					250					255		
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	260						265					270			
Phe	Asn	Ser	Phe	Lys	Lys	Ile	Ala	Arg	Ser	Met	Gly	Tyr	Asn	Glu	Asp

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Asp	Leu	Pro	Leu	Val	Ser	Phe	Gln	Ser	Val	Ser	Lys	Gly	Tyr	Tyr	Gly
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Pro	Val	Arg	Glu	Gln	Ile	Tyr	Lys	Val	Ala	Ser	Val	Asn	Leu	Cys	Ser
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Ala	Gly	Asp	Ala	Ser	Tyr	Ala	Ser	Tyr	Lys	Ala	Glu	Lys	Asp	Gly	Ile
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385					390					395					400
Phe	Pro	Gln	Leu	Ser	Leu	Pro	Gln	Lys	Ala	Ile	Asp	Ala	Ala	Lys	Ala
				405					410					415	
Ala	Asn	Lys	Ala	Pro	Asp	Ala	Phe	Tyr	Ala	Leu	Arg	Leu	Leu	Glu	Ala
			420					425					430		
Thr	Gly	Ile	Val	Val	Val	Pro	Gly	Ser	Gly	Phe	Gly	Gln	Val	Pro	Gly
		435					440					445			
Thr	Trp	His	Ile	Arg	Cys	Thr	Ile	Leu	Pro	Gln	Glu	Glu	Lys	Ile	Pro
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Tyr	Arg	Asp													

<210> 57
 <211> 2559
 <212> DNA
 <213> *Oryza sativa*

<400> 57

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