

CD088PCT.ST25.txt
SEQUENCE LISTING

<110> CropDesign N.V.

<120> Stress Tolerance

<130> CD-088-PCT

<150> EP 03076064.9

<151> 2003-04-11

<160> 10

<170> PatentIn version 3.2

<210> 1

<211> 1344

<212> DNA

<213> Beta vulgaris

<220>

<221> misc_feature

<222> (3)..(3)

<223> n is a, c, g, or t

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acgatcgtag	agtctctgtt	tttcaactgt	ttaaactctt	caaacaattt	tctctctcct	180
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gagaaattga	atgagacact	tgaaatgcta	gagaagaaag	agcagcttct	aatgaaaaag	360
gctactgcag	agggtgaaaa	ggccaaagag	ttcacaaggg	caaagaataa	acgtgctgct	420
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caactacgaa	ttcatgatca	gatcataatg	cttgattctg	caaaagcaac	gacagagaca	540
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gagcttgaag	aacttgaagg	agctgagttg	gaggaacaac	ttctacaacc	atttacaact	780
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<211> 224

<212> PRT

<213> Beta vulgaris

<400> 2

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Ala Ala Thr Thr Glu Thr Thr Leu Ser Thr Leu Glu Lys Leu Asn Glu
20 25 30

Thr Leu Glu Met Leu Glu Lys Lys Glu Gln Leu Leu Met Lys Lys Ala
35 40 45

Thr Ala Glu Val Glu Lys Ala Lys Glu Phe Thr Arg Ala Lys Asn Lys
50 55 60

Arg Ala Ala Ile Gln Cys Leu Lys Arg Lys Arg Leu Tyr Glu Gln Gln
65 70 75 80

Val Glu Gln Val Gly Asn Phe Gln Leu Arg Ile His Asp Gln Ile Ile
85 90 95

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

Ser Gly Ala Ser Ala Met Lys Ala Met Gln Lys Ala Thr Asn Ile Asp
115 120 125

Asp Val Asp Lys Thr Met Asp Glu Ile Asn Glu Gln Thr Asp Asn Leu
130 135 140

Arg Gln Ile Gln Glu Ala Leu Ala Thr Pro Val Gly Ala Thr Asp Phe
145 150 155 160

Asp Glu Asp Glu Leu Glu Ala Glu Leu Glu Glu Leu Glu Gly Ala Glu
165 170 175

Leu Glu Glu Gln Leu Leu Gln Pro Phe Thr Thr Ala Pro Thr Ala Pro
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tcgagttaac ctaatcactc cattcttatt tcctctcgga aaaaaaccta atcaatcaac 240
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gttgcaacgt tagacaaatt gaggtagaca ctcgaaatgt tggaaaaaaa agaacaggtg 420
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CD088PCT.ST25.txt

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<210> 4
<211> 154
<212> PRT
<213> Beta vulgaris

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20 25 30

Lys Glu Gln Val Leu Leu Lys Lys Ala Gly Ala Glu Val Glu Lys Ala
35 40 45

Lys Glu Phe Thr Arg Ala Lys Asn Lys Arg Ala Ala Ile Thr Cys Leu
50 55 60

Lys Arg Lys Arg Leu Tyr Glu Gln Gln Ile Glu Gln Leu Gly Asn Met
65 70 75 80

Gln Leu Arg Ile His Asp Gln Met Ile Leu Leu Glu Gly Ala Lys Ala
85 90 95

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

Ala Met Gln Lys Ala Thr Asn Ile Asp Asn Val Asp Lys Thr Met Asp
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Glu Ile Asn Glu Gln Thr Glu Asn Leu Lys Gln Ile Gln Glu Ala Leu
130 135 140

Ser Ala Pro Ile Gly Ala Ala Ala Asp Phe
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<223> n is a, c, g, or t

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cgtcaatctc gtaagtgcga gaaagaagaa aaagctgaga aactcaaagt caagaaagca      180
atcgagaaaag gaaacatgga tggagctcga atttacgccg aaaacgcaat tcgtaagcgt      240
actgaacaga tgaactactt gcgcctcgct tctcgccctg acgccgctcg ttcgcgcctc      300
gatactcaag ctaagatgca aaccatcgga aaatcgatgg gatcaattgt taaatcgctt      360
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agctttactg atgatcaacc ctctgtgata tggggggttg atgataattt gctctatatt      780
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ggccttttgt gggttgaaga aggaaaaaga cagaaacgac ttaattacct acttgaaaaa      960
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<210> 6

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<212> PRT

<213> Beta vulgaris

<400> 6

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1              5              10              15

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Thr Ser Lys Ser Leu Gln Arg Gln Ser Arg Lys Cys Glu Lys Glu Glu
20              25              30

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Lys Ala Glu Lys Leu Lys Val Lys Lys Ala Ile Glu Lys Gly Asn Met
35              40              45

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Asp Gly Ala Arg Ile Tyr Ala Glu Asn Ala Ile Arg Lys Arg Thr Glu
50              55              60

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Gln Met Asn Tyr Leu Arg Leu Ala Ser Arg Leu Asp Ala Val Val Ser
65              70              75              80

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Arg Leu Asp Thr Gln Ala Lys Met Gln Thr Ile Gly Lys Ser Met Gly
85              90              95

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Ser Ile Val Lys Ser Leu Glu Ser Ser Leu Asn Thr Gly Asn Leu Gln
100             105             110

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Lys Met Ser Glu Thr Met Asp Asn Phe Glu Lys Gln Phe Val Asn Met
115             120             125

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Glu Val Gln Ala Glu Phe Met Glu Ser Ser Met Ala Gly Ser Thr Ser
130             135             140

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Leu Ser Thr Pro Glu Thr Glu Val Asn Ser Leu Met Gln Gln Val Ala
145 150 155 160

Asp Asp Tyr Gly Leu Glu Val Ser Val Gly Leu Pro Gln Ala Ala Gly
165 170 175

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180 185 190

Leu Thr Arg Arg Leu Ala Glu Leu Lys Ala Arg Gly
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ccagtagccg agaaaccagc tgagaagcca gctgagaagg cagttctacc acctgaagct 180
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ctaacagaac cagaatctgt tgaggagaca caaaagaag ctgaagttgt agtggagaa 780
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<210> 8
<211> 427
<212> PRT
<213> Beta vulgaris

<400> 8
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Leu	Pro	Pro	Glu	Ala	Glu	Lys	Leu	Ala	Ala	Ala	Glu	Ser	Ala	Glu	Ala	35	40	45
Glu	Lys	Pro	Ala	Asp	Ser	Ala	Glu	Ala	Lys	Ile	Ala	Gln	Gln	Val	Ser	50	55	60
Phe	Lys	Glu	Glu	Thr	Asn	Val	Ala	Ser	Glu	Leu	Pro	Glu	Leu	His	Arg	65	70	75
Lys	Ala	Leu	Glu	Asp	Leu	Lys	Lys	Leu	Ile	Gln	Glu	Ala	Leu	Glu	Lys	85	90	95
His	Glu	Phe	Ser	Ser	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Pro	Ala	Lys	100	105	110
Val	Glu	Glu	Lys	Ala	Glu	Glu	Lys	Lys	Glu	Glu	Gln	Pro	Pro	Ser	Thr	115	120	125
Thr	Ser	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Ala	Val	Ser	Asp	Glu	Val	Ala	130	135	140
Val	Ala	Pro	Pro	Ser	Glu	Glu	Ala	Pro	Lys	Thr	Asp	Glu	Ala	Ser	Pro	145	150	155
Lys	Val	Glu	Glu	Glu	Pro	Ala	Lys	Ile	Val	Glu	Gln	Pro	Pro	Thr	Thr	165	170	175
Pro	Ala	Glu	Glu	Pro	Glu	Pro	Ala	Lys	Thr	Pro	Glu	Val	Val	Val	Ala	180	185	190
Glu	Glu	Glu	Lys	Thr	Gly	Glu	Asp	Ile	Lys	Glu	Thr	Ile	Val	Val	Glu	195	200	205
Val	Ala	Thr	Thr	Thr	Ala	Ala	Pro	Val	Leu	Thr	Glu	Pro	Glu	Ser	Val	210	215	220
Glu	Glu	Thr	Pro	Lys	Glu	Ala	Glu	Val	Val	Val	Glu	Glu	Ser	Pro	Lys	225	230	235
Glu	Pro	Glu	Glu	Val	Ser	Ile	Trp	Gly	Ile	Pro	Leu	Leu	Ala	Asp	Glu	245	250	255
Arg	Ser	Asp	Val	Ile	Leu	Leu	Lys	Phe	Leu	Arg	Ala	Arg	Asp	Tyr	Arg	260	265	270
Val	Lys	Asp	Ala	Phe	Thr	Met	Ile	Arg	Asn	Thr	Ala	Arg	Trp	Arg	Lys	275	280	285
Glu	Phe	Glu	Val	Asp	Ser	Leu	Leu	Asp	Glu	Asp	Leu	Gly	Asn	Asp	Tyr	290	295	300
Glu	Lys	Val	Val	Phe	Thr	His	Gly	Val	Asp	Lys	Gln	Gly	Arg	Pro	Val	305	310	315
Cys	Tyr	Asn	Val	Phe	Gly	Glu	Phe	Gln	Asn	Lys	Glu	Leu	Tyr	Gln	Asn			

Thr	Phe	Ser	Asp	Ala	Glu	Lys	Arg	Lys	Lys	Phe	Leu	Arg	Trp	Leu	Ile	325	330	335
			340					345					350					
Gln	Phe	Leu	Glu	Lys	Thr	Ile	Arg	Thr	Leu	Asp	Phe	Ser	Pro	Glu	Gly			
		355					360					365						
Ile	Asn	Ser	Phe	Val	Leu	Val	Asn	Asp	Leu	Lys	Asn	Ser	Pro	Gly	Tyr			
	370					375					380							
Gly	Lys	Arg	Asp	Leu	Tyr	Lys	Val	Ile	Asp	Lys	Phe	Leu	Glu	Ile	Leu			
385					390					395					400			
Gln	Asp	Asn	Tyr	Pro	Glu	Phe	Ala	Ala	Lys	Gln	Leu	Cys	Ile	Asn	Val			
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 <223> n is a, c, g, or t

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ggatgaatat	tccaatagaa	aatctttctg	tcttgctatc	tccaggagag	ggcctagcct	180
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gattgtagag	aggatgagca	tgatatcaaa	tgacagcatat	gccaggaaga	atatggtggc	1620
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gaccggaatc	tgtcgatttt	tatttcttca	tcagaaattt	gatgtttcta	tagatagtcc	1860
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aataatgctc	gagctggttag	aagctccagt	atgggaacag	gttcacttca	cttatttttac	1980
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<400> 10
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 35 40 45
 Ser Val Lys Asp Ala Lys Val Ser Ser Pro Ser Lys Val Lys Ser Pro
 50 55 60
 Lys Thr Pro Phe Arg Ser Ser Ala Gln Gly Lys Glu Thr Ile Gly Ser
 65 70 75 80
 Ser Ser Arg Thr Leu Ala Ser Pro Ser Pro Phe Lys Lys Ser Leu Ser
 85 90 95
 Asp Arg Lys Lys Lys Leu Pro Ser Asn Leu Asp Thr Asp Ser Glu Met
 100 105 110
 Cys Ser Leu Gln Asp Glu Ser Glu Glu Val Ser Gly Lys Thr Arg Ile
 115 120 125
 Arg Val Gln Pro Glu Pro Glu Asp His Asp Ser Ile Glu Ala Ser Ser
 130 135 140
 Ser Glu Ala Gly Ser Ser Ser Ser Gly Pro Ser Asn Arg Leu Ala Asn
 145 150 155 160
 Arg Asn Thr Gln Arg Phe Gly Leu Gly Arg Gln Asp Ser Ala Ala Ser
 165 170 175
 Ser Ala Ser Phe Ser Leu Asn Lys Thr Asn Gln Gly Gln Arg Asn Gly
 180 185 190
 Gly Gly Gly Gly Ala Ser Ala Asn Arg Tyr Asn Leu Arg Gln Leu Lys
 195 200 205
 Cys Asn Ser Ile Ser Asp Val Val Pro Ser Gly Ser Pro Gln Ser Ala
 210 215 220
 Glu Ser Ser Leu Ser Lys Lys Arg Asp Thr Gly Cys Arg Lys Arg Asn
 225 230 235 240

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Gly	Glu	Ala	Glu	Ser	Ser	Leu	Pro	Val	Arg	Gly	Lys	Lys	Ile	Asn	Gly		
				245					250					255			
Ala	Thr	Gln	Asp	Asp	Arg	Arg	Asn	Asp	Tyr	Pro	Asn	Arg	Gly	Ile	Ser		
			260					265					270				
Ile	Ser	Asp	Thr	Arg	Arg	Thr	Arg	Ser	Ser	Ser	Pro	Gly	Asn	Asn	Asp		
		275					280					285					
Val	Thr	Ser	Val	Arg	Ser	Arg	Arg	Ser	Val	Ala	Arg	Thr	Arg	Leu	Ser		
	290					295					300						
Asn	Gln	Asp	Thr	Arg	Asp	Arg	Leu	Pro	Leu	Val	Glu	Ser	Pro	Leu	Arg		
305					310					315					320		
Asn	Pro	Ser	Ser	Pro	Leu	Pro	Glu	Ser	Ser	Thr	Gly	Gly	Thr	Asp	Phe		
				325					330					335			
Ser	Leu	Glu	Asn	Gln	Phe	Ser	Gly	Arg	Thr	Pro	Ala	Gly	Ser	Leu	Ser		
			340					345					350				
Ser	Tyr	Asn	Arg	Pro	Gly	Gly	Gly	Ser	Glu	His	Met	Arg	Pro	Ser	Arg		
		355					360					365					
Ser	Ile	Asp	Pro	Tyr	Glu	Ala	Gly	Ile	Ala	Arg	Ser	Phe	Met	Asn	Arg		
	370					375					380						
Asp	Thr	Leu	Arg	Gln	Tyr	Asn	Leu	Asp	Gly	Ile	Ala	Glu	Met	Leu	Leu		
385					390					395					400		
Ala	Leu	Glu	Arg	Ile	Glu	Gln	Glu	Glu	Asp	Pro	Thr	Tyr	Glu	Gln	Leu		
				405					410					415			
Leu	Val	Leu	Glu	Thr	Asn	Leu	Phe	Leu	Gly	Gly	Leu	Ser	Phe	His	Asp		
			420					425					430				
Gln	His	Arg	Asp	Met	Arg	Leu	Asp	Ile	Asp	Asn	Met	Ser	Tyr	Glu	Glu		
		435					440					445					
Leu	Leu	Ala	Leu	Glu	Glu	Ser	Met	Gly	Thr	Val	Arg	Gln	Pro	Cys	Gln		
	450					455					460						
Lys	Met	Ile	Trp	Leu	Ser	Val	Leu	Lys	Gly	Thr	Ser	Thr	Arg	Val	Leu		
465					470					475					480		
Gln	Ile	Val	Glu	Arg	Met	Ser	Met	Ile	Ser	Asn	Ala	Ala	Tyr	Ala	Arg		
				485					490					495			
Lys	Asn	Met	Val	Ala	Gly	Lys	Lys										
			500														