

# SEQUENCE LISTING

<110> Bayer BioScience N.V.  
Laga, Benjamin  
den Boer, Bart  
Lambert, Bart

<120> Brassica plant comprising a mutant INDEHISCENT allele

<130> BCS 08-2010

<160> 28

<170> PatentIn version 3.3

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<213> Brassica napus wild type IND-A1 coding sequence

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Glu His His His Leu Leu Met Asn Trp Asn Lys Pro Ile Asp Leu Ile	
20 25 30	
aca gaa gaa aac tct ttt aac cac aat cct cat ttc ata gta gat cca	144
Thr Glu Glu Asn Ser Phe Asn His Asn Pro His Phe Ile Val Asp Pro	
35 40 45	
cct tcc gaa acc cta agc cac ttc cag ccc ccg ccg aca atc ttc tcc	192
Pro Ser Glu Thr Leu Ser His Phe Gln Pro Pro Pro Thr Ile Phe Ser	
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gat cac gga gga gga gag gaa gca gaa gaa gaa gaa gaa gaa gaa gga	240
Asp His Gly Gly Gly Glu Glu Ala Glu Glu Glu Glu Glu Glu Glu Gly	
65 70 75 80	
gag gaa gag atg gat ccg atg aag aag atg caa tac gcg att gct gcc	288
Glu Glu Glu Met Asp Pro Met Lys Lys Met Gln Tyr Ala Ile Ala Ala	
85 90 95	
atg cag ccc gta gac ctc gat cca gcc acc gtt cct aag ccg aac cgc	336
Met Gln Pro Val Asp Leu Asp Pro Ala Thr Val Pro Lys Pro Asn Arg	
100 105 110	
cgt aac gta agg gta agc gac gac cct cag acg gtg gtg gct cgt cgg	384
Arg Asn Val Arg Val Ser Asp Asp Pro Gln Thr Val Val Ala Arg Arg	
115 120 125	
cgt aga gaa agg ata agc gag aag atc cgg ata ttg aag agg atg gtg	432
Arg Arg Glu Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys Arg Met Val	
130 135 140	
cca ggc ggt gca aag atg gac act gcc tcc atg ctc gac gaa gcc atc	480
Pro Gly Gly Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ile	
145 150 155 160	
cgc tac acc aag ttc ttg aaa cgg cag gtg agg cta gct tct tca gcc	528
Arg Tyr Thr Lys Phe Leu Lys Arg Gln Val Arg Leu Ala Ser Ser Ala	
165 170 175	

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 180 185

558

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 <213> Brassica napus wild type IND-A1 coding sequence  
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Met Ser Gly Ser Lys Ala Asp Ala Ala Ile Ala Pro Ile Val Met Met  
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Glu His His His Leu Leu Met Asn Trp Asn Lys Pro Ile Asp Leu Ile  
 20 25 30

Thr Glu Glu Asn Ser Phe Asn His Asn Pro His Phe Ile Val Asp Pro  
 35 40 45

Pro Ser Glu Thr Leu Ser His Phe Gln Pro Pro Pro Thr Ile Phe Ser  
 50 55 60

Asp His Gly Gly Gly Glu Glu Ala Glu Glu Glu Glu Glu Glu Gly  
 65 70 75 80

Glu Glu Glu Met Asp Pro Met Lys Lys Met Gln Tyr Ala Ile Ala Ala  
 85 90 95

Met Gln Pro Val Asp Leu Asp Pro Ala Thr Val Pro Lys Pro Asn Arg  
 100 105 110

Arg Asn Val Arg Val Ser Asp Asp Pro Gln Thr Val Val Ala Arg Arg  
 115 120 125

Arg Arg Glu Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys Arg Met Val  
 130 135 140

Pro Gly Gly Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ile  
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Arg Tyr Thr Lys Phe Leu Lys Arg Gln Val Arg Leu Ala Ser Ser Ala  
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Ser His Ser Ala Trp Ser Ser Tyr Val  
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 tct ggt tca aaa gca gat gca gca gcc ata gcc cca ata gtc atg atg 96  
 Ser Gly Ser Lys Ala Asp Ala Ala Ala Ile Ala Pro Ile Val Met Met  
 20 25 30  
 gag cct cat cat ctc ctt atg aac tgg aac aaa cct att gat ctc att 144  
 Glu Pro His His Leu Leu Met Asn Trp Asn Lys Pro Ile Asp Leu Ile  
 35 40 45  
 aca caa gaa aac tct ttt aac cac aat cct cat ttc atg gta gat cca 192  
 Thr Gln Glu Asn Ser Phe Asn His Asn Pro His Phe Met Val Asp Pro  
 50 55 60  
 cct tcc gaa acc cta agc cac ttc cag ccc ccg ccg aca gtc ttc tcc 240  
 Pro Ser Glu Thr Leu Ser His Phe Gln Pro Pro Pro Thr Val Phe Ser  
 65 70 75 80  
 gat ccc gga gga gga gag gaa gca gaa gac gaa gaa gga gag gaa gag 288  
 Asp Pro Gly Gly Gly Glu Glu Ala Glu Asp Glu Glu Gly Glu Glu Glu  
 85 90 95  
 ata gat gag atg aag gag atg caa tac gcg att gct gcc atg cag ccc 336  
 Ile Asp Glu Met Lys Glu Met Gln Tyr Ala Ile Ala Ala Met Gln Pro  
 100 105 110  
 gta gac atc gat cca gcc acc gtt cct aag ccg aac cgc cgt aac gta 384  
 Val Asp Ile Asp Pro Ala Thr Val Pro Lys Pro Asn Arg Arg Asn Val  
 115 120 125  
 agg gta agc gag gac ccc cag acg gtg gtg gct cgt cgg cgt aga gaa 432  
 Arg Val Ser Glu Asp Pro Gln Thr Val Val Ala Arg Arg Arg Arg Glu  
 130 135 140  
 agg ata agc gag aag atc cgg ata ttg aag agg atg gtg cca ggc ggt 480  
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 145 150 155 160  
 gca aag atg gac act gcc tcc atg ctt gac gaa gcc atc cgc tac acc 528  
 Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ile Arg Tyr Thr  
 165 170 175  
 aag ttc ttg aaa cgg cag gtg agg ctt ctt cag cct cac act cag ctt 576  
 Lys Phe Leu Lys Arg Gln Val Arg Leu Leu Gln Pro His Thr Gln Leu  
 180 185 190  
 ggg gct cct atg tct gac cct tct cgc ctt tgt tat tac cac aac tcg 624  
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 Asp Thr  
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<213> Brassica napus wild type IND-C1 coding sequence

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 20 25 30  
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 35 40 45  
 Thr Gln Glu Asn Ser Phe Asn His Asn Pro His Phe Met Val Asp Pro  
 50 55 60  
 Pro Ser Glu Thr Leu Ser His Phe Gln Pro Pro Pro Thr Val Phe Ser  
 65 70 75 80  
 Asp Pro Gly Gly Gly Glu Glu Ala Glu Asp Glu Glu Gly Glu Glu Glu  
 85 90 95  
 Ile Asp Glu Met Lys Glu Met Gln Tyr Ala Ile Ala Ala Met Gln Pro  
 100 105 110  
 Val Asp Ile Asp Pro Ala Thr Val Pro Lys Pro Asn Arg Arg Asn Val  
 115 120 125  
 Arg Val Ser Glu Asp Pro Gln Thr Val Val Ala Arg Arg Arg Arg Glu  
 130 135 140  
 Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys Arg Met Val Pro Gly Gly  
 145 150 155 160  
 Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ile Arg Tyr Thr  
 165 170 175  
 Lys Phe Leu Lys Arg Gln Val Arg Leu Leu Gln Pro His Thr Gln Leu  
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 Gly Ala Pro Met Ser Asp Pro Ser Arg Leu Cys Tyr Tyr His Asn Ser  
 195 200 205  
 Asp Thr  
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tatcacatat ttaaacgtca gttttttttt tttttttggg gggggggggg ggggtaatat	180
aaaaatataa ttaacaaaaa aaaattatga aacaattagc atgtaaaaca ctaatctttt	240
ggttgtgaca aaacgttttc acaaattgttc tataaataaa ttcaagtgc ttttatctgc	300
aaaatatata ctttcactca taaaataaga gcgttttaaaa cattcataca cgcactacat	360
tgacatgaca aaagaaatcc gcaaatacac atgatgtatg tcgaaaaaaa caaaaaatac	420
acatgatgta tatatagaga ggatagtatc taggaaataa gactatatta tatatataaa	480
gaaaatagag aaaagataaa aatataaatt ggtatgtata aaagaaaggc ctatgcgtct	540
ctagtccaaa aactctatat atg tct ggc tca aaa gca gat gca gcc ata gcc	593
Met Ser Gly Ser Lys Ala Asp Ala Ala Ile Ala	
1 5 10	
cca ata gtc atg atg gag cat cat cat ctc ctt atg aat tgg aac aaa	641
Pro Ile Val Met Met Glu His His His Leu Leu Met Asn Trp Asn Lys	
15 20 25	
cct att gat ctc att aca gaa gaa aac tct ttt aac cac aat cct cat	689
Pro Ile Asp Leu Ile Thr Glu Glu Asn Ser Phe Asn His Asn Pro His	
30 35 40	
ttc ata gta gat cca cct tcc gaa acc cta agc cac ttc cag ccc ccg	737
Phe Ile Val Asp Pro Pro Ser Glu Thr Leu Ser His Phe Gln Pro Pro	
45 50 55	
ccg aca atc ttc tcc gat cac gga gga gga gag gaa gca gaa gaa gaa	785
Pro Thr Ile Phe Ser Asp His Gly Gly Gly Glu Glu Ala Glu Glu Glu	
60 65 70 75	
gaa gaa gaa gaa gga gag gaa gag atg gat ccg atg aag aag atg caa	833
Glu Glu Glu Glu Gly Glu Glu Glu Met Asp Pro Met Lys Lys Met Gln	
80 85 90	
tac gcg att gct gcc atg cag ccc gta gac ctc gat cca gcc acc gtt	881
Tyr Ala Ile Ala Ala Met Gln Pro Val Asp Leu Asp Pro Ala Thr Val	
95 100 105	
cct aag ccg aac cgc cgt aac gta agg gta agc gac gac cct cag acg	929
Pro Lys Pro Asn Arg Arg Asn Val Arg Val Ser Asp Asp Pro Gln Thr	
110 115 120	
gtg gtg gct cgt cgg cgt aga gaa agg ata agc gag aag atc cgg ata	977
Val Val Ala Arg Arg Arg Arg Glu Arg Ile Ser Glu Lys Ile Arg Ile	
125 130 135	
ttg aag agg atg gtg cca ggc ggt gca aag atg gac act gcc tcc atg	1025
Leu Lys Arg Met Val Pro Gly Gly Ala Lys Met Asp Thr Ala Ser Met	
140 145 150 155	
ctc gac gaa gcc atc cgc tac acc aag ttc ttg aaa cgg cag gtg agg	1073
Leu Asp Glu Ala Ile Arg Tyr Thr Lys Phe Leu Lys Arg Gln Val Arg	
160 165 170	
cta gct tct tca gcc tca cac tca gct tgg agc tcc tat gtc tga	1118
Leu Ala Ser Ser Ala Ser His Ser Ala Trp Ser Ser Tyr Val	
175 180 185	
cccttcttgc ctttgttatt accacaactc ggatacctaa ttataattct atcacgcgtt	1178
tcattgtgat atatatagat aaatggtcga ataaggattt cgatcgaaga ttgtatgtac	1238
aataaatgat gtgtgtatatt caattaatgt atgatatata tatatatatg tatgcagtat	1298
gcatttatat tctattctct ataaggaggc aacattgccg gattagggct ttgatcttat	1358

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 agcctttctc taatccctaa gattatagct actgaaacaa tgaaacaatg aagaatcagt 1538  
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 <212> PRT  
 <213> Brassica napus wild type IND-A1 genomic sequence

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Met Ser Gly Ser Lys Ala Asp Ala Ala Ile Ala Pro Ile Val Met Met  
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Glu His His His Leu Leu Met Asn Trp Asn Lys Pro Ile Asp Leu Ile  
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Thr Glu Glu Asn Ser Phe Asn His Asn Pro His Phe Ile Val Asp Pro  
 35 40 45

Pro Ser Glu Thr Leu Ser His Phe Gln Pro Pro Pro Thr Ile Phe Ser  
 50 55 60

Asp His Gly Gly Gly Glu Glu Ala Glu Glu Glu Glu Glu Glu Gly  
 65 70 75 80

Glu Glu Glu Met Asp Pro Met Lys Lys Met Gln Tyr Ala Ile Ala Ala  
 85 90 95

Met Gln Pro Val Asp Leu Asp Pro Ala Thr Val Pro Lys Pro Asn Arg  
 100 105 110

Arg Asn Val Arg Val Ser Asp Asp Pro Gln Thr Val Val Ala Arg Arg  
 115 120 125

Arg Arg Glu Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys Arg Met Val  
 130 135 140

Pro Gly Gly Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ile  
 145 150 155 160

Arg Tyr Thr Lys Phe Leu Lys Arg Gln Val Arg Leu Ala Ser Ser Ala  
 165 170 175

Ser His Ser Ala Trp Ser Ser Tyr Val  
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<210> 7  
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 <222> (497)..(1126)

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actcaagctt ggtccagagc ataaaaaaat taaagccatc gcttttggtat cacatatttta      180
aacgtcagtt tttttttggg gaagtaatat aaaaatataa ttaacaagaa aatttatgaa      240
ataattagca tgtaaaacac tagtcttttg gttgtgacaa aacgttttca caaatgttct      300
ataaataaat tcaagcacat tttatctgca aaatatatac tttcactcat aaaataagag      360
cgtttaaaac attcatatac gcactacatt gacatgacaa aagaaatccg caaatacaaa      420
catatttagt tcggatatat ctaggaaata agactatatt atatatataa agaaattaga      480
aaaaaagaaa attggt atg tat aaa aga aag gtc tat gcg tct cta gtc caa      532
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                1          5          10

aaa ctc tat atg tct ggt tca aaa gca gat gca gca gcc ata gcc cca      580
Lys Leu Tyr Met Ser Gly Ser Lys Ala Asp Ala Ala Ala Ile Ala Pro
                15          20          25

ata gtc atg atg gag cct cat cat ctc ctt atg aac tgg aac aaa cct      628
Ile Val Met Met Glu Pro His His Leu Leu Met Asn Trp Asn Lys Pro
                30          35          40

att gat ctc att aca caa gaa aac tct ttt aac cac aat cct cat ttc      676
Ile Asp Leu Ile Thr Gln Glu Asn Ser Phe Asn His Asn Pro His Phe
                45          50          55          60

atg gta gat cca cct tcc gaa acc cta agc cac ttc cag ccc ccg ccg      724
Met Val Asp Pro Pro Ser Glu Thr Leu Ser His Phe Gln Pro Pro Pro
                65          70          75

aca gtc ttc tcc gat ccc gga gga gga gag gaa gca gaa gac gaa gaa      772
Thr Val Phe Ser Asp Pro Gly Gly Gly Glu Glu Ala Glu Asp Glu Glu
                80          85          90

gga gag gaa gag ata gat gag atg aag gag atg caa tac gcg att gct      820
Gly Glu Glu Glu Ile Asp Glu Met Lys Glu Met Gln Tyr Ala Ile Ala
                95          100          105

gcc atg cag ccc gta gac atc gat cca gcc acc gtt cct aag ccg aac      868
Ala Met Gln Pro Val Asp Ile Asp Pro Ala Thr Val Pro Lys Pro Asn
                110          115          120

cgc cgt aac gta agg gta agc gag gac ccc cag acg gtg gtg gct cgt      916
Arg Arg Asn Val Arg Val Ser Glu Asp Pro Gln Thr Val Val Ala Arg
                125          130          135          140

cgg cgt aga gaa agg ata agc gag aag atc cgg ata ttg aag agg atg      964
Arg Arg Arg Glu Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys Arg Met
                145          150          155

gtg cca ggc ggt gca aag atg gac act gcc tcc atg ctt gac gaa gcc      1012
Val Pro Gly Gly Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala
                160          165          170

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atc cgc tac acc aag ttc ttg aaa cgg cag gtg agg ctt ctt cag cct	1060
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175 180 185	
cac act cag ctt ggg gct cct atg tct gac cct tct cgc ctt tgt tat	1108
His Thr Gln Leu Gly Ala Pro Met Ser Asp Pro Ser Arg Leu Cys Tyr	
190 195 200	
tac cac aac tcg gat acc taattataat tctatcacgc gtttcatgtt	1156
Tyr His Asn Ser Asp Thr	
205 210	
gatatatata gataaatggt tgaataagga tttcgcacga agattgtatg gctattgatt	1216
acattatata ttgtacaata aatgatgtgt gtatttctat taatgtatat atgatatata	1276
tctgttttgca gtatgcattt atatttctatt ctttataggg aggcaacatg ccggattagg	1336
gctttgatcg tatgcaagtt ttccgaccaa aaatatgaaa tacttgtttg gatataacat	1396
atgaatcgga taagtgttac tagttatata actggaaaaa attgtttggt ataagaattc	1456
ccgggagAAC caagcctttc tctaattccct aagatcatag ctactgaaat aatgaaaaaa	1516
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 <213> Brassica napus wild type IND-C1 genomic sequence  
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20 25 30	
Glu Pro His His Leu Leu Met Asn Trp Asn Lys Pro Ile Asp Leu Ile	
35 40 45	
Thr Gln Glu Asn Ser Phe Asn His Asn Pro His Phe Met Val Asp Pro	
50 55 60	
Pro Ser Glu Thr Leu Ser His Phe Gln Pro Pro Pro Thr Val Phe Ser	
65 70 75 80	
Asp Pro Gly Gly Gly Glu Glu Ala Glu Asp Glu Glu Gly Glu Glu Glu	
85 90 95	
Ile Asp Glu Met Lys Glu Met Gln Tyr Ala Ile Ala Ala Met Gln Pro	
100 105 110	
Val Asp Ile Asp Pro Ala Thr Val Pro Lys Pro Asn Arg Arg Asn Val	
115 120 125	
Arg Val Ser Glu Asp Pro Gln Thr Val Val Ala Arg Arg Arg Arg Glu	



130

135

140

Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys Arg Met Val Pro Gly Gly  
145 150 155 160

Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala Ile Arg Tyr Thr  
165 170 175

Lys Phe Leu Lys Arg Gln Val Arg Leu Leu Gln Pro His Thr Gln Leu  
180 185 190

Gly Ala Pro Met Ser Asp Pro Ser Arg Leu Cys Tyr Tyr His Asn Ser  
195 200 205

Asp Thr  
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<220>  
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tcg tcc aaa agc aga tcc aac cac agc ccc aaa aga agc atg atg gag 96  
Ser Ser Lys Ser Arg Ser Asn His Ser Pro Lys Arg Ser Met Met Glu  
20 25 30  
cct cag cct cac cat ctc ctc atg gat tgg aac aaa gct aat gat ctt 144  
Pro Gln Pro His His Leu Leu Met Asp Trp Asn Lys Ala Asn Asp Leu  
35 40 45  
ctc aca caa gaa cac gca gct ttt ctc aat gat cct cac cat ctc atg 192  
Leu Thr Gln Glu His Ala Ala Phe Leu Asn Asp Pro His His Leu Met  
50 55 60  
tta gat cca cct ccc gaa acc cta att cac ttg gac gaa gac gaa gag 240  
Leu Asp Pro Pro Pro Glu Thr Leu Ile His Leu Asp Glu Asp Glu Glu  
65 70 75 80  
tac gat gaa gac atg gat gcg atg aag gag atg cag tac atg atc gcc 288  
Tyr Asp Glu Asp Met Asp Ala Met Lys Glu Met Gln Tyr Met Ile Ala  
85 90 95  
gtc atg cag ccc gta gac atc gac cct gcc acg gtc cct aag ccg aac 336  
Val Met Gln Pro Val Asp Ile Asp Pro Ala Thr Val Pro Lys Pro Asn  
100 105 110  
cgc cgt aac gta agg ata agc gac gat cct cag acg gtg gtt gct cgt 384  
Arg Arg Asn Val Arg Ile Ser Asp Asp Pro Gln Thr Val Val Ala Arg  
115 120 125  
cgg cgt cgg gaa agg atc agc gag aag atc cga att ctc aag agg atc 432  
Arg Arg Arg Glu Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys Arg Ile  
130 135 140

gtg cct ggt ggt gcg aag atg gac aca gct tcc atg ctc gac gaa gcc 480  
Val Pro Gly Gly Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala 160  
145 150 155

ata cgt tac acc aag ttc ttg aaa cgg cag gtg agg att ctt cag cct 528  
Ile Arg Tyr Thr Lys Phe Leu Lys Arg Gln Val Arg Ile Leu Gln Pro 175  
165 170

cac tct cag att gga gct cct atg gct aac ccc tct tac ctt tgt tat 576  
His Ser Gln Ile Gly Ala Pro Met Ala Asn Pro Ser Tyr Leu Cys Tyr 190  
180 185

tac cac aac tcc caa ccc tga 597  
Tyr His Asn Ser Gln Pro 195

<210> 10  
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20 25 30

Pro Gln Pro His His Leu Leu Met Asp Trp Asn Lys Ala Asn Asp Leu  
35 40 45

Leu Thr Gln Glu His Ala Ala Phe Leu Asn Asp Pro His His Leu Met  
50 55 60

Leu Asp Pro Pro Pro Glu Thr Leu Ile His Leu Asp Glu Asp Glu Glu  
65 70 75 80

Tyr Asp Glu Asp Met Asp Ala Met Lys Glu Met Gln Tyr Met Ile Ala  
85 90 95

Val Met Gln Pro Val Asp Ile Asp Pro Ala Thr Val Pro Lys Pro Asn  
100 105 110

Arg Arg Asn Val Arg Ile Ser Asp Asp Pro Gln Thr Val Val Ala Arg  
115 120 125

Arg Arg Arg Glu Arg Ile Ser Glu Lys Ile Arg Ile Leu Lys Arg Ile  
130 135 140

Val Pro Gly Gly Ala Lys Met Asp Thr Ala Ser Met Leu Asp Glu Ala  
145 150 155 160

Ile Arg Tyr Thr Lys Phe Leu Lys Arg Gln Val Arg Ile Leu Gln Pro  
165 170 175

His Ser Gln Ile Gly Ala Pro Met Ala Asn Pro Ser Tyr Leu Cys Tyr  
180 185 190

Tyr His Asn Ser Gln Pro  
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