

BPS66376PC-2009022554  
SEQUENCE LISTING

<110> BASF Plant Science GmbH  
Motyka, Shawn

<120> Compositions and Methods of Using RNA Interference for control of  
Nematodes

<130> BPS66376PC

<160> 107

<170> PatentIn version 3.4

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 Gly Gly Ser Pro Ile Glu Cys Trp Val Asn Pro His Ser Arg Glu Ser  
 50 55 60  
 Met Glu Glu Tyr Ile Glu Ala Phe Cys Trp Ile Gln Asn Thr Tyr Trp  
 65 70 75 80  
 Val Pro Met Tyr Glu His Ile Pro Asp Ser His Glu Ala Arg Glu Gly  
 85 90 95  
 Gln Gln Ile Gly Tyr Tyr Gln Trp Val Pro Phe Ile Leu Ile Ala Gln  
 100 105 110  
 Ala Leu Met Phe Ser Leu Pro Cys Ile Leu Trp Arg Leu Leu Asn Trp  
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 Gln Asn Gly Thr Asn Ile Gln Gln Leu Ile Ser Ala Ala Cys Glu Ala  
 130 135 140  
 Arg Ser Val Ile Asp Ala Asp Glu Arg Glu Arg Val Val Gly Ala Val  
 145 150 155 160  
 Ala Arg Thr Phe Val Glu Met Leu Asp Leu Arg Glu Ile Gln Asn Arg  
 165 170 175  
 Pro His Pro Tyr Ala Ser Ser Leu Ala Arg Phe Asn Pro Ile Arg Leu  
 180 185 190

Met Asn Gly His Leu Val Cys Ser Leu Tyr Leu Phe Thr Lys Val Cys  
 195 200 205

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

Val Gln Cys Ala Leu Ile Ile Asn Ile Ile Asn Glu Lys Val Phe Ala  
 275 280 285

Phe Phe Trp Leu Trp Tyr Cys Leu Leu Leu Cys Ala Thr Thr Cys Ser  
 290 295 300

Ala Leu Phe Trp Leu Ser Asn Ile Leu Leu His Ile Ala Arg Val Asp  
 305 310 315 320

Tyr Val Leu Lys Phe Met Gln Ile Ala Glu His Ser Glu Gln Gln Arg  
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Ser Ser Gly Arg Thr Pro Lys Leu Ser Gln Gln Lys Trp Ala Met Val  
 340 345 350

Glu Glu Gly Glu Met Pro Gln Phe Thr Lys Arg Pro Phe Arg Val Pro  
 355 360 365

Ser Ala His Ser Val Asp Lys Phe Val Asp Glu Phe Leu Lys Ser Asp  
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Gly Leu Phe Ile Leu Arg Leu Val Ala Thr Asn Ala Gly Glu Leu Val  
 385 390 395 400

Val Val Asp Ile Val Lys Cys Leu Trp Arg Glu Phe Ser Ser Arg Gln  
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Phe His Ile Arg Pro Leu Val Tyr Glu Asn Glu Leu Ser Glu Glu Arg  
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Arg Arg Glu Asp Glu Asp Ser His His Ser Leu Leu Leu Asn Val Tyr  
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Ser Ser Arg Gly Asn Gly Pro Thr His Gln Gln Gln Gln Arg Lys Gln  
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Ser Gln Gln Leu Arg Tyr Ser Thr Asn Gly Asn Ser Leu Gly Leu Pro  
 Seite 3

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Val Gly Thr Pro Ser Pro Val  
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ttgttcacca aagtgtgcta ttccgtcaac attatgctcc aatttgctct tctcaatgcc 180  
gcactgacct caaaagacca ttttctgttt gggtttcaag ttctgtccga cttttacgag 240  
ggaaaaccgt ggacaaagtc gggccatttt ccacgagtga ctctctgtga cttcgaagtg 300  
cgttatttgg ccaatttgaa cagatacact gtacaatgcg ctctgatcat taacattatc 360  
aacgaaaagg tgttcgcttt cttttggctt tggtagtgc tgcttttatg tgccacaacc 420  
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Gly His Leu Val Cys Ser Leu Tyr Leu Phe Thr Lys Val Cys Tyr Ser  
35 40 45

Val Asn Ile Met Leu Gln Phe Ala Leu Leu Asn Ala Ala Leu Thr Ser  
50 55 60

Lys Asp His Phe Leu Phe Gly Phe Gln Val Leu Ser Asp Leu Tyr Glu  
65 70 75 80

Gly Lys Pro Trp Thr Lys Ser Gly His Phe Pro Arg Val Thr Leu Cys  
85 90 95

Asp Phe Glu Val Arg Tyr Leu Ala Asn Leu Asn Arg Tyr Thr Val Gln  
100 105 110

Cys Ala Leu Ile Ile Asn Ile Ile Asn Glu Lys Val Phe Ala Phe Phe  
 115 120 125

Trp Leu Trp Tyr Cys Leu Leu Leu Cys Ala Thr Thr Cys Ser Ala Leu  
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Phe Trp Leu Ser Asn Ile Leu Leu His Ile Ala Arg Val Asp Tyr Val  
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Leu Lys Phe Met Gln Ile Ala Glu His  
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 ccgctgttgg cattgctctt gatgaaactg ccgtaattgc cgtacaacgt cgcgttcccg 180  
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 cagccagatg gaagtatgag aatggctatg aaatgccaat ttcggaactc gcgcgtaaaa 360  
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 agcatctgac ggcaattgag gagagagact gaggacgaaa gtgattttaa aacaacattt 780  
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 20 25 30

Asn Thr Ala Thr Leu Ser Ala Val Gly Ile Ala Leu Asp Glu Thr Ala  
           35                  40                  45

Val Ile Ala Val Gln Arg Arg Val Pro Asp Lys Leu Val Asp Pro Ser  
       50                  55                  60

Ser Val Lys Ser Ile Tyr Lys Leu Ser Ser Thr Val Ser Cys Gly Val  
       65                  70                  75                  80

Ile Gly Ile Val Pro Asp Ala Met Phe Gln Val Arg Arg Ala Gln Ser  
           85                  90                  95

Glu Ala Ala Arg Trp Lys Tyr Glu Asn Gly Tyr Glu Met Pro Ile Ser  
           100                  105                  110

Glu Leu Ala Arg Lys Met Ala Glu Ile Asn Gln Tyr Tyr Thr Gln Val  
       115                  120                  125

Ala Glu Leu Arg Ser Leu Gly Thr Leu Met Leu Met Ile Ser Tyr Asp  
       130                  135                  140

Asp Glu Lys Gly Ala Ser Val Phe Ser Ile Asp Pro Ala Gly His Tyr  
       145                  150                  155                  160

Ile Ser Val Arg Gly Tyr Gly Ile Gly Val Lys Gln Gln Gln Ile Asn  
           165                  170                  175

Gly Phe Leu Glu Lys Lys Leu Lys Ser Lys Asp Arg Lys Phe Gly Asp  
           180                  185                  190

Thr Glu Val Ile Gln Leu Ala Leu Glu Ala Leu Gln Thr Gly Leu Gly  
       195                  200                  205

Ile Asp Leu Lys Ala Asp Glu Val Glu Val Ile Val Ala Thr Lys Thr  
       210                  215                  220

Asp Pro Lys Gly Val Lys Val Ser Asp Lys Ser Ile Glu Glu His Leu  
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Thr Ala Ile Ala Glu Arg Asp  
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<212> DNA

<213> Heterodera glycines

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

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 <213> Globodera rostochiensis

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



Ile Ser Val Arg Gly Tyr Gly Ile Gly Val Lys Gln Gln Leu Val Asn  
165 170 175

Gly Phe Leu Glu Lys Lys Leu Lys Ala Lys Asp Arg Lys Phe Gly Glu  
180 185 190

Ala Glu Val Ile Gln Leu Ala Leu Glu  
195 200

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35 40 45

Ser Gly Arg Gly Glu His Gln Asn Val Gln Val Thr Asn Asp Gly Ala  
50 55 60

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

Val Asp Ile Ser Leu Thr Gln Asp Lys Glu Val Gly Asp Gly Thr Thr  
85 90 95

Ser Val Thr Val Phe Ala Ala Glu Leu Leu Arg Glu Ala Glu Val Met  
100 105 110

Ile Gly Gln Arg Ile His Pro Gln Val Ile Val Ser Gly Tyr Arg Lys  
115 120 125

Ala Val Arg Val Ala Lys Asp Ala Leu Glu Asn Ala Ala Gln Ala Ser  
130 135 140

Gly Glu His Leu Arg Glu Asp Leu Leu Lys Ile Ala Lys Thr Ser Leu  
145 150 155 160

Gly Ser Lys Ile Leu Ser Gln His Ser Asn His Phe Ala Lys Leu Ala  
165 170 175

Val Asp Ala Val Leu Arg Leu Gly Pro Asn Gly Ala Leu Asp Ser Ile  
180 185 190

Gln Val Ile Lys Lys Leu Gly Gly Ser Met Glu Asp Ser Tyr Leu Asp  
195 200 205

Glu Gly Phe Leu Leu Glu Lys Lys Ala Gly Met Tyr Gln Pro Gln Arg  
 210 215 220  
 Ile Glu Asp Ala Lys Ile Leu Ile Ala Asn Ser Pro Met Asp Gln Asp  
 225 230 235 240  
 Lys Ile Lys Val Phe Gly Ser Arg Ile Arg Val Asp Ser Val Ala Lys  
 245 250 255  
 Ile Ala Glu Leu Glu Gln Ala Glu Lys Asp Lys Met Lys Gln Lys Val  
 260 265 270  
 Glu Asn Ile Cys Asn His Gly Ile Asn Val Phe Ile Asn Arg Gln Leu  
 275 280 285  
 Ile Tyr Asn Tyr Pro Glu Gln Leu Phe Ala Asp Arg Lys Val Met Ala  
 290 295 300  
 Ile Glu His Ala Asp Phe Glu Gly Ile Glu Arg Leu Ala Leu Val Leu  
 305 310 315 320  
 Gly Gly Glu Ile Ala Ser Thr Phe Asp Ser Pro Ser Glu Val Lys Leu  
 325 330 335  
 Gly Ser Cys Glu Leu Ile Glu Glu Val Thr Val Gly Glu Asp Thr Leu  
 340 345 350  
 Leu Arg Phe Ser Gly Val Pro Leu Gly Asn Ala Cys Ser Val Val Leu  
 355 360 365  
 Arg Gly Ser Thr Gln Gln Ile Ile Asp Glu Ala Glu Arg Ser Leu His  
 370 375 380  
 Asp Ala Leu Cys Val Leu Ser Thr His Val Lys Asp Gln Arg Val Val  
 385 390 395 400  
 Pro Gly Ala Gly Ala Ser Glu Met Leu Met Ala Met Ala Val Met Gly  
 405 410 415  
 Glu Ser Gln Lys Val Ala Gly Lys Glu Ser Ile Ala Met Glu Ala Phe  
 420 425 430  
 Ala Arg Ala Leu Ala Lys Leu Pro Thr Ile Ile Cys Asp Asn Ala Gly  
 435 440 445  
 Leu Asp Ser Ala Glu Ile Ile Ser His Val Arg Ala Glu His Ser Lys  
 450 455 460  
 Gly Asn Arg Gln Phe Gly Ile Asp Val Glu Asn Gly Arg Met Ala Asp  
 465 470 475 480

Val Tyr Glu Leu Gly Val Leu Glu Ser Tyr Asn Val Lys Leu Gly Val  
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Leu Cys Ser Gly Ala Glu Ala Ala Glu Gln Leu Leu Arg Val Asp Cys  
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Ile Ile Lys Cys Ala Pro Arg Pro Arg Thr Lys Asp Arg Arg Pro Cys  
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 agaaagtgga gaatatttgc aatcacggca tcaatgtgtt catcaatcgt cagctcattt 180  
 acaattaccc cgaacaattg ttcgctgata ggaaagtgat ggccatcgaa cagcccgact 240  
 ttgagggcat cgaacgattg gcacttgtat taggtggcga aattgcttca acatttgaca 300  
 gtccatcgga ggtgaaattg ggtagctgag aactcattga agaagtcacc gttggcgaag 360  
 acactttgct ccgcttttcc ggtgtccgcg ttggcaatgc atgttccggt gtgcttcgtg 420  
 ggtccacca gcaaatcatt gatgaagcag aacgttcggt gcacgacgag ctttgtgtgc 480  
 tgagtacgca tgtgaaagac 500

<210> 14  
 <211> 166  
 <212> PRT  
 <213> Heterodera glycines

<400> 14  
 Leu Ile Ala Asn Ser Pro Met Asp Gln Asp Lys Ile Lys Val Phe Gly  
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 Ser Arg Ile Arg Val Asp Ser Val Ala Lys Ile Ala Glu Leu Glu Gln  
                   20                                  25                                  30  
 Ala Glu Lys Asp Lys Met Lys Gln Lys Val Glu Asn Ile Cys Asn His  
                   35                                  40                                  45  
 Gly Ile Asn Val Phe Ile Asn Arg Gln Leu Ile Tyr Asn Tyr Pro Glu  
                   50                                  55                                  60  
 Gln Leu Phe Ala Asp Arg Lys Val Met Ala Ile Glu His Ala Asp Phe  
 65                  70                                  75                                  80  
 Glu Gly Ile Glu Arg Leu Ala Leu Val Leu Gly Gly Glu Ile Ala Ser  
                   85                                  90                                  95

Thr Phe Asp Ser Pro Ser Glu Val Lys Leu Gly Ser Cys Glu Leu Ile  
 100 105 110

Glu Glu Val Thr Val Gly Glu Asp Thr Leu Leu Arg Phe Ser Gly Val  
 115 120 125

Pro Leu Gly Asn Ala Cys Ser Val Val Leu Arg Gly Ser Thr Gln Gln  
 130 135 140

Ile Ile Asp Glu Ala Glu Arg Ser Leu His Asp Ala Leu Cys Val Leu  
 145 150 155 160

Ser Thr His Val Lys Asp  
 165

<210> 15  
 <211> 585  
 <212> DNA  
 <213> Heterodera schachtii

<400> 15  
 atcgagcgat tggcactcgt tttaggcatg tttcgtcgca attcctattc ctaatttgaa 60  
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 tccatcggag gtgaaattgg gtagctgcaa actcattgaa gaagtcaccg ttggcgaaga 180  
 cactttgctc cgcttttccg gtgtcccgct tggcaatgctg tgttccggtg tgcttcgtgg 240  
 gtccaccag caaatcattg atgaagcgga acgttcgttg cacgacgcgc tttgtgtgct 300  
 gagtacgcat gtgaaagacc aacgcgtggg gcccgggcg ggcgcacatcg aaatgtcat 360  
 ggcaatggca gtgatggcg aaagtcaaaa ggtggccggg aaggagtcca tcgcaatgga 420  
 agcattcgca cgggcactcg ccaaattgcc cacaatcatt tgcgacaacg ccggactgga 480  
 cagtgccgaa atcatttcgc atgtgcgagc cgaacacagc aaagggaatc accaatttgg 540  
 cattgatgtt gaaaatggtc gtatggcgga tgtttacgag ttggg 585

<210> 16  
 <211> 164  
 <212> PRT  
 <213> Heterodera schachtii

<400> 16

Gly Gly Glu Ile Ala Ser Thr Phe Asp Ser Pro Ser Glu Val Lys Leu  
 1 5 10 15

Gly Ser Cys Lys Leu Ile Glu Glu Val Thr Val Gly Glu Asp Thr Leu  
 20 25 30

Leu Arg Phe Ser Gly Val Pro Leu Gly Asn Ala Cys Ser Val Val Leu  
 35 40 45

Arg Gly Ser Thr Gln Gln Ile Ile Asp Glu Ala Glu Arg Ser Leu His  
 50 55 60

Asp Ala Leu Cys Val Leu Ser Thr His Val Lys Asp Gln Arg Val Val  
65 70 75 80

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

Glu Ser Gln Lys Val Ala Gly Lys Glu Ser Ile Ala Met Glu Ala Phe  
100 105 110

Ala Arg Ala Leu Ala Lys Leu Pro Thr Ile Ile Cys Asp Asn Ala Gly  
115 120 125

Leu Asp Ser Ala Glu Ile Ile Ser His Val Arg Ala Glu His Ser Lys  
130 135 140

Gly Asn His Gln Phe Gly Ile Asp Val Glu Asn Gly Arg Met Ala Asp  
145 150 155 160

Val Tyr Glu Leu

<210> 17  
<211> 1590  
<212> DNA  
<213> Caenorhabditis elegans

<400> 17  
atgcttccag tccaaatttt aaaggacaat gctcaagagg aacgaggaga gagcgctcgt 60  
ctcagctcat tcgtgggtgc aatcgccatc ggagatcttg tcaagtctac tcttggaacca 120  
aagggaatgg acaaaattct catcagtggg aaccagaaaa gcgcaggagg aatcaaagtt 180  
accaacgatg gagcaacgat cctgaagtca atcgggtgttg acaatccagc tgctaagggtt 240  
cttggtgata tgtcaatgac acaggatcac gaagttggag atggtactac ttcagtaact 300  
gtcctggccg cagagctcct caaagaagcc gagaaacttg tcaatcaacg tattcatcca 360  
cagacgatca tttctggata tagacgtgct ctcgggattg ctcaagaatc cttgaaaaag 420  
tccagcattg aatccggaga taatattcgt gatgatcttt tgaagattgc ccgtactact 480  
cttggtatcta agattctcag tcaacacaaa gagcactttg ctcaactcgc cgttgatgca 540  
gttttgagac tcaagggatc tggaaatttg gatgccattc aaattatcaa gaagctcgga 600  
ggatccatga atgaatctta tctcgacgag ggtttccttc tcgaaaaact ccctggaatg 660  
ttccaaccaa gaagagttga gaaagcaaag attctcattg ccaacacacc aatggacact 720  
gacaaagtga aagttttcgg atcaagagtg agagtagatg gtgttgccaa ggttgctgaa 780  
ctcgaagctg ctgagaaatt gaagatgaaa gaaaaagttg acaaaattct ggcccataac 840  
tgtaatgtct tcatcaaccg tcagttgatc tacaactacc cagagcaact ttttgccgat 900  
gctaaggtta tggctattga acacgccgat tttgaaggaa tcgagaggct tgctcttggtt 960  
ctcggaggag aaattgtttc cacatttgat tcaccacaaa ctgctcaatt cggatcttgt 1020

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 gaaagatccc tccatgatgc cctttgtgtt ctcgttactc acgtgaaaga atcaaagact 1200  
 gttgccggag ctggagcgag cgaaattttg atgagttcag ccatcgccgt cgaagctcaa 1260  
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 ccaaccatca tttgcgacaa tgctggactt gactcggctg aacttgtcac aagactccgt 1380  
 gcagagcacg ccaatggacg tcacaatatg ggaatcgaca tcgagaaagg agaggttgct 1440  
 gatgttacga aattgggcgt tattgagtct tacaatgtga agttgtgcat ggtttcttcc 1500  
 gccgctgaag ccacggaaca aattcttcgc gtcgacgata tcatcaaggc agctccacgt 1560  
 gcccgtgctc aagataaccg accatgctaa 1590

<210> 18  
 <211> 529  
 <212> PRT  
 <213> Caenorhabditis elegans

<400> 18

Met Leu Pro Val Gln Ile Leu Lys Asp Asn Ala Gln Glu Glu Arg Gly  
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Glu Ser Ala Arg Leu Ser Ser Phe Val Gly Ala Ile Ala Ile Gly Asp  
 20 25 30

Leu Val Lys Ser Thr Leu Gly Pro Lys Gly Met Asp Lys Ile Leu Ile  
 35 40 45

Ser Gly Asn Pro Glu Ser Ala Gly Gly Ile Lys Val Thr Asn Asp Gly  
 50 55 60

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

Leu Val Asp Met Ser Met Thr Gln Asp His Glu Val Gly Asp Gly Thr  
 85 90 95

Thr Ser Val Thr Val Leu Ala Ala Glu Leu Leu Lys Glu Ala Glu Lys  
 100 105 110

Leu Val Asn Gln Arg Ile His Pro Gln Thr Ile Ile Ser Gly Tyr Arg  
 115 120 125

Arg Ala Leu Gly Ile Ala Gln Glu Ser Leu Lys Lys Ser Ser Ile Glu  
 130 135 140

Ser Gly Asp Asn Ile Arg Asp Asp Leu Leu Lys Ile Ala Arg Thr Thr  
 145 150 155 160

Leu Gly Ser Lys Ile Leu Ser Gln His Lys Glu His Phe Ala Gln Leu  
 Seite 15

165

170

175

Ala Val Asp Ala Val Leu Arg Leu Lys Gly Ser Gly Asn Leu Asp Ala  
 180 185 190  
 Ile Gln Ile Ile Lys Lys Leu Gly Gly Ser Met Asn Glu Ser Tyr Leu  
 195 200 205  
 Asp Glu Gly Phe Leu Leu Glu Lys Leu Pro Gly Met Phe Gln Pro Arg  
 210 215 220  
 Arg Val Glu Lys Ala Lys Ile Leu Ile Ala Asn Thr Pro Met Asp Thr  
 225 230 235 240  
 Asp Lys Val Lys Val Phe Gly Ser Arg Val Arg Val Asp Gly Val Ala  
 245 250 255  
 Lys Val Ala Glu Leu Glu Ala Ala Glu Lys Leu Lys Met Lys Glu Lys  
 260 265 270  
 Val Asp Lys Ile Leu Ala His Asn Cys Asn Val Phe Ile Asn Arg Gln  
 275 280 285  
 Leu Ile Tyr Asn Tyr Pro Glu Gln Leu Phe Ala Asp Ala Lys Val Met  
 290 295 300  
 Ala Ile Glu His Ala Asp Phe Glu Gly Ile Glu Arg Leu Ala Leu Val  
 305 310 315 320  
 Leu Gly Gly Glu Ile Val Ser Thr Phe Asp Ser Pro Gln Thr Ala Gln  
 325 330 335  
 Phe Gly Ser Cys Asp Leu Ile Glu Glu Ile Met Ile Gly Glu Asp Arg  
 340 345 350  
 Leu Leu Arg Phe Ser Gly Val Lys Leu Gly Glu Ala Cys Ser Val Val  
 355 360 365  
 Leu Arg Gly Ala Thr Gln Gln Ile Leu Asp Glu Ser Glu Arg Ser Leu  
 370 375 380  
 His Asp Ala Leu Cys Val Leu Val Thr His Val Lys Glu Ser Lys Thr  
 385 390 395 400  
 Val Ala Gly Ala Gly Ala Ser Glu Ile Leu Met Ser Ser Ala Ile Ala  
 405 410 415  
 Val Glu Ala Gln Lys Val Ala Gly Lys Glu Ser Leu Ala Val Glu Ala  
 420 425 430  
 Phe Gly Arg Ala Leu Ala Gln Leu Pro Thr Ile Ile Cys Asp Asn Ala  
 435 440 445



Gly Leu Asp Ser Ala Glu Leu Val Thr Arg Leu Arg Ala Glu His Ala  
 450 455 460

Asn Gly Arg His Asn Met Gly Ile Asp Ile Glu Lys Gly Glu Val Ala  
 465 470 475 480

Asp Val Thr Lys Leu Gly Val Ile Glu Ser Tyr Asn Val Lys Leu Cys  
 485 490 495

Met Val Ser Ser Ala Ala Glu Ala Thr Glu Gln Ile Leu Arg Val Asp  
 500 505 510

Asp Ile Ile Lys Ala Ala Pro Arg Ala Arg Ala Gln Asp Asn Arg Pro  
 515 520 525

Cys

<210> 19  
 <211> 1508  
 <212> DNA  
 <213> Heterodera glycines

<400> 19  
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 tcaaacaaaa acctattatt ctctaaaacc aattaatgga cgtggacgat ttgctagatt 120  
 ccttttccaa atcaacgggtc acagcggaca acgaattcgg tgtcaccagt gccaccgccg 180  
 ttggtggtgg gggtgctgag gatggcattg gcgcccagca gcagcagcag tgggaggcgg 240  
 cacagcacc gcattttggc cgcaactaca aaaatgaggg ccgagtggcc gcgctgcagc 300  
 gccaacgccg tcaggaacac ttggagagac agcattttggc tcgcgaggat tggctgaggc 360  
 gccgccgtga aattgaagat gatgagtcgt cgtcattttt gcgtcgtgtg cggcagaaaa 420  
 ggcagaaccc gtacaaggac atgttgatgt tcagcgattg gcttgttgac attccaggca 480  
 ctttgtccac cgagtggaca atgcttccgt cgccggtcgg acgtcgcact ttggttgtgg 540  
 ccaacagagg cgaaacgcga gtgtacttca aaaatgggca tttggccacc aattttcatt 600  
 cacttttgcc gggaggaaat gccaaaacga aaggttctct gaccattttg gacgccattt 660  
 ttgacgcgaa gaagcggaag ttgtacctgc ttgatttgct ctggtggaac aagctgatgt 720  
 acacggacat ggaattcacc gcgcgtcgct tctttctcca gtcgcgcatt gacgaaatga 780  
 acgaggacat tgagcggaaa aacagcaggg ccagcatcag caaaaatcag gaacgaaatg 840  
 gttgcaaaat tgcggagcag gacaaaatgt cgtcttccga aatctcgccg tacgaaatgt 900  
 caccgccgag cgacacgtcg cctgaacaaa acgccgtcga gccaaaatct cgccgtgaca 960  
 ttaaatttgt gcctgtgccc tcttgcgctt gttctccgga cgaaattggc caatttatgc 1020  
 gcaccctttt tacattccgt atcgacgggc tgctgttcta ctacaactcg gccttttaca 1080  
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ttcgagacgc ccctcgttgg ttggcttaag ccgtggatgc ttccagaggt ccttggagtg 1200
ccggtgcccc agctgtacaa ggaggaaatg gcatgcggaa gttcccagga gttcattgac 1260
cagttcaaca aggagcacgg gcacgtttcg tcggcggaaa aatatcggca gaaagcgcag 1320
tcgccggaca tgacaatgga cgaggcgaac gcaaatgccg acgaatggac ggagggcaaa 1380
gagatgggca cggcatggaa ggaggaggga gaagagcaga gcaaaaatgg aggataaaga 1440
gatgaaaacg gcacaagaga agcggacgga ccgagacttc ggcacttttt gacccaaaaa 1500
aaaaaaaaa 1508

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<210> 20
<211> 357
<212> PRT
<213> Heterodera glycines
<400> 20

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Met Asp Val Asp Asp Leu Leu Asp Ser Phe Ser Lys Ser Thr Val Thr
1          5          10          15

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Ala Asp Asn Glu Phe Gly Val Thr Ser Ala Thr Ala Val Gly Gly Gly
20          25          30

```

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Gly Ala Glu Asp Gly Ile Gly Ala Gln Gln Gln Gln Gln Trp Glu Ala
35          40          45

```

```

Ala Gln His Pro His Phe Gly Arg Asn Tyr Lys Asn Glu Gly Arg Val
50          55          60

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Ala Ala Leu Gln Arg Gln Arg Arg Gln Glu His Leu Glu Arg Gln His
65          70          75          80

```

```

Leu Ala Arg Glu Asp Trp Leu Arg Arg Arg Arg Glu Ile Glu Asp Asp
85          90          95

```

```

Glu Ser Ser Ser Phe Leu Arg Arg Val Arg Gln Lys Arg Gln Asn Pro
100          105          110

```

```

Tyr Lys Asp Met Leu Met Phe Ser Asp Trp Leu Val Asp Ile Pro Gly
115          120          125

```

```

Thr Leu Ser Thr Glu Trp Thr Met Leu Pro Ser Pro Val Gly Arg Arg
130          135          140

```

```

Thr Leu Val Val Ala Asn Arg Gly Glu Thr Arg Val Tyr Phe Lys Asn
145          150          155          160

```

```

Gly His Leu Ala Thr Asn Phe His Ser Leu Leu Pro Gly Gly Asn Ala
165          170          175

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```

Lys Thr Lys Gly Ser Leu Thr Ile Leu Asp Ala Ile Phe Asp Ala Lys
180          185          190

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Lys Arg Lys<sub>195</sub> Leu Tyr Leu Leu Asp<sub>200</sub> Leu Leu Trp Trp Asn<sub>205</sub> Lys Leu Met  
 Tyr Thr<sub>210</sub> Asp Met Glu Phe Thr<sub>215</sub> Ala Arg Arg Phe<sub>220</sub> Phe Leu Gln Ser Arg  
 Ile Asp Glu Met Asn Glu<sub>230</sub> Asp Ile Glu Arg Lys<sub>235</sub> Asn Ser Arg Ala Ser<sub>240</sub>  
 Ile Ser Lys Asn<sub>245</sub> Gln Glu Arg Asn Gly Cys<sub>250</sub> Lys Ile Ala Glu Gln<sub>255</sub> Asp  
 Lys Met Ser Ser<sub>260</sub> Ser Glu Ile Ser Pro<sub>265</sub> Tyr Glu Met Ser Pro<sub>270</sub> Pro Ser  
 Asp Thr Ser<sub>275</sub> Pro Glu Gln Asn Ala<sub>280</sub> Val Glu Pro Lys Ser<sub>285</sub> Arg Arg Asp  
 Ile Lys<sub>290</sub> Phe Val Pro Val Pro<sub>295</sub> Ser Cys Ala Cys Ser<sub>300</sub> Pro Asp Glu Ile  
 Gly Gln Phe Met Arg Thr<sub>310</sub> Leu Phe Thr Phe Arg<sub>315</sub> Ile Asp Gly Leu Leu<sub>320</sub>  
 Phe Tyr Tyr Asn Ser<sub>325</sub> Ala Phe Tyr Ile Pro<sub>330</sub> Glu Gln Val Ala Glu<sub>335</sub> Phe  
 Cys Phe Gln Leu<sub>340</sub> Phe Leu Phe Glu Phe<sub>345</sub> Phe Leu Val Phe Arg<sub>350</sub> Asp Ala  
 Pro Arg Trp<sub>355</sub> Leu Ala

<210> 21  
 <211> 160  
 <212> DNA  
 <213> Heterodera glycines

<400> 21  
 gaattcaccg cgcgtcgctt ctttctccag tcgcgattg acgaaatgaa cgaggacatt 60  
 gagcgga aaa acagcagggc cagcatcagc aaaaatcagg aacgaaatgg ttgcaaaatt 120  
 gcggagcagg acaaaatgtc gtcttccgaa atctcgccgt 160

<210> 22  
 <211> 53  
 <212> PRT  
 <213> Heterodera glycines

<400> 22

Glu Phe Thr Ala Arg Arg Phe Phe Leu Gln Ser Arg Ile Asp Glu Met  
 1 5 10 15

Asn Glu Asp Ile Glu Arg Lys Asn Ser Arg Ala Ser Ile Ser Lys Asn  
                   20                                  25                                  30

Gln Glu Arg Asn Gly Cys Lys Ile Ala Glu Gln Asp Lys Met Ser Ser  
                   35                                  40                                  45

Ser Glu Ile Ser Pro  
           50

<210> 23  
 <211> 1686  
 <212> DNA  
 <213> Heterodera glycines

<400> 23  
 ttgtcatcca tttatttgtg cttatattgt gcaatcaata tttgcccttt gccctccgtc 60  
 cctcttcgct tattttttta ttttgtgtct tcacaacttg aataaaataa ttgtttatac 120  
 acttcgccgc tgacttatgg tgaagcaaca ggaacgcata tcttttcctt tctcagttga 180  
 ctcaaagcgt tttttacttt tgcccaccga ttttgtggat gaaaaaagca aattttttcaa 240  
 ccgtcagttt ctcaccattt atcgggcacg gattaattgt cttaaagact taattaaaaa 300  
 aaatgcgcga aatattcttg cttctacctc caataattct gttcaaatcg atgatttatc 360  
 aaatttttct gccggcaatg atattttgct gatcgggtgtt gttttcaaga aaatgaaatt 420  
 ccgtcaaagc attcttttac agttttcgga tgattcgaat gttcccatta aaatggggag 480  
 aaaagcgggc gacaaccttt gcgatgacga ggacatactc caattggagg acgaccagca 540  
 gactgttaaa ttgcttgtaa acattgacaa acattgtttt gtcactggcg atgtcattgg 600  
 agtgatcggc tgtcaggagg atgtatcaga caattttgaa gtgcgaatga ttatttacct 660  
 ggaaatgagc cctcaattgg aatggccttt ggttgagcat gattgttata ttgtttttat 720  
 gtccggcatt tcattagttg gcaattttga caacgatgtc caaacgtttt cggcactgat 780  
 gcagtttcag cgggtggataa acggggaggt ggaggtgtca aaggacggca ctgatttgag 840  
 tgatgagggc gaggacgagt cggacacttt gcgcaacatc gccagacttg tcattgctgg 900  
 tgattttgcg cgttttgcac agaatgacat tgaaactcag cgagtttcga tgattggcgc 960  
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 ccaacagcca attccccccg cgggtgttcac tttggcggcg ccgttccaac caatgcttaa 1140  
 cacagtgacc aatccctaca gtttcgagct caacggagtc cgtttttttg ggacatcagg 1200  
 tcaaaacatc aatgatttgc ggcggttgac acgcggaaag gacacattag cattgatgga 1260  
 acgcacgttg gaaatgggct atattttccc gacagtcccc gacactcttc ccggatttcc 1320  
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 tcagccaacc tttgaaaaac gaatcgttga atttggcgga aaaccaacga aaagatgttg 1440  
 ccttttggct gttcctaagt tttgcaagac aaaatcagtt attctgctga atttacggac 1500

tcttgaatcc aatgaatact gttttggtgc aaatttcaat gaatcagggtc aatagaagtt 1560  
 cgagaagggt catttgatct caattttatg cttgcattta tttaaaagcg attggccaat 1620  
 tactccaaac gtcactttca ttgataaaca cataaaattg caaaaaaaaa aaaaaaaaaa 1680  
 aaaaaa 1686

<210> 24  
 <211> 472  
 <212> PRT  
 <213> Heterodera glycines  
 <400> 24

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

210

215

220

Val Glu Val Ser Lys Asp Gly Thr Asp Leu Ser Asp Glu Gly Glu Asp  
 225 230 235 240  
 Glu Ser Asp Thr Leu Arg Asn Ile Ala Arg Leu Val Ile Ala Gly Asp  
 245 250 255  
 Phe Ala Arg Phe Ala Gln Asn Asp Ile Glu Thr Gln Arg Val Ser Met  
 260 265 270  
 Ile Gly Ala Glu Leu Asp Ser Asp Met Asp Ser Phe Ser Gln Phe Asp  
 275 280 285  
 Lys Phe Leu Ala Thr Leu Leu Gln Asn Leu Arg Val Asp Leu Met Pro  
 290 295 300  
 Gly Ala Ser Asp Pro Val Gln Cys Met Ile Pro Gln Gln Pro Ile Pro  
 305 310 315 320  
 Pro Ala Val Phe Thr Leu Ala Ala Pro Phe Gln Pro Met Leu Asn Thr  
 325 330 335  
 Val Thr Asn Pro Tyr Ser Phe Glu Leu Asn Gly Val Arg Phe Leu Gly  
 340 345 350  
 Thr Ser Gly Gln Asn Ile Asn Asp Leu Arg Arg Leu Thr Arg Gly Lys  
 355 360 365  
 Asp Thr Leu Ala Leu Met Glu Arg Thr Leu Glu Met Gly Tyr Ile Phe  
 370 375 380  
 Pro Thr Val Pro Asp Thr Leu Pro Gly Phe Pro Phe Ser Gly Arg Asp  
 385 390 395 400  
 Pro Leu Val Leu Asp Gln Ile Pro His Ile Tyr Phe Val Gly Asn Gln  
 405 410 415  
 Pro Thr Phe Glu Lys Arg Ile Val Glu Phe Gly Gly Lys Pro Thr Lys  
 420 425 430  
 Arg Cys Cys Leu Leu Ala Val Pro Lys Phe Cys Lys Thr Lys Ser Val  
 435 440 445  
 Ile Leu Leu Asn Leu Arg Thr Leu Glu Ser Asn Glu Tyr Cys Phe Gly  
 450 455 460  
 Ala Asn Phe Asn Glu Ser Gly Gln  
 465 470

<210> 25  
 <211> 224

<212> DNA  
 <213> Heterodera glycines  
 <400> 25  
 cgcgacccgc ttgttttggg ccaaattccg cacatttatt tcgtcgggaa tcagccaacc 60  
 ttgaaaaaac gaatcgttga atttggcgga aaaccaacga aaagatgttg ctttttggct 120  
 gttcctaagt ttgcaagac aaaatcagtt attctgctga atttacggac tcttgaatcc 180  
 aatgaatact gttttggtgc aaatttcaat gaatcaggtc aata 224

<210> 26  
 <211> 74  
 <212> PRT  
 <213> Heterodera glycines  
 <400> 26  
 Arg Asp Pro Leu Val Leu Asp Gln Ile Pro His Ile Tyr Phe Val Gly  
 1 5 10 15  
 Asn Gln Pro Thr Phe Glu Lys Arg Ile Val Glu Phe Gly Gly Lys Pro  
 20 25 30  
 Thr Lys Arg Cys Cys Leu Leu Ala Val Pro Lys Phe Cys Lys Thr Lys  
 35 40 45  
 Ser Val Ile Leu Leu Asn Leu Arg Thr Leu Glu Ser Asn Glu Tyr Cys  
 50 55 60  
 Phe Gly Ala Asn Phe Asn Glu Ser Gly Gln  
 65 70

<210> 27  
 <211> 575  
 <212> DNA  
 <213> Heterodera glycines  
 <400> 27  
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 cgatcactcg ttgtaaactc aagctcctca agtatgaccg gattaaggac tatcttttaa 180  
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<210> 28  
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&lt;212&gt; PRT

&lt;213&gt; Heterodera glycines

&lt;400&gt; 28

Gly Gln Asp Pro Glu Lys Lys Arg Lys Tyr His Gly Pro Pro Val Pro  
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Thr Arg Ile Gly Lys Arg Lys Lys Gly Ser Arg Gly Pro Asp Thr Ala  
 20 25 30

Asn Lys Met Pro Thr Val Thr Pro Ile Thr Arg Cys Lys Leu Lys Leu  
 35 40 45

Leu Lys Tyr Asp Arg Ile Lys Asp Tyr Leu Leu Met Glu Glu Glu Phe  
 50 55 60

Ile Lys Asn Met Glu Arg Leu Lys Pro Gln Asp Glu Arg Gln Glu Glu  
 65 70 75 80

Glu Arg Val Lys Val Asp Asp Leu Arg Gly Thr Pro Met Ser Val Gly  
 85 90 95

Ser Leu Glu Glu Val Ile Asp Asp Gln His Ala Ile Val Ser Thr Asn  
 100 105 110

Val Gly Ser Glu His Tyr Val Asn Ile Leu Ser Phe Val Asp Lys Glu  
 115 120 125

Gln Leu Glu Pro Gly Cys Ala Val Leu Leu Asn His Lys Thr His Ser  
 130 135 140

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

Lys Leu Glu Lys Ala Pro Thr Glu Thr Tyr Ala Asp Val Gly Gly Leu  
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Glu Gln Gln Ile Gln Glu Ile Lys Glu Ala Val Glu Leu Pro Leu  
 180 185 190

&lt;210&gt; 29

&lt;211&gt; 498

&lt;212&gt; DNA

&lt;213&gt; Heterodera glycines

&lt;400&gt; 29

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cgtttgaagc ctcaggacga acgtcaggag gaagagcgtg tttaaagttga cgaccttcgt	240
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 cttgagccgg gctgtgccgt tctgtgaat cacaaaaccc actcaatcgt cggcgttctt 420  
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 <211> 166  
 <212> PRT  
 <213> Heterodera glycines  
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Ser Arg Gly Pro Asp Thr Ala Asn Lys Met Pro Thr Val Thr Pro Ile  
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Thr Arg Cys Lys Leu Lys Leu Leu Lys Tyr Asp Arg Ile Lys Asp Tyr  
 35 40 45

Leu Leu Met Glu Glu Glu Phe Ile Lys Asn Met Glu Arg Leu Lys Pro  
 50 55 60

Gln Asp Glu Arg Gln Glu Glu Arg Val Lys Val Asp Asp Leu Arg  
 65 70 75 80

Gly Thr Pro Met Ser Val Gly Ser Leu Glu Glu Val Ile Asp Asp Gln  
 85 90 95

His Ala Ile Val Ser Thr Asn Val Gly Ser Glu His Tyr Val Asn Ile  
 100 105 110

Leu Ser Phe Val Asp Lys Glu Gln Leu Glu Pro Gly Cys Ala Val Leu  
 115 120 125

Leu Asn His Lys Thr His Ser Ile Val Gly Val Leu Ala Glu Asp Ala  
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Asp Pro Met Val Ser Val Met Lys Leu Glu Lys Ala Pro Thr Glu Thr  
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Tyr Ala Asp Val Gly Gly  
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<210> 31  
 <211> 1332  
 <212> DNA  
 <213> Caenorhabditis briggsae

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 gaaaagaaag aaaagaagaa gtatgaggct ccaattccat caagaatcgg aaaaaagaag 120  
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<210> 32  
 <211> 443  
 <212> PRT  
 <213> Caenorhabditis briggsae

<400> 32

Met Gly Gln Gln Gln Ser Gly Phe Gly Gly Arg Gly Asn Asp Arg Gly  
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Ser Gly Asp Asn Glu Lys Lys Glu Lys Lys Lys Tyr Glu Ala Pro Ile  
 20 25 30

Pro Ser Arg Ile Gly Lys Lys Lys Lys Gly Ser Lys Gly Pro Asp Ala  
 35 40 45

Ala Ser Lys Leu Pro Ala Val Thr Pro His Ala Arg Cys Arg Leu Lys  
 50 55 60

Leu Leu Lys Ser Glu Arg Ile Lys Asp Tyr Leu Leu Met Glu Gln Glu  
 65 70 75 80

Phe Ile Gln Asn Gln Glu Arg Leu Lys Pro Gln Glu Glu Arg Gln Glu  
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 Glu Glu Arg Ala Lys Val Asp Glu Leu Arg Gly Thr Pro Met Ala Val  
 100 105 110  
 Gly Ser Leu Glu Glu Ile Ile Asp Asp Gln His Ala Ile Val Ser Thr  
 115 120 125  
 Asn Val Gly Ser Glu His Tyr Val Asn Ile Met Ser Phe Val Asp Lys  
 130 135 140  
 Glu Gln Leu Glu Pro Gly Cys Ser Val Leu Leu Asn His Lys Asn His  
 145 150 155 160  
 Ala Val Ile Gly Val Leu Ser Asp Asp Thr Asp Pro Met Val Ser Val  
 165 170 175  
 Met Lys Leu Glu Lys Ala Pro Gln Glu Thr Tyr Ala Asp Val Gly Gly  
 180 185 190  
 Leu Asp Gln Gln Ile Gln Glu Ile Lys Glu Ala Val Glu Leu Pro Leu  
 195 200 205  
 Thr His Pro Glu Tyr Tyr Glu Glu Met Gly Ile Arg Pro Pro Lys Gly  
 210 215 220  
 Val Ile Leu Tyr Gly Cys Pro Gly Thr Gly Lys Thr Leu Leu Ala Lys  
 225 230 235 240  
 Ala Val Ala Asn Gln Thr Ser Ala Thr Phe Leu Arg Ile Val Gly Ser  
 245 250 255  
 Glu Leu Ile Gln Lys Tyr Leu Gly Asp Gly Pro Lys Met Val Arg Glu  
 260 265 270  
 Leu Phe Arg Val Ala Glu Glu Asn Ala Pro Ser Ile Val Phe Ile Asp  
 275 280 285  
 Glu Ile Asp Ala Val Gly Thr Lys Arg Tyr Asp Ser Asn Ser Gly Gly  
 290 295 300  
 Glu Arg Glu Ile Gln Arg Thr Met Leu Glu Leu Leu Asn Gln Leu Asp  
 305 310 315 320  
 Gly Phe Asp Ser Arg Gly Asp Val Lys Val Leu Met Ala Thr Asn Arg  
 325 330 335  
 Ile Glu Ser Leu Asp Pro Ala Leu Ile Arg Pro Gly Arg Ile Asp Arg  
 340 345 350

Lys Ile Glu Phe Pro Leu Pro Asp Glu Lys Thr Lys Arg Arg Ile Phe  
 355 360 365

Gln Ile His Thr Ser Arg Met Thr Leu Gly Asp Asp Val Asn Leu Glu  
 370 375 380

Glu Phe Ile Thr Ala Lys Asp Glu Leu Ser Gly Ala Asp Ile Lys Ala  
 385 390 395 400

Met Cys Thr Glu Ala Gly Leu Leu Ala Leu Arg Glu Arg Arg Met Arg  
 405 410 415

Val Thr Met Glu Asp Phe Gln Lys Ser Lys Glu Asn Val Leu Tyr Arg  
 420 425 430

Lys Lys Glu Gly Ala Pro Glu Glu Leu Tyr Leu  
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 <213> Caenorhabditis elegans

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 tgccgtctga agttgctgaa gagcgaaaga atcaaggatt atttgttgat ggagcaagaa 240  
 ttcatcaaaa accaggagcg tttgaagcca caagaggaga gacaagaaga agagcgcgcc 300  
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<210> 34  
 <211> 443  
 <212> PRT  
 <213> Caenorhabditis elegans  
 <400> 34

Met Gly Gln Gln Gln Ser Gly Phe Gly Gly Arg Gly Asn Asp Arg Gly  
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Ala Gly Asp Gly Glu Lys Lys Glu Lys Lys Lys Tyr Glu Ala Pro Ile  
 20 25 30

Pro Ser Arg Ile Gly Lys Lys Lys Lys Gly Ser Lys Gly Pro Asp Ala  
 35 40 45

Ala Ser Lys Leu Pro Ala Val Thr Pro His Ala Arg Cys Arg Leu Lys  
 50 55 60

Leu Leu Lys Ser Glu Arg Ile Lys Asp Tyr Leu Leu Met Glu Gln Glu  
 65 70 75 80

Phe Ile Gln Asn Gln Glu Arg Leu Lys Pro Gln Glu Glu Arg Gln Glu  
 85 90 95

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

Gly Ser Leu Glu Glu Ile Ile Asp Asp Gln His Ala Ile Val Ser Thr  
 115 120 125

Asn Val Gly Ser Glu His Tyr Val Asn Ile Met Ser Phe Val Asp Lys  
 130 135 140

Glu Gln Leu Glu Pro Gly Cys Ser Val Leu Leu Asn His Lys Asn His  
 145 150 155 160

Ala Val Ile Gly Val Leu Ser Asp Asp Thr Asp Pro Met Val Ser Val  
 165 170 175

Met Lys Leu Glu Lys Ala Pro Gln Glu Thr Tyr Ala Asp Val Gly Gly  
 180 185 190

Leu Asp Gln Gln Ile Gln Glu Ile Lys Glu Ala Val Glu Leu Pro Leu  
 195 200 205

Thr His Pro Glu Tyr Tyr Glu Glu Met Gly Ile Arg Pro Pro Lys Gly  
 Seite 29

210

215

220

Val Ile Leu Tyr Gly Cys Pro Gly Thr Gly Lys Thr Leu Leu Ala Lys  
 225 230 235 240

Ala Val Ala Asn Gln Thr Ser Ala Thr Phe Leu Arg Ile Val Gly Ser  
 245 250 255

Glu Leu Ile Gln Lys Tyr Leu Gly Asp Gly Pro Lys Met Val Arg Glu  
 260 265 270

Leu Phe Arg Val Ala Glu Glu Asn Ala Pro Ser Ile Val Phe Ile Asp  
 275 280 285

Glu Ile Asp Ala Val Gly Thr Lys Arg Tyr Asp Ser Asn Ser Gly Gly  
 290 295 300

Glu Arg Glu Ile Gln Arg Thr Met Leu Glu Leu Leu Asn Gln Leu Asp  
 305 310 315 320

Gly Phe Asp Ser Arg Gly Asp Val Lys Val Leu Met Ala Thr Asn Arg  
 325 330 335

Ile Glu Ser Leu Asp Pro Ala Leu Ile Arg Pro Gly Arg Ile Asp Arg  
 340 345 350

Lys Ile Glu Phe Pro Leu Pro Asp Glu Lys Thr Lys Arg Arg Ile Phe  
 355 360 365

Gln Ile His Thr Ser Arg Met Thr Leu Gly Lys Glu Val Asn Leu Glu  
 370 375 380

Glu Phe Ile Thr Ala Lys Asp Glu Leu Ser Gly Ala Asp Ile Lys Ala  
 385 390 395 400

Met Cys Thr Glu Ala Gly Leu Leu Ala Leu Arg Glu Arg Arg Met Arg  
 405 410 415

Val Thr Met Glu Asp Phe Gln Lys Ser Lys Glu Asn Val Leu Tyr Arg  
 420 425 430

Lys Lys Glu Gly Ala Pro Glu Glu Leu Tyr Leu  
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<210> 35  
 <211> 1263  
 <212> DNA  
 <213> Meloidogyne hapla

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<210> 36  
 <211> 420  
 <212> PRT  
 <213> Meloidogyne hapla

<400> 36

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Arg Lys Lys Gly Ser Lys Gly Pro Glu Ala Ser Asn Lys Met Pro Asn  
 20 25 30

Val Ala Pro Leu Thr Arg Cys Lys Leu Arg Leu Leu Lys Tyr Glu Arg  
 35 40 45

Ile Lys Asp Tyr Leu Leu Met Glu Glu Glu Phe Ile Arg Asn Gln Glu  
 50 55 60

Arg Leu Lys Pro Gln Glu Glu Arg Gln Glu Glu Glu Arg Thr Lys Val  
 65 70 75 80

Asp Glu Met Arg Gly Ser Pro Met Ala Val Gly Thr Leu Glu Glu Val  
 Seite 31

Ile Asp Asp Gln His Ala Ile Phe Ser Thr Asn Val Gly Ser Glu His  
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 Tyr Val Asn Ile Leu Ser Phe Val Asp Lys Glu Gln Leu Glu Pro Gly  
 115 120 125  
 Cys Ala Val Leu Leu Asn His Lys Thr His Ala Val Val Gly Val Leu  
 130 135 140  
 Ala Asp Asp Thr Asp Pro Met Val Ser Val Met Lys Leu Glu Lys Ala  
 145 150 155 160  
 Pro Thr Glu Thr Tyr Ala Asp Val Gly Gly Leu Glu Gln Gln Ile Gln  
 165 170 175  
 Glu Ile Lys Glu Ala Val Glu Leu Pro Leu Thr His Pro Glu Tyr Tyr  
 180 185 190  
 Glu Glu Ile Gly Ile Lys Pro Pro Lys Gly Val Ile Leu Tyr Gly Pro  
 195 200 205  
 Pro Gly Thr Gly Lys Thr Leu Leu Ala Lys Ala Val Ala Asn Gln Thr  
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 Ser Ala Thr Phe Leu Arg Val Val Gly Ser Glu Leu Ile Gln Lys Tyr  
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 245 250 255  
 Glu His Ala Pro Ser Ile Val Phe Ile Asp Glu Ile Asp Ala Ile Gly  
 260 265 270  
 Thr Lys Arg Tyr Glu Ser Asn Ser Gly Gly Glu Arg Glu Ile Gln Arg  
 275 280 285  
 Thr Met Leu Glu Leu Leu Asn Gln Leu Asp Gly Phe Asp Ser Arg Gly  
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 Asp Val Lys Val Leu Met Ala Thr Asn Arg Ile Asp Ser Leu Asp Pro  
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 Ala Leu Ile Arg Pro Gly Arg Ile Asp Arg Lys Ile Glu Phe Pro Leu  
 325 330 335  
 Pro Asp Glu Lys Thr Lys Arg Arg Ile Phe Gly Ile His Thr Ala Arg  
 340 345 350  
 Met Gln Leu Glu Asn Val Asn Leu Glu Glu Phe Ile Glu Ala Lys Asp  
 355 360 365



Asp Leu Ser Gly Ala Asp Val Lys Ala Val Cys Thr Glu Ala Gly Leu  
 370 375 380

Leu Ala Leu Arg Asp Arg Arg Met Arg Val Thr Met Glu Asp Met Lys  
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Lys Ala Lys Glu Asn Val Leu Tyr Arg Lys Lys Asp Gly Ala Pro Glu  
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Ser Met Tyr Leu  
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 <211> 658  
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 <213> Meloidogyne incognita

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 <213> Meloidogyne incognita

<400> 38

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Gln Gly Glu Gly Asp Lys Lys Arg Arg Phe Gly Pro Pro Ile Pro Thr  
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Arg Phe Gly Lys Arg Lys Lys Gly Ser Lys Gly Pro Glu Ala Ser Asn  
 35 40 45

Lys Met Pro Asn Val Thr Pro Val Thr Arg Cys Lys Leu Arg Leu Leu  
 50 55 60

Lys Tyr Glu Arg Ile Lys Asp Tyr Leu Leu Met Glu Glu Glu Phe Ile  
65 70 75 80

Arg Asn Gln Glu Arg His Lys Pro Gln Glu Glu Arg Gln Glu Glu Glu  
85 90 95

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

Leu Glu Glu Ile Ile Asp Asp Gln His Ala Val Val Ser Thr Asn Val  
115 120 125

Gly Ser Glu His Tyr Val Asn Ile Leu Ser Phe Val Asp Lys Glu Gln  
130 135 140

Leu Glu Pro Arg Cys Ala Val Leu Leu Asn His Lys Thr His Ala Val  
145 150 155 160

Val Gly Val Leu Ala Asp Asp Thr Asp Pro Met Val Ser Val Met Lys  
165 170 175

Leu Glu Lys Ala Pro Thr Glu Thr Tyr Ala Asp Val Gly Gly Leu Glu  
180 185 190

Gln Gln Ile Gln Glu Ile Lys Glu Ala Val Glu Leu Pro Leu Thr His  
195 200 205

Pro Glu Tyr Tyr Glu Glu Ile Gly Ile Lys Pro  
210 215

<210> 39  
<211> 1444  
<212> DNA  
<213> Heterodera glycines

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gaaggacatt gatgaaattc agaagcgcac aaacactctt tgcggagtga aagagagcga 240  
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aaaa	1444

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 <212> PRT  
 <213> Heterodera glycines  
 <400> 40

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

130

135

140

Arg Asn Lys Tyr Gln Ile His Leu Pro Leu Pro Ala Lys Ile Asp Ala  
 145 150 155 160

Ser Val Thr Met Met Gln Val Glu Asp Lys Pro Asp Val Thr Tyr Ala  
 165 170 175

Asp Ile Gly Gly Cys Glu Glu Gln Ile Lys Lys Leu Arg Glu Val Val  
 180 185 190

Glu Phe Pro Leu Leu Gln Pro Glu Arg Phe Thr Ser Leu Gly Ile Glu  
 195 200 205

Pro Pro Lys Gly Val Leu Phe Phe Gly Pro Pro Gly Thr Gly Lys Thr  
 210 215 220

Leu Cys Ala Arg Ala Val Ala Asn Arg Thr Asp Ala Cys Phe Ile Arg  
 225 230 235 240

Val Ile Gly Ser Glu Leu Val Lys Lys Tyr Val Gly Glu Gly Ala Arg  
 245 250 255

Met Val Arg Glu Leu Phe Ser Leu Ala Lys Thr Lys Lys Ala Cys Ile  
 260 265 270

Leu Phe Phe Asp Glu Val Asp Ala Ile Gly Gly Ala Arg Phe Asp Asp  
 275 280 285

Gly Lys Gly Gly Asp Asn Glu Val Gln Arg Thr Met Leu Glu Leu Val  
 290 295 300

Asn Gln Leu Asp Gly Phe Asp Ser Arg Gly Ala Ile Lys Val Leu Met  
 305 310 315 320

Ala Thr Asn Arg Pro Asp Thr Leu Asp Pro Ala Leu Ile Arg Pro Gly  
 325 330 335

Arg Ile Asp Arg Arg Ile Glu Phe Ser Leu Pro Asp Leu Lys Ala Arg  
 340 345 350

Gly Asn Ile Leu Gln Ile His Thr Lys Arg Met Ser Val Asp Arg Asn  
 355 360 365

Ile Arg Tyr Glu Leu Ile Ala Arg Leu Cys Pro Asn Thr Thr Gly Ala  
 370 375 380

Asp Leu Arg Ser Val Cys Thr Glu Ala Gly Met Phe Ala Leu Arg Ala  
 385 390 395 400

Arg Arg Lys Val Ile Thr Glu Gln Asp Phe Leu Lys Ala Val Gln Lys  
 405 410 415

Val Val Lys Ser Tyr Ala Lys Phe Ser Ser Thr Pro Ala Tyr Met Thr  
                   420                                  425                                  430

His Asn

<210> 41  
 <211> 368  
 <212> DNA  
 <213> Heterodera glycines

<400> 41  
 ctttgctttg ttgaatttct tccactcaaa aatgtccagc gatattgtcg agaaaaagga 60  
 gacaaacccc aatgagacgg atgacaaaac caaagaaata aaatcgcttg acgaggatga 120  
 aattgccgca cttagtaatt acaacatggg accgtacgcg gatcagttga agcaggcgga 180  
 gaaggacatt gatgaaattc agaagcgcac aaacactctt tgcggagtga aagagagcga 240  
 cacggggctg gcgccgccca ttctttggga cattgcggcc gacaaaatgg ccatgtccca 300  
 tgagcagccg ctgcaggtgg ctcgctgcac aaaaatcatc aaagaagaga gcaaagaaac 360  
 gcgttaca 368

<210> 42  
 <211> 122  
 <212> PRT  
 <213> Heterodera glycines

<400> 42  
 Phe Ala Leu Leu Asn Phe Phe His Ser Lys Met Ser Ser Asp Ile Val  
 1                  5                                  10                                  15  
 Glu Lys Lys Glu Thr Asn Pro Asn Glu Thr Asp Asp Lys Thr Lys Glu  
                   20                                  25                                  30  
 Ile Lys Ser Leu Asp Glu Asp Glu Ile Ala Ala Leu Ser Asn Tyr Asn  
                   35                                  40                                  45  
 Met Gly Pro Tyr Ala Asp Gln Leu Lys Gln Ala Glu Lys Asp Ile Asp  
                   50                                  55                                  60  
 Glu Ile Gln Lys Arg Ile Asn Thr Leu Cys Gly Val Lys Glu Ser Asp  
 65                                  70                                  75                                  80  
 Thr Gly Leu Ala Pro Pro Ile Leu Trp Asp Ile Ala Ala Asp Lys Met  
                   85                                  90                                  95  
 Ala Met Ser His Glu Gln Pro Leu Gln Val Ala Arg Cys Thr Lys Ile  
                   100                                  105                                  110  
 Ile Lys Glu Glu Ser Lys Glu Thr Arg Tyr  
                   115                                  120

<210> 43  
 <211> 636  
 <212> DNA  
 <213> Heterodera glycines

<400> 43  
 cacgaaaatg tggcgccac tgacattgag gagggaatgc gagtgggtgt ggaccgcaac 60  
 aaataccaga ttcatttgcc ttgcccggca aagattgacg cgtccgttac gatgatgcaa 120  
 gtggaggaca agccggacgt tacctacgcg gacattggcg ggtgcgaaga acagatcaaa 180  
 aagttgcgtg aagtgggtcga gtttccgttg cttcagcctg agcgtttcac gagtttgggc 240  
 attgagcctc cgaagggcgt tttgtttttt ggtccgccgg gcaccggcaa aactttgtgt 300  
 gcccgcgcgg tcgccaatcg gacggacgcg tgtttcatcc gcgtcatcgg ttccgaatta 360  
 gtcaaaaaat acgttggcga aggcgcgcgc atggtgcgcg agctgttttc gctggctaaa 420  
 acgaaaaagg cgtgcattct cttcttcgac gaagtcgacg ccatcggcgg agcgcgattt 480  
 gacgacggaa aagggggcga caacgaagtg caacggacga tgctcgagtt ggtcaaccaa 540  
 ctggacggat tcgactcacg cggggccatc aaggttttga tggccaccaa cagaccggac 600  
 acactcgacc cggcgctcat tcgtcccggt cgcatt 636

<210> 44  
 <211> 212  
 <212> PRT  
 <213> Heterodera glycines

<400> 44

His Glu Asn Val Ala Pro Thr Asp Ile Glu Glu Gly Met Arg Val Gly  
 1 5 10 15

Val Asp Arg Asn Lys Tyr Gln Ile His Leu Pro Leu Pro Ala Lys Ile  
 20 25 30

Asp Ala Ser Val Thr Met Met Gln Val Glu Asp Lys Pro Asp Val Thr  
 35 40 45

Tyr Ala Asp Ile Gly Gly Cys Glu Glu Gln Ile Lys Lys Leu Arg Glu  
 50 55 60

Val Val Glu Phe Pro Leu Leu Gln Pro Glu Arg Phe Thr Ser Leu Gly  
 65 70 75 80

Ile Glu Pro Pro Lys Gly Val Leu Phe Phe Gly Pro Pro Gly Thr Gly  
 85 90 95

Lys Thr Leu Cys Ala Arg Ala Val Ala Asn Arg Thr Asp Ala Cys Phe  
 100 105 110

Ile Arg Val Ile Gly Ser Glu Leu Val Lys Lys Tyr Val Gly Glu Gly  
 115 120 125

Ala Arg Met Val Arg Glu Leu Phe Ser Leu Ala Lys Thr Lys Lys Ala  
 130 135 140

Cys Ile Leu Phe Phe Asp Glu Val Asp Ala Ile Gly Gly Ala Arg Phe  
 145 150 155 160

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

Leu Val Asn Gln Leu Asp Gly Phe Asp Ser Arg Gly Ala Ile Lys Val  
 180 185 190

Leu Met Ala Thr Asn Arg Pro Asp Thr Leu Asp Pro Ala Leu Ile Arg  
 195 200 205

Pro Gly Arg Ile  
 210

<210> 45  
 <211> 547  
 <212> DNA  
 <213> Heterodera schachtii

<400> 45  
 caaagatacg cgttatgtga tcaatgtgaa gcagttcgcc aagttcgtcg tggacttgca 60  
 cgaaaatgtg gcgcccactg acattgagga gggaatgcga gtaggggtgg accgcaacaa 120  
 ataccagatt catttgcctt tgccggcaaa gattgacgcg tccgttacga tgatgcaagt 180  
 ggaggacaag ccggacgtta cctacgcgga cattggcggg tgcgaagagc agatcaaaaa 240  
 gttgcgtgaa gtggtcgagt ttccgttgct tcagccggaa cgtttcacga gtttgggcat 300  
 tgagcctccg aagggcgtct tgttttttgg tccgccgggc accggcaaaa ctttgtgtgc 360  
 ccgcgcggtc gccaatcgga cggacgctt tttcatccgc gtcatcggtt ccgaattggt 420  
 caaaaaatac gttggcgaag gcgcgcgcat ggtgcgcgag ctgttttcgc tggcgaagac 480  
 gaaaaaggcg tgcattctct tcttcgacga agtcgacgcc atcggcgag ctcgttttga 540  
 tgacgga 547

<210> 46  
 <211> 182  
 <212> PRT  
 <213> Heterodera schachtii

<400> 46

Lys Asp Thr Arg Tyr Val Ile Asn Val Lys Gln Phe Ala Lys Phe Val  
 1 5 10 15

Val Asp Leu His Glu Asn Val Ala Pro Thr Asp Ile Glu Glu Gly Met  
 20 25 30

Arg Val Gly Val Asp Arg Asn Lys Tyr Gln Ile His Leu Pro Leu Pro  
 35 40 45

Ala Lys Ile Asp Ala Ser Val Thr Met Met Gln Val Glu Asp Lys Pro  
 50 55 60  
 Asp Val Thr Tyr Ala Asp Ile Gly Gly Cys Glu Glu Gln Ile Lys Lys  
 65 70 75 80  
 Leu Arg Glu Val Val Glu Phe Pro Leu Leu Gln Pro Glu Arg Phe Thr  
 85 90 95  
 Ser Leu Gly Ile Glu Pro Pro Lys Gly Val Leu Phe Phe Gly Pro Pro  
 100 105 110  
 Gly Thr Gly Lys Thr Leu Cys Ala Arg Ala Val Ala Asn Arg Thr Asp  
 115 120 125  
 Ala Cys Phe Ile Arg Val Ile Gly Ser Glu Leu Val Lys Lys Tyr Val  
 130 135 140  
 Gly Glu Gly Ala Arg Met Val Arg Glu Leu Phe Ser Leu Ala Lys Thr  
 145 150 155 160  
 Lys Lys Ala Cys Ile Leu Phe Phe Asp Glu Val Asp Ala Ile Gly Gly  
 165 170 175  
 Ala Arg Phe Asp Asp Gly  
 180

<210> 47  
 <211> 566  
 <212> DNA  
 <213> Globodera rostochiensis

<400> 47  
 gaatcgaacc accgaagggc gttctgttct ttggtccgcc gggcaccggc aaaacgcttt 60  
 gcgcccgcgc ggtggccaat cggacggacg cgtgtttcat tcgcgtcatc ggttccgagc 120  
 tgggtcaagaa gtacgtcggc gaaggcgccc gcatgggtgcg tgagctgttc tcgcttgcca 180  
 agacgaaaaa ggcgtgcatt ctcttcttcg acgaggtgga cgccatcggc ggggcgcgct 240  
 ttgatgacgg aaaaggcggc gacaacgaag tgcagcggac aatgctcgag ctggtcaacc 300  
 agctggacgg gtttgattcg cgcggggcca ttaaggtttt gatggccacc aacagaccgg 360  
 acacgctcga cccggccctc attcggcctg gtcgtattga tcgacgcatt gagttctggt 420  
 tgcccgaact aaaggcccgt gggaacattc ttcaaattca caccaaaccg atgagcgttg 480  
 accgaaacat tcgatacgaa ttgattgcgc ggctctgccc gaacacgaca ggtgccgatt 540  
 tgcgaagcgt ttgcactgag gcggga 566

<210> 48  
 <211> 189  
 <212> PRT  
 <213> Globodera rostochiensis



&lt;400&gt; 48

Gly Ile Glu Pro Pro Lys Gly Val Leu Phe Phe Gly Pro Pro Gly Thr  
 1 5 10 15

Gly Lys Thr Leu Cys Ala Arg Ala Val Ala Asn Arg Thr Asp Ala Cys  
 20 25 30

Phe Ile Arg Val Ile Gly Ser Glu Leu Val Lys Lys Tyr Val Gly Glu  
 35 40 45

Gly Ala Arg Met Val Arg Glu Leu Phe Ser Leu Ala Lys Thr Lys Lys  
 50 55 60

Ala Cys Ile Leu Phe Phe Asp Glu Val Asp Ala Ile Gly Gly Ala Arg  
 65 70 75 80

Phe Asp Asp Gly Lys Gly Gly Asp Asn Glu Val Gln Arg Thr Met Leu  
 85 90 95

Glu Leu Val Asn Gln Leu Asp Gly Phe Asp Ser Arg Gly Ala Ile Lys  
 100 105 110

Val Leu Met Ala Thr Asn Arg Pro Asp Thr Leu Asp Pro Ala Leu Ile  
 115 120 125

Arg Pro Gly Arg Ile Asp Arg Arg Ile Glu Phe Cys Leu Pro Asp Leu  
 130 135 140

Lys Ala Arg Gly Asn Ile Leu Gln Ile His Thr Lys Arg Met Ser Val  
 145 150 155 160

Asp Arg Asn Ile Arg Tyr Glu Leu Ile Ala Arg Leu Cys Pro Asn Thr  
 165 170 175

Thr Gly Ala Asp Leu Arg Ser Val Cys Thr Glu Ala Gly  
 180 185

&lt;210&gt; 49

&lt;211&gt; 583

&lt;212&gt; DNA

&lt;213&gt; Globodera rostochiensis

&lt;400&gt; 49

ggcggggaca acgaagtgca gcggacaatg ctcgagctgg tcaaccagct ggacggggtt 60  
 gattcgcgcg gggccattaa ggttttgatg gccaccaaca gaccggacac gctcgacccg 120  
 gccttcattc ggcctggtcg tattgatcga cgcattgagt tctgtttgcc cgacctaaag 180  
 gcccgtggga acatttttca aattcacacc aaacggatga gcgttgaccg aaacattcga 240  
 tacgaattga ttgcgggggt ctgccgaac acgacaggtg ccgatttgcg aagcgtttgc 300  
 actgaggcgg gaatgttcgt tttgcgcgcg cgtcgaaagg ttatcacgga gcaagacttc 360  
 ctcaaggccg tccaaaaagt ggtgaaaagc tatgggaagt tcagctcaac accggcctat 420

atgacgcaca attaattgga cattttgtca ttttgatgaa atggacgggtt gataattttt 480  
 tgtttgttta cacacattca attcgtcatt tgttcattcg aaaagaagcg tggaaccgtc 540  
 aaaaaaaaaa aaaaaaacca aaaaagaaac atgtcggccg cct 583

<210> 50  
 <211> 144  
 <212> PRT  
 <213> Globodera rostochiensis

<400> 50

Gly Gly Asp Asn Glu Val Gln Arg Thr Met Leu Glu Leu Val Asn Gln  
 1 5 10 15

Leu Asp Gly Phe Asp Ser Arg Gly Ala Ile Lys Val Leu Met Ala Thr  
 20 25 30

Asn Arg Pro Asp Thr Leu Asp Pro Ala Phe Ile Arg Pro Gly Arg Ile  
 35 40 45

Asp Arg Arg Ile Glu Phe Cys Leu Pro Asp Leu Lys Ala Arg Gly Asn  
 50 55 60

Ile Phe Gln Ile His Thr Lys Arg Met Ser Val Asp Arg Asn Ile Arg  
 65 70 75 80

Tyr Glu Leu Ile Ala Gly Phe Cys Pro Asn Thr Thr Gly Ala Asp Leu  
 85 90 95

Arg Ser Val Cys Thr Glu Ala Gly Met Phe Val Leu Arg Ala Arg Arg  
 100 105 110

Lys Val Ile Thr Glu Gln Asp Phe Leu Lys Ala Val Gln Lys Val Val  
 115 120 125

Lys Ser Tyr Gly Lys Phe Ser Ser Thr Pro Ala Tyr Met Thr His Asn  
 130 135 140

<210> 51  
 <211> 1297  
 <212> DNA  
 <213> Meloidogyne hapla

<400> 51

aaggaagtta aagctttggg agaggaagaa atagccgctt taaaaagtta caatttgggg 60  
 ccgtattctg agaaattgag gcaagtcgag actgacattc aagaagcggtt aaagaatatc 120  
 aacacacttt gcggtgtcaa agaaagcgat actggccttg ctctcctgc tctttgggat 180  
 cttgttgctg ataaaactgc cattgctcaa gagcaacctc ttcaggttgc aagatgtaca 240  
 aaaataatta aaactgaggg tcaagatcca cgttatatga ttaatgtcaa acaatttgcc 300  
 aaatttggtg ttgatttggc ctctgcagtt gctccaactg acattgaaga aggaatgcgt 360

BPS66376PC-2009022554

gttgggtgttg atcgaaataa atatcagatt catattcctt taccagcaaa aattgatcct 420  
tcagtgacaa tgatgacagt tgaagagaag ccagatgtga cttatgctga cgttgggtgtt 480  
tgtaaagaac aaatagaaaa gcttcgagaa gttgtcgaaa tgcctctact tcatcctgaa 540  
cgtttcgtga atattggtat tgaacctcct aaggggtgtac tcttttatgg tcctcctggg 600  
acaggaaaga cgctttgtgc tcgtgctgtt gcaaatacga ctgatgcttg gtttattcgc 660  
gtaattgggt ctgaattggt acaaaaatat gttgggtgaag gagcgagaat ggttcgtgaa 720  
ttattcgaga tggcaaaaac gaagaaggct tgtattatct tctttgatga agtcgatgct 780  
attggtggag ctcgttttga tgatggaatg ggaggggata atgaagtaca acggacaatg 840  
ctggaattga tcaatcagtt ggatggattt gattcgcgcg gtgcaattaa agttttaatg 900  
gccacaaatc gtcccgtac tttggatccc gcacttgtag ggccaggacg tattgatcgt 960  
cgtattgaat tcgccgtgcc tgatctggaa gcacgtgcaa atattctaaa gattcataca 1020  
aaacggatga gtgttgatcg gagtattcgt tacgaattga tatcgcgctt ttgcccgaat 1080  
acaacagggt ctgatattcg ctctgtctgt acagaagccg gaatgtttgc attacgtgcc 1140  
ccccgtaaag tgataactga aaaagatttt attgacgctg ttcagaaagt ggtgaaagga 1200  
tatgcaaagt ttagttcaac tccaagttat atgacacata attaaaatca atttctttga 1260  
atttgggctt ttgataaatg tttcttaaata aaaaaaa 1297

<210> 52  
<211> 414  
<212> PRT  
<213> Meloidogyne hapla  
<400> 52

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

115

Gln Ile His Ile Pro Leu Pro Ala Lys Ile Asp Pro Ser Val Thr Met  
130 135 140

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

Cys Lys Glu Gln Ile Glu Lys Leu Arg Glu Val Val Glu Met Pro Leu  
165 170 175

Leu His Pro Glu Arg Phe Val Asn Ile Gly Ile Glu Pro Pro Lys Gly  
180 185 190

Val Leu Phe Tyr Gly Pro Pro Gly Thr Gly Lys Thr Leu Cys Ala Arg  
195 200 205

Ala Val Ala Asn Arg Thr Asp Ala Trp Phe Ile Arg Val Ile Gly Ser  
210 215 220

Glu Leu Val Gln Lys Tyr Val Gly Glu Gly Ala Arg Met Val Arg Glu  
225 230 235 240

Leu Phe Glu Met Ala Lys Thr Lys Lys Ala Cys Ile Ile Phe Phe Asp  
245 250 255

Glu Val Asp Ala Ile Gly Gly Ala Arg Phe Asp Asp Gly Met Gly Gly  
260 265 270

Asp Asn Glu Val Gln Arg Thr Met Leu Glu Leu Ile Asn Gln Leu Asp  
275 280 285

Gly Phe Asp Ser Arg Gly Ala Ile Lys Val Leu Met Ala Thr Asn Arg  
290 295 300

Pro Asp Thr Leu Asp Pro Ala Leu Val Arg Pro Gly Arg Ile Asp Arg  
305 310 315 320

Arg Ile Glu Phe Ala Val Pro Asp Leu Glu Ala Arg Ala Asn Ile Leu  
325 330 335

Lys Ile His Thr Lys Arg Met Ser Val Asp Arg Ser Ile Arg Tyr Glu  
340 345 350

Leu Ile Ser Arg Leu Cys Pro Asn Thr Thr Gly Ala Asp Ile Arg Ser  
355 360 365

Val Cys Thr Glu Ala Gly Met Phe Ala Leu Arg Ala Pro Arg Lys Val  
370 375 380

Ile Thr Glu Lys Asp Phe Ile Asp Ala Val Gln Lys Val Val Lys Gly  
385 390 395 400

Tyr Ala Lys Phe Ser Ser Thr Pro Ser Tyr Met Thr His Asn  
 405 410

<210> 53  
 <211> 1308  
 <212> DNA  
 <213> Caenorhabditis elegans

<400> 53  
 atgccagatc accttgagaga tgacatgctc aaaactaaaa aagatgatac caaggaggaa 60  
 gagaagaatt tccaggctct cgacgaagga gacattgctg ttttgaaaag atacgggcaa 120  
 ggtccatacg cggaacagct caaaacattg gacgcggata ttgaaaactg tctgaagaag 180  
 gtgaacgaac tttctggagt gaaagaatca gacaccgggt tggctccacc agctctatgg 240  
 gatattgctg ctgataaaca agcaatgcag caagaacagc ctctccaagt tgccagatgc 300  
 aaaaaatta tcaccagcga caagcacgat ccgcgttact tgatcaacgt aaaacagttc 360  
 gctaagtttg ttgtagacct tgctgattcc gttgcaccta ctgatattga ggagggcatg 420  
 agagtaggag tagaccgtaa caagtatcaa attcatcttc cgttgcccgc caaaattgat 480  
 ccaaccgtca caatgatgca ggttgaagaa aaaccagatg taacatattc ggatgtcgga 540  
 ggctgcaagg atcaaattga aaagcttcga gaagttgtcg agactccact tcttcatccc 600  
 gagcgttacg ttaatctcgg aatcgagcca caaaaggag ttttgctcta cgggccacca 660  
 ggaacaggaa agacgctttg cgctcgtgcc gttgccaatc gaacagatgc ttgcttcatt 720  
 cgtgttattg gatcagagtt ggttcagaaa tatgtcggag aaggagctcg aatgggttcgt 780  
 gagttgttcg aaatggctcg taccaagaag gcatgtctta tcttctttga tgaaattgat 840  
 gctgttgag gtgctcgttt tgatgatgga caaggagggtg acaatgaagt tcaacgtact 900  
 atgctcgagt tgattaacca acttgacgga ttcgatccac gtggaaacat caaggtgctt 960  
 atggcaacaa acagaccgga cactctcgat cccgctctca tgagacctgg tcgattggat 1020  
 cgtaaagtcg aattcgctct tccagacctt gcaggctcgtg ctcacattct caagattcat 1080  
 gcaaaacaaa tgagcgttga aagagatatt cgttatgatt tacttgctcg tctgtgccca 1140  
 aacagtacag gagccgaaat tcgctcagtc tgcaccgaag ctggaatgtt tgcaattcgt 1200  
 gctagaagaa aggtggcaac tgaaaaagat ttccttgaag ctatcaataa ggttgtcaag 1260  
 ggatagcca aattcagcgc cactccaaga tatctgacac ataattaa 1308

<210> 54  
 <211> 435  
 <212> PRT  
 <213> Caenorhabditis elegans

<400> 54

Met Pro Asp His Leu Gly Asp Asp Met Arg Lys Thr Lys Lys Asp Asp  
 1 5 10 15

Thr Lys Glu Glu Glu Lys Asn Phe Gln Ala Leu Asp Glu Gly Asp Ile  
 Seite 45

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

Ile Asn Gln Leu Asp Gly Phe Asp Pro Arg Gly Asn Ile Lys Val Leu  
305 310 315 320

Met Ala Thr Asn Arg Pro Asp Thr Leu Asp Pro Ala Leu Met Arg Pro  
325 330 335

Gly Arg Leu Asp Arg Lys Val Glu Phe Ala Leu Pro Asp Leu Ala Gly  
340 345 350

Arg Ala His Ile Leu Lys Ile His Ala Lys Gln Met Ser Val Glu Arg  
355 360 365

Asp Ile Arg Tyr Asp Leu Leu Ala Arg Leu Cys Pro Asn Ser Thr Gly  
370 375 380

Ala Glu Ile Arg Ser Val Cys Thr Glu Ala Gly Met Phe Ala Ile Arg  
385 390 395 400

Ala Arg Arg Lys Val Ala Thr Glu Lys Asp Phe Leu Glu Ala Ile Asn  
405 410 415

Lys Val Val Lys Gly Tyr Ala Lys Phe Ser Ala Thr Pro Arg Tyr Leu  
420 425 430

Thr His Asn  
435

<210> 55  
<211> 1308  
<212> DNA  
<213> Caenorhabditis briggsae

<400> 55  
atgccagatc accttgagga tgatatgcgt aaaacaaaga agggcgagac aaccgaagaa 60  
gagaaaaact tccaagcact cgacgaagga gatattgctg ttttgaagag atacggtcaa 120  
gggtccatatg ccgagcagct gaaacagttg gatactgaca ttgaaaactg tttgaagaag 180  
gtcaatgagc tatccggcgt gaaagaatcg gatacaggat tggcaccgcc agcgttatgg 240  
gatattgctg ctgacaagca agctatgcag caagaacaac ctcttcaggt cgccagatgc 300  
acgaaaatta tcaccagtga caagcatgat ccaagatatt tgatcaatgt gaaacagttc 360  
gcaaaattcg tcgttgatct tgctgattcc gttgcgcaa ctgatattga ggaaggaatg 420  
agagtcggag tcgatcgcaa caagtatcaa attcatcttc cacttcagc aaaaattgat 480  
ccaaccgtaa caatgatgca agttgaagag aagccagatg tgacatactc tgacgttgga 540  
ggttgcaagg atcaaattga aaaacttcgt gaagtagtcg aaactccact tcttcatcca 600  
gagcgctacg tgaatctcgg aattgaacca ccaaaaggag tgctgctcta cgggtcccct 660  
ggaactggta aaactctttg cgctcgtgct gttgccaatc gtaccgatgc ttgcttcatt 720  
cgagttatcg gatccgaact cgttcaaaag tacgtcggag aaggagctcg tatggttcgt 780

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gagcttttcg aaatggctcg caccaaaaag gcgtgtctta tcttcttcga tgaaatcgac 840  
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atgcttgaat tgattaacca gcttgatggt ttcgacccaa gaggaacat taaggtactg 960  
atggcaacaa acagaccaga tacacttgac cctgccctca tgagaccagg tcgcctggat 1020  
cgtaaagtcg aattcgctct tcctgatctt gtgggacgtg ctcacattct caagattcat 1080  
gctaagcaga tgagtgtgga aagagacatt cgctacgact tgcttgctcg tctttgccct 1140  
aacagtactg gagctgaaat tcgttcagtg tgcaccgaag ctggaatggt cgctattcgt 1200  
gccagaagaa aggttgccac cgaaaaggat ttcctcgaag ctatcaataa agttgtgaag 1260  
ggatatgcca aattcagtcg aacaccgaga tacctcacac ataactga 1308

<210> 56  
<211> 435  
<212> PRT  
<213> Caenorhabditis briggsae

<400> 56

Met Pro Asp His Leu Gly Asp Asp Met Arg Lys Thr Lys Lys Gly Glu  
1 5 10 15

Thr Thr Glu Glu Glu Lys Asn Phe Gln Ala Leu Asp Glu Gly Asp Ile  
20 25 30

Ala Val Leu Lys Arg Tyr Gly Gln Gly Pro Tyr Ala Glu Gln Leu Lys  
35 40 45

Gln Leu Asp Thr Asp Ile Glu Asn Cys Leu Lys Lys Val Asn Glu Leu  
50 55 60

Ser Gly Val Lys Glu Ser Asp Thr Gly Leu Ala Pro Pro Ala Leu Trp  
65 70 75 80

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

Val Ala Arg Cys Thr Lys Ile Ile Thr Ser Asp Lys His Asp Pro Arg  
100 105 110

Tyr Leu Ile Asn Val Lys Gln Phe Ala Lys Phe Val Val Asp Leu Ala  
115 120 125

Asp Ser Val Ala Pro Thr Asp Ile Glu Glu Gly Met Arg Val Gly Val  
130 135 140

Asp Arg Asn Lys Tyr Gln Ile His Leu Pro Leu Pro Ala Lys Ile Asp  
145 150 155 160

Pro Thr Val Thr Met Met Gln Val Glu Glu Lys Pro Asp Val Thr Tyr  
165 170 175



Ser Asp Val Gly Gly Cys Lys Asp Gln Ile Glu Lys Leu Arg Glu Val  
 180 185 190  
 Val Glu Thr Pro Leu Leu His Pro Glu Arg Tyr Val Asn Leu Gly Ile  
 195 200 205  
 Glu Pro Pro Lys Gly Val Leu Leu Tyr Gly Pro Pro Gly Thr Gly Lys  
 210 215 220  
 Thr Leu Cys Ala Arg Ala Val Ala Asn Arg Thr Asp Ala Cys Phe Ile  
 225 230 235 240  
 Arg Val Ile Gly Ser Glu Leu Val Gln Lys Tyr Val Gly Glu Gly Ala  
 245 250 255  
 Arg Met Val Arg Glu Leu Phe Glu Met Ala Arg Thr Lys Lys Ala Cys  
 260 265 270  
 Leu Ile Phe Phe Asp Glu Ile Asp Ala Val Gly Gly Ala Arg Phe Asp  
 275 280 285  
 Asp Gly Gln Gly Gly Asp Asn Glu Val Gln Arg Thr Met Leu Glu Leu  
 290 295 300  
 Ile Asn Gln Leu Asp Gly Phe Asp Pro Arg Gly Asn Ile Lys Val Leu  
 305 310 315 320  
 Met Ala Thr Asn Arg Pro Asp Thr Leu Asp Pro Ala Leu Met Arg Pro  
 325 330 335  
 Gly Arg Leu Asp Arg Lys Val Glu Phe Ala Leu Pro Asp Leu Val Gly  
 340 345 350  
 Arg Ala His Ile Leu Lys Ile His Ala Lys Gln Met Ser Val Glu Arg  
 355 360 365  
 Asp Ile Arg Tyr Asp Leu Leu Ala Arg Leu Cys Pro Asn Ser Thr Gly  
 370 375 380  
 Ala Glu Ile Arg Ser Val Cys Thr Glu Ala Gly Met Phe Ala Ile Arg  
 385 390 395 400  
 Ala Arg Arg Lys Val Ala Thr Glu Lys Asp Phe Leu Glu Ala Ile Asn  
 405 410 415  
 Lys Val Val Lys Gly Tyr Ala Lys Phe Ser Ala Thr Pro Arg Tyr Leu  
 420 425 430  
 Thr His Asn  
 435

<210> 57  
 <211> 1652  
 <212> DNA  
 <213> Heterodera glycines

<400> 57  
 ggtttaatta cccaagtttg agtgaagata aaagtaatta atggaccctt ttcaccggaa 60  
 cgaggctaaa gttgaggtcg ccgttgagcc accaacggcg atagaccaac gggaggacga 120  
 cataatgcaa acgggcagat ttggagacgg ccgattggtg aagatggaag tggactatag 180  
 cgctcaagtg gacagtcagt tgatagtggc agacaatttg gccaaggagg ggaagactgc 240  
 cgaggcaatt gagtccttgg aaaagctgga aaaggacagt cgcataaatt gcgacatgcg 300  
 ttccaaccag cgcctgttgt gccacatggt caaattggca tttgacgcga ataattggca 360  
 attgctctgc gaaactgcga agacatttg caagaagcgt ctgctgatca agtcgagcat 420  
 caagaaaatg gtccaagaat gctgcgaaat ggtgccaaaa gcgccagacg cgtcgtccaa 480  
 atcgacgctc atcgacacac tccgcgcagt gactgcggga aagatttacc tagaggtcga 540  
 aagagcgcgg ctgaccaaac aagtggccga aaagttggaa gccgagggaa aattggacga 600  
 agcgcgcgaa atgatgatgg aactgcaagt ggagacgtac ggcacgatgg aagtggagga 660  
 aaagggtcaat tatttgctgc atcaaatgcg cttttccatt gccataatc attttacgcg 720  
 tgcttcaatt atttcacgta aaatcagcac aaaatttttc gaacgcgaag gcactcaagt 780  
 gcaattgatg aaattggaat tttaaaata tatggtgcaa atcggactga gcgaaaacaa 840  
 ctatttggat gtgtgcaaac actttctggc aattcttaac actccgcaga tccaagaaaa 900  
 caacgtcaag aaaattgaga ttctcaagtg tgctgtgttt tacttgctgc tttcggctca 960  
 tgacaacgaa aaatgggaac ttttgcatcg agtgaatgcg atgagagaat tggaacaaat 1020  
 acccaaacac aaagaactgc tggaactgtt catccaccag gaattgatct tttggagcaa 1080  
 aaccattgag tccgaattcg ccccaatttt attcgctgct caaccgccgg tcgaagtcatt 1140  
 ttcggattcg tttctcccggt ccaccacgt gtttccgatg accaaagagg atggtcaaaa 1200  
 gcgcagagaa cgccttcatt actgtgtggg ggaacataat gtgcgaatgg tggccaaata 1260  
 ttactcgcgg atcactttcc aacgaatggc caaacttctc gaattcggaa ttgagcaaat 1320  
 ggaagccttt gtgtgcaaaa tgattgtcga cggagtaatc cccgaagtga aaattcaccg 1380  
 cccttcgcaa attattttatt tgagcccgaa aaagaacggc gcagaagtgc tggacgaatg 1440  
 ggtttttaac gttcgcaaat tgaccgacac aatgaacaaa gtcagtcagc tgatcgcaaa 1500  
 ggaggaaaatg gttcacggat tgcaaatctc tcagcggatt tgaccgatga tatcgatata 1560  
 aagaatcaat tgattgtttt attattgttt tcccaaaaaa ataaacgaat taacaaaaaa 1620  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1652

<210> 58  
 <211> 500  
 <212> PRT  
 <213> Heterodera glycines

&lt;400&gt; 58

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

Lys His Phe Leu Ala Ile Leu Asn Thr Pro Gln Ile Gln Glu Asn Asn  
 275 280 285

Val Lys Lys Ile Glu Ile Leu Lys Cys Val Val Phe Tyr Leu Leu Leu  
 290 295 300

Ser Ala His Asp Asn Glu Lys Trp Glu Leu Leu His Arg Val Asn Ala  
 305 310 315 320

Met Arg Glu Leu Glu Gln Ile Pro Lys His Lys Glu Leu Leu Glu Leu  
 325 330 335

Phe Ile His Gln Glu Leu Ile Phe Trp Ser Lys Thr Ile Glu Ser Glu  
 340 345 350

Phe Ala Pro Ile Leu Phe Ala Ala Gln Pro Pro Val Glu Val Ile Ser  
 355 360 365

Asp Ser Phe Leu Pro Ser Thr His Val Phe Pro Met Thr Lys Glu Asp  
 370 375 380

Gly Gln Lys Arg Arg Glu Arg Leu His Asp Cys Val Gly Glu His Asn  
 385 390 395 400

Val Arg Met Val Ala Lys Tyr Tyr Ser Arg Ile Thr Phe Gln Arg Met  
 405 410 415

Ala Lys Leu Leu Glu Phe Gly Ile Glu Gln Met Glu Ala Phe Val Cys  
 420 425 430

Lys Met Ile Val Asp Gly Val Ile Pro Glu Val Lys Ile His Arg Pro  
 435 440 445

Ser Gln Ile Ile Tyr Leu Ser Pro Lys Lys Asn Gly Ala Glu Val Leu  
 450 455 460

Asp Glu Trp Val Phe Asn Val Arg Lys Leu Thr Asp Thr Met Asn Lys  
 465 470 475 480

Val Ser Gln Leu Ile Ala Lys Glu Glu Met Val His Gly Leu Gln Ile  
 485 490 495

Ser Gln Arg Ile  
 500

<210> 59

<211> 537

<212> DNA

<213> Heterodera glycines

<400> 59

tcggactgag cgaaaacaac tatttgatg tgtgcaaaca ctttctggca attcttaaca

60

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ctccgcagat ccaagaaaac aacgtcaaga aaattgagat tctcaagtgt gtcgtgtttt 120  
 acttgctgct ttcggctcat gacaacgaaa aatgggaact tttgcatcga gtgaatgcga 180  
 tgagagaatt ggaacaaata cccaaacaca aagaactgct ggaactgttc atccaccagg 240  
 aattgatctt ttggagcaaa accattgagt ccgaattcgc cccaatttta ttcgctgctc 300  
 aaccgccggt cgaagtcatt tcggattcgt ttctcccgtc caccacgtg tttccgatga 360  
 ccaaagagga tgggtcaaaag cgcagagaac gccttcatga ctgtgtgggg gaacataatg 420  
 tgccaatggt ggccaaatat tactcgcgga tcactttcca acgaatggcc aaactttctcg 480  
 aattcggaat tgagcaaatg gaagcctttg tgtgcaaat gattgtcgac ggagtaa 537

<210> 60  
 <211> 178  
 <212> PRT  
 <213> Heterodera glycines  
 <400> 60

Gly Leu Ser Glu Asn Asn Tyr Leu Asp Val Cys Lys His Phe Leu Ala  
 1 5 10 15

Ile Leu Asn Thr Pro Gln Ile Gln Glu Asn Asn Val Lys Lys Ile Glu  
 20 25 30

Ile Leu Lys Cys Val Val Phe Tyr Leu Leu Leu Ser Ala His Asp Asn  
 35 40 45

Glu Lys Trp Glu Leu Leu His Arg Val Asn Ala Met Arg Glu Leu Glu  
 50 55 60

Gln Ile Pro Lys His Lys Glu Leu Leu Glu Leu Phe Ile His Gln Glu  
 65 70 75 80

Leu Ile Phe Trp Ser Lys Thr Ile Glu Ser Glu Phe Ala Pro Ile Leu  
 85 90 95

Phe Ala Ala Gln Pro Pro Val Glu Val Ile Ser Asp Ser Phe Leu Pro  
 100 105 110

Ser Thr His Val Phe Pro Met Thr Lys Glu Asp Gly Gln Lys Arg Arg  
 115 120 125

Glu Arg Leu His Asp Cys Val Gly Glu His Asn Val Arg Met Val Ala  
 130 135 140

Lys Tyr Tyr Ser Arg Ile Thr Phe Gln Arg Met Ala Lys Leu Leu Glu  
 145 150 155 160

Phe Gly Ile Glu Gln Met Glu Ala Phe Val Cys Lys Met Ile Val Asp  
 165 170 175

Gly Val

<210> 61  
 <211> 790  
 <212> DNA  
 <213> Heterodera glycines

<400> 61  
 aaaatccgta gccgagggaa aattggacga agcgcgcgaa atgatgcttg aactgcaagt 60  
 ggagacgtac ggcacgatgg aagtggagga aaaggtcaat tatttgctgc atcaaatgcg 120  
 cctttccatt gccaataatc attttacgcg tgcttcaatt atttcacgta aaatcagcac 180  
 aaaatttttc gaacgcgaag gcactcaagt gcaattgatg aaattggaat ttacaaaata 240  
 tatggtgcaa atcggactga gcgaaaacaa ctatttggat gtgtgcaaac actttctggc 300  
 aattcttaac actccgcaga tccaagaaaa caacgtcaag aaaattgaga ttctcaagtg 360  
 tgtcgtgttt tacttgctgc tttcggctca tgacaacgaa aaatgggaac ttttgcacgc 420  
 agtgaatgcg atgagagaat tggaacaaat acccaaacac aaagaactgc tggaactggt 480  
 catccaccag gaattgatct tttggagcaa aaccattgag tccgaattcg cccaattttt 540  
 attcgtgct caaccgccgg tcgaagtcatt ttcggattcg tttctcccgt ccaccacgt 600  
 gtttccgatg accaaagagg atggtcaaaa gcgcagagaa cgccttcacg actgtgtggg 660  
 ggaacataat gtgcgaatgg tggccaaata ttactcgcg atcactttcc aacgaatggc 720  
 caaacttctc gaattcggaa ttgagcaaat gggagccttt gtgtgcaaaa tgattgtcga 780  
 cggagtaatc 790

<210> 62  
 <211> 263  
 <212> PRT  
 <213> Heterodera glycines

<400> 62  
 Lys Ser Val Ala Glu Gly Lys Leu Asp Glu Ala Arg Glu Met Met Leu  
 1 5 10 15  
 Glu Leu Gln Val Glu Thr Tyr Gly Thr Met Glu Val Glu Glu Lys Val  
 20 25 30  
 Asn Tyr Leu Leu His Gln Met Arg Leu Ser Ile Ala Asn Asn His Phe  
 35 40 45  
 Thr Arg Ala Ser Ile Ile Ser Arg Lys Ile Ser Thr Lys Phe Phe Glu  
 50 55 60  
 Arg Glu Gly Thr Gln Val Gln Leu Met Lys Leu Glu Phe Tyr Lys Tyr  
 65 70 75 80  
 Met Val Gln Ile Gly Leu Ser Glu Asn Asn Tyr Leu Asp Val Cys Lys  
 85 90 95

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

<210> 63  
 <211> 672  
 <212> DNA  
 <213> Globodera rostochiensis

<400> 63  
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 ggaactgatt ttctggagta aagccattga gtccaaatat gcaccaatth tgtttgagc 120  
 tgatccgcct cccgaacttg tccgggacac gttgctgccg tctactcacg tgttcccgat 180  
 gaccaagcg gatggtcgaa ggcgtagaga acgtcttcac gactgtgtgg gcgaacataa 240  
 tgtgaggatg gtgtcgaagt actactcgcg gattacgttt caacgtatgg ccaaactgct 300  
 cgaatttggc gttgagcaaa tggaaacttt tgtgtgcaaa atgattgtcg acggagttat 360  
 tcctgaggcg aaaattcacc gccctcgca aataatttat ttgagtccga agaagaacag 420  
 tgtggaagtg ctagacgcgt gggtttttaa tgttcgcaaa ttgaccgaca caatgaacaa 480  
 agtgagtcag ctgactgcaa aggaggaaat ggtgcccgga ttgcaaattg cgcagcgagt 540  
 ttgacgatca gcagaagttg aacgaatgtt ttgcaacttt tgttattaaa tacattttat 600

tgttttgcag gagatcaatg aggtttttaa aaaaaaaaaa aaaccccggg tgaggggaca 660  
 tgtcggccgc ct 672

<210> 64  
 <211> 180  
 <212> PRT  
 <213> Globodera rostochiensis

<400> 64

Met Arg Glu Leu Glu His Leu Pro Thr His Lys Glu Leu Leu Glu Leu  
 1 5 10 15

Phe Ile His Gln Glu Leu Ile Phe Trp Ser Lys Ala Ile Glu Ser Lys  
 20 25 30

Tyr Ala Pro Ile Leu Phe Gly Ala Asp Pro Pro Pro Glu Leu Val Arg  
 35 40 45

Asp Thr Leu Leu Pro Ser Thr His Val Phe Pro Met Thr Gln Ala Asp  
 50 55 60

Gly Arg Arg Arg Arg Glu Arg Leu His Asp Cys Val Gly Glu His Asn  
 65 70 75 80

Val Arg Met Val Ser Lys Tyr Tyr Ser Arg Ile Thr Phe Gln Arg Met  
 85 90 95

Ala Lys Leu Leu Glu Phe Gly Val Glu Gln Met Glu Thr Phe Val Cys  
 100 105 110

Lys Met Ile Val Asp Gly Val Ile Pro Glu Ala Lys Ile His Arg Pro  
 115 120 125

Ser Gln Ile Ile Tyr Leu Ser Pro Lys Lys Asn Ser Val Glu Val Leu  
 130 135 140

Asp Ala Trp Val Phe Asn Val Arg Lys Leu Thr Asp Thr Met Asn Lys  
 145 150 155 160

Val Ser Gln Leu Thr Ala Lys Glu Glu Met Val Pro Gly Leu Gln Ile  
 165 170 175

Ala Gln Arg Val  
 180

<210> 65  
 <211> 1473  
 <212> DNA  
 <213> Caenorhabditis elegans

<400> 65

atggccgaca gacgcgaacc gatcccggtt gaccgggtcg atgtcggaga actaagcgaa 60



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cttgacaatt tggctcattt ggccgctcat ggtggagatg gtcgtttgtt caaaatggag	120
caggactact cgaaacaagt cgacgaagca cttctgaaag cccgagatat cgctcaaaag	180
gacgctgttg ctgctgtaga gagtctgaac aacatcgaaa agctcactcg tcttggagct	240
gacatgaaga gcaatacacg cgttgttcaa tatatgacga agctttgttt cgaagggcag	300
aaatgggatc ttcttatgga aacaatcatg acgctttcaa agaaaagact tctcatcaaa	360
atggctatcg caaagatggt ccgtgatgct gtcgcaatga ttgacaaaat gccaacggag	420
gacctcaaga tgaagcttat tgaaactctt cgcactgtta cagctggaaa gatctatgtg	480
gaagtggAAC gtgctcgctt cacctcgatg gttgtgaaga agttggagag agaggggaaag	540
cttgacgaag ctgcaacat gcttcttgaa cttcaagtgg aaacatatgg ctccatggaa	600
atgCGagaga aggtgcaata cttctcgag caaatgagat attctctcgt tcgtaatgat	660
tttgtgcgag ccactattat ctctaagaaa atcaatatca agttcttcaa caagtcagac	720
gaagatgaag tacagaacct gaagctgaaa tactacgatt cgatgatccg tatcggaactt	780
cacgatggaa actatctgga cgtgtgccgt catcatcgtg aaatttatga gacgaaaaag	840
attaaagctg attcagccaa ggcgacctca catcttcgtt ctgccattgt ctactgtctt	900
ttggctccgc acacaaacga gcaatgggat ctctcaacc gaattgccat tcaaagagaa	960
ttggaaaccg ttccagacta caagatcatt ctggatcttt tcatcaacca agaactcatt	1020
tctttcaaag gaaccattgt cgaaagtac gagaagcttt taagacgtgg aacaactagc	1080
tcaccagaca ccggaatttt cgacaaatca actgaaggag agaagcggtg gtctgatttg	1140
caccttcgtg ttggagagca caacatgctg atgattgccA agtactatac tcaaatact	1200
ttcgaacgtc tcgctgagct cctcgacttc ccagttgatg aaatggaatc atttgtgtgt	1260
aacctcattg ttaccggtca gatcaccgga gcaaaacttc atcgcccttc ccgtattgtc	1320
aatcttcgtt tgaaaaaggc aaatgttgag caattggatg tatgggCGag caacgtgcac	1380
aaactgacgg atacattgaa caaagtttcc catctcattc tgaaagagca aatggttcac	1440
aagaacttgg atctcgCGgc cccacgggca taa	1473

<210> 66  
 <211> 490  
 <212> PRT  
 <213> Caenorhabditis elegans  
 <400> 66

Met	Ala	Asp	Arg	Arg	Glu	Pro	Ile	Pro	Val	Asp	Pro	Val	Asp	Val	Gly
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Glu	Leu	Ser	Glu	Leu	Asp	Asn	Leu	Ala	His	Leu	Ala	Ala	His	Gly	Gly
			20					25					30		

Asp	Gly	Arg	Leu	Phe	Lys	Met	Glu	Gln	Asp	Tyr	Ser	Lys	Gln	Val	Asp
		35					40					45			

Glu	Ala	Leu	Leu	Lys	Ala	Arg	Asp	Ile	Ala	Gln	Lys	Asp	Ala	Val	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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50

55

60

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

Asp Met Lys Ser Asn Thr Arg Val Val Gln Tyr Met Thr Lys Leu Cys  
 85 90 95

Phe Glu Gly Gln Lys Trp Asp Leu Leu Met Glu Thr Ile Met Thr Leu  
 100 105 110

Ser Lys Lys Arg Leu Leu Ile Lys Met Ala Ile Ala Lys Met Val Arg  
 115 120 125

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

Lys Leu Ile Glu Thr Leu Arg Thr Val Thr Ala Gly Lys Ile Tyr Val  
 145 150 155 160

Glu Val Glu Arg Ala Arg Leu Thr Ser Met Val Val Lys Lys Leu Glu  
 165 170 175

Arg Glu Gly Lys Leu Asp Glu Ala Ala Thr Met Leu Leu Glu Leu Gln  
 180 185 190

Val Glu Thr Tyr Gly Ser Met Glu Met Arg Glu Lys Val Gln Tyr Leu  
 195 200 205

Leu Glu Gln Met Arg Tyr Ser Leu Val Arg Asn Asp Phe Val Arg Ala  
 210 215 220

Thr Ile Ile Ser Lys Lys Ile Asn Ile Lys Phe Phe Asn Lys Ser Asp  
 225 230 235 240

Glu Asp Glu Val Gln Asn Leu Lys Leu Lys Tyr Tyr Asp Ser Met Ile  
 245 250 255

Arg Ile Gly Leu His Asp Gly Asn Tyr Leu Asp Val Cys Arg His His  
 260 265 270

Arg Glu Ile Tyr Glu Thr Lys Lys Ile Lys Ala Asp Ser Ala Lys Ala  
 275 280 285

Thr Ser His Leu Arg Ser Ala Ile Val Tyr Cys Leu Leu Ala Pro His  
 290 295 300

Thr Asn Glu Gln Trp Asp Leu Leu Asn Arg Ile Ala Ile Gln Arg Glu  
 305 310 315 320

Leu Glu Thr Val Pro Asp Tyr Lys Ile Ile Leu Asp Leu Phe Ile Asn  
 325 330 335

Gln Glu Leu Ile Ser Phe Lys Gly Thr Ile Val Ala Lys Tyr Glu Lys  
                   340                                  345                                  350

Leu Leu Arg Arg Gly Thr Thr Ser Ser Pro Asp Thr Gly Ile Phe Asp  
                   355                                  360                                  365

Lys Ser Thr Glu Gly Glu Lys Arg Trp Ser Asp Leu His Leu Arg Val  
           370                                  375                                  380

Gly Glu His Asn Met Arg Met Ile Ala Lys Tyr Tyr Thr Gln Ile Thr  
   385                                  390                                  395                                  400

Phe Glu Arg Leu Ala Glu Leu Leu Asp Phe Pro Val Asp Glu Met Glu  
                   405                                  410                                  415

Ser Phe Val Cys Asn Leu Ile Val Thr Gly Gln Ile Thr Gly Ala Lys  
                   420                                  425                                  430

Leu His Arg Pro Ser Arg Ile Val Asn Leu Arg Leu Lys Lys Ala Asn  
                   435                                  440                                  445

Val Glu Gln Leu Asp Val Trp Ala Ser Asn Val His Lys Leu Thr Asp  
           450                                  455                                  460

Thr Leu Asn Lys Val Ser His Leu Ile Leu Lys Glu Gln Met Val His  
   465                                  470                                  475                                  480

Lys Asn Leu Asp Leu Ala Ala Pro Arg Ala  
                   485                                  490

<210> 67  
 <211> 1476  
 <212> DNA  
 <213> Caenorhabditis briggsae

<400> 67  
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 ctcgacagtt tggctcattt ggcggctcat ggcggagatg gtcgtctttt caaaatggag 120  
 caagattaca caaaacaagt agacgaagcg ctctctaaag ctcgtgatct ggctcaaaaa 180  
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 aaatgggatc ttctgatgga aactatcatg acactctcca agaagagact tctcatcaag 360  
 atggccatcg ccaaaatggt tcgtgacgca gtcgcatga tagataagat gccaaagcgac 420  
 gatctcaaaa tgaaactcat cgaaaccctt cgcactgtca ccgctggcaa aatctatggt 480  
 gaagttgagc gtgctcgtct tacatctatg gttgtcaaga agttggaagc tgagggaaag 540  
 cttgatgagg ccgctacgat gcttctcgag cttcaagtcg agacatatgg ttctatggag 600  
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tacgttcgtg caacaatcat ttccaagaag attaacatta aatTTTTTcaa caaatctgac 720
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cacgacggaa actatttTga tgtctgtcgc caccatcgtg aaattttacga aaccataaag 840
atcagagcgg atccggcaaa agcggcatcg caccttcgct cggctatcgt ctactgtctt 900
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<210> 68  
 <211> 491  
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 <213> Caenorhabditis briggsae

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Glu Thr Thr Asp Leu Asp Ser Leu Ala His Leu Ala Ala His Gly Gly  
 20 25 30

Asp Gly Arg Leu Phe Lys Met Glu Gln Asp Tyr Thr Lys Gln Val Asp  
 35 40 45

Glu Ala Leu Leu Lys Ala Arg Asp Leu Ala Gln Lys Asp Val Leu Ala  
 50 55 60

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

Asp Met Lys Ser Asn Thr Arg Val Val Gln Tyr Met Thr Lys Leu Cys  
 85 90 95

Phe Glu Gly Gln Lys Trp Asp Leu Leu Met Glu Thr Ile Met Thr Leu  
 100 105 110

Ser Lys Lys Arg Leu Leu Ile Lys Met Ala Ile Ala Lys Met Val Arg  
 115 120 125

Asp Ala Val Ala Met Ile Asp Lys Met Pro Ser Asp Asp Leu Lys Met  
 130 135 140  
 Lys Leu Ile Glu Thr Leu Arg Thr Val Thr Ala Gly Lys Ile Tyr Val  
 145 150 155 160  
 Glu Val Glu Arg Ala Arg Leu Thr Ser Met Val Val Lys Lys Leu Glu  
 165 170 175  
 Ala Glu Gly Lys Leu Asp Glu Ala Ala Thr Met Leu Leu Glu Leu Gln  
 180 185 190  
 Val Glu Thr Tyr Gly Ser Met Glu Met Lys Glu Lys Val Ser Tyr Leu  
 195 200 205  
 Leu Glu Gln Met Arg His Ser Leu Val Arg Asn Asp Tyr Val Arg Ala  
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 Thr Ile Ile Ser Lys Lys Ile Asn Ile Lys Phe Phe Asn Lys Ser Asp  
 225 230 235 240  
 Ala Glu Asp Val Gln Asp Leu Lys Leu Lys Tyr Tyr Asp Leu Met Ile  
 245 250 255  
 Arg Ile Gly Leu His Asp Gly Asn Tyr Leu Asp Val Cys Arg His His  
 260 265 270  
 Arg Glu Ile Tyr Glu Thr Ile Lys Ile Arg Ala Asp Pro Ala Lys Ala  
 275 280 285  
 Ala Ser His Leu Arg Ser Ala Ile Val Tyr Cys Leu Leu Ala Pro His  
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 Asn Asn Glu Gln Trp Asp Leu Leu Asn Arg Ile Ala Ile Gln Arg Glu  
 305 310 315 320  
 Leu Glu Thr Val Pro Asp Tyr Lys Ile Ile Leu Asp Leu Phe Ile Asn  
 325 330 335  
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 340 345 350  
 Leu Leu Arg Arg Gly Thr Pro Thr Ser Pro Asp Thr Gly Ile Phe Asp  
 355 360 365  
 Lys Ser Gln Glu Gly Glu Lys Arg Trp Ser Asp Leu His Leu Arg Val  
 370 375 380  
 Gly Glu His Asn Met Arg Met Ile Ala Lys Tyr Tyr Thr Gln Ile Thr  
 385 390 395 400  
 Phe Glu Arg Leu Ala Glu Leu Leu Asp Phe Pro Val Asp Glu Met Glu  
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405

410

415

Ser Phe Val Cys Asn Leu Ile Val Ser Gly Gln Ile Ile Gly Ala Lys  
                   420                  425                  430

Leu His Arg Pro Ser Arg Ile Val Asn Leu Arg Leu Lys Lys Ala Asn  
           435                  440                  445

Val Glu Gln Leu Asp Val Trp Ala Ser Asn Val His Lys Leu Thr Asp  
       450                  455                  460

Thr Leu Asn Lys Val Ser His Leu Ile Leu Lys Glu Gln Met Val His  
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Lys Asn Leu Asp Leu Ser Ala Ala Pro Arg Ala  
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 gttccaagag acgttataat cgtattgcaat catattgcttg cgtattgattt ccaacagttt 180  
 tgtttcgttg ataggaggaa ctcaacactc tagggtagtg attggtagac actatttagca 240  
 caaaaaatat taatttttact ctgattgttta ccaaaaaagt taccaatcaa atattttaaga 300  
 gatcgtactc ttccacggcg actctaaaaa ccaagatat aggttagact cataactact 360  
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 atttaaaatt tgaaaagtta ataattgatcc acacattttt tctaattattt aatttagtaa 600  
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 aaatttttaa tagtaattca tacacttttt aatatttaata ttagtatttt cttaaattcca 780  
 aattttaatc ttacaattta aatatctact ttaacataat acaaatataa ttttaatttca 840  
 ttgtattaaa ttcaaatata atttgattat aataaaatac aatttaattc taaaagtcc 900  
 atcttagatt ttaattttcc ttttttagttt tgaaaattaa aaattttaaat ttattagata 960  
 tatattgttac tttttcagtt ttcctattta ttttaagaaaa aaatattttt taacacatgt 1020  
 caacttgtaa acaatagact gaacacgtca ttttatatta tgttttagttt tgaaaattaa 1080  
 agttaattaa atattttatat ttcttttttt tagcttttct aattattttt aaaatagtaa 1140  
 atatttttaa tacaaatcaa tatctgaaca atagatttga tacataacat aatcctataa 1200

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 cactaaaagc taccactttg gcaaatcact catttatatt attatatact atcacctcaa 1380  
 ttcaatcgaa acctcaaaat aacactaata tatacacaaa gaaacaacag aataacaccg 1440  
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 aaaaaactag gaataataat aaaaaaatgg aatgatgtgg aggaagctct ttactctttg 1860  
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 ggtatattag gccataatat tataggtaac atgaaatatc aaatgacacg caagagtttt 180  
 gtcaaaaatg aaaccatcac acatcagaga ttatggcaaa taatgttttg tgtgtctctt 240  
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<210> 71  
 <211> 1476  
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<400> 71  
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<223> n is a, c, g, or t

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23



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38

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<400> 78  
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26

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26

<210> 82  
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46

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 <210> 84  
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 <210> 85  
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<212> DNA

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<210> 97  
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<222> (18)..(18)  
<223> n is a, c, g, or t

<400> 102  
atnacggagc aagacttnct caaggc 26

<210> 103  
<211> 26  
<212> DNA  
<213> Unknown

<220>  
<223> motif

<220>  
<221> misc\_feature  
<222> (6)..(6)  
<223> n is a, c, g, or t

<220>  
<221> misc\_feature  
<222> (12)..(12)  
<223> n is a, c, g, or t

<400> 103  
tcaacnccgg cntatatgac gcacaa 26

<210> 104  
<211> 1425  
<212> DNA  
<213> Heterodera glycines

<400> 104  
ggtttaatta cccaagtttg agatatttat taattatcat catttttggt ttacaaaatg 60  
ggtcaaaacc aaccgcaggg aggtgggcca aagccaggcg atgacaaagg acaggaccct 120  
gaaaaaaaaac ggaaatacca tggaccgccg gttccaacgc gaattggaaa acgcaagaag 180  
ggctctcgtg gtcccgacac agcaaacaaa atgcccaccg tgactccgat cactcgttgt 240  
aaactcaagc tcctcaagta tgaccggatt aaggactatc ttttaatgga ggaagaattc 300  
ataaagaaca tggagcgttt gaagcctcag gacgaacgac aggaggaaga gcgtgttaaa 360  
gttgacgacc ttcgtgggac tccaatgtct gtcggatcat tggaagaagt cattgacgat 420

BPS66376PC-2009022554

caacacgcaa ttgtttccac gaatgtcggc agtgaacatt acgtcaacat tttgtcattt 480  
 gtggacaaag aacagcttga gccgggctgt gccgttctgc tgaatcacia aaccactca 540  
 atcgtcggcg ttcttgcgga ggacgccgat ccgatgggtg cggatgatgaa attggagaaa 600  
 gcaccgaccg agacttacgc tgacgttggt ggcctcgagc agcaaattca ggagatcaaa 660  
 gaggcggtgg agttgccgtt gacacacccg gaatattacg aggaaatggg catcaaaccg 720  
 cccaaaggcg tcattctcta cgggtcgcgc ggcactggca aaacgctgct tgcaaaggcc 780  
 gttgccaacc aaacttctgc cacctttttg cgcgtcgttg gctccgaact catccaaaag 840  
 tatttgggag acggggccga aatgggtccg gaattgtttc gcgttgacaga agaacatgcg 900  
 ccgtcaatcg ttttcatcga cgaaatcgac gccattggaa ccaaacggta cgattcgaat 960  
 tccggcggag agcgcgagat tcagcgcacg atgctggaac tgctcaatca gttggacggc 1020  
 tttgactcgc gtggcgacgt caaagtgtcg atggcgacca atcggatcga ctcgttggac 1080  
 ccggcactta tccgtcccgg acgaatcgac cgcaaaatcg aattcccact tccggacgaa 1140  
 aagaccaagc ggaggatttt ccacattcac actgctcggg tgcaactgga aaatgtggac 1200  
 ttggaggaat ttatagcagc caaagacgat ctgtcgggag ccgacataaa ggcaatgtgc 1260  
 actgaggcgg gtttgcttgc actgcgcgaa cggcgaatga aagtgacaat ggacgacatg 1320  
 cgaaaggcga aggaaaatgt tctttaccgg aagaaagaca acgcacccga aacgatgtat 1380  
 ctttgaaggg ttcccaaat tggaatttgt gttgactttt attca 1425

<210> 105  
 <211> 442  
 <212> PRT  
 <213> Heterodera glycines

<400> 105

Met Gly Gln Asn Gln Pro Gln Gly Gly Gly Arg Lys Pro Gly Asp Asp  
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Lys Gly Gln Asp Pro Glu Lys Lys Arg Lys Tyr His Gly Pro Pro Val  
 20 25 30

Pro Thr Arg Ile Gly Lys Arg Lys Lys Gly Ser Arg Gly Pro Asp Thr  
 35 40 45

Ala Asn Lys Met Pro Thr Val Thr Pro Ile Thr Arg Cys Lys Leu Lys  
 50 55 60

Leu Leu Lys Tyr Asp Arg Ile Lys Asp Tyr Leu Leu Met Glu Glu Glu  
 65 70 75 80

Phe Ile Lys Asn Met Glu Arg Leu Lys Pro Gln Asp Glu Arg Gln Glu  
 85 90 95

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

Gly Ser Leu Glu Glu Val Ile Asp Asp Gln His Ala Ile Val Ser Thr  
 115 120 125  
 Asn Val Gly Ser Glu His Tyr Val Asn Ile Leu Ser Phe Val Asp Lys  
 130 135 140  
 Glu Gln Leu Glu Pro Gly Cys Ala Val Leu Leu Asn His Lys Thr His  
 145 150 155 160  
 Ser Ile Val Gly Val Leu Ala Glu Asp Ala Asp Pro Met Val Ser Val  
 165 170 175  
 Met Lys Leu Glu Lys Ala Pro Thr Glu Thr Tyr Ala Asp Val Gly Gly  
 180 185 190  
 Leu Glu Gln Gln Ile Gln Glu Ile Lys Glu Ala Val Glu Leu Pro Leu  
 195 200 205  
 Thr His Pro Glu Tyr Tyr Glu Glu Met Gly Ile Lys Pro Pro Lys Gly  
 210 215 220  
 Val Ile Leu Tyr Gly Ser Pro Gly Thr Gly Lys Thr Leu Leu Ala Lys  
 225 230 235 240  
 Ala Val Ala Asn Gln Thr Ser Ala Thr Phe Leu Arg Val Val Gly Ser  
 245 250 255  
 Glu Leu Ile Gln Lys Tyr Leu Gly Asp Gly Pro Lys Met Val Arg Glu  
 260 265 270  
 Leu Phe Arg Val Ala Glu Glu His Ala Pro Ser Ile Val Phe Ile Asp  
 275 280 285  
 Glu Ile Asp Ala Ile Gly Thr Lys Arg Tyr Asp Ser Asn Ser Gly Gly  
 290 295 300  
 Glu Arg Glu Ile Gln Arg Thr Met Leu Glu Leu Leu Asn Gln Leu Asp  
 305 310 315 320  
 Gly Phe Asp Ser Arg Gly Asp Val Lys Val Leu Met Ala Thr Asn Arg  
 325 330 335  
 Ile Asp Ser Leu Asp Pro Ala Leu Ile Arg Pro Gly Arg Ile Asp Arg  
 340 345 350  
 Lys Ile Glu Phe Pro Leu Pro Asp Glu Lys Thr Lys Arg Arg Ile Phe  
 355 360 365  
 His Ile His Thr Ala Arg Met Gln Leu Glu Asn Val Asp Leu Glu Glu  
 370 375 380

Phe Ile Ala Ala Lys Asp Asp Leu Ser Gly Ala Asp Ile Lys Ala Met  
 385 390 395 400

Cys Thr Glu Ala Gly Leu Leu Ala Leu Arg Glu Arg Arg Met Lys Val  
 405 410 415

Thr Met Asp Asp Met Arg Lys Ala Lys Glu Asn Val Leu Tyr Arg Lys  
 420 425 430

Lys Asp Asn Ala Pro Glu Thr Met Tyr Leu  
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<210> 106  
 <211> 23  
 <212> DNA  
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<220>  
 <223> motif sequence

<220>  
 <221> misc\_feature  
 <222> (6)..(6)  
 <223> n is a, c, g, or t

<220>  
 <221> misc\_feature  
 <222> (12)..(12)  
 <223> n is a, c, g, or t

<400> 106  
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23

<210> 107  
 <211> 38  
 <212> DNA  
 <213> Unknown

<220>  
 <223> motif sequence

<220>  
 <221> misc\_feature  
 <222> (12)..(12)  
 <223> n is a, c, g, or t

<220>  
 <221> misc\_feature  
 <222> (21)..(21)  
 <223> n is a, c, g, or t

<400> 107  
 gaagaacatg cnccgtcaat ngttttcatc gacgaaat

38