

SEQUENCE LISTING

<110> Boehringer Ingelheim International GmbH

<120> Method for controlling insect populations

<130> 14_0090_PCT

<160> 54

<170> PatentIn version 3.3

<210> 1

<211> 1308

<212> DNA

<213> Artificial

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<223> Synthetic Sex Peptide

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<221> CDS

<222> (1)..(1308)

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gcc agc ccg gaa atg gaa atg gaa ctg gcc gat ccg cgt cag atg gtc 96

Ala Ser Pro Glu Met Glu Met Glu Leu Ala Asp Pro Arg Gln Met Val

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cgc gga ttt cat ctg cca acc aac gag tcg cag ttg gag att ccc gac 144

Arg Gly Phe His Leu Pro Thr Asn Glu Ser Gln Leu Glu Ile Pro Asp

35 40 45

tat ggc aac gag agc ctg gac tat ccc aac tac cag cag atg gtc ggc 192

Tyr Gly Asn Glu Ser Leu Asp Tyr Pro Asn Tyr Gln Gln Met Val Gly

50 55 60

gga ccg tgt cgc atg gag gac aac aat atc agc tat tgg aat ctc acc 240

Gly Pro Cys Arg Met Glu Asp Asn Asn Ile Ser Tyr Trp Asn Leu Thr

65 70 75 80

tgc gat tcg cca ctg gag tac gct atg ccg ctc tat ggc tac tgt atg 288

Cys Asp Ser Pro Leu Glu Tyr Ala Met Pro Leu Tyr Gly Tyr Cys Met

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ccc ttc ctg ctg atc atc acc att atc tgc aac tcc ctg att gtg ctc 336

Pro Phe Leu Leu Ile Ile Thr Ile Ile Ser Asn Ser Leu Ile Val Leu

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gtt ttg agc aag aag agc atg gcc acg ccc acc aat ttt gtg cta atg 384

Val Leu Ser Lys Lys Ser Met Ala Thr Pro Thr Asn Phe Val Leu Met

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gga atg gct ata tgc gat atg ctg acg gtt ata ttt ccg gca ccc ggt 432

Gly Met Ala Ile Cys Asp Met Leu Thr Val Ile Phe Pro Ala Pro Gly

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ctc tgg tat atg tac aca ttc ggc aat cat tat aag ccc ctg cat ccg 480

Leu Trp Tyr Met Tyr Thr Phe Gly Asn His Tyr Lys Pro Leu His Pro

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gtc tcc atg tgt ctg gcc tac agc att ttc aat gag ata atg cca gcc 528

Val Ser Met Cys Leu Ala Tyr Ser Ile Phe Asn Glu Ile Met Pro Ala

165

170

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atg tgc cac acc atc tcc gtt tgg cta act ctg gcc ctc gcc gtt caa 576

Met Cys His Thr Ile Ser Val Trp Leu Thr Leu Ala Leu Ala Val Gln

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185

190

aga tac atc tac gtt tgc cac gcc ccc atg gcc cga acg tgg tgc acg 624

Arg Tyr Ile Tyr Val Cys His Ala Pro Met Ala Arg Thr Trp Cys Thr

195

200

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atg ccg cgt gtg agg cgg tgc acg gcg tat att gca ttg ctg gcg ttt 672

Met Pro Arg Val Arg Arg Cys Thr Ala Tyr Ile Ala Leu Leu Ala Phe

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215

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ctg cac caa ctg ccc aga ttc ttc gac agg acg tac atg ccg ctg gtg 720

Leu His Gln Leu Pro Arg Phe Phe Asp Arg Thr Tyr Met Pro Leu Val

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atc gag tgg aac ggc agc cca acg gag gtg tgc cac ttg gag acg tgc 768

Ile Glu Trp Asn Gly Ser Pro Thr Glu Val Cys His Leu Glu Thr Ser

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atg tgg gtg cac gat tac att gga gtg gac cta tac tac aca agc tac 816

Met Trp Val His Asp Tyr Ile Gly Val Asp Leu Tyr Tyr Thr Ser Tyr

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Tyr Leu Phe Arg Val Leu Phe Val His Leu Leu Pro Cys Ile Ile Leu

275 280 285

gtt acc ctg aac att ctg ctg ttc gcg gcg atg cgg cag gca cag gag 912
Val Thr Leu Asn Ile Leu Leu Phe Ala Ala Met Arg Gln Ala Gln Glu
290 295 300

cgc cga aag ctc ctc ttc cgg gag aac cgg aag aag gag tgc aag aaa 960
Arg Arg Lys Leu Leu Phe Arg Glu Asn Arg Lys Lys Glu Cys Lys Lys
305 310 315 320

ctg agg gag acc aat tgc acc acg ctg atg cta att gtg gtc gtg tcg 1008
Leu Arg Glu Thr Asn Cys Thr Thr Leu Met Leu Ile Val Val Val Ser
325 330 335

gtg ttc ctt cta gcc gag ata ccc att gct gtg gtc act gcg atg cac 1056
Val Phe Leu Leu Ala Glu Ile Pro Ile Ala Val Val Thr Ala Met His
340 345 350

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Ile Val Ser Ser Leu Ile Ile Glu Phe Leu Asp Tyr Gly Leu Ala Asn
355 360 365

att tgc atc atg ctg acg aac ttc ttc ctg gta ttc agc tat ccg atc 1152
Ile Cys Ile Met Leu Thr Asn Phe Phe Leu Val Phe Ser Tyr Pro Ile
370 375 380

aac ttc ggc att tac tgc ggc atg tcg cgc cag ttt cgg gag act ttc 1200
Asn Phe Gly Ile Tyr Cys Gly Met Ser Arg Gln Phe Arg Glu Thr Phe
385 390 395 400

aag gag ata ttc ctc ggt cgg ctg atg gcc aaa aag gat agc tcc aca 1248
Lys Glu Ile Phe Leu Gly Arg Leu Met Ala Lys Lys Asp Ser Ser Thr
405 410 415

aaa tac tcg atc gtt aat ggc gcc cgc acc tgc acc aac acc aac gag 1296
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 35 40 45

Tyr Gly Asn Glu Ser Leu Asp Tyr Pro Asn Tyr Gln Gln Met Val Gly
 50 55 60

Gly Pro Cys Arg Met Glu Asp Asn Asn Ile Ser Tyr Trp Asn Leu Thr
 65 70 75 80

Cys Asp Ser Pro Leu Glu Tyr Ala Met Pro Leu Tyr Gly Tyr Cys Met
 85 90 95

Pro Phe Leu Leu Ile Ile Thr Ile Ile Ser Asn Ser Leu Ile Val Leu
 100 105 110

Val Leu Ser Lys Lys Ser Met Ala Thr Pro Thr Asn Phe Val Leu Met
 115 120 125

Gly Met Ala Ile Cys Asp Met Leu Thr Val Ile Phe Pro Ala Pro Gly
 130 135 140

Leu Trp Tyr Met Tyr Thr Phe Gly Asn His Tyr Lys Pro Leu His Pro
 145 150 155 160

Val Ser Met Cys Leu Ala Tyr Ser Ile Phe Asn Glu Ile Met Pro Ala
 165 170 175

Met Cys His Thr Ile Ser Val Trp Leu Thr Leu Ala Leu Ala Val Gln
 180 185 190

Arg Tyr Ile Tyr Val Cys His Ala Pro Met Ala Arg Thr Trp Cys Thr
 195 200 205

Met Pro Arg Val Arg Arg Cys Thr Ala Tyr Ile Ala Leu Leu Ala Phe
 210 215 220

Leu His Gln Leu Pro Arg Phe Phe Asp Arg Thr Tyr Met Pro Leu Val
 225 230 235 240

Ile Glu Trp Asn Gly Ser Pro Thr Glu Val Cys His Leu Glu Thr Ser
 245 250 255

Met Trp Val His Asp Tyr Ile Gly Val Asp Leu Tyr Tyr Thr Ser Tyr
 260 265 270

Tyr Leu Phe Arg Val Leu Phe Val His Leu Leu Pro Cys Ile Ile Leu
 275 280 285

Val Thr Leu Asn Ile Leu Leu Phe Ala Ala Met Arg Gln Ala Gln Glu
 290 295 300

Arg Arg Lys Leu Leu Phe Arg Glu Asn Arg Lys Lys Glu Cys Lys Lys
 305 310 315 320

Leu Arg Glu Thr Asn Cys Thr Thr Leu Met Leu Ile Val Val Val Ser
 325 330 335

Val Phe Leu Leu Ala Glu Ile Pro Ile Ala Val Val Thr Ala Met His
 340 345 350

Ile Val Ser Ser Leu Ile Ile Glu Phe Leu Asp Tyr Gly Leu Ala Asn
 355 360 365

Ile Cys Ile Met Leu Thr Asn Phe Phe Leu Val Phe Ser Tyr Pro Ile
 370 375 380

Asn Phe Gly Ile Tyr Cys Gly Met Ser Arg Gln Phe Arg Glu Thr Phe
 385 390 395 400

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

tca aca ttt gct gca aac agc gga gac gcc tca agt ggt ggc gaa cga 144
 Ser Thr Phe Ala Ala Asn Ser Gly Asp Ala Ser Ser Gly Gly Glu Arg
 35 40 45

atg ctg tat tac ttc gat ggt agc gac gat gat agc act gcg tct aag 192
 Met Leu Tyr Tyr Phe Asp Gly Ser Asp Asp Asp Ser Thr Ala Ser Lys
 50 55 60

caa cag ttt cac agc ctc caa cac cag cag aaa gcg gca ctt ttg ctg 240
 Gln Gln Phe His Ser Leu Gln His Gln Gln Lys Ala Ala Leu Leu Leu
 65 70 75 80

ggc gag aac atc aca acc tcc aca atg tat tcc tca ctg gat cct ggc 288
 Gly Glu Asn Ile Thr Thr Ser Thr Met Tyr Ser Ser Leu Asp Pro Gly
 85 90 95

atc tac aat ccg ata gag gca gaa aac gag act gac ttc ctc tat atc 336
 Ile Tyr Asn Pro Ile Glu Ala Glu Asn Glu Thr Asp Phe Leu Tyr Ile
 100 105 110

aac gga cca agc agt agt tat ggt tat acg gaa ggt cac aac ggc aca 384
 Asn Gly Pro Ser Ser Ser Tyr Gly Tyr Thr Glu Gly His Asn Gly Thr
 115 120 125

ctc ccg tac ggc gat gac tac tat cag agc tgt atg gga atg tac ggt 432
 Leu Pro Tyr Gly Asp Asp Tyr Tyr Gln Ser Cys Met Gly Met Tyr Gly
 130 135 140

aac gtt acg tat ctg aac gtg tcc tgt gaa aca att cta aac tat agt 480
 Asn Val Thr Tyr Leu Asn Val Ser Cys Glu Thr Ile Leu Asn Tyr Ser
 145 150 155 160

ata cca ctc tac gga tac tgt act ccc atc ttc atc cta att aca ctg 528
 Ile Pro Leu Tyr Gly Tyr Cys Thr Pro Ile Phe Ile Leu Ile Thr Leu
 165 170 175

act gcc aac tcg ctg atc gtg att gtc ctc agc aaa cgc agc atg gca 576
 Thr Ala Asn Ser Leu Ile Val Ile Val Leu Ser Lys Arg Ser Met Ala
 180 185 190

tcg ccg acc aac ttc gtg ctg atg gct atg gct ctt tgc gat atg ttt 624
 Ser Pro Thr Asn Phe Val Leu Met Ala Met Ala Leu Cys Asp Met Phe
 195 200 205

acc ctg ata ttc ccg gcg cca ggc ctg ctg tac atg tac acg ttt ggc 672
 Thr Leu Ile Phe Pro Ala Pro Gly Leu Leu Tyr Met Tyr Thr Phe Gly
 210 215 220

aat cac tac aag cca tta tcg ccg att acc gcc tgc tac gtg tgg aac 720
 Asn His Tyr Lys Pro Leu Ser Pro Ile Thr Ala Cys Tyr Val Trp Asn
 225 230 235 240

gcg ctg aac gag cac tta ccg gca atg ttc cac aca gca tca gtc tgg 768
 Ala Leu Asn Glu His Leu Pro Ala Met Phe His Thr Ala Ser Val Trp
 245 250 255

ctt acg tta gcg ttg gct gta cag agg tac gtc tat gtt tgc cat gct 816
 Leu Thr Leu Ala Leu Ala Val Gln Arg Tyr Val Tyr Val Cys His Ala
 260 265 270

ccc ata gct cga acg tgg tgc acg att cct cgg gtg aaa aaa tgt atc 864
 Pro Ile Ala Arg Thr Trp Cys Thr Ile Pro Arg Val Lys Lys Cys Ile
 275 280 285

gcc tac atc tgc ata gca gca cta att cat cag agc acc agg ttt ttc 912
 Ala Tyr Ile Cys Ile Ala Ala Leu Ile His Gln Ser Thr Arg Phe Phe
 290 295 300

gat aaa tca tac agc ctg gtg aca atc gaa tgg aac ggc cat tcg acg 960
 Asp Lys Ser Tyr Ser Leu Val Thr Ile Glu Trp Asn Gly His Ser Thr
 305 310 315 320

gag gtt tgc cac acc gag acc tca agc tgg gtg cac gac tac gta ggc 1008
 Glu Val Cys His Thr Glu Thr Ser Ser Trp Val His Asp Tyr Val Gly
 325 330 335

gaa gat gtg tac tat acc ttc tac ttt tcg ttc cgg ata ttg ttc gtg 1056
 Glu Asp Val Tyr Tyr Thr Phe Tyr Phe Ser Phe Arg Ile Leu Phe Val
 340 345 350

cat ctg ata ccg tgc ggg agt ttg gtt gcg ttg aac gtg ctg ctt ttc 1104
 His Leu Ile Pro Cys Gly Ser Leu Val Ala Leu Asn Val Leu Leu Phe
 355 360 365

aag gca atg cgc caa gcg caa cag aag cgc gaa cgt ctc ttc aaa gat 1152
 Lys Ala Met Arg Gln Ala Gln Gln Lys Arg Glu Arg Leu Phe Lys Asp
 370 375 380

acc gcc aaa aag cga gaa tgc aag cga gtc cgg gac tcc aac tgc acc 1200
 Thr Ala Lys Lys Arg Glu Cys Lys Arg Val Arg Asp Ser Asn Cys Thr
 385 390 395 400

aca ctt atg ttg ata gtc gtg gtg aca gtt ttc ctc atc gtg gaa ata 1248
 Thr Leu Met Leu Ile Val Val Val Thr Val Phe Leu Ile Val Glu Ile
 405 410 415

cca ctc gct gtg att acg gcc tta cac atc atc tcc tcg ctc att tat 1296
 Pro Leu Ala Val Ile Thr Ala Leu His Ile Ile Ser Ser Leu Ile Tyr
 420 425 430

gag ttc ctc gac tac tac att gcg aac ctg ttc atc ctg ttt gcg aac 1344
 Glu Phe Leu Asp Tyr Tyr Ile Ala Asn Leu Phe Ile Leu Phe Ala Asn
 435 440 445

ttt ttc ctc atc gtt agc tat cca atc aat ttt gca atc tac tgc ggg 1392
 Phe Phe Leu Ile Val Ser Tyr Pro Ile Asn Phe Ala Ile Tyr Cys Gly
 450 455 460

atg tca cgt cag ttc cgg gag acg ttc aag gaa att ttc gtc aaa tcg 1440
 Met Ser Arg Gln Phe Arg Glu Thr Phe Lys Glu Ile Phe Val Lys Ser
 465 470 475 480

agc aaa caa atc ccg agc gga aaa aag gat tgt ggc tcc tcg cgg tat 1488
 Ser Lys Gln Ile Pro Ser Gly Lys Lys Asp Cys Gly Ser Ser Arg Tyr
 485 490 495

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<213> Aedes aegypti

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Ser Thr Phe Ala Ala Asn Ser Gly Asp Ala Ser Ser Gly Gly Glu Arg
 35 40 45

Met Leu Tyr Tyr Phe Asp Gly Ser Asp Asp Asp Ser Thr Ala Ser Lys
 50 55 60

Gln Gln Phe His Ser Leu Gln His Gln Gln Lys Ala Ala Leu Leu Leu
 65 70 75 80

Gly Glu Asn Ile Thr Thr Ser Thr Met Tyr Ser Ser Leu Asp Pro Gly
 85 90 95

Ile Tyr Asn Pro Ile Glu Ala Glu Asn Glu Thr Asp Phe Leu Tyr Ile
 100 105 110

Asn Gly Pro Ser Ser Ser Tyr Gly Tyr Thr Glu Gly His Asn Gly Thr
 115 120 125

Leu Pro Tyr Gly Asp Asp Tyr Tyr Gln Ser Cys Met Gly Met Tyr Gly
 130 135 140

Asn Val Thr Tyr Leu Asn Val Ser Cys Glu Thr Ile Leu Asn Tyr Ser
 145 150 155 160

Ile Pro Leu Tyr Gly Tyr Cys Thr Pro Ile Phe Ile Leu Ile Thr Leu
 165 170 175

Thr Ala Asn Ser Leu Ile Val Ile Val Leu Ser Lys Arg Ser Met Ala
 180 185 190

Ser Pro Thr Asn Phe Val Leu Met Ala Met Ala Leu Cys Asp Met Phe
 195 200 205

Thr Leu Ile Phe Pro Ala Pro Gly Leu Leu Tyr Met Tyr Thr Phe Gly
 210 215 220

Asn His Tyr Lys Pro Leu Ser Pro Ile Thr Ala Cys Tyr Val Trp Asn
 225 230 235 240

Ala Leu Asn Glu His Leu Pro Ala Met Phe His Thr Ala Ser Val Trp
 245 250 255

Leu Thr Leu Ala Leu Ala Val Gln Arg Tyr Val Tyr Val Cys His Ala
 260 265 270

Pro Ile Ala Arg Thr Trp Cys Thr Ile Pro Arg Val Lys Lys Cys Ile
 275 280 285

Ala Tyr Ile Cys Ile Ala Ala Leu Ile His Gln Ser Thr Arg Phe Phe
 290 295 300

Asp Lys Ser Tyr Ser Leu Val Thr Ile Glu Trp Asn Gly His Ser Thr
 305 310 315 320

Glu Val Cys His Thr Glu Thr Ser Ser Trp Val His Asp Tyr Val Gly
 325 330 335

Glu Asp Val Tyr Tyr Thr Phe Tyr Phe Ser Phe Arg Ile Leu Phe Val
 340 345 350

His Leu Ile Pro Cys Gly Ser Leu Val Ala Leu Asn Val Leu Leu Phe
 355 360 365

Lys Ala Met Arg Gln Ala Gln Gln Lys Arg Glu Arg Leu Phe Lys Asp
 370 375 380

Thr Ala Lys Lys Arg Glu Cys Lys Arg Val Arg Asp Ser Asn Cys Thr
 385 390 395 400

Thr Leu Met Leu Ile Val Val Val Thr Val Phe Leu Ile Val Glu Ile
 405 410 415

Pro Leu Ala Val Ile Thr Ala Leu His Ile Ile Ser Ser Leu Ile Tyr
 420 425 430

Glu Phe Leu Asp Tyr Tyr Ile Ala Asn Leu Phe Ile Leu Phe Ala Asn
 435 440 445

Phe Phe Leu Ile Val Ser Tyr Pro Ile Asn Phe Ala Ile Tyr Cys Gly
 450 455 460

Met Ser Arg Gln Phe Arg Glu Thr Phe Lys Glu Ile Phe Val Lys Ser
 465 470 475 480

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cag tac cta tct aat atg ata gag cca aaa aaa aac aga gca ccg att 96
 Gln Tyr Leu Ser Asn Met Ile Glu Pro Lys Lys Asn Arg Ala Pro Ile
 20 25 30

att cta ttc aac tct cca cac atg gca act tat tac tat ttc aat gaa 144
 Ile Leu Phe Asn Ser Pro His Met Ala Thr Tyr Tyr Tyr Phe Asn Glu
 35 40 45

tca acg cct ctt tcg tca caa ata ttc ttt cca aaa gaa agc tca gaa 192
 Ser Thr Pro Leu Ser Ser Gln Ile Phe Phe Pro Lys Glu Ser Ser Glu
 50 55 60

aac tat aat act act ggt atc aac acg agt act tcc tac acg gtt cat 240
 Asn Tyr Asn Thr Thr Gly Ile Asn Thr Ser Thr Ser Tyr Thr Val His
 65 70 75 80

atg aat gaa ttg aat aac gac tcg aca tac agt tac tat aat tgc cta 288
 Met Asn Glu Leu Asn Asn Asp Ser Thr Tyr Ser Tyr Tyr Asn Cys Leu
 85 90 95

gca tca gaa gga aac acg tct tac ttg aat gtg tca tgt gaa acc att 336
 Ala Ser Glu Gly Asn Thr Ser Tyr Leu Asn Val Ser Cys Glu Thr Ile
 100 105 110

ctt aat tat agc att ccg ttg tat gga tat tgt ata ccc ttt ctt ttg 384

Leu Asn Tyr Ser Ile Pro Leu Tyr Gly Tyr Cys Ile Pro Phe Leu Leu
 115 120 125

ctg gtt acc ctc aca gca aat tct tta ata att att atc ctc aat aaa 432
 Leu Val Thr Leu Thr Ala Asn Ser Leu Ile Ile Ile Ile Leu Asn Lys
 130 135 140

aga agc atg gcg tca cca aca aat tgt att ctt atg gca atg gct ctt 480
 Arg Ser Met Ala Ser Pro Thr Asn Cys Ile Leu Met Ala Met Ala Leu
 145 150 155 160

tgt gat atg ttt acc ctt ctt ttt ccg gca cct ggt ttg ata tac atg 528
 Cys Asp Met Phe Thr Leu Leu Phe Pro Ala Pro Gly Leu Ile Tyr Met
 165 170 175

tat aca ttt gga aac cat tac aaa cca ttg tca cct tta ata gcg tgc 576
 Tyr Thr Phe Gly Asn His Tyr Lys Pro Leu Ser Pro Leu Ile Ala Cys
 180 185 190

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 Tyr Val Trp Asn Ala Leu Asn Glu Ile Leu Pro Ala Met Cys His Thr
 195 200 205

gca tca gta tgg ctt aca tta gct tta gct ttg caa aga tac ata tac 672
 Ala Ser Val Trp Leu Thr Leu Ala Leu Ala Leu Gln Arg Tyr Ile Tyr
 210 215 220

gtt tgc cat gca cct gcc cga aat tgg tgt act att cct aga gta aaa 720
 Val Cys His Ala Pro Ala Arg Asn Trp Cys Thr Ile Pro Arg Val Lys
 225 230 235 240

aaa tgc att ggt tat atc tgt gct act gct ttt tta cac caa agc agt 768
 Lys Cys Ile Gly Tyr Ile Cys Ala Thr Ala Phe Leu His Gln Ser Ser
 245 250 255

aga ttt ttt gac aag tct tat agt cta ata aca ata atg tgg aat ggc 816
 Arg Phe Phe Asp Lys Ser Tyr Ser Leu Ile Thr Ile Met Trp Asn Gly
 260 265 270

caa atg aca aac gta tgt cat gtt gaa aca gca aat tgg ata cac aaa 864
 Gln Met Thr Asn Val Cys His Val Glu Thr Ala Asn Trp Ile His Lys
 275 280 285

tac acc agc gaa gat ttt tat tac aca ttc tat ttt tcc ttt cgc att 912
 Tyr Thr Ser Glu Asp Phe Tyr Tyr Thr Phe Tyr Phe Ser Phe Arg Ile
 290 295 300

tta ttt gtc cat tta aca ccc tgt gcc agt ctg gta gct cta aat gtt 960

Leu Phe Val His Leu Thr Pro Cys Ala Ser Leu Val Ala Leu Asn Val
 305 310 315 320

ttc ctt ttt agg gcc atg aaa caa gct caa aag aag aga gaa cgg ctt 1008
 Phe Leu Phe Arg Ala Met Lys Gln Ala Gln Lys Lys Arg Glu Arg Leu
 325 330 335

ttt aag gac aac aag aaa cgt gaa tgt aaa cgg atc cgc gat tct aac 1056
 Phe Lys Asp Asn Lys Lys Arg Glu Cys Lys Arg Ile Arg Asp Ser Asn
 340 345 350

tgt act act ctt atg tta atc gtt gtg gtt acc gtc ttc tta gtt gta 1104
 Cys Thr Thr Leu Met Leu Ile Val Val Val Thr Val Phe Leu Val Val
 355 360 365

gaa ata cca cta ggt gtt att aca gca ctt cat att ata tca tct ctc 1152
 Glu Ile Pro Leu Gly Val Ile Thr Ala Leu His Ile Ile Ser Ser Leu
 370 375 380

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 Ile Tyr Glu Phe Leu Asp Tyr Tyr Val Ala Asn Leu Phe Ile Leu Phe
 385 390 395 400

gct aat ttt ttt cta ata gtc agt tat cca ata aat ttt gcg att tat 1248
 Ala Asn Phe Phe Leu Ile Val Ser Tyr Pro Ile Asn Phe Ala Ile Tyr
 405 410 415

tgc gga atg tcg cgt caa ttt cgt gag aca ttc aaa gga ata ttt gtt 1296
 Cys Gly Met Ser Arg Gln Phe Arg Glu Thr Phe Lys Gly Ile Phe Val
 420 425 430

caa tca gat tct caa atc aaa ata aca aaa gaa tat ggt tca tcg aag 1344
 Gln Ser Asp Ser Gln Ile Lys Ile Thr Lys Glu Tyr Gly Ser Ser Lys
 435 440 445

tat tcg tta gta aat gga ccg aga acg tgt aca aat gaa act gtg att 1392
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<212> PRT

<213> Anopheles gambiae

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 35 40 45

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

Asn Tyr Asn Thr Thr Gly Ile Asn Thr Ser Thr Ser Tyr Thr Val His
 65 70 75 80

Met Asn Glu Leu Asn Asn Asp Ser Thr Tyr Ser Tyr Tyr Asn Cys Leu
 85 90 95

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

Leu Asn Tyr Ser Ile Pro Leu Tyr Gly Tyr Cys Ile Pro Phe Leu Leu
 115 120 125

Leu Val Thr Leu Thr Ala Asn Ser Leu Ile Ile Ile Ile Leu Asn Lys
 130 135 140

Arg Ser Met Ala Ser Pro Thr Asn Cys Ile Leu Met Ala Met Ala Leu
 145 150 155 160

Cys Asp Met Phe Thr Leu Leu Phe Pro Ala Pro Gly Leu Ile Tyr Met
 165 170 175

Tyr Thr Phe Gly Asn His Tyr Lys Pro Leu Ser Pro Leu Ile Ala Cys
 180 185 190

Tyr Val Trp Asn Ala Leu Asn Glu Ile Leu Pro Ala Met Cys His Thr
195 200 205

Ala Ser Val Trp Leu Thr Leu Ala Leu Ala Leu Gln Arg Tyr Ile Tyr
210 215 220

Val Cys His Ala Pro Ala Arg Asn Trp Cys Thr Ile Pro Arg Val Lys
225 230 235 240

Lys Cys Ile Gly Tyr Ile Cys Ala Thr Ala Phe Leu His Gln Ser Ser
245 250 255

Arg Phe Phe Asp Lys Ser Tyr Ser Leu Ile Thr Ile Met Trp Asn Gly
260 265 270

Gln Met Thr Asn Val Cys His Val Glu Thr Ala Asn Trp Ile His Lys
275 280 285

Tyr Thr Ser Glu Asp Phe Tyr Tyr Thr Phe Tyr Phe Ser Phe Arg Ile
290 295 300

Leu Phe Val His Leu Thr Pro Cys Ala Ser Leu Val Ala Leu Asn Val
305 310 315 320

Phe Leu Phe Arg Ala Met Lys Gln Ala Gln Lys Lys Arg Glu Arg Leu
325 330 335

Phe Lys Asp Asn Lys Lys Arg Glu Cys Lys Arg Ile Arg Asp Ser Asn
340 345 350

Cys Thr Thr Leu Met Leu Ile Val Val Val Thr Val Phe Leu Val Val
355 360 365

Glu Ile Pro Leu Gly Val Ile Thr Ala Leu His Ile Ile Ser Ser Leu
370 375 380

Ile Tyr Glu Phe Leu Asp Tyr Tyr Val Ala Asn Leu Phe Ile Leu Phe
385 390 395 400

Ala Asn Phe Phe Leu Ile Val Ser Tyr Pro Ile Asn Phe Ala Ile Tyr
405 410 415

Cys Gly Met Ser Arg Gln Phe Arg Glu Thr Phe Lys Gly Ile Phe Val
420 425 430

Gln Ser Asp Ser Gln Ile Lys Ile Thr Lys Glu Tyr Gly Ser Ser Lys
435 440 445

Tyr Ser Leu Val Asn Gly Pro Arg Thr Cys Thr Asn Glu Thr Val Ile
450 455 460

<210> 7
<211> 1221
<212> DNA
<213> Bombyx mori

<220>
<221> CDS
<222> (1)..(1221)

<400> 7
atg gcg gtc acc ata gac aat tca acg aac gac ttc gaa ttc cag aag 48
Met Ala Val Thr Ile Asp Asn Ser Thr Asn Asp Phe Glu Phe Gln Lys
1 5 10 15

cca ttc aac tac tca att aac gag aac atc acc tac ttc gat tac acg 96
Pro Phe Asn Tyr Ser Ile Asn Glu Asn Ile Thr Tyr Phe Asp Tyr Thr
20 25 30

aac ttc act tcg gac gat ttc tgc gca tca aac aac tca cac gta tac 144
Asn Phe Thr Ser Asp Asp Phe Cys Ala Ser Asn Asn Ser His Val Tyr
35 40 45

tta aac gtc acc tgt gag ttc gct ata agc tat gct gag cct atg tac 192
Leu Asn Val Thr Cys Glu Phe Ala Ile Ser Tyr Ala Glu Pro Met Tyr
50 55 60

g g g t a c a t c g c a c c g t t t c t g c t a g c t a c a a c g a c a g t t g c c a a c a c c 240
 Gly Tyr Ile Ala Pro Phe Leu Leu Ala Thr Thr Thr Val Ala Asn Thr
 65 70 75 80

c t g a t c g t g g t g c t a t c g c g g a g g c a c a t g a g g a c g c c c a c c a a t 288
 Leu Ile Val Val Val Leu Ser Arg Arg His Met Arg Thr Pro Thr Asn
 85 90 95

g c c g t g c t g a t g g c g a t g g c t c t t g c g a t a t g t t c a c c a t g c t g t t c 336
 Ala Val Leu Met Ala Met Ala Leu Cys Asp Met Phe Thr Met Leu Phe
 100 105 110

c c g g c g c c c g t g g c t a t t c t a c a t g t a c a c t t t t g g a a c c a c t a c a a g 384
 Pro Ala Pro Trp Leu Phe Tyr Met Tyr Thr Phe Gly Asn His Tyr Lys
 115 120 125

c c g c t a a g t c c c g t c a g a g c c t g c c a a g c t t g g a a t t a c a t g a a c g a g 432
 Pro Leu Ser Pro Val Arg Ala Cys Gln Ala Trp Asn Tyr Met Asn Glu
 130 135 140

g t c a t t c c a g c g a t g t t c c a c a c g g c t a g t a t c t g g t t g a c g t t a g c c 480
 Val Ile Pro Ala Met Phe His Thr Ala Ser Ile Trp Leu Thr Leu Ala
 145 150 155 160

t t a g c c g t c c a g a g a t a t a t c t a c g t t t g c c a c g c g c c g t c g c c a g g 528
 Leu Ala Val Gln Arg Tyr Ile Tyr Val Cys His Ala Pro Val Ala Arg
 165 170 175

a c c t g g t g t a c c a t g c c c c g g g t g a t g a a a t g t c t g a t c t a c a t a g g a 576
 Thr Trp Cys Thr Met Pro Arg Val Met Lys Cys Leu Ile Tyr Ile Gly
 180 185 190

a t a g c g g c g t t t c t t c a t c a g c t a c c g c g g t t c t t c g a c a g a t g c t a c 624
 Ile Ala Ala Phe Leu His Gln Leu Pro Arg Phe Phe Asp Arg Cys Tyr
 195 200 205

a c t c c c c a c a a g a c t g t g t g g c g g g g c g g t g g a g g a a g t c t g c a g a 672
 Thr Pro His Lys Thr Val Trp Arg Gly Arg Val Glu Glu Val Cys Arg
 210 215 220

a t c g a g a t g g c g t c t t g g g t g a a a g c g c t c t c c g t c g a c g c c t a t t t c 720
 Ile Glu Met Ala Ser Trp Val Lys Ala Leu Ser Val Asp Ala Tyr Phe
 225 230 235 240

a t c t c c t a c t t c g g c t t c a g a g t t t t g t t c g t c c a c t t a a t c c g t g c 768
 Ile Ser Tyr Phe Gly Phe Arg Val Leu Phe Val His Leu Ile Pro Cys
 245 250 255

aca tct tta gtt gtc ctg aac gtg ctc ctc ttc agg gcc atg agg acg 816
 Thr Ser Leu Val Val Leu Asn Val Leu Leu Phe Arg Ala Met Arg Thr
 260 265 270

gcc caa ata aac aga cag aag ctg ttc aaa gaa aac cga aaa tcg gag 864
 Ala Gln Ile Asn Arg Gln Lys Leu Phe Lys Glu Asn Arg Lys Ser Glu
 275 280 285

tgc aag aga ctc aga gat tct aac tgc acc acc ctg atg ttg ata gtc 912
 Cys Lys Arg Leu Arg Asp Ser Asn Cys Thr Thr Leu Met Leu Ile Val
 290 295 300

gtg gtc acg gtt ttc ctc ctc gtg gaa ata ccc gtg gcc gtc gtc act 960
 Val Val Thr Val Phe Leu Leu Val Glu Ile Pro Val Ala Val Val Thr
 305 310 315 320

atc ctc cac ata ata tcc agc acg att gtc gag atc ttg gac tac cat 1008
 Ile Leu His Ile Ile Ser Ser Thr Ile Val Glu Ile Leu Asp Tyr His
 325 330 335

atc gcg aat att ctc gtt ctg gta acg aat ttc ttc att atc gtt tcc 1056
 Ile Ala Asn Ile Leu Val Leu Val Thr Asn Phe Phe Ile Ile Val Ser
 340 345 350

tat cca atc aac ttt gct ata tat tgc ggt atg tcg cgt caa ttc agg 1104
 Tyr Pro Ile Asn Phe Ala Ile Tyr Cys Gly Met Ser Arg Gln Phe Arg
 355 360 365

gag acc ttc aaa gaa ttg ttt atc aga ggc acg gtt act agt agg aag 1152
 Glu Thr Phe Lys Glu Leu Phe Ile Arg Gly Thr Val Thr Ser Arg Lys
 370 375 380

aac ggt ggc tcc agt agg tac tct ctt gtc aat ggc ccg agg acc tgt 1200
 Asn Gly Gly Ser Ser Arg Tyr Ser Leu Val Asn Gly Pro Arg Thr Cys
 385 390 395 400

aca aac gaa act gtg ctt taa 1221
 Thr Asn Glu Thr Val Leu
 405

<210> 8

<211> 406

<212> PRT

<213> Bombyx mori

<400> 8

Met Ala Val Thr Ile Asp Asn Ser Thr Asn Asp Phe Glu Phe Gln Lys
 1 5 10 15

Pro Phe Asn Tyr Ser Ile Asn Glu Asn Ile Thr Tyr Phe Asp Tyr Thr
 20 25 30

Asn Phe Thr Ser Asp Asp Phe Cys Ala Ser Asn Asn Ser His Val Tyr
 35 40 45

Leu Asn Val Thr Cys Glu Phe Ala Ile Ser Tyr Ala Glu Pro Met Tyr
 50 55 60

Gly Tyr Ile Ala Pro Phe Leu Leu Ala Thr Thr Thr Val Ala Asn Thr
 65 70 75 80

Leu Ile Val Val Val Leu Ser Arg Arg His Met Arg Thr Pro Thr Asn
 85 90 95

Ala Val Leu Met Ala Met Ala Leu Cys Asp Met Phe Thr Met Leu Phe
 100 105 110

Pro Ala Pro Trp Leu Phe Tyr Met Tyr Thr Phe Gly Asn His Tyr Lys
 115 120 125

Pro Leu Ser Pro Val Arg Ala Cys Gln Ala Trp Asn Tyr Met Asn Glu
 130 135 140

Val Ile Pro Ala Met Phe His Thr Ala Ser Ile Trp Leu Thr Leu Ala
 145 150 155 160

Leu Ala Val Gln Arg Tyr Ile Tyr Val Cys His Ala Pro Val Ala Arg
 165 170 175

Thr Trp Cys Thr Met Pro Arg Val Met Lys Cys Leu Ile Tyr Ile Gly
 180 185 190

Ile Ala Ala Phe Leu His Gln Leu Pro Arg Phe Phe Asp Arg Cys Tyr
 195 200 205

Thr Pro His Lys Thr Val Trp Arg Gly Arg Val Glu Glu Val Cys Arg
 210 215 220

Ile Glu Met Ala Ser Trp Val Lys Ala Leu Ser Val Asp Ala Tyr Phe
 225 230 235 240

Ile Ser Tyr Phe Gly Phe Arg Val Leu Phe Val His Leu Ile Pro Cys
 245 250 255

Thr Ser Leu Val Val Leu Asn Val Leu Leu Phe Arg Ala Met Arg Thr
 260 265 270

Ala Gln Ile Asn Arg Gln Lys Leu Phe Lys Glu Asn Arg Lys Ser Glu
 275 280 285

Cys Lys Arg Leu Arg Asp Ser Asn Cys Thr Thr Leu Met Leu Ile Val
 290 295 300

Val Val Thr Val Phe Leu Leu Val Glu Ile Pro Val Ala Val Val Thr
 305 310 315 320

Ile Leu His Ile Ile Ser Ser Thr Ile Val Glu Ile Leu Asp Tyr His
 325 330 335

Ile Ala Asn Ile Leu Val Leu Val Thr Asn Phe Phe Ile Ile Val Ser
 340 345 350

Tyr Pro Ile Asn Phe Ala Ile Tyr Cys Gly Met Ser Arg Gln Phe Arg
 355 360 365

Glu Thr Phe Lys Glu Leu Phe Ile Arg Gly Thr Val Thr Ser Arg Lys
 370 375 380

Asn Gly Gly Ser Ser Arg Tyr Ser Leu Val Asn Gly Pro Arg Thr Cys
 385 390 395 400

Thr Asn Glu Thr Val Leu
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<210> 9
 <211> 1176
 <212> DNA
 <213> Tribolium castaneum

<220>
 <221> CDS
 <222> (1)..(1176)

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 1 5 10 15
 tac gcg aac gaa acc gta cca aat gtt acg tca gtg gaa aaa gtc cag 96
 Tyr Ala Asn Glu Thr Val Pro Asn Val Thr Ser Val Glu Lys Val Gln
 20 25 30
 tac att aac atc acg atg gaa atg cct att gcc tac gct gtg ccc tta 144
 Tyr Ile Asn Ile Thr Met Glu Met Pro Ile Ala Tyr Ala Val Pro Leu
 35 40 45
 tat ggc tac gtt atg ccg ttc tta ttg ata ata act att atc gcg aat 192
 Tyr Gly Tyr Val Met Pro Phe Leu Leu Ile Ile Thr Ile Ile Ala Asn
 50 55 60
 act tta atc gtc gtt gtg ctg agc aaa agg cag atg agg act cca aca 240
 Thr Leu Ile Val Val Val Leu Ser Lys Arg Gln Met Arg Thr Pro Thr
 65 70 75 80
 aac gtc gtt ttg atg gcg atg gct ctt tgt gat atg ttc acg gtt tta 288
 Asn Val Val Leu Met Ala Met Ala Leu Cys Asp Met Phe Thr Val Leu
 85 90 95
 ata ccg gct cct tgg ctt atc tac atg tac tcc ttt ggg aac cac tac 336
 Ile Pro Ala Pro Trp Leu Ile Tyr Met Tyr Ser Phe Gly Asn His Tyr
 100 105 110
 aag ccc ctt tgg cct ata agt ctt tgt tac gcc tgg ttt gtt atg cac 384

Lys Pro Leu Trp Pro Ile Ser Leu Cys Tyr Ala Trp Phe Val Met His
 115 120 125

gag gta att ccc aac atg ttc cac acg gcg agc att tgg cta aca ttg 432
 Glu Val Ile Pro Asn Met Phe His Thr Ala Ser Ile Trp Leu Thr Leu
 130 135 140

gcc ctc gct gtt cag agg tac att ttc gta tgc cat gcg cct ctt gca 480
 Ala Leu Ala Val Gln Arg Tyr Ile Phe Val Cys His Ala Pro Leu Ala
 145 150 155 160

cga aaa ttg tgc acc atg tct aac gtc tac aag tgt ctt atc tat att 528
 Arg Lys Leu Cys Thr Met Ser Asn Val Tyr Lys Cys Leu Ile Tyr Ile
 165 170 175

cta gtc ata gca gct ctt cat cag ggt ttc cgg ttt ttt gac tca gaa 576
 Leu Val Ile Ala Ala Leu His Gln Gly Phe Arg Phe Phe Asp Ser Glu
 180 185 190

tat agc acg gtg gac gtg cta tgg aac aac cac aca aca cat gtg tgc 624
 Tyr Ser Thr Val Asp Val Leu Trp Asn Asn His Thr Thr His Val Cys
 195 200 205

aaa aga gag cat gca cat tgg gtg aag gaa tac gtg acc gag gat ttc 672
 Lys Arg Glu His Ala His Trp Val Lys Glu Tyr Val Thr Glu Asp Phe
 210 215 220

tac ttc gta act tat ttc atg ttc agg gta tta ttt gtg cat cta att 720
 Tyr Phe Val Thr Tyr Phe Met Phe Arg Val Leu Phe Val His Leu Ile
 225 230 235 240

cct tgt gta gct ctc gtg att ttg aat atc cta ttg ttt cga gca ctg 768
 Pro Cys Val Ala Leu Val Ile Leu Asn Ile Leu Leu Phe Arg Ala Leu
 245 250 255

aaa caa gcg caa cag cga agg gag caa ctg ctt tcc aaa aag aat caa 816
 Lys Gln Ala Gln Gln Arg Arg Glu Gln Leu Leu Ser Lys Lys Asn Gln
 260 265 270

aag aac gaa tgc aag aag tta aga gac tct aat tgc acc act ctg atg 864
 Lys Asn Glu Cys Lys Lys Leu Arg Asp Ser Asn Cys Thr Thr Leu Met
 275 280 285

ctg ata gtc gta gta act gtg ttt ctt att gta gag att ccg cta gtg 912
 Leu Ile Val Val Val Thr Val Phe Leu Ile Val Glu Ile Pro Leu Val
 290 295 300

gtg gtt act ttg ttg cat ata ata tcc agc acg ttt att gag ttt ctg 960

Val Val Thr Leu Leu His Ile Ile Ser Ser Thr Phe Ile Glu Phe Leu
 305 310 315 320

gac tac tat gta gcg aat acg tta att ctt ttt acc aat ttt ttc ata 1008
 Asp Tyr Tyr Val Ala Asn Thr Leu Ile Leu Phe Thr Asn Phe Phe Ile
 325 330 335

atc tta agt tac ccg att aat ttc gct att tat tgt ggc atg tcg cga 1056
 Ile Leu Ser Tyr Pro Ile Asn Phe Ala Ile Tyr Cys Gly Met Ser Arg
 340 345 350

caa ttt aga gag act ttt aag gaa ttg ttt ata cgg ggc gcc gtt acg 1104
 Gln Phe Arg Glu Thr Phe Lys Glu Leu Phe Ile Arg Gly Ala Val Thr
 355 360 365

acc aga aat gga tcg tct agg tat tcg ctg gtc aat gga cct cga act 1152
 Thr Arg Asn Gly Ser Ser Arg Tyr Ser Leu Val Asn Gly Pro Arg Thr
 370 375 380

tgt acc aat gaa act gtt ttg taa 1176
 Cys Thr Asn Glu Thr Val Leu
 385 390

<210> 10
 <211> 391
 <212> PRT
 <213> Tribolium castaneum

<400> 10

Met Gly Glu Met Ala Ser Asn Ser Thr Leu Ile Phe Pro Asn Gln Thr
 1 5 10 15

Tyr Ala Asn Glu Thr Val Pro Asn Val Thr Ser Val Glu Lys Val Gln
 20 25 30

Tyr Ile Asn Ile Thr Met Glu Met Pro Ile Ala Tyr Ala Val Pro Leu
 35 40 45

Tyr Gly Tyr Val Met Pro Phe Leu Leu Ile Ile Thr Ile Ile Ala Asn
 50 55 60

Thr Leu Ile Val Val Val Leu Ser Lys Arg Gln Met Arg Thr Pro Thr

65

70

75

80

Asn Val Val Leu Met Ala Met Ala Leu Cys Asp Met Phe Thr Val Leu
 85 90 95

Ile Pro Ala Pro Trp Leu Ile Tyr Met Tyr Ser Phe Gly Asn His Tyr
 100 105 110

Lys Pro Leu Trp Pro Ile Ser Leu Cys Tyr Ala Trp Phe Val Met His
 115 120 125

Glu Val Ile Pro Asn Met Phe His Thr Ala Ser Ile Trp Leu Thr Leu
 130 135 140

Ala Leu Ala Val Gln Arg Tyr Ile Phe Val Cys His Ala Pro Leu Ala
 145 150 155 160

Arg Lys Leu Cys Thr Met Ser Asn Val Tyr Lys Cys Leu Ile Tyr Ile
 165 170 175

Leu Val Ile Ala Ala Leu His Gln Gly Phe Arg Phe Phe Asp Ser Glu
 180 185 190

Tyr Ser Thr Val Asp Val Leu Trp Asn Asn His Thr Thr His Val Cys
 195 200 205

Lys Arg Glu His Ala His Trp Val Lys Glu Tyr Val Thr Glu Asp Phe
 210 215 220

Tyr Phe Val Thr Tyr Phe Met Phe Arg Val Leu Phe Val His Leu Ile
 225 230 235 240

Pro Cys Val Ala Leu Val Ile Leu Asn Ile Leu Leu Phe Arg Ala Leu
 245 250 255

Lys Gln Ala Gln Gln Arg Arg Glu Gln Leu Leu Ser Lys Lys Asn Gln

260 265 270

Lys Asn Glu Cys Lys Lys Leu Arg Asp Ser Asn Cys Thr Thr Leu Met
275 280 285

Leu Ile Val Val Val Thr Val Phe Leu Ile Val Glu Ile Pro Leu Val
290 295 300

Val Val Thr Leu Leu His Ile Ile Ser Ser Thr Phe Ile Glu Phe Leu
305 310 315 320

Asp Tyr Tyr Val Ala Asn Thr Leu Ile Leu Phe Thr Asn Phe Phe Ile
325 330 335

Ile Leu Ser Tyr Pro Ile Asn Phe Ala Ile Tyr Cys Gly Met Ser Arg
340 345 350

Gln Phe Arg Glu Thr Phe Lys Glu Leu Phe Ile Arg Gly Ala Val Thr
355 360 365

Thr Arg Asn Gly Ser Ser Arg Tyr Ser Leu Val Asn Gly Pro Arg Thr
370 375 380

Cys Thr Asn Glu Thr Val Leu
385 390

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<211> 1050
<212> DNA
<213> Pediculus humanus corporis

<220>
<221> CDS
<222> (1)..(1050)
<223> Partial Sequence

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ttc gct caa ccc tta tac ggt tac ata gta cct ttt tta ctg gtc ata 48

Phe Ala Gln Pro Leu Tyr Gly Tyr Ile Val Pro Phe Leu Leu Val Ile
1 5 10 15

aca atc ata gca aac aca tta ata gtc gtg gtt tta tca aag aga cac 96
Thr Ile Ile Ala Asn Thr Leu Ile Val Val Val Leu Ser Lys Arg His
20 25 30

atg aga acg ccg aca aat ttt gtt ttg atg gtc atg gca cta tcc gac 144
Met Arg Thr Pro Thr Asn Phe Val Leu Met Val Met Ala Leu Ser Asp
35 40 45

atg ttc acg cta tta ttt ccc gct ccc tgg ctt ttt tac atg tac aca 192
Met Phe Thr Leu Leu Phe Pro Ala Pro Trp Leu Phe Tyr Met Tyr Thr
50 55 60

ttt ggc aat cac tac aaa ccg ttg tgg cct gtc gcc gcg tgt tat tta 240
Phe Gly Asn His Tyr Lys Pro Leu Trp Pro Val Ala Ala Cys Tyr Leu
65 70 75 80

tgg aac gca atg aaa gaa gat ata cct gca tta ttt cac acg gca tcg 288
Trp Asn Ala Met Lys Glu Asp Ile Pro Ala Leu Phe His Thr Ala Ser
85 90 95

ata tgg ttg aca tta gca ttg gct gta caa agg tac ata tac gtt tgt 336
Ile Trp Leu Thr Leu Ala Leu Ala Val Gln Arg Tyr Ile Tyr Val Cys
100 105 110

cac gca ccg gtg gct cgc act tgg tgc acg atg cca aga gtc atc aaa 384
His Ala Pro Val Ala Arg Thr Trp Cys Thr Met Pro Arg Val Ile Lys
115 120 125

tgc gtg gct tgg atc tac gta ttc gcg acc ctt cat caa tct tct aga 432
Cys Val Ala Trp Ile Tyr Val Phe Ala Thr Leu His Gln Ser Ser Arg
130 135 140

ttt ttc gat cga act tac act tcg ata aac ata acg tgg aac ggt gtg 480
Phe Phe Asp Arg Thr Tyr Thr Ser Ile Asn Ile Thr Trp Asn Gly Val
145 150 155 160

cct gat gtg gcc gtt tgc aaa gtt aat tta gcc acg tgg gtc acc gac 528
Pro Asp Val Ala Val Cys Lys Val Asn Leu Ala Thr Trp Val Thr Asp
165 170 175

atc gtg acc gaa gat gtt tat ttt acc gtt tat tat tgc ttt cgc gtt 576
Ile Val Thr Glu Asp Val Tyr Phe Thr Val Tyr Tyr Cys Phe Arg Val
180 185 190

gtt ttt gta cat tct ctg ccc tgt gtt tcg ctg gtg gtc aat gta 624

Val Phe Val His Ser Leu Pro Cys Val Ser Leu Val Val Leu Asn Val
 195 200 205

ttg ttg ttt cgt gcc atg aga gcc gcg caa ctt aaa aga aag gaa ttg 672
 Leu Leu Phe Arg Ala Met Arg Ala Ala Gln Leu Lys Arg Lys Glu Leu
 210 215 220

ttt aaa gaa aat cgc aag tgc gaa agt aaa aaa ata cgg gat tcg aac 720
 Phe Lys Glu Asn Arg Lys Cys Glu Ser Lys Lys Ile Arg Asp Ser Asn
 225 230 235 240

tgc acc act ttg atg ctc att gtc gtc gtt acc gtc ttc cta gct gta 768
 Cys Thr Thr Leu Met Leu Ile Val Val Val Thr Val Phe Leu Ala Val
 245 250 255

gaa ata cca tta gcc gtt ata acc gtt ttg cat atc ata tcg agt ggt 816
 Glu Ile Pro Leu Ala Val Ile Thr Val Leu His Ile Ile Ser Ser Gly
 260 265 270

ata acc gaa ata tta gat tac aat ata gca aac gta ttg att tta ttt 864
 Ile Thr Glu Ile Leu Asp Tyr Asn Ile Ala Asn Val Leu Ile Leu Phe
 275 280 285

tca aac ttt ttt atc att gtt agt tat cca att aat ttt gcc att tat 912
 Ser Asn Phe Phe Ile Ile Val Ser Tyr Pro Ile Asn Phe Ala Ile Tyr
 290 295 300

tgt gga atg tca cga caa ttt agg gaa act ttt aaa gag ctt ttc ata 960
 Cys Gly Met Ser Arg Gln Phe Arg Glu Thr Phe Lys Glu Leu Phe Ile
 305 310 315 320

cgt gga gcg ata acg acg aga aga aac gat gga agt tca aga tat tca 1008
 Arg Gly Ala Ile Thr Thr Arg Arg Asn Asp Gly Ser Ser Arg Tyr Ser
 325 330 335

ttg gtg aat gga cct cgc acg tgc acc aac gaa act gtc cta 1050
 Leu Val Asn Gly Pro Arg Thr Cys Thr Asn Glu Thr Val Leu
 340 345 350

<210> 12

<211> 350

<212> PRT

<213> Pediculus humanus corporis

<400> 12

Phe Ala Gln Pro Leu Tyr Gly Tyr Ile Val Pro Phe Leu Leu Val Ile

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Thr Ile Ile Ala Asn Thr Leu Ile Val Val Val Leu Ser Lys Arg His
20 25 30

Met Arg Thr Pro Thr Asn Phe Val Leu Met Val Met Ala Leu Ser Asp
35 40 45

Met Phe Thr Leu Leu Phe Pro Ala Pro Trp Leu Phe Tyr Met Tyr Thr
50 55 60

Phe Gly Asn His Tyr Lys Pro Leu Trp Pro Val Ala Ala Cys Tyr Leu
65 70 75 80

Trp Asn Ala Met Lys Glu Asp Ile Pro Ala Leu Phe His Thr Ala Ser
85 90 95

Ile Trp Leu Thr Leu Ala Leu Ala Val Gln Arg Tyr Ile Tyr Val Cys
100 105 110

His Ala Pro Val Ala Arg Thr Trp Cys Thr Met Pro Arg Val Ile Lys
115 120 125

Cys Val Ala Trp Ile Tyr Val Phe Ala Thr Leu His Gln Ser Ser Arg
130 135 140

Phe Phe Asp Arg Thr Tyr Thr Ser Ile Asn Ile Thr Trp Asn Gly Val
145 150 155 160

Pro Asp Val Ala Val Cys Lys Val Asn Leu Ala Thr Trp Val Thr Asp
165 170 175

Ile Val Thr Glu Asp Val Tyr Phe Thr Val Tyr Tyr Cys Phe Arg Val
180 185 190

Val Phe Val His Ser Leu Pro Cys Val Ser Leu Val Val Leu Asn Val

195 200 205

Leu Leu Phe Arg Ala Met Arg Ala Ala Gln Leu Lys Arg Lys Glu Leu
210 215 220

Phe Lys Glu Asn Arg Lys Cys Glu Ser Lys Lys Ile Arg Asp Ser Asn
225 230 235 240

Cys Thr Thr Leu Met Leu Ile Val Val Val Thr Val Phe Leu Ala Val
245 250 255

Glu Ile Pro Leu Ala Val Ile Thr Val Leu His Ile Ile Ser Ser Gly
260 265 270

Ile Thr Glu Ile Leu Asp Tyr Asn Ile Ala Asn Val Leu Ile Leu Phe
275 280 285

Ser Asn Phe Phe Ile Ile Val Ser Tyr Pro Ile Asn Phe Ala Ile Tyr
290 295 300

Cys Gly Met Ser Arg Gln Phe Arg Glu Thr Phe Lys Glu Leu Phe Ile
305 310 315 320

Arg Gly Ala Ile Thr Thr Arg Arg Asn Asp Gly Ser Ser Arg Tyr Ser
325 330 335

Leu Val Asn Gly Pro Arg Thr Cys Thr Asn Glu Thr Val Leu
340 345 350

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<211> 1125
<212> DNA
<213> Culex pipiens

<220>
<221> CDS
<222> (1)..(1125)

<223> Partial sequence

<400> 13

tgc atg gga atg gaa gga aat gtt tcc tac ttg aac gtg tgg tgt gag 48
Cys Met Gly Met Glu Gly Asn Val Ser Tyr Leu Asn Val Ser Cys Glu
1 5 10 15

act att ctc aac tac agc atc cca ctg tac ggc tac tgc aca ccg atc 96
Thr Ile Leu Asn Tyr Ser Ile Pro Leu Tyr Gly Tyr Cys Thr Pro Ile
20 25 30

ttc atc cta att aca ctg act gcc aac tct tta atc gtg att gtc ctg 144
Phe Ile Leu Ile Thr Leu Thr Ala Asn Ser Leu Ile Val Ile Val Leu
35 40 45

agc aaa cgc agc atg gcc tct cct acc aac ttt gtt ctg atg gcg atg 192
Ser Lys Arg Ser Met Ala Ser Pro Thr Asn Phe Val Leu Met Ala Met
50 55 60

gca ctt tgc gac atg ttt act ctg tta ttt ccg gca ccc ggc cta ctg 240
Ala Leu Cys Asp Met Phe Thr Leu Leu Phe Pro Ala Pro Gly Leu Leu
65 70 75 80

tac atg tac acg ttc ggc aat cat tac aag cca tta tgg ccc atc gcc 288
Tyr Met Tyr Thr Phe Gly Asn His Tyr Lys Pro Leu Ser Pro Ile Ala
85 90 95

gcc tgc tat gtg tgg aat gct ctg aat gag atc ctt ccg gca atg ttc 336
Ala Cys Tyr Val Trp Asn Ala Leu Asn Glu Ile Leu Pro Ala Met Phe
100 105 110

cac acg gca tgg gtt tgg ctg acg ttg gcg ctt gcg gtg cag agg tac 384
His Thr Ala Ser Val Trp Leu Thr Leu Ala Leu Ala Val Gln Arg Tyr
115 120 125

gtg tac gtc tgt cat gcc cca atc gcc cgg acg tgg tgc aca atc ccg 432
Val Tyr Val Cys His Ala Pro Ile Ala Arg Thr Trp Cys Thr Ile Pro
130 135 140

agg gtg aaa aag tgt atc gcc tac atc tgt cta gct gca tta att cat 480
Arg Val Lys Lys Cys Ile Ala Tyr Ile Cys Leu Ala Ala Leu Ile His
145 150 155 160

cag agc acc aga ttt ttc gat aaa tcc tac agc ttg gtg cag atc gaa 528
Gln Ser Thr Arg Phe Phe Asp Lys Ser Tyr Ser Leu Val Gln Ile Glu
165 170 175

tgg aac ggg cag ctt acc gaa gtg tgt cac acg gac acc gcc ggc tgg 576

Trp Asn Gly Gln Leu Thr Glu Val Cys His Thr Asp Thr Ala Gly Trp
 180 185 190

gtg cac gat tac gtc ggc gag gac ttt tac tac acg ttt tat ttt tcg 624
 Val His Asp Tyr Val Gly Glu Asp Phe Tyr Tyr Thr Phe Tyr Phe Ser
 195 200 205

ttc cga ata ctg ttc gtg cac ctg atc ccg tgc ggc agc ctg gtg gcg 672
 Phe Arg Ile Leu Phe Val His Leu Ile Pro Cys Gly Ser Leu Val Ala
 210 215 220

ttg aac gtt ctg ctg ttc aaa gcg atg cga caa gcc cag caa aag cgc 720
 Leu Asn Val Leu Leu Phe Lys Ala Met Arg Gln Ala Gln Gln Lys Arg
 225 230 235 240

gaa agg ctc ttc aag gac act gcc aaa aag cgc gaa tgt aaa cgg cag 768
 Glu Arg Leu Phe Lys Asp Thr Ala Lys Lys Arg Glu Cys Lys Arg Gln
 245 250 255

agg gac tcg aac tgt acc acg ctg atg ctc atc gtc gtt gta act gtg 816
 Arg Asp Ser Asn Cys Thr Thr Leu Met Leu Ile Val Val Val Thr Val
 260 265 270

ttc cta atc gtt gaa att cca ctc ggt gtg ata acg gcc tta cac ata 864
 Phe Leu Ile Val Glu Ile Pro Leu Gly Val Ile Thr Ala Leu His Ile
 275 280 285

att tcc tcg ctc atc tac gag ttt tta gac tac tac att gca aac ttg 912
 Ile Ser Ser Leu Ile Tyr Glu Phe Leu Asp Tyr Tyr Ile Ala Asn Leu
 290 295 300

ttt att ctt ttt gca aac ttt ttc ctc atc gtc agt tac cct atc aat 960
 Phe Ile Leu Phe Ala Asn Phe Phe Leu Ile Val Ser Tyr Pro Ile Asn
 305 310 315 320

ttc gcc att tac tgc ggg atg tcg cgc cag ttt cgg gag acc ttc aaa 1008
 Phe Ala Ile Tyr Cys Gly Met Ser Arg Gln Phe Arg Glu Thr Phe Lys
 325 330 335

gaa atc ttt gtc aaa tct agc aaa caa atc cca ggt ggc agc agc aag 1056
 Glu Ile Phe Val Lys Ser Ser Lys Gln Ile Pro Gly Gly Ser Ser Lys
 340 345 350

aaa gac tgc gga tca tcg cga tac tcc ctg gtc aac gga cct cgg aca 1104
 Lys Asp Cys Gly Ser Ser Arg Tyr Ser Leu Val Asn Gly Pro Arg Thr
 355 360 365

ttc acc aac gag acg gta cta 1125

Phe Thr Asn Glu Thr Val Leu
370 375

<210> 14
<211> 375
<212> PRT
<213> Culex pipiens

<400> 14

Cys Met Gly Met Glu Gly Asn Val Ser Tyr Leu Asn Val Ser Cys Glu
1 5 10 15

Thr Ile Leu Asn Tyr Ser Ile Pro Leu Tyr Gly Tyr Cys Thr Pro Ile
20 25 30

Phe Ile Leu Ile Thr Leu Thr Ala Asn Ser Leu Ile Val Ile Val Leu
35 40 45

Ser Lys Arg Ser Met Ala Ser Pro Thr Asn Phe Val Leu Met Ala Met
50 55 60

Ala Leu Cys Asp Met Phe Thr Leu Leu Phe Pro Ala Pro Gly Leu Leu
65 70 75 80

Tyr Met Tyr Thr Phe Gly Asn His Tyr Lys Pro Leu Ser Pro Ile Ala
85 90 95

Ala Cys Tyr Val Trp Asn Ala Leu Asn Glu Ile Leu Pro Ala Met Phe
100 105 110

His Thr Ala Ser Val Trp Leu Thr Leu Ala Leu Ala Val Gln Arg Tyr
115 120 125

Val Tyr Val Cys His Ala Pro Ile Ala Arg Thr Trp Cys Thr Ile Pro
130 135 140

Arg Val Lys Lys Cys Ile Ala Tyr Ile Cys Leu Ala Ala Leu Ile His

145 150 155 160

Gln Ser Thr Arg Phe Phe Asp Lys Ser Tyr Ser Leu Val Gln Ile Glu
165 170 175

Trp Asn Gly Gln Leu Thr Glu Val Cys His Thr Asp Thr Ala Gly Trp
180 185 190

Val His Asp Tyr Val Gly Glu Asp Phe Tyr Tyr Thr Phe Tyr Phe Ser
195 200 205

Phe Arg Ile Leu Phe Val His Leu Ile Pro Cys Gly Ser Leu Val Ala
210 215 220

Leu Asn Val Leu Leu Phe Lys Ala Met Arg Gln Ala Gln Gln Lys Arg
225 230 235 240

Glu Arg Leu Phe Lys Asp Thr Ala Lys Lys Arg Glu Cys Lys Arg Gln
245 250 255

Arg Asp Ser Asn Cys Thr Thr Leu Met Leu Ile Val Val Val Thr Val
260 265 270

Phe Leu Ile Val Glu Ile Pro Leu Gly Val Ile Thr Ala Leu His Ile
275 280 285

Ile Ser Ser Leu Ile Tyr Glu Phe Leu Asp Tyr Tyr Ile Ala Asn Leu
290 295 300

Phe Ile Leu Phe Ala Asn Phe Phe Leu Ile Val Ser Tyr Pro Ile Asn
305 310 315 320

Phe Ala Ile Tyr Cys Gly Met Ser Arg Gln Phe Arg Glu Thr Phe Lys
325 330 335

Glu Ile Phe Val Lys Ser Ser Lys Gln Ile Pro Gly Gly Ser Ser Lys

340 345 350

Lys Asp Cys Gly Ser Ser Arg Tyr Ser Leu Val Asn Gly Pro Arg Thr
 355 360 365

Phe Thr Asn Glu Thr Val Leu
 370 375

<210> 15
 <211> 1515
 <212> DNA
 <213> *Drosophila pseudoobscura*

<220>
 <221> CDS
 <222> (1)..(1515)

<400> 15
 atg ggc ggc gat caa ggg gtg cta att gaa ttg cag gaa atg tca acg 48
 Met Gly Gly Asp Gln Gly Val Leu Ile Glu Leu Gln Glu Met Ser Thr
 1 5 10 15

gca gtc acg aaa acc gtc gcg gcc gcc gct gcg gcc atg ctg ggg tcc 96
 Ala Val Thr Lys Thr Val Ala Ala Ala Ala Ala Ala Met Leu Gly Ser
 20 25 30

agc atg gac aat aac tct gcc tat tcg tac gat ata tcc gca acg gac 144
 Ser Met Asp Asn Asn Ser Ala Tyr Ser Tyr Asp Ile Ser Ala Thr Asp
 35 40 45

gtg ctc tat cag tgg agt gcc aat gcg gcg gca gcc gcc gcc ggc ggg 192
 Val Leu Tyr Gln Trp Ser Ala Asn Ala Ala Ala Ala Ala Ala Gly Gly
 50 55 60

gca cgt atc gcc cac acc atg ccg ccc tca gtg gcg acc ctg cct cca 240
 Ala Arg Ile Ala His Thr Met Pro Pro Ser Val Ala Thr Leu Pro Pro
 65 70 75 80

gcc acg aat cac ggc tcc atg cat cag tcc gtg ccg ctt ccc gga atc 288
 Ala Thr Asn His Gly Ser Met His Gln Ser Val Pro Leu Pro Gly Ile
 85 90 95

gga caa cgc ctc gct ccc aac gag acg cag ttc gga ctg ctc gac tac 336
 Gly Gln Arg Leu Ala Pro Asn Glu Thr Gln Phe Gly Leu Leu Asp Tyr

100 105 110

ggg atg agc agc atg aac gac agc ctg gac tac gcc tcc tac cag cag 384
Gly Met Ser Ser Met Asn Asp Ser Leu Asp Tyr Ala Ser Tyr Gln Gln
115 120 125

cag atg ggc gag gac ggg cag tgc cgg cag atg gac gcc aac gtg agc 432
Gln Met Gly Glu Asp Gly Gln Cys Arg Gln Met Asp Ala Asn Val Ser
130 135 140

tac tgg aac ctc acc tgc gac tgc ccc ctg gac tac gcc ctg ccc cta 480
Tyr Trp Asn Leu Thr Cys Asp Ser Pro Leu Asp Tyr Ala Leu Pro Leu
145 150 155 160

tac ggc tac tgc atg ccg ttc ctg ctg ata atc acc atc ata tgc aac 528
Tyr Gly Tyr Cys Met Pro Phe Leu Leu Ile Ile Thr Ile Ile Ser Asn
165 170 175

acc ctg atc gtc cta gtc ctc agc aag aag agc atg gcc acg ccg aca 576
Thr Leu Ile Val Leu Val Leu Ser Lys Lys Ser Met Ala Thr Pro Thr
180 185 190

aac ttg gtg ctc atg ggc atg gct ata tgc gat atg ctg acg gtt ata 624
Asn Phe Val Leu Met Gly Met Ala Ile Cys Asp Met Leu Thr Val Ile
195 200 205

ttc ccg gca ccg gga ctc tgg tat atg tac aca ttg ggc aat cat tat 672
Phe Pro Ala Pro Gly Leu Trp Tyr Met Tyr Thr Phe Gly Asn His Tyr
210 215 220

aag cct ctg cat ccg gtc tcc atg tgt ctg gcc tac agc att ttc aac 720
Lys Pro Leu His Pro Val Ser Met Cys Leu Ala Tyr Ser Ile Phe Asn
225 230 235 240

gag att atg cca gcc atg tgc cac acc atc tcc gtg tgg cta acc ctg 768
Glu Ile Met Pro Ala Met Cys His Thr Ile Ser Val Trp Leu Thr Leu
245 250 255

gcc ctg gcc gtg caa aga tat atc tac gtg tgc cac gcc ccc atg gcc 816
Ala Leu Ala Val Gln Arg Tyr Ile Tyr Val Cys His Ala Pro Met Ala
260 265 270

cgc acc tgg tgc act atg ccg cgg gtg aag cgc tgc acg gtg tac atc 864
Arg Thr Trp Cys Thr Met Pro Arg Val Lys Arg Cys Thr Val Tyr Ile
275 280 285

gca ctg ctg gcg ttc ctg cac cag ctg cca cga ttc ttc gac cgc acc 912
Ala Leu Leu Ala Phe Leu His Gln Leu Pro Arg Phe Phe Asp Arg Thr

290 295 300

ttt ctg ccc ctt cag atc gag tgg aac gga aac gag acg gag gtg tgt 960
Phe Leu Pro Leu Gln Ile Glu Trp Asn Gly Asn Glu Thr Glu Val Cys
305 310 315 320

cac ctg gag acg tcg atg tgg gtg cac gag tac atc ggc atg gac ctg 1008
His Leu Glu Thr Ser Met Trp Val His Glu Tyr Ile Gly Met Asp Leu
 325 330 335

tac tac acg agc tac tac ctg ttc cgg gtg ctg ttc gtg cac ctg ctg 1056
Tyr Tyr Thr Ser Tyr Tyr Leu Phe Arg Val Leu Phe Val His Leu Leu
 340 345 350

ccg tgc atc atc ctg gtg acg ctc aac atc ctg ctg ttc gcg gcg atg 1104
Pro Cys Ile Ile Leu Val Thr Leu Asn Ile Leu Leu Phe Ala Ala Met
 355 360 365

cgg cag gcc cag gag cgg cgg aag ctg ctg ttc cgc gag aac cgc aag 1152
Arg Gln Ala Gln Glu Arg Arg Lys Leu Leu Phe Arg Glu Asn Arg Lys
 370 375 380

aag gag tgc aag aag ctg cgc gag tcc aac tgc acc acg ctg atg ctg 1200
Lys Glu Cys Lys Lys Leu Arg Glu Ser Asn Cys Thr Thr Leu Met Leu
385 390 395 400

atc gtg gtg gtg acc gtg ttc ctc atc gcc gag ata ccc att gcc gtg 1248
Ile Val Val Val Thr Val Phe Leu Ile Ala Glu Ile Pro Ile Ala Val
 405 410 415

gtc acg gcc atg cac atc gtg agc tcg ctg atc atc gag ttc ctc gac 1296
Val Thr Ala Met His Ile Val Ser Ser Leu Ile Ile Glu Phe Leu Asp
 420 425 430

tac ggc atc gcc aac atc ttc atc atg ctg acc aac ttc ttc ctg gtg 1344
Tyr Gly Ile Ala Asn Ile Phe Ile Met Leu Thr Asn Phe Phe Leu Val
 435 440 445

gtg agc tac ccg atc aac ttt ggc atc tac tgc ggc atg tcg cgc cag 1392
Val Ser Tyr Pro Ile Asn Phe Gly Ile Tyr Cys Gly Met Ser Arg Gln
 450 455 460

ttc cgc gag acc ttc aag gag ata ttc ctc ggc cgc atc att gcc aag 1440
Phe Arg Glu Thr Phe Lys Glu Ile Phe Leu Gly Arg Ile Ile Ala Lys
465 470 475 480

aag gac agc tcc tcc aag tac tcg atc gtc aat gga ccc cgt acc tgc 1488
Lys Asp Ser Ser Ser Lys Tyr Ser Ile Val Asn Gly Pro Arg Thr Cys

485

490

495

acc aat acc aac gag acg gtc cta tag

1515

Thr Asn Thr Asn Glu Thr Val Leu

500

<210> 16

<211> 504

<212> PRT

<213> *Drosophila pseudoobscura*

<400> 16

Met Gly Gly Asp Gln Gly Val Leu Ile Glu Leu Gln Glu Met Ser Thr

1

5

10

15

Ala Val Thr Lys Thr Val Ala Ala Ala Ala Ala Ala Met Leu Gly Ser

20

25

30

Ser Met Asp Asn Asn Ser Ala Tyr Ser Tyr Asp Ile Ser Ala Thr Asp

35

40

45

Val Leu Tyr Gln Trp Ser Ala Asn Ala Ala Ala Ala Ala Gly Gly

50

55

60

Ala Arg Ile Ala His Thr Met Pro Pro Ser Val Ala Thr Leu Pro Pro

65

70

75

80

Ala Thr Asn His Gly Ser Met His Gln Ser Val Pro Leu Pro Gly Ile

85

90

95

Gly Gln Arg Leu Ala Pro Asn Glu Thr Gln Phe Gly Leu Leu Asp Tyr

100

105

110

Gly Met Ser Ser Met Asn Asp Ser Leu Asp Tyr Ala Ser Tyr Gln Gln

115

120

125

Gln Met Gly Glu Asp Gly Gln Cys Arg Gln Met Asp Ala Asn Val Ser

130

135

140

Tyr Trp Asn Leu Thr Cys Asp Ser Pro Leu Asp Tyr Ala Leu Pro Leu
 145 150 155 160

Tyr Gly Tyr Cys Met Pro Phe Leu Leu Ile Ile Thr Ile Ile Ser Asn
 165 170 175

Thr Leu Ile Val Leu Val Leu Ser Lys Lys Ser Met Ala Thr Pro Thr
 180 185 190

Asn Phe Val Leu Met Gly Met Ala Ile Cys Asp Met Leu Thr Val Ile
 195 200 205

Phe Pro Ala Pro Gly Leu Trp Tyr Met Tyr Thr Phe Gly Asn His Tyr
 210 215 220

Lys Pro Leu His Pro Val Ser Met Cys Leu Ala Tyr Ser Ile Phe Asn
 225 230 235 240

Glu Ile Met Pro Ala Met Cys His Thr Ile Ser Val Trp Leu Thr Leu
 245 250 255

Ala Leu Ala Val Gln Arg Tyr Ile Tyr Val Cys His Ala Pro Met Ala
 260 265 270

Arg Thr Trp Cys Thr Met Pro Arg Val Lys Arg Cys Thr Val Tyr Ile
 275 280 285

Ala Leu Leu Ala Phe Leu His Gln Leu Pro Arg Phe Phe Asp Arg Thr
 290 295 300

Phe Leu Pro Leu Gln Ile Glu Trp Asn Gly Asn Glu Thr Glu Val Cys
 305 310 315 320

His Leu Glu Thr Ser Met Trp Val His Glu Tyr Ile Gly Met Asp Leu
 325 330 335

Tyr Tyr Thr Ser Tyr Tyr Leu Phe Arg Val Leu Phe Val His Leu Leu
 340 345 350

Pro Cys Ile Ile Leu Val Thr Leu Asn Ile Leu Leu Phe Ala Ala Met
 355 360 365

Arg Gln Ala Gln Glu Arg Arg Lys Leu Leu Phe Arg Glu Asn Arg Lys
 370 375 380

Lys Glu Cys Lys Lys Leu Arg Glu Ser Asn Cys Thr Thr Leu Met Leu
 385 390 395 400

Ile Val Val Val Thr Val Phe Leu Ile Ala Glu Ile Pro Ile Ala Val
 405 410 415

Val Thr Ala Met His Ile Val Ser Ser Leu Ile Ile Glu Phe Leu Asp
 420 425 430

Tyr Gly Ile Ala Asn Ile Phe Ile Met Leu Thr Asn Phe Phe Leu Val
 435 440 445

Val Ser Tyr Pro Ile Asn Phe Gly Ile Tyr Cys Gly Met Ser Arg Gln
 450 455 460

Phe Arg Glu Thr Phe Lys Glu Ile Phe Leu Gly Arg Ile Ile Ala Lys
 465 470 475 480

Lys Asp Ser Ser Ser Lys Tyr Ser Ile Val Asn Gly Pro Arg Thr Cys
 485 490 495

Thr Asn Thr Asn Glu Thr Val Leu
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<210> 17

<211> 177

<212> DNA
 <213> *Drosophila melanogaster*

<220>
 <221> CDS
 <222> (1)..(177)

<400> 17
 atg aaa act cta gcc cta ttc ttg gtt ctc gtt tgc gta ctc ggc ttg 48
 Met Lys Thr Leu Ala Leu Phe Leu Val Leu Val Cys Val Leu Gly Leu
 1 5 10 15
 gtc cag tcc tgg gaa tgg ccg tgg aat agg aag cct aca aag ttt cca 96
 Val Gln Ser Trp Glu Trp Pro Trp Asn Arg Lys Pro Thr Lys Phe Pro
 20 25 30
 att cca agc ccc aat cct cct ttc gta ggt gat aag tgg tgc cgt ctt 144
 Ile Pro Ser Pro Asn Pro Pro Phe Val Gly Asp Lys Trp Cys Arg Leu
 35 40 45
 aat ttg ggg ccc gcc tgg ggt gga aga tgt taa 177
 Asn Leu Gly Pro Ala Trp Gly Gly Arg Cys
 50 55

<210> 18
 <211> 58
 <212> PRT
 <213> *Drosophila melanogaster*

<400> 18
 Met Lys Thr Leu Ala Leu Phe Leu Val Leu Val Cys Val Leu Gly Leu
 1 5 10 15
 Val Gln Ser Trp Glu Trp Pro Trp Asn Arg Lys Pro Thr Lys Phe Pro
 20 25 30
 Ile Pro Ser Pro Asn Pro Pro Phe Val Gly Asp Lys Trp Cys Arg Leu
 35 40 45
 Asn Leu Gly Pro Ala Trp Gly Gly Arg Cys
 50 55

<210> 19
<211> 9
<212> PRT
<213> *Drosophila melanogaster*

<400> 19

Asp Pro Lys Gln Asp Phe Met Arg Phe
1 5

<210> 20
<211> 9
<212> PRT
<213> *Drosophila melanogaster*

<400> 20

Thr Pro Ala Glu Asp Phe Met Arg Phe
1 5

<210> 21
<211> 7
<212> PRT
<213> *Drosophila melanogaster*

<400> 21

Asn Gln Lys Thr Met Ser Phe
1 5

<210> 22
<211> 9
<212> PRT
<213> *Drosophila melanogaster*

<400> 22

Phe Asp Asp Tyr Gly His Met Arg Phe
1 5

<210> 23
<211> 14
<212> PRT

<213> *Drosophila melanogaster*

<400> 23

Gly Gly Asp Asp Gln Phe Asp Asp Tyr Gly His Met Arg Phe
1 5 10

<210> 24

<211> 10

<212> PRT

<213> *Drosophila melanogaster*

<400> 24

Thr Asp Val Asp His Val Phe Leu Arg Phe
1 5 10

<210> 25

<211> 17

<212> PRT

<213> *Drosophila melanogaster*

<400> 25

Gln Leu Gln Ser Asn Gly Glu Pro Ala Tyr Arg Val Arg Thr Pro Arg
1 5 10 15

Leu

<210> 26

<211> 8

<212> PRT

<213> *Drosophila melanogaster*

<400> 26

Ser Val Pro Phe Lys Pro Arg Leu
1 5

<210> 27

<211> 36

<212> PRT

<213> Artificial

<220>

<223> Synthetic sex peptide

<400> 27

Trp Glu Trp Pro Trp Asn Arg Lys Pro Thr Lys Phe Pro Ile Pro Ser
1 5 10 15

Pro Asn Pro Arg Asp Lys Trp Cys Arg Leu Asn Leu Gly Pro Ala Trp
20 25 30

Gly Gly Arg Cys
35

<210> 28

<211> 31

<212> PRT

<213> Artificial

<220>

<223> Synthetic DUP99P

<400> 28

Gln Asp Arg Asn Asp Thr Glu Trp Ile Gln Ser Gln Lys Asp Arg Glu
1 5 10 15

Lys Trp Cys Arg Leu Asn Leu Gly Pro Tyr Leu Gly Gly Arg Cys
20 25 30

<210> 29

<211> 22

<212> PRT

<213> Artificial

<220>

<223> N-terminal sex peptide receptor peptide

<400> 29

Pro Thr Asn Glu Ser Gln Leu Glu Ile Pro Asp Tyr Gly Asn Glu Ser

1 5 10 15

Leu Asp Tyr Pro Asn Cys
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<210> 30
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Primer forward

<400> 30
atgggcggcg atcaaggggt 20

<210> 31
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Primer reverse

<400> 31
ggcaccaaca tcaccaatta 20

<210> 32
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Primer forward

<400> 32
atgtcaattg atgctgcggt a 21

<210> 33
<211> 20
<212> DNA
<213> Artificial

<220>

<223> Primer reverse

<400> 33

cgttggttct gtgtgacaaa

20

<210> 34

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Primer forward

<400> 34

atgattgaaa aaaataattt caag

24

<210> 35

<211> 19

<212> DNA

<213> Artificial

<220>

<223> Primer reverse

<400> 35

cctgctatct aaccacagt

19

<210> 36

<211> 20

<212> DNA

<213> Artificial

<220>

<223> Primer forward

<400> 36

atggcgggtca ccatagacaa

20

<210> 37

<211> 20

<212> DNA

<213> Artificial

<220>

<223> Primer reverse

<400> 37

ggcttaaagc acagtttcgt

20

<210> 38

<211> 21

<212> DNA

<213> Artificial

<220>

<223> Primer forward

<400> 38

atgggcgaga tggcgtcgaa c

21

<210> 39

<211> 21

<212> DNA

<213> Artificial

<220>

<223> Primer reverse

<400> 39

tcaacattga gttgtccta a

21

<210> 40

<211> 9

<212> PRT

<213> Drosophila melanogaster

<400> 40

Ala Trp Gln Ser Leu Gln Ser Ser Trp

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5

<210> 41

<211> 9

<212> PRT

<213> Drosophila melanogaster

<400> 41

Ala Trp Lys Ser Met Asn Val Ala Trp
1 5

<210> 42
<211> 12
<212> PRT
<213> *Drosophila melanogaster*

<400> 42

Glu Ala Gln Gly Trp Asn Lys Phe Arg Gly Ala Trp
1 5 10

<210> 43
<211> 11
<212> PRT
<213> *Drosophila melanogaster*

<400> 43

Glu Pro Thr Trp Asn Asn Leu Lys Gly Met Trp
1 5 10

<210> 44
<211> 10
<212> PRT
<213> *Drosophila melanogaster*

<400> 44

Asp Gln Trp Gln Lys Leu His Gly Gly Trp
1 5 10

<210> 45
<211> 9
<212> PRT
<213> *Aedes aegypti*

<400> 45

Thr Trp Lys Asn Leu Gln Gly Gly Trp
1 5

<210> 46
 <211> 9
 <212> PRT
 <213> Aedes aegypti

<400> 46

Ala Trp Asn Lys Ile Asn Gly Gly Trp
 1 5

<210> 47
 <211> 16
 <212> PRT
 <213> Aedes aegypti

<400> 47

Arg Val Asn Ala Gly Pro Ala Gln Trp Asn Lys Phe Arg Gly Ser Trp
 1 5 10 15

<210> 48
 <211> 11
 <212> PRT
 <213> Aedes aegypti

<400> 48

Glu Pro Gly Trp Asn Asn Leu Lys Gly Leu Trp
 1 5 10

<210> 49
 <211> 11
 <212> PRT
 <213> Aedes aegypti

<400> 49

Ser Glu Lys Trp Asn Lys Leu Ser Ser Ser Trp
 1 5 10

<210> 50
 <211> 9
 <212> PRT

<213> Anopheles gambiae

<400> 50

Ser Trp Ser Lys Met Asn Ala Ala Trp
1 5

<210> 51

<211> 17

<212> PRT

<213> Anopheles gambiae

<400> 51

Leu Ser Gly Gly Asn Arg Asn Ser Gly Trp Thr Lys Phe Gly Ala Ala
1 5 10 15

Trp

<210> 52

<211> 11

<212> PRT

<213> Anopheles gambiae

<400> 52

Glu Pro Gly Trp Asn Asn Leu Lys Gly Leu Trp
1 5 10

<210> 53

<211> 11

<212> PRT

<213> Anopheles gambiae

<400> 53

Ala Asp Lys Trp Asp Lys Leu Ala Ser Ala Trp
1 5 10

<210> 54

<211> 36

<212> PRT

<213> Artificial

<220>

<223> Synthetic sex peptide

<220>

<221> misc_feature

<222> (9)..(9)

<223> Xaa is hydroxyproline

<220>

<221> misc_feature

<222> (13)..(13)

<223> Xaa is hydroxyproline

<220>

<221> misc_feature

<222> (15)..(15)

<223> Xaa is hydroxyproline

<220>

<221> misc_feature

<222> (17)..(17)

<223> Xaa is hydroxyproline

<220>

<221> misc_feature

<222> (19)..(19)

<223> Xaa is hydroxyproline

<400> 54

Trp Glu Trp Pro Trp Asn Arg Lys Xaa Thr Lys Phe Xaa Ile Xaa Ser

1

5

10

15

Xaa Asn Xaa Arg Asp Lys Trp Cys Arg Leu Asn Leu Gly Pro Ala Trp

20

25

30

Gly Gly Arg Cys

35