

RDQL-J6430-Sequence-Listing_ST25.txt
SEQUENCE LISTING

<110> Sime Darby Technology Centre Sdn Bhd
<120> Methods for Obtaining Oil Palm Plants that Have Tolerance to
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<130> RDQL-J6430
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<170> PatentIn version 3.5
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<213> Elaeis guineensis

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<223> Mannosyl-oligosaccharide 1,2-alpha-mannosidase MNS3-like isoform
X1 polynucleotide

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<213> Elaeis guineensis

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polynucleotide

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<223> Putative disease resistance protein RGA3 polynucleotide

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<212> DNA

<213> Elaeis guineensis

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tagtggtgac aactctgtgt tgtatgacca cgatttagag agctatgcac tgtttgatat      660
gaatggttgc caagtccttc aacagctggt aattagagtt ggagaaatgt ttgagagaat      720
tctcaaagag acagtgaag taagggatga acatgctgag gacatgtctc tgctccaagc      780
tatttctatt gttttgaaca gaaatccaga tctaaggcaa gaggggcccgg cacatgaagt      840
gttgacgtgg tatatatgca gaatggaggc atggtttgct gcagacgtgg atactatatc      900
tttgaaaagc tgggatcagg agcatgttct ttctggtggc catggactta tgggtgcaagg      960
atactatcct gttatcaaaa cccttgcaaa tgatctggat atcaaaactga accacagggg      1020
gaaaaaaatt gtccagcgtt gtaacaaagt aatggtcacc gtggaggatg gctcaaattt      1080
tgtggctgat gctgctatta tctactgttc tcttgggggt ctcaaagcaa atgtgatcga      1140
atgtgaacc aagctaccag aatggaaagt ctcagcaatc tctgatcttg gtgttgcaa      1200
tgagaataag attgctcttc acttttagtac tgttttttg cccaatgtag aagttctagg      1260
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acatcctgtt cttgtgtaca tggctgctgg aagggttgct tatgatattg agaaactttc      1380
tgatgaagaa gctgttaaat ttgtgatgtt acagcttcag aaaatgctac cagatgctac      1440
agagccggtt caatacttg tttctagggt gggtagagac ccagattccc ttgggtccta      1500
ttcttgtgac ttggttggga agccagctga cttgtatgag agatttcgag ctctgtgga      1560
taatatatat tttgctggag aagcagcaag tgttgatcac tctgggtccg tccatggagc      1620
ttacacagca ggtatcatag ctgcagagga ctgccgaagg cgtctactac tgcaacatgg      1680

```

RDQL-J6430-Sequence-Listing_ST25.txt

aatgtcagat ctcttcagg ctgtattaag ggaggaaatg actgaagcca tggccccct 1740
 ccaaatatct aggatgtaat agattaataa aagcagtaga ctacctggaa attaa 1795

<210> 9
 <211> 2510
 <212> DNA
 <213> Elaeis guineensis

<220>
 <221> misc_feature
 <222> (1)..(2510)
 <223> Putative lipoxxygenase 5 polynucleotide

<400> 9
 caagaaccaa gtcagcagag aaaggaggtg ggggacgcac ctcttcttta acccaaacat 60
 ccacacaagt gagatttttg gaagcaaaaa aaaaagaaga agctaattggc ggcttctatc 120
 gaaagcttg gacattcttt gatccaaaga ttgcctctcc ttccttcctc gagctctcga 180
 atttttcgag gggagcagag caacctcggc ttccaacctg ctctgtttcc gttgacacaa 240
 aggagtcttc atagggtgaa tagagctgtg agagctccgg tggcggcggc ggtcacagag 300
 aaagtgggta aggtgggtggc agagaagcca gtgaggttta aggttcgggc agcgttgacg 360
 gtgaggaaga agaaagagga ggatttgaaa gagaagattg caagccagct cgatgccttc 420
 tcggataaga ttggaaggaa cgtcgttttg gagctcgtca gcaccgagat cgatccatgg 480
 acacaaaagc cgaagagaag caacaaggca gtgcttaggg actgggttga gaagaagaat 540
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 aaaattcacc ccagcgagag ggtcttcttc aacaacaagc catatttgcc agcagagaca 780
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 gaaggccttc gctggaagaa gaccttgag gaccaactct tccataagat tccatttggtg 1260
 agcaagattg aagagtccag cgaggccctg ctccgattcg acaccccgga catcataaca 1320
 aaggacaagt ttgcgtggct gcgagatgac gagttcgctc ggcaggcact cgccggcatt 1380

RDQL-J6430-Sequence-Listing_ST25.txt

```

aaccccgctca acgtagagag gcttcaggtg ttccctcctg ttagcaagct cgatcccacc 1440
atatatggtc ctctgaatc tgccatcaaa gaggagcaca ttattggcca tctcgggtggc 1500
atgtcagttc aacaggcact ggaggagaac aagctattca tgttggatta ccatgatggt 1560
tacctcccat ttcttgaccg gatcaatgcc caagatggga ggaaagccta tggcacaaga 1620
actctatttt tcctcactca acttgggact ctgaagccaa tagccattga gctcagtctc 1680
ccaccagcaa cccctggttg ctcgagagcg aaacgtgtcc tcacaccacc caccgatgcc 1740
acaacaact ggctctggca actcgccaag gccacgtct gctccaatga tgctgggggc 1800
caccaacttg tcaaccactg gttgaggaca catgctgtct tggagccctt cataatagct 1860
gcgcatcgac aactaagcgc gatgcatcca atcttcaagc tgctcaagcc ccatatgcgt 1920
tacacccttg agatcaatgc tcttgctcgc caaatcctca tcagtgggtg tggagtcac 1980
gagtctggct tcacccttg atcatgttg atggagatga gtgtctcttt ctatcgggat 2040
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gaggacccta gccaacccca tgggctaaag cttctcatag aggactacc ctacgccaac 2160
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gccgaccttg cctccctgct caccaccctc ctctggctcg cgtcggctca gcacgccgcg 2400
ctcaacttcg ggcagtacc gctcggcggc tacatccga accggcccc tctcatgcgc 2460
cggctcgtcc ccgccgagg cgaccccgag tacgacaact tcctcgccga 2510

```

```

<210> 10
<211> 1137
<212> DNA
<213> Elaeis guineensis

```

```

<220>
<221> misc_feature
<222> (1)..(1137)
<223> 12-oxophytodienoate reductase 1-like polynucleotide

```

```

<400> 10
ggctgcaaca aaacagggga gaggaagag aaggcagagg agagggagga aggagaggca 60
gtagaagata tccctcttct cactccatac aagatgggag gattcctgct ttcgcatagg 120
gtagtattgg caccattgac aaggcagaga tcctatggat atattccaca acaacatgct 180
atthtgtact actcccagag gacttccaaa gggggctttt tgatatctga aggcactgtg 240
gtatcaaaca cgggcatagg gtataaagat atccccggta tttggactag agagcaggtg 300
gaagcatgga aaccaatagt gaatgctgta catgagaagg gtggtatttt ctttttacag 360

```

RDQL-J6430-Sequence-Listing_ST25.txt

attgggcaca tgggaaggat ctcaaattat gggttccagc ctaatggaca agcaccatc	420
tcaagtactg acaagccaat cactcctcag actccagaag atgatttctc ccctcctcga	480
cgcttgagca ctgatgaaat tcctcttata gtcaatgatt ttagagttgc tgcaaggaat	540
gctattgaag ctggctttga tggagttgag atccatgcgg cattcggtca tctactcgag	600
cagttcatga aagacaacat caacgaccga acagatgaat atggtggaag cttgcagaac	660
cgctgccggt tcgcattgga agtagttgag gctgtagtcg atgaaatcgg agccagtaga	720
gttggcatga gattatctct ctttgagac atcatggaga gtggagactc agaccctgag	780
ggctttgcac tgtacatggc tgaatcactg aacaagtttg gcgttctcta ctgcatgtg	840
attgaaccaa acatggaagt tgtggatgga aagcagcaaa taccacatgt gcatctttcc	900
atgagaaagg ctttcaaagg tacattcatc cttgctgggg gatttgatag agaagaagg	960
aacaaggtaa tcaagaagg ttatgctgat ctagtggcat atggccgctc attcatagct	1020
aatcctgact tgccaagag atttgaattc aatgctcctc tcaacaagta tgataggtct	1080
actattttac actatcagta cccggttggt gggtagtag actaccatt cttgaa	1137

<210> 11
 <211> 1299
 <212> DNA
 <213> Elaeis guineensis

<220>
 <221> misc_feature
 <222> (1)..(1299)
 <223> ORF 4 in reading frame 3 on reverse strand extending from base
 873 to base 2171 of Mannosyl-oligosaccharide
 1,2-alpha-mannosidase MNS3-like isoform X1 polynucleotide

<400> 11	
aaaaacaacc ttatggaaag aatcagtaca aaagggcagg tcaatttatt tgaaactacc	60
attcgtgttt taggggggct tcttagtgct tatcatttaa gtgggggtga acatggcacc	120
ttggaagaca gtggaatcct catgactcgt caaggagcta agccagagat cttcttaaaa	180
atagcaaaga atttagctga cagactgttg tctgcgttta cttcaagtcc aacatcaatt	240
cctttcagtg atgtcattct tcatgatagt acagcccatc ctgctcctga cggcatgagc	300
agtacttcag aagtttcaac cttacaactt gagtttaact acctcagtaa aatttcaggt	360
gatccaaaat atggttcaga ggcaatgaaa atattggaac atttaaggac acttcccaag	420
gtggaaggtc tgggtgcctat ttacatcagt cccaatctg gtcaatttaa tggagagaac	480
attcggctgg gatctcgtgg tgacagttac tatgagtact taattaaagt gtggattcag	540
caaaaatctg gtcacaatag ccagctaaag tatctatatg agatgtatac agaagcaatg	600
aaaggggtca gacatcttct tggttcgaaa tctgtaccca aggggctagt tttgttggg	660

RDQL-J6430-Sequence-Listing_ST25.txt

```

gagctgccct atggatctaa tgggtggcttc agtcccaaaa tggatcacct ggtgtgtttc      720
cttccaggca cccttgcaact tgggtgaacc aaaggatatca caaagaaaaa ggcagttgaa      780
ggtaatttat taactgcaga agacttgag aatttaaagc ttgctgaaga tctggcaaaa      840
acatgctttg aaatgtattc tgtgacttct actggtcttt ctctgaaat tgtttatttc      900
catgttgagg gtggttctga agggggacct gatggcggt acaaaagctc cgtgtatgta      960
aatgatataa ttatcaaaca caatgatcgt cataatcttt tgcgtccaga aactgtggaa     1020
tcattgtttg tgttgatcg tattactgaa gatccaaaat accgcgaatg gggctggcag     1080
atctttcagg ctttgaaaa atatacaaag gtggattctg gaggttatgc ttgtttggat     1140
gatgtcacia caatacccc tccaaaaaga gacaagatgg agactttctt cttgggggaa     1200
acattgaagt atttatattt gttgtttgga gacaataatg ttcttcctct ggataagttt     1260
gtattcaaca cagaagccca cccctttcca cttaactga                               1299

```

```

<210> 12
<211> 1344
<212> DNA
<213> Elaeis guineensis

```

```

<220>
<221> misc_feature
<222> (1)..(1344)
<223> ORF 1 in reading frame 2 on reverse strand extending from base 2
      to base 1345 of Alpha-1,3-mannosyl-glycoprotein
      2-beta-N-acetylglucosaminyltransferase-like isoform X3
      polynucleotide

```

```

<400> 12
gcggcaatgg cgagaaatat ctgacgacgtc cgactcctcc tcttcgtggc agccactgcc      60
tttatattca tccagatgcg cttttttgca acacagtctg agtatgcaga tcgcctagct     120
tctgctgtgg agtctgaaag ccagtgacac agtcagatga gattgttgat tgatcagatt     180
agcatacaac aaggaaaaat tgttgcccta gaagaggcga agaagcttca agatgaagag     240
tatgttcact tgaaggccct agttcaagat cttgaaaaaa aaggctcttca gagcttggtg     300
aaccacttag aggtacctgt agcagcagtt gttataatgg cttgtaatcg cccagactat     360
ttacaaagga cggttcaatc tgttttaaaa taccagactt cagttgcatc caaatttcca     420
ctatttgat cccaggatgg gacaaatcca gatgttaaaa acgtggcttt gagctttaaa     480
cagatcacat atttgcagca cttggatttt acacctgtgc atacggaaag gcctggagaa     540
ttaattgcat actacaagat cgcaagacac tacaagtggg ctttgatga attatttatc     600
aagcataatt tcaatcgagt aatcatatta gaagatgaca tggagattgc cccggatttt     660
tttaattatt ttgaggccac agcttctata ctcgacagtg acaagacaat catggctgtt     720

```

RDQL-J6430-Sequence-Listing_ST25.txt

```

tcttcttggga atgacaatgg acaagtgcaa tttgtgcatg atcctaaaac tctttatcgc      780
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ccgaagtggc ctaaagctta ttgggatgac tggattaggc ttaaggagat acacggagag      900
cgtcaattta ttcgtccaga agttttaga acttacaatt tcggtgagca tggctctagt      960
atggggcagt tctttaaaca atatttggag ccaatcaaat tgaatgatgt tcatgttgat     1020
tggaggacaa tggatctaag ctacctgaca gaggacaaat ttgtgagaca ctttgctaaa     1080
ctagtcgcag atgccaaacc tgttcatggt ggacctgatg cagttttaaa agcacataac     1140
atagatggtg atgtacggat ccaatataga gatcaagctg actttgaaca aattgcacga     1200
ggatttggga tatttgaaga atggaaggat ggcatccca ggacagcata taaaggagtt     1260
gtagtgttcc ggcataaac ttcaaggcgt atatatcttg tgggccaga ttctcttaag     1320
ctacttgggc ttgaggatgc ttga                                     1344

```

```

<210> 13
<211> 927
<212> DNA
<213> Elaeis guineensis

```

```

<220>
<221> misc_feature
<222> (1)..(927)
<223> ORF 1 in reading frame 2 on reverse strand extending from base 2
      to base 928 of Probable WRKY transcription factor 40
      polynucleotide

```

```

<400> 13
aagcttcaaa gcaacacata cccaatttgt caacaggctt cattcatcat ggactcctcg      60
ctgagccttg atctcaaggt cggttctctc cggttcccca ccgaagttcc aaaagtgtta     120
cgcaatagtc ccaagcatga ggaagagggg cttcttatga aaagagaggt tgggtgttctt     180
gaggcagagc tcaatcgggt ttctgaggag aatagaagac taaatgagaa gattgccatc     240
atttatgaag attgtgcaa cctgcagagc cagctaatag atttgatgac caccatgcgc     300
tcagataggg ggtcgggtctc gccggaaagg aagaggaaga gtgagaactc tgccctgaat     360
ggctacagtg atgtggctaa tggaatgacc aattggatgg gacgtcagat tgaaagcaac     420
tcaagcggaa attcttgcaa gcgagcgaga gaagattgtg atctgaaggt ctctaggctc     480
tgcgttcgca ccgatccatc ggattcaagc cttattgtaa aagatgggta tcaatggaga     540
aaatatggtc agaaggtgac aagagacaat ccatgtccaa gggcctactt cagatgctca     600
tttgctcctg cttgccctgt caagaagaag gtgcaaagaa gtgtagagga tagatcgatc     660
ctggttgcaa cttatgaagg cgagcacaac catggttacc cttctcagct tccagcacc     720
aatggttcca gccgtggtgg ctcggtctct cgccattctt ccggcccag caacgtaaca     780

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RDQL-J6430-Sequence-Listing_ST25.txt
 cttgatctca caccagtgagg atcgacagcag gaggttgagt caccagagct tccgcggagt 840
 ttggtggagc aagtggcggt gtcattgacg aaggatccag ggtttaaagc cgactggcc 900
 accgccgttt ctgggaacat tcttttag 927

<210> 14
 <211> 792
 <212> DNA
 <213> Elaeis guineensis

<220>
 <221> misc_feature
 <222> (1)..(792)
 <223> ORF 4 in reading frame 2 on reverse strand extending from base
 683 to base 1474 of Probable WRKY transcription factor 53
 polynucleotide

<400> 14
 catggctccc ccttgtgtg taactgcagg aagacactgc ccaagtggac cagccacatc 60
 aaggtgtgcc caggggaagg agttgaagg cctttggacg atggctatag ctggaggaaa 120
 tatgggcaga aagaaatact tggagccaaa catccaagag gctactatag gtgcacgcac 180
 cgcaacactc agggctgccc agcaacaaaa caggtgcaga gatccgatga gaacccgctg 240
 gtcttcgatg tcacctacca tgggtctcac acatgcctcc agaggtccca agcagtccca 300
 agatcagcgt cccgggaaca agagctgaaa caaaacaaac ctaattccca ggagcattct 360
 cagcagcagg accacaacct gcttctaacc ttccaaagag gcctcaaagt aataacccaa 420
 ggcttgact cggaagctca ggaccagaaa tcattatcct tctcctccc ttccactcca 480
 gtcagtgccg taaaggctga gaaccatatt tttcctgcc ctccaacact ggatagtggc 540
 ttcatgggca gcttctcttc atcattcttc tcacaaacaa catcagagtc caactatttc 600
 tcagtatccc cttgcagcat gagtaactat ggtggggggc tcaatcttca gacggccgag 660
 tctgacctca ccgaaataat gtcggctgca acctcagcca ccaattctcc tctgatggac 720
 atggatttca tgcttgaacc gctggagttc gatccaaaat ttcaacttga tgtttccagc 780
 ttcttctcat aa 792

<210> 15
 <211> 471
 <212> DNA
 <213> Elaeis guineensis

<220>
 <221> misc_feature
 <222> (1)..(471)
 <223> ORF 1 in reading frame 1 on direct strand extending from base 1
 to base 471 of Dirigent protein 5-like polynucleotide

<400> 15

RDQL-J6430-Sequence-Listing_ST25.txt

```

acaatgcagg gatcaccaac accatccgcc aagtcttggt cccttctcct cctttccttt      60
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tgcaagcgcc tgggtgctcta ctaccacgac atcctcttca atggaaccaa cgtatctaata      180
gccacctctg ctgccgtcgc caaccaaaca gccctcggag attacaaatt tggcatgttc      240
gtagtgttcg acgaccccat gaccgaagac caccacctgc tgtccaagcc ggtggcccgg      300
gctcagggct tctacttcta cgatatgaag aaagagtaca acgcatgggt tgcgtacacg      360
cttggtgttca actccactga gtacggccag gggactataa acataatggg ggccgacctg      420
atgggcccct tagctggggt ttcgagcggg aataggctcg aggtaatttg a              471

```

```

<210> 16
<211> 1191
<212> DNA
<213> Elaeis guineensis

```

```

<220>
<221> misc_feature
<222> (1)..(1191)
<223> ORF 1 in reading frame 2 on direct strand extending from base 146
      to base 1336 of G-type lectin S-receptor-like
      serine/threonine-protein kinase polynucleotide

```

```

<400> 16
caacttcaga ttctcttttg aaacatcatg tctctcagta catatctggt ggtgaagtat      60
gtcaggaaac gaatagcaag gagaatacaa gaacaaaatg acattgtttc acccgtattg      120
gaaacaagaa atcttttgcc atatgcaaac gagcttacia ttgtcatgga ggatggcagt      180
ggcctagact caccattatt tgattttaac atgataatag cagcaacaaa caactttagc      240
aaggaaaata agcttgagga gggaggattt ggtccagttt acaagggaaa gcttccaggc      300
ggtcaagaaa tagcagtga gaggctatcc aagaggtctg ggcagggtt aaaggaattc      360
aagaatgagg tggaactgat atccaagctc caacacagga acctagttag gcttctgggt      420
tgctgcatat atggagatga gaagcttttg atctatgagt tcatgcccaa caagagcttg      480
gatgcctttc tcttcgatgc aaccaggaaa gttctattag actggaaaag ccgctgcaac      540
attggttgaag ggattgctcg ggggctgctg taccttcaca gagattctag attaaggatc      600
attcaccgag atctgaaagc gagcaatggt ctattagacg aacaatttaa tcccagaata      660
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gttggttgaa caattggcta catgtcccct gagtatgcca tggaagggca gatttcggag      780
aaatccgatg tcttcagctt tgggtgtttg cttttagaag ttgtgagtgg taagaggaaac      840
aatcattttg tcgacaacga gaaaggtctg aacctcttgg gatatgcatg gacactgtgg      900
aaggaaaaca gagtcctcga gttgatcgat ccatcattgg gtgactcatg gtcttactca      960

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RDQL-J6430-Sequence-Listing_ST25.txt

gaagtgtctca ggatcattaa agtggggctc ttatgtgtgc aagaattccc aacagacagg	1020
ccatccatgt ctttggtagt gtctatgctt acaagtgatg cgaatgttcc agttccaaaa	1080
caggctgcat tctttggaag gagaagtcac tcagattcca tttcatcaac cgaaagcaag	1140
gagacatggt cagcaaatgg tctcactatt accaaactag agtgcagata a	1191

<210> 17
 <211> 1263
 <212> DNA
 <213> Elaeis guineensis

<220>
 <221> misc_feature
 <222> (1)..(1263)
 <223> ORF 1 in reading frame 2 on reverse strand extending from base
 131 to base 1393 of Putative disease resistance protein RGA3
 polynucleotide

<400> 17	
ggttgtgcaa tggcgagcgc tttcctctct tccatcatat caaaaaccag ccaagttttg	60
ggctctgttc atagatgggc agcctcgccg tcttcgccat cagatccacg cagcagtgtc	120
ttggaagatc tggaggagct ggagagaaca ttgaaaagga tccaggcagt gctccatgac	180
gcggaggaga gggagatacg agaagaagcc gtcaagctct ggctgaagga gctcaaagaa	240
gtggcttatg acgcggaaga tgtgctggac gagtaccagt acgaggtact gcgagcccaa	300
gcggaaggcg gagcttcccg caagaggaag cgagtggaag caggggacga tgaggaagag	360
gtaagtactt ctctttccac catagttaat gtttcaattc ccgatggcat gggggataga	420
atcaggaaga tcaggaagag gttcgatgag atctcggagg atcggaaacg cctccgttta	480
agcgaggaag atggagagcg acgggtctct ggagctccgt acccagcacc aaccagtcac	540
atggtggatg aatcacgtac ttttggaagg aaacatgaca agaagaaaat aattgatttg	600
ctgctttctg agggatatgg aaatggatc tctgtcattc caattgtcgg caagggagga	660
ctgggaaaaa ccaccatcgc tcagctggtc tacaatgact ccaagggtcaa agaatatattt	720
gatcggactg gatggggttg tgtatccgat gatattgatg ttccgaggct aacaaaggcc	780
atcatcgagt ctattactgg aactccatgt aagcttacag aaatcagccc acttcaaaat	840
acactcaagc aaaagggtgaa ggggaagaaa gtgttgcttg tgctggacga tgtctggaac	900
gaggaacaaa gcctttggga gtccttgagt atcccccttcg ttggcgaaga aacagtaaga	960
attatcgtga cttgtagaaa tgagaagggt gcggagatca tgcagacaga ggatccttat	1020
tgtcctggct acttgctgct ggagcagtct tggtcattat tcaggcatta tgcatttggt	1080
ggtcgagacc ctgaagaaca accacacttg gcggataccg gtaagcagat tgtcaagaag	1140
tgttccggtt taccattggc tgtgaagaca ctaggaagcc ttctaagaca tgaggcagat	1200

RDQL-J6430-Sequence-Listing_ST25.txt
gaagatagtt ggacggaggt cttacaaagc gatcaatgta tgggaactag agaagaacaa 1260
tga 1263

<210> 18
<211> 1524
<212> DNA
<213> *Elaeis guineensis*

<220>
<221> misc_feature
<222> (1)..(1524)
<223> ORF 2 in reading frame 2 on direct strand extending from base 236
to base 1759 of Polyamine oxidase polynucleotide

<400> 18
gcggcggttcg ggggattcgg atcgccgtct ttgatcgcca ggatggagcg caagaccctc 60
ccgggcccgcg acaatttcgc catcagcggg atttttctca cacacattga gaggcaacag 120
tcttccccac cttcagtcatt tgtgattggg ggaggccttt cagggatcgc agctgcacgt 180
gcattgacga atgcttcatt taaggttatt ttgtagagt cacgcaatcg gcttggtggc 240
cgagtgcata ctgactattc ttttggtgtt cctgttgaca tgggggcatc atggctgcat 300
ggtgtttgca atgaaaattc tctggcacca tttattcgtg gtctgggcct aagattatac 360
cgcactagtgt gtgacaactc tgtgttgtat gaccacgatt tagagagcta tgcactgttt 420
gatatgaatg gttgccaaagt ccctcaacag ctggtaatta gagttggaga aatgtttgag 480
agaattctca aagagacagt gaaagtaagg gatgaacatg ctgaggacat gtctctgctc 540
caagctatctt ctattgtttt gaacagaaat ccagatctaa ggcaagaggg gccggcacat 600
gaagtgttgc agtgggtatat atgcagaatg gaggcattgg ttgctgcaga cgtggatact 660
atatctttga aaagctggga tcaggagcat gttctttctg gtggccatgg acttatggtg 720
caaggatact atcctgttat caaaaccctt gcaaatgatac tggatatcaa actgaaccac 780
aggggtgaaa aaattgtcca gcgttgtaac aaagtaatgg tcaccgtgga ggatggctca 840
aattttgtgg ctgatgctgc tattatcact gttcctcttg gggttctcaa agcaaatgtg 900
atcgaatttg aaccgaagct accagaatgg aaagtctcag caatctctga tcttggtgtt 960
ggcaatgaga ataagattgc tcttcacttt agtactgttt tttggcccaa tgtagaagtt 1020
ctaggaatgg tcgctccaac atcttatgcc tgtggctact ttctcaatct ccacaaggca 1080
acaggacatc ctgttcttgt gtacatggct gctggaaggg ttgcttatga tattgagaaa 1140
ctttctgatg aagaagctgt taaatttgtg atgttacagc ttcagaaaat gctaccagat 1200
gctacagagc cggttcaata cttggtttct aggtggggta cagaccaga ttcccttggg 1260
tcctattctt gtgacttggg tgggaagcca gctgacttgt atgagagatt tcgagctcct 1320
gtggataata tatattttgc tggagaagca gcaagtgttg atcactctgg gtccgtccat 1380

RDQL-J6430-Sequence-Listing_ST25.txt

```

ggagcttaca cagcaggtat catagctgca gaggactgcc gaaggcgtct actactgcaa      1440
catggaatgt cagatctctt ccaggctgta ttaagggagg aaatgactga agccatggtc      1500
cccctccaaa tatctaggat gtaa                                             1524

```

```

<210> 19
<211> 2436
<212> DNA
<213> Elaeis guineensis

```

```

<220>
<221> misc_feature
<222> (1)..(2436)
<223> ORF 1 in reading frame 1 on direct strand extending from base 73
      to base 2508 of Putative lipoxygenase 5 polynucleotide

```

```

<400> 19
gattttggga agcaaaaaaa aaagaagaag ctaatggcgg cttctatcga aagcttgggc      60
acttctttga tccaaagatt gcctctcctt ccttcctcga gctctcgaat ttttcgaggg      120
gagcagagca acctcggcctt ccaacctgct ctgtttccgt tgacacaaaag gagtcttcat      180
agggtgaata gagctgtgag agctccggtg gcggcggcgg tcacagagaa agtggtgaag      240
gtggtggcag agaagccagt gaggtttaag gttcgggcag cgttgacggt gaggaagaag      300
aaagaggagg atttgaaaga gaagattgca agccagctcg atgccttctc ggataagatt      360
ggaaggaacg tcgttttggg gctcgtcagc accgagatcg atccatggac acaaaagccg      420
aagagaagca acaaggcagt gcttagggac tggtttgaga agaagaatgt gaagggggag      480
agggtggtgt acacagctga attcatggtg gactccagct tcggcatgcc gggagccatc      540
acggtgctga atcggcacca gaaggagttc ttcttagaaa gcatcgtcgt cgagggcctc      600
gcctgtggtc ctgtccactt ctcttgctac tcctgggtcc aaccaccaa aattcacccc      660
agcgagaggg tcttcttcaa caacaagcca tatttgccag cagagacacc tcctggtctg      720
aaggaactaa gggagagggg gttggaggag ctaagaggcg acggaacggg cgagaggaag      780
ctcactgata gaatttacga ttctgatact tataatgact taggcaaccc tgacaagggg      840
ttcgagtacg caaggccgat cgccggagga gacaaaatgc catatccaag aagatgtaga      900
acagggaggt cccaaccaa tacagatgtg catgcagaga gcagaaggga gtatccctcg      960
ccaatatatg tgcctcgtga tgaagcattt gaggagggta agcaagagat gttatcggcc     1020
ggtgcactga aagcattgct ccacaacctt gtgccatctt tcgtcgcacg catttctccg     1080
gagagccatg acttcaaggc cttccacgac atcgacaacc tcttcaaaga aggccttcgc     1140
tggaagaaga ccttgagga ccaactcttc cataagattc catttgtgag caagattgaa     1200
gagtccagcg aggccctgct ccgattcgac accccggaca tcataacaaa ggacaagttt     1260

```

RDQL-J6430-Sequence-Listing_ST25.txt

gcgtggctgc gagatgacga gttcgctcgg caggcactcg ccggcattaa ccccgtaac	1320
gtagagaggc ttcaggtgtt cctcctgtt agcaagctcg atcccacat atatggtcct	1380
cctgaatctg ccatcaaaga ggagcacatt attggccatc tcggtggcat gtcagtccaa	1440
caggcactgg aggagaacaa gctattcatg ttggattacc atgatgttta cctcccattt	1500
cttgaccgga tcaatgccca agatgggagg aaagcctatg gcacaagaac tctatttttc	1560
ctcactcaac ttgggactct gaagccaata gccattgagc tcagtctccc accagcaacc	1620
cctggttgct cgagagcgaa acgtgtcctc acaccacca ccgatgccac aaacaactgg	1680
ctctggcaac tcgccaaggc ccacgtctgc tccaatgatg ctgggggtcca ccaacttgct	1740
aaccactggt tgaggacaca tgcgtgcttg gagcccttca taatagctgc gcatcgacaa	1800
ctaagcgca tgcatccaat cttcaagctg ctcaagcccc atatgctta cacccttgag	1860
atcaatgctc ttgctcgcca aatcctcatc agtggtggtg gagtcacga gtctggcttc	1920
accctggat catgttgcat ggagatgagt gtctctttct atcgggatca ctggcgtttt	1980
gatcgagagg gcctccctgc cgatctcatt agaagaggca tggcaataga ggaccctagc	2040
caaccccatg ggctaaagct tctcatagag gactaccctc acgccaacga tggcctcctc	2100
ctttggtccg cctccaggc ctgggtccgg acctacgtcc aggcctacta cccgaacccc	2160
cacgtcgtcc aagccgaccc cgagctccaa gcctggtacg ccgaagccgt ccgctggtggc	2220
cacgccgaca agagcggcgc cgactggtgg ccccggtca gctccccgc cgacctggc	2280
tcctgtctca ccacctcct ctggctcgcg tcggtcagc acgccgcgt caacttcggg	2340
cagtaccgc tcggcggcta catccgaac cggccccctc tcatgcgccg gctcgtcccc	2400
gccgagggcg accccgagta cgacaacttc ctgcgc	2436

<210> 20
 <211> 1149
 <212> DNA
 <213> Elaeis guineensis

<220>
 <221> misc_feature
 <222> (1)..(1149)
 <223> ORF 1 in reading frame 1 on direct strand extending from base 1
 to base 1137 of 12-oxophytodienoate reductase 1-like
 polynucleotide

<400> 20	
ggctgcaaca aaacagggga gaggaagag aaggcagagg agagggagga aggagaggca	60
gtagaagata tcctctttct cactccatac aagatgggag gattcctgct ttcgcatagg	120
gtagtattgg caccattgac aaggcagaga tcctatggat atattccaca acaacatgct	180
atthttgtact actcccagag gacttccaaa gggggccttt tgatatctga aggcactgtg	240

RDQL-J6430-Sequence-Listing_ST25.txt

```

gtatcaaaca cgggcatagg gtataaagat atccccggta ttgggactag agagcagggtg      300
gaagcatgga aaccaatagt gaatgctgta catgagaagg gtggtatattt ctttttacag      360
attgggcaca tgggaaggat ctcaaattat ggtttccagc ctaatggaca agcacccatc      420
tcaagtactg acaagccaat cactcctcag actccagaag atgattttctc ccctcctcga      480
cgcttgagca ctgatgaaat tcctcttata gtcaatgatt ttagagttgc tgcaaggaat      540
gctattgaag ctggctttga tggagttgag atccatgcgg cattcgggtca tctactcgag      600
cagttcatga aagacaacat caacgaccga acagatgaat atggtggaag cttgcagaac      660
cgctgccggt tcgcattgga agtagttgag gctgtagtcg atgaaatcgg agccagtaga      720
gttgcatga gattatctct ctttgcagac atcatggaga gtggagactc agaccctgag      780
ggctctgcac tgtacatggc tgaatcactg aacaagtttg gcgttctcta ctgcatgtg      840
attgaaccaa acatggaagt tgtggatgga aagcagcaaa taccacatgt gcatctttcc      900
atgagaaaagg ctttcaaagg tacattcatc cttgctgggg gatttgatag agaagaagg      960
aacaaggtaa tcaaagaagg ttatgctgat ctagtggcat atggccgctc attcatagct     1020
aatcctgact tgcccaagag atttgaattc aatgctcctc tcaacaagta tgataggtct     1080
actattttac actatcagta cccggttggt gggtatgtag actaccatt cttgaaatcc     1140
ttaaactaa                                     1149

```

<210> 21
 <211> 432
 <212> PRT
 <213> Elaeis guineensis

<220>
 <221> MISC_FEATURE
 <222> (1)..(432)
 <223> Translation of ORF 4 in reading frame 3 on reverse strand of
 Mannosyl-oligosaccharide 1,2- α -mannosidase MNS3-like isoform
 X1 polynucleotide

<400> 21

Lys Asn Asn Leu Met Glu Arg Ile Ser Thr Lys Gly Gln Val Asn Leu
 1 5 10 15

Phe Glu Thr Thr Ile Arg Val Leu Gly Gly Leu Leu Ser Ala Tyr His
 20 25 30

Leu Ser Gly Gly Glu His Gly Thr Leu Glu Asp Ser Gly Ile Ser Met
 35 40 45

Thr Arg Gln Gly Ala Lys Pro Glu Ile Phe Leu Lys Ile Ala Lys Asn
 50 55 60

RDQL-J6430-Sequence-Listing_ST25.txt

Leu Ala Asp Arg Leu Leu Ser Ala Phe Thr Ser Ser Pro Thr Ser Ile
 65 70 75 80
 Pro Phe Ser Asp Val Ile Leu His Asp Ser Thr Ala His Pro Ala Pro
 85 90 95
 Asp Gly Met Ser Ser Thr Ser Glu Val Ser Thr Leu Gln Leu Glu Phe
 100 105 110
 Asn Tyr Leu Ser Lys Ile Ser Gly Asp Pro Lys Tyr Gly Ser Glu Ala
 115 120 125
 Met Lys Ile Leu Glu His Leu Arg Thr Leu Pro Lys Val Glu Gly Leu
 130 135 140
 Val Pro Ile Tyr Ile Ser Pro Gln Ser Gly Gln Phe Asn Gly Glu Asn
 145 150 155 160
 Ile Arg Leu Gly Ser Arg Gly Asp Ser Tyr Tyr Glu Tyr Leu Ile Lys
 165 170 175
 Val Trp Ile Gln Gln Lys Ser Gly His Asn Ser Gln Leu Lys Tyr Leu
 180 185 190
 Tyr Glu Met Tyr Thr Glu Ala Met Lys Gly Val Arg His Leu Leu Val
 195 200 205
 Arg Lys Ser Val Pro Lys Gly Leu Val Phe Val Gly Glu Leu Pro Tyr
 210 215 220
 Gly Ser Asn Gly Gly Phe Ser Pro Lys Met Asp His Leu Val Cys Phe
 225 230 235 240
 Leu Pro Gly Thr Leu Ala Leu Gly Ala Thr Lys Gly Ile Thr Lys Lys
 245 250 255
 Lys Ala Val Glu Gly Asn Leu Leu Thr Ala Glu Asp Leu Glu Asn Leu
 260 265 270
 Lys Leu Ala Glu Asp Leu Ala Lys Thr Cys Phe Glu Met Tyr Ser Val
 275 280 285
 Thr Ser Thr Gly Leu Ser Pro Glu Ile Val Tyr Phe His Val Glu Gly
 290 295 300
 Gly Ser Glu Gly Gly Pro Asp Gly Gly Asn Lys Ser Ser Val Tyr Val
 305 310 315 320

RDQL-J6430-Sequence-Listing_ST25.txt

Asn Asp Ile Ile Ile Lys His Asn Asp Arg His Asn Leu Leu Arg Pro
325 330 335

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

Lys Tyr Arg Glu Trp Gly Trp Gln Ile Phe Gln Ala Phe Glu Lys Tyr
355 360 365

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

Ile Pro Pro Pro Lys Arg Asp Lys Met Glu Thr Phe Phe Leu Gly Glu
385 390 395 400

Thr Leu Lys Tyr Leu Tyr Leu Leu Phe Gly Asp Asn Asn Val Leu Pro
405 410 415

Leu Asp Lys Phe Val Phe Asn Thr Glu Ala His Pro Phe Pro Leu Asn
420 425 430

<210> 22
<211> 447
<212> PRT
<213> Elaeis guineensis

```
<220>
<221> MISC_FEATURE
<222> (1)..(447)
<223> Translation of ORF 1 in reading frame 2 on reverse strand of
Alpha-1,3-mannosyl-glycoprotein
2-beta-N-acetylglucosaminyltransferase-like isoform X3
polynucleotide
```

<400> 22

Ala Ala Met Ala Arg Asn Ile Cys Asp Val Arg Leu Leu Leu Phe Val
1 5 10 15

Ala Ala Thr Ala Phe Ile Phe Ile Gln Met Arg Leu Phe Ala Thr Gln
20 25 30

Ser Glu Tyr Ala Asp Arg Leu Ala Ser Ala Val Glu Ser Glu Ser Gln
35 40 45

Cys Thr Ser Gln Met Arg Leu Leu Ile Asp Gln Ile Ser Ile Gln Gln
50 55 60

Gly Lys Ile Val Ala Leu Glu Glu Ala Lys Lys Leu Gln Asp Glu Glu

RDQL-J6430-Sequence-Listing_ST25.txt																		
65						70						75						80
Tyr	Val	His	Leu	Lys ₈₅	Ala	Leu	Val	Gln	Asp ₉₀	Leu	Glu	Lys	Lys	Gly ₉₅	Leu			
Gln	Ser	Leu	Leu ₁₀₀	Asn	His	Leu	Glu	Val ₁₀₅	Pro	Val	Ala	Ala	Val ₁₁₀	Val	Ile			
Met	Ala	Cys ₁₁₅	Asn	Arg	Pro	Asp	Tyr ₁₂₀	Leu	Gln	Arg	Thr	Val ₁₂₅	Gln	Ser	Val			
Leu	Lys ₁₃₀	Tyr	Gln	Thr	Ser	Val ₁₃₅	Ala	Ser	Lys	Phe	Pro ₁₄₀	Leu	Phe	Val	Ser			
Gln ₁₄₅	Asp	Gly	Thr	Asn	Pro ₁₅₀	Asp	Val	Lys	Asn	Val ₁₅₅	Ala	Leu	Ser	Phe	Lys ₁₆₀			
Gln	Ile	Thr	Tyr	Leu ₁₆₅	Gln	His	Leu	Asp	Phe ₁₇₀	Thr	Pro	Val	His	Thr ₁₇₅	Glu			
Arg	Pro	Gly	Glu ₁₈₀	Leu	Ile	Ala	Tyr	Tyr ₁₈₅	Lys	Ile	Ala	Arg	His ₁₉₀	Tyr	Lys			
Trp	Ala	Leu ₁₉₅	Asp	Glu	Leu	Phe	Ile ₂₀₀	Lys	His	Asn	Phe	Asn ₂₀₅	Arg	Val	Ile			
Ile	Leu ₂₁₀	Glu	Asp	Asp	Met	Glu ₂₁₅	Ile	Ala	Pro	Asp	Phe ₂₂₀	Phe	Asn	Tyr	Phe			
Glu ₂₂₅	Ala	Thr	Ala	Ser	Ile ₂₃₀	Leu	Asp	Ser	Asp	Lys ₂₃₅	Thr	Ile	Met	Ala	Val ₂₄₀			
Ser	Ser	Trp	Asn	Asp ₂₄₅	Asn	Gly	Gln	Val	Gln ₂₅₀	Phe	Val	His	Asp	Pro ₂₅₅	Lys			
Thr	Leu	Tyr	Arg ₂₆₀	Ser	Asp	Phe	Phe	Pro ₂₆₅	Gly	Leu	Gly	Trp	Met ₂₇₀	Leu	Ser			
Lys	Ser	Ile ₂₇₅	Trp	Asp	Glu	Leu	Ser ₂₈₀	Pro	Lys	Trp	Pro	Lys ₂₈₅	Ala	Tyr	Trp			
Asp	Asp ₂₉₀	Trp	Ile	Arg	Leu	Lys ₂₉₅	Glu	Ile	His	Gly	Glu ₃₀₀	Arg	Gln	Phe	Ile			
Arg ₃₀₅	Pro	Glu	Val	Cys	Arg ₃₁₀	Thr	Tyr	Asn	Phe	Gly ₃₁₅	Glu	His	Gly	Ser	Ser ₃₂₀			

RDQL-J6430-Sequence-Listing_ST25.txt

Met Gly Gln Phe Phe Lys Gln Tyr Leu Glu Pro Ile Lys Leu Asn Asp
325 330 335

Val His Val Asp Trp Arg Thr Met Asp Leu Ser Tyr Leu Thr Glu Asp
340 345 350

Lys Phe Val Arg His Phe Ala Lys Leu Val Ala Asp Ala Lys Pro Val
355 360 365

His Gly Gly Pro Asp Ala Val Leu Lys Ala His Asn Ile Asp Gly Asp
370 375 380

Val Arg Ile Gln Tyr Arg Asp Gln Ala Asp Phe Glu Gln Ile Ala Arg
385 390 395 400

Gly Phe Gly Ile Phe Glu Glu Trp Lys Asp Gly Ile Pro Arg Thr Ala
405 410 415

Tyr Lys Gly Val Val Val Phe Arg His Gln Thr Ser Arg Arg Ile Tyr
420 425 430

Leu Val Gly Pro Asp Ser Leu Lys Leu Leu Gly Leu Glu Asp Ala
435 440 445

<210> 23
<211> 308
<212> PRT
<213> Elaeis guineensis

```
<220>
<221> MISC_FEATURE
<222> (1)..(308)
<223> Translation of ORF 1 in reading frame 2 on reverse strand of
      Probable WRKY transcription factor 40 polynucleotide
```

<400> 23

Lys Leu Gln Ser Asn Thr Tyr Pro Ile Cys Gln Gln Ala Ser Phe Ile
1 5 10 15

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

Pro Thr Glu Val Pro Lys Val Leu Arg Asn Ser Pro Lys His Glu Glu
35 40 45

Glu Gly Leu Leu Met Lys Arg Glu Val Gly Val Leu Glu Ala Glu Leu
50 55 60

Asn Arg Val Ser Glu Glu Asn Arg Arg Leu Asn Glu Lys Ile Ala Ile
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RDQL-J6430-Sequence-Listing_ST25.txt																
65					70					75					80	
Ile	Tyr	Glu	Asp	Cys 85	Ala	Asn	Leu	Gln	Ser 90	Gln	Leu	Ile	Asp	Leu 95	Met	
Thr	Thr	Met	Arg 100	Ser	Asp	Arg	Gly	Ser 105	Val	Ser	Pro	Glu	Arg 110	Lys	Arg	
Lys	Ser	Glu 115	Asn	Ser	Ala	Leu	Asn 120	Gly	Tyr	Ser	Asp	Val 125	Ala	Asn	Gly	
Met	Thr 130	Asn	Trp	Met	Gly	Arg 135	Gln	Ile	Glu	Ser	Asn 140	Ser	Ser	Gly	Asn	
Ser 145	Cys	Lys	Arg	Ala	Arg 150	Glu	Asp	Cys	Asp	Leu 155	Lys	Val	Ser	Arg	Leu 160	
Cys	Val	Arg	Thr	Asp 165	Pro	Ser	Asp	Ser	Ser 170	Leu	Ile	Val	Lys	Asp 175	Gly	
Tyr	Gln	Trp	Arg 180	Lys	Tyr	Gly	Gln	Lys 185	Val	Thr	Arg	Asp	Asn 190	Pro	Cys	
Pro	Arg	Ala 195	Tyr	Phe	Arg	Cys	Ser 200	Phe	Ala	Pro	Ala	Cys 205	Pro	Val	Lys	
Lys	Lys 210	Val	Gln	Arg	Ser	Val 215	Glu	Asp	Arg	Ser	Ile 220	Leu	Val	Ala	Thr	
Tyr 225	Glu	Gly	Glu	His	Asn 230	His	Gly	Tyr	Pro	Ser 235	Gln	Leu	Pro	Ala	Pro 240	
Asn	Gly	Ser	Ser	Arg 245	Gly	Gly	Ser	Val	Ser 250	Arg	His	Ser	Ser	Gly 255	Pro	
Ser	Asn	Val	Thr 260	Leu	Asp	Leu	Thr	Arg 265	Val	Gly	Ser	Gln	Gln 270	Glu	Val	
Glu	Ser	Pro 275	Glu	Leu	Pro	Arg	Ser 280	Leu	Val	Glu	Gln	Val 285	Ala	Leu	Ser	
Leu	Thr 290	Lys	Asp	Pro	Gly	Phe 295	Lys	Ala	Ala	Leu	Ala 300	Thr	Ala	Val	Ser	
Gly 305	Asn	Ile	Leu													

RDQL-J6430-Sequence-Listing_ST25.txt

<210> 24
 <211> 263
 <212> PRT
 <213> Elaeis guineensis

<220>
 <221> MISC_FEATURE
 <222> (1)..(263)
 <223> Translation of ORF 4 in reading frame 2 on reverse strand of
 Probable WRKY transcription factor 53 polynucleotide

<400> 24

His Gly Ser Pro Leu Val Cys Asn Cys Arg Lys Thr Leu Pro Lys Trp
 1 5 10 15

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

Asp Asp Gly Tyr Ser Trp Arg Lys Tyr Gly Gln Lys Glu Ile Leu Gly
 35 40 45

Ala Lys His Pro Arg Gly Tyr Tyr Arg Cys Thr His Arg Asn Thr Gln
 50 55 60

Gly Cys Pro Ala Thr Lys Gln Val Gln Arg Ser Asp Glu Asn Pro Leu
 65 70 75 80

Val Phe Asp Val Thr Tyr His Gly Ser His Thr Cys Leu Gln Arg Ser
 85 90 95

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

Lys Pro Asn Ser Gln Glu His Ser Gln Gln Gln Asp His Asn Leu Leu
 115 120 125

Leu Thr Phe Gln Arg Gly Leu Lys Val Ile Thr Gln Gly Leu Asp Ser
 130 135 140

Glu Ala Gln Asp Gln Lys Ser Leu Ser Phe Ser Phe Pro Ser Thr Pro
 145 150 155 160

Val Ser Ala Val Lys Ala Glu Asn His Ile Phe Ser Cys Pro Pro Thr
 165 170 175

Leu Asp Ser Gly Phe Met Gly Ser Phe Ser Ser Ser Phe Leu Ser Gln
 180 185 190

Thr Thr Ser Glu Ser Asn Tyr Phe Ser Val Ser Pro Cys Ser Met Ser
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RDQL-J6430-Sequence-Listing_ST25.txt
200 205

195 200 205

Asn Tyr Gly Gly Gly Leu Asn Leu Gln Thr Ala Glu Ser Asp Leu Thr
210 215 220

Glu Ile Met Ser Ala Ala Thr Ser Ala Thr Asn Ser Pro Leu Met Asp
225 230 235 240

Met Asp Phe Met Leu Glu Pro Leu Glu Phe Asp Pro Lys Phe Gln Leu
245 250 255

Asp Val Ser Ser Phe Phe Ser
260

```
<210> 25
<211> 156
<212> PRT
<213> Elaeis guineensis
```

```
<220>
<221> MISC_FEATURE
<222> (1)..(156)
<223> Translation of ORF 1 in reading frame 1 on direct strand of
Dirigent protein 5-like polynucleotide
```

<400> 25

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

RDQL-J6430-Sequence-Listing_ST25.txt

Gly Gln Gly Thr Ile Asn Ile Met Gly Ala Asp Leu Met Gly Pro Leu
 130 135 140

Ala Gly Phe Ser Ser Gly Asn Arg Ser Glu Val Ile
 145 150 155

<210> 26
 <211> 396
 <212> PRT
 <213> Elaeis guineensis

<220>
 <221> MISC_FEATURE
 <222> (1)..(396)
 <223> Translation of ORF 1 in reading frame 2 on direct strand of
 G-type lectin S-receptor-like serine/threonine-protein kinase
 polynucleotide

<400> 26

Gln Leu Gln Ile Leu Phe Gly Asn Ile Met Ser Leu Ser Thr Tyr Leu
 1 5 10 15

Leu Val Lys Tyr Val Arg Lys Arg Ile Ala Arg Arg Ile Gln Glu Gln
 20 25 30

Asn Asp Ile Val Ser Pro Val Leu Glu Thr Arg Asn Leu Leu Pro Tyr
 35 40 45

Ala Asn Glu Leu Thr Ile Val Met Glu Asp Gly Ser Gly Leu Asp Ser
 50 55 60

Pro Leu Phe Asp Phe Asn Met Ile Ile Ala Ala Thr Asn Asn Phe Ser
 65 70 75 80

Lys Glu Asn Lys Leu Gly Glu Gly Gly Phe Gly Pro Val Tyr Lys Gly
 85 90 95

Lys Leu Pro Gly Gly Gln Glu Ile Ala Val Lys Arg Leu Ser Lys Arg
 100 105 110

Ser Gly Gln Gly Leu Lys Glu Phe Lys Asn Glu Val Glu Leu Ile Ser
 115 120 125

Lys Leu Gln His Arg Asn Leu Val Arg Leu Leu Gly Cys Cys Ile Tyr
 130 135 140

Gly Asp Glu Lys Leu Leu Ile Tyr Glu Phe Met Pro Asn Lys Ser Leu
 145 150 155 160

RDQL-J6430-Sequence-Listing_ST25.txt

Asp Ala Phe Leu Phe Asp Ala Thr Arg Lys Val Leu Leu Asp Trp Lys
 165 170 175
 Ser Arg Cys Asn Ile Val Glu Gly Ile Ala Arg Gly Leu Leu Tyr Leu
 180 185 190
 His Arg Asp Ser Arg Leu Arg Ile Ile His Arg Asp Leu Lys Ala Ser
 195 200 205
 Asn Val Leu Leu Asp Glu Gln Phe Asn Pro Arg Ile Ser Asp Phe Gly
 210 215 220
 Met Ala Arg Ile Phe Gly Arg Asp Gln Ser Leu Glu Arg Thr Asp Arg
 225 230 235 240
 Val Val Gly Thr Ile Gly Tyr Met Ser Pro Glu Tyr Ala Met Glu Gly
 245 250 255
 Gln Ile Ser Glu Lys Ser Asp Val Phe Ser Phe Gly Val Leu Leu Leu
 260 265 270
 Glu Val Val Ser Gly Lys Arg Asn Asn His Phe Val Asp Asn Glu Lys
 275 280 285
 Gly Leu Asn Leu Leu Gly Tyr Ala Trp Thr Leu Trp Lys Glu Asn Arg
 290 295 300
 Val Leu Glu Leu Ile Asp Pro Ser Leu Gly Asp Ser Trp Ser Tyr Ser
 305 310 315 320
 Glu Val Leu Arg Ile Ile Lys Val Gly Leu Leu Cys Val Gln Glu Phe
 325 330 335
 Pro Thr Asp Arg Pro Ser Met Ser Leu Val Val Ser Met Leu Thr Ser
 340 345 350
 Asp Ala Asn Val Pro Val Pro Lys Gln Ala Ala Phe Phe Gly Arg Arg
 355 360 365
 Ser His Ser Asp Ser Ile Ser Ser Thr Glu Ser Lys Glu Thr Trp Ser
 370 375 380
 Ala Asn Gly Leu Thr Ile Thr Lys Leu Glu Cys Arg
 385 390 395

<210> 27

RDQL-J6430-Sequence-Listing_ST25.txt

<211> 420

<212> PRT

<213> *Elaeis guineensis*

<220>

<221> MISC_FEATURE

<222> (1)..(420)

<223> Translation of ORF 1 in reading frame 2 on reverse strand of
Putative disease resistance protein RGA3 polynucleotide

<400> 27

Gly Cys Ala Met Ala Ser Ala Phe Leu Ser Ser Ile Ile Ser Lys Thr
1 5 10 15

Ser Gln Val Leu Gly Ser Val His Arg Trp Ala Ala Ser Pro Ser Ser
20 25 30

Pro Ser Asp Pro Arg Ser Ser Val Leu Glu Asp Leu Glu Glu Leu Glu
35 40 45

Arg Thr Leu Lys Arg Ile Gln Ala Val Leu His Asp Ala Glu Glu Arg
50 55 60

Glu Ile Arg Glu Glu Ala Val Lys Leu Trp Leu Lys Glu Leu Lys Glu
65 70 75 80

Val Ala Tyr Asp Ala Glu Asp Val Leu Asp Glu Tyr Gln Tyr Glu Val
85 90 95

Leu Arg Ala Gln Ala Glu Gly Gly Ala Ser Arg Lys Arg Lys Arg Val
100 105 110

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

Val Asn Val Ser Ile Pro Asp Gly Met Gly Asp Arg Ile Arg Lys Ile
130 135 140

Arg Lys Arg Phe Asp Glu Ile Ser Glu Asp Arg Lys Arg Leu Arg Leu
145 150 155 160

Ser Glu Glu Asp Gly Glu Arg Arg Val Ser Gly Ala Pro Tyr Pro Ala
165 170 175

Pro Thr Ser His Met Val Asp Glu Ser Arg Thr Phe Gly Arg Lys His
180 185 190

Asp Lys Lys Lys Ile Ile Asp Leu Leu Leu Ser Glu Gly Met Gly Asn
195 200 205

RDQL-J6430-Sequence-Listing_ST25.txt

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

<210> 28
 <211> 507
 <212> PRT
 <213> Elaeis guineensis

RDQL-J6430-Sequence-Listing_ST25.txt

<220>
 <221> MISC_FEATURE
 <222> (1)..(507)
 <223> Translation of ORF 2 in reading frame 2 on direct strand of
 Polyamine oxidase polynucleotide

<400> 28

Ala Ala Phe Gly Gly Phe Gly Ser Pro Ser Leu Ile Ala Arg Met Glu
 1 5 10 15

Arg Lys Thr Leu Pro Gly Arg Asp Asn Phe Ala Ile Ser Gly Ile Phe
 20 25 30

Leu Thr His Ile Glu Arg Gln Gln Ser Ser Pro Pro Ser Val Ile Val
 35 40 45

Ile Gly Gly Gly Phe Ser Gly Ile Ala Ala Ala Arg Ala Leu Thr Asn
 50 55 60

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

Arg Val His Thr Asp Tyr Ser Phe Gly Cys Pro Val Asp Met Gly Ala
 85 90 95

Ser Trp Leu His Gly Val Cys Asn Glu Asn Ser Leu Ala Pro Phe Ile
 100 105 110

Arg Gly Leu Gly Leu Arg Leu Tyr Arg Thr Ser Gly Asp Asn Ser Val
 115 120 125

Leu Tyr Asp His Asp Leu Glu Ser Tyr Ala Leu Phe Asp Met Asn Gly
 130 135 140

Cys Gln Val Pro Gln Gln Leu Val Ile Arg Val Gly Glu Met Phe Glu
 145 150 155 160

Arg Ile Leu Lys Glu Thr Val Lys Val Arg Asp Glu His Ala Glu Asp
 165 170 175

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

Leu Arg Gln Glu Gly Pro Ala His Glu Val Leu Gln Trp Tyr Ile Cys
 195 200 205

Arg Met Glu Ala Trp Phe Ala Ala Asp Val Asp Thr Ile Ser Leu Lys
 210 215 220

RDQL-J6430-Sequence-Listing_ST25.txt

Ser Trp Asp Gln Glu His Val Leu Ser Gly Gly His Gly Leu Met Val
 225 230 235 240
 Gln Gly Tyr Tyr Pro Val Ile Lys Thr Leu Ala Asn Asp Leu Asp Ile
 245 250 255
 Lys Leu Asn His Arg Val Lys Lys Ile Val Gln Arg Cys Asn Lys Val
 260 265 270
 Met Val Thr Val Glu Asp Gly Ser Asn Phe Val Ala Asp Ala Ala Ile
 275 280 285
 Ile Thr Val Pro Leu Gly Val Leu Lys Ala Asn Val Ile Glu Phe Glu
 290 295 300
 Pro Lys Leu Pro Glu Trp Lys Val Ser Ala Ile Ser Asp Leu Gly Val
 305 310 315 320
 Gly Asn Glu Asn Lys Ile Ala Leu His Phe Ser Thr Val Phe Trp Pro
 325 330 335
 Asn Val Glu Val Leu Gly Met Val Ala Pro Thr Ser Tyr Ala Cys Gly
 340 345 350
 Tyr Phe Leu Asn Leu His Lys Ala Thr Gly His Pro Val Leu Val Tyr
 355 360 365
 Met Ala Ala Gly Arg Val Ala Tyr Asp Ile Glu Lys Leu Ser Asp Glu
 370 375 380
 Glu Ala Val Lys Phe Val Met Leu Gln Leu Gln Lys Met Leu Pro Asp
 385 390 395 400
 Ala Thr Glu Pro Val Gln Tyr Leu Val Ser Arg Trp Gly Thr Asp Pro
 405 410 415
 Asp Ser Leu Gly Ser Tyr Ser Cys Asp Leu Val Gly Lys Pro Ala Asp
 420 425 430
 Leu Tyr Glu Arg Phe Arg Ala Pro Val Asp Asn Ile Tyr Phe Ala Gly
 435 440 445
 Glu Ala Ala Ser Val Asp His Ser Gly Ser Val His Gly Ala Tyr Thr
 450 455 460
 Ala Gly Ile Ile Ala Ala Glu Asp Cys Arg Arg Arg Leu Leu Leu Gln
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RDQL-J6430-Sequence-Listing-ST25.txt

465 470 475 480

His Gly Met Ser Asp Leu Phe Gln Ala Val Leu Arg Glu Glu Met Thr
485 490 495

Glu Ala Met Val Pro Leu Gln Ile Ser Arg Met
500 505

<210> 29
<211> 812
<212> PRT
<213> Elaeis guineensis

<220>
<221> MISC_FEATURE
<222> (1)..(812)
<223> Translation of ORF 1 in reading frame 1 on direct strand of
Putative lipoxygenase 5 polynucleotide

<400> 29

Asp Phe Gly Lys Gln Lys Lys Lys Lys Lys Leu Met Ala Ala Ser Ile
1 5 10 15

Glu Ser Leu Gly Thr Ser Leu Ile Gln Arg Leu Pro Leu Leu Pro Ser
20 25 30

Ser Ser Ser Arg Ile Phe Arg Gly Glu Gln Ser Asn Leu Gly Phe Gln
35 40 45

Pro Ala Leu Phe Pro Leu Thr Gln Arg Ser Leu His Arg Val Asn Arg
50 55 60

Ala Val Arg Ala Pro Val Ala Ala Ala Val Thr Glu Lys Val Val Lys
65 70 75 80

Val Val Ala Glu Lys Pro Val Arg Phe Lys Val Arg Ala Ala Leu Thr
85 90 95

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

Leu Asp Ala Phe Ser Asp Lys Ile Gly Arg Asn Val Val Leu Glu Leu
115 120 125

Val Ser Thr Glu Ile Asp Pro Trp Thr Gln Lys Pro Lys Arg Ser Asn
130 135 140

Lys Ala Val Leu Arg Asp Trp Phe Glu Lys Lys Asn Val Lys Gly Glu
145 150 155 160

RDQL-J6430-Sequence-Listing_ST25.txt

Arg Val Val Tyr Thr Ala Glu Phe Met Val Asp Ser Ser Phe Gly Met
 165 170 175
 Pro Gly Ala Ile Thr Val Leu Asn Arg His Gln Lys Glu Phe Phe Leu
 180 185 190
 Glu Ser Ile Val Val Glu Gly Phe Ala Cys Gly Pro Val His Phe Ser
 195 200 205
 Cys Tyr Ser Trp Val Gln Pro Thr Lys Ile His Pro Ser Glu Arg Val
 210 215 220
 Phe Phe Asn Asn Lys Pro Tyr Leu Pro Ala Glu Thr Pro Pro Gly Leu
 225 230 235 240
 Lys Glu Leu Arg Glu Arg Glu Leu Glu Glu Leu Arg Gly Asp Gly Thr
 245 250 255
 Gly Glu Arg Lys Leu Thr Asp Arg Ile Tyr Asp Phe Asp Thr Tyr Asn
 260 265 270
 Asp Leu Gly Asn Pro Asp Lys Gly Phe Glu Tyr Ala Arg Pro Ile Ala
 275 280 285
 Gly Gly Asp Lys Met Pro Tyr Pro Arg Arg Cys Arg Thr Gly Arg Ser
 290 295 300
 Pro Thr Asn Thr Asp Val His Ala Glu Ser Arg Arg Glu Tyr Pro Ser
 305 310 315 320
 Pro Ile Tyr Val Pro Arg Asp Glu Ala Phe Glu Glu Gly Lys Gln Glu
 325 330 335
 Met Leu Ser Ala Gly Ala Leu Lys Ala Leu Leu His Asn Leu Val Pro
 340 345 350
 Ser Phe Val Ala Ser Ile Ser Pro Glu Ser His Asp Phe Lys Ala Phe
 355 360 365
 His Asp Ile Asp Asn Leu Phe Lys Glu Gly Leu Arg Trp Lys Lys Thr
 370 375 380
 Leu Gln Asp Gln Leu Phe His Lys Ile Pro Phe Val Ser Lys Ile Glu
 385 390 395 400

RDQL-J6430-Sequence-Listing_ST25.txt
 405 410 415

Lys Asp Lys Phe Ala Trp Leu Arg Asp Asp Glu Phe Ala Arg Gln Ala
 420 425 430

Leu Ala Gly Ile Asn Pro Val Asn Val Glu Arg Leu Gln Val Phe Pro
 435 440 445

Pro Val Ser Lys Leu Asp Pro Thr Ile Tyr Gly Pro Pro Glu Ser Ala
 450 455 460

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

Gln Ala Leu Glu Glu Asn Lys Leu Phe Met Leu Asp Tyr His Asp Val
 485 490 495

Tyr Leu Pro Phe Leu Asp Arg Ile Asn Ala Gln Asp Gly Arg Lys Ala
 500 505 510

Tyr Gly Thr Arg Thr Leu Phe Phe Leu Thr Gln Leu Gly Thr Leu Lys
 515 520 525

Pro Ile Ala Ile Glu Leu Ser Leu Pro Pro Ala Thr Pro Gly Cys Ser
 530 535 540

Arg Ala Lys Arg Val Leu Thr Pro Pro Thr Asp Ala Thr Asn Asn Trp
 545 550 555 560

Leu Trp Gln Leu Ala Lys Ala His Val Cys Ser Asn Asp Ala Gly Val
 565 570 575

His Gln Leu Val Asn His Trp Leu Arg Thr His Ala Cys Leu Glu Pro
 580 585 590

Phe Ile Ile Ala Ala His Arg Gln Leu Ser Ala Met His Pro Ile Phe
 595 600 605

Lys Leu Leu Lys Pro His Met Arg Tyr Thr Leu Glu Ile Asn Ala Leu
 610 615 620

Ala Arg Gln Ile Leu Ile Ser Gly Gly Gly Val Ile Glu Ser Gly Phe
 625 630 635 640

Thr Pro Gly Ser Cys Cys Met Glu Met Ser Val Ser Phe Tyr Arg Asp
 645 650 655

RDQL-J6430-Sequence-Listing_ST25.txt

His Trp Arg Phe Asp Arg Glu Gly Leu Pro Ala Asp Leu Ile Arg Arg
660 665 670

Gly Met Ala Ile Glu Asp Pro Ser Gln Pro His Gly Leu Lys Leu Leu
675 680 685

Ile Glu Asp Tyr Pro Tyr Ala Asn Asp Gly Leu Leu Leu Trp Ser Ala
690 695 700

Leu Gln Ala Trp Val Arg Thr Tyr Val Gln Ala Tyr Tyr Pro Asn Pro
705 710 715 720

His Val Val Gln Ala Asp Pro Glu Leu Gln Ala Trp Tyr Ala Glu Ala
725 730 735

Val Arg Val Gly His Ala Asp Lys Ser Gly Ala Asp Trp Trp Pro Arg
740 745 750

Leu Ser Ser Pro Ala Asp Leu Ala Ser Leu Leu Thr Thr Leu Leu Trp
755 760 765

Leu Ala Ser Ala Gln His Ala Ala Leu Asn Phe Gly Gln Tyr Pro Leu
770 775 780

Gly Gly Tyr Ile Pro Asn Arg Pro Pro Leu Met Arg Arg Leu Val Pro
785 790 795 800

Ala Glu Gly Asp Pro Glu Tyr Asp Asn Phe Leu Ala
805 810

<210> 30
<211> 382
<212> PRT
<213> Elaeis guineensis

<220>
<221> MISC_FEATURE
<222> (1)..(382)
<223> Translation of ORF 1 in reading frame 1 on direct strand of
12-oxophytodienoate reductase 1-like polynucleotide

<400> 30

Gly Cys Asn Lys Thr Gly Glu Arg Lys Glu Lys Ala Glu Glu Arg Glu
1 5 10 15

Glu Gly Glu Ala Val Glu Asp Ile Pro Leu Leu Thr Pro Tyr Lys Met
20 25 30

Gly Gly Phe Leu Leu Ser His Arg Val Val Leu Ala Pro Leu Thr Arg
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RDQL-J6430-Sequence-Listing_ST25.txt
40 45

Protein Sequence: E15C9_0125.txt															
35															
Gln	Arg	Ser	Tyr	Gly	Tyr	Ile	Pro	Gln	Gln	His	Ala	Ile	Leu	Tyr	Tyr
50															
Ser	Gln	Arg	Thr	Ser	Lys	Gly	Gly	Phe	Leu	Ile	Ser	Glu	Gly	Thr	Val
65															
Val	Ser	Asn	Thr	Gly	Ile	Gly	Tyr	Lys	Asp	Ile	Pro	Gly	Ile	Trp	Thr
80															
Arg	Glu	Gln	Val	Glu	Ala	Trp	Lys	Pro	Ile	Val	Asn	Ala	Val	His	Glu
100															
Lys	Gly	Gly	Ile	Phe	Phe	Leu	Gln	Ile	Gly	His	Met	Gly	Arg	Ile	Ser
115															
Asn	Tyr	Gly	Phe	Gln	Pro	Asn	Gly	Gln	Ala	Pro	Ile	Ser	Ser	Thr	Asp
130															
Lys	Pro	Ile	Thr	Pro	Gln	Thr	Pro	Glu	Asp	Asp	Phe	Ser	Pro	Pro	Arg
145															
Arg	Leu	Ser	Thr	Asp	Glu	Ile	Pro	Leu	Ile	Val	Asn	Asp	Phe	Arg	Val
160															
Ala	Ala	Arg	Asn	Ala	Ile	Glu	Ala	Gly	Phe	Asp	Gly	Val	Glu	Ile	His
180															
Ala	Ala	Phe	Gly	His	Leu	Leu	Glu	Gln	Phe	Met	Lys	Asp	Asn	Ile	Asn
195															
Asp	Arg	Thr	Asp	Glu	Tyr	Gly	Gly	Ser	Leu	Gln	Asn	Arg	Cys	Arg	Phe
210															
Ala	Leu	Glu	Val	Val	Glu	Ala	Val	Val	Asp	Glu	Ile	Gly	Ala	Ser	Arg
225															
Val	Gly	Met	Arg	Leu	Ser	Leu	Phe	Ala	Asp	Ile	Met	Glu	Ser	Gly	Asp
240															
Ser	Asp	Pro	Glu	Gly	Leu	Ala	Leu	Tyr	Met	Ala	Glu	Ser	Leu	Asn	Lys
260															
Phe	Gly	Val	Leu	Tyr	Cys	His	Val	Ile	Glu	Pro	Asn	Met	Glu	Val	Val
275															
285															

RDQL-J6430-Sequence-Listing_ST25.txt

Asp Gly Lys Gln Gln Ile Pro His Val His Leu Ser Met Arg Lys Ala
 290 295 300

Phe Lys Gly Thr Phe Ile Leu Ala Gly Gly Phe Asp Arg Glu Glu Gly
 305 310 315 320

Asn Lys Val Ile Lys Glu Gly Tyr Ala Asp Leu Val Ala Tyr Gly Arg
 325 330 335

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

Pro Leu Asn Lys Tyr Asp Arg Ser Thr Ile Leu His Tyr Gln Tyr Pro
 355 360 365

Val Val Gly Tyr Val Asp Tyr Pro Phe Leu Glu Ser Leu Asn
 370 375 380

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

<220>
 <223> Forward Primer

<220>
 <221> misc_feature
 <222> (1)..(20)
 <223> Forward primer of Mannosyl-oligosaccharide 1,2-alpha-mannosidase
 MNS3-like isoform X1 polynucleotide

<400> 31
 tcggaaatct gtacccaagg 20

<210> 32
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Reverse Primer

<220>
 <221> misc_feature
 <222> (1)..(20)
 <223> Reverse primer of Mannosyl-oligosaccharide 1,2-alpha-mannosidase
 MNS3-like isoform X1 polynucleotide

<400> 32
 gggactgaag ccaccattag 20

<210> 33

RDQL-J6430-Sequence-Listing_ST25.txt

<211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Forward Primer

 <220>
 <221> misc_feature
 <222> (1)..(21)
 <223> Forward primer of Alpha-1,3-mannosyl-glycoprotein
 2-beta-N-acetylglucosaminyltransferase-like isoform X3
 polynucleotide

 <400> 33
 gcagcacttg gattttacac c 21

 <210> 34
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Reverse Primer

 <220>
 <221> misc_feature
 <222> (1)..(24)
 <223> Reverse primer of Alpha-1,3-mannosyl-glycoprotein
 2-beta-N-acetylglucosaminyltransferase-like isoform X3
 polynucleotide

 <400> 34
 tcttgcatc ttgtagtatg caat 24

 <210> 35
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Forward Primer

 <220>
 <221> misc_feature
 <222> (1)..(20)
 <223> Forward primer of Probable WRKY transcription factor 40
 polynucleotide

 <400> 35
 aacctgcaga gccagctaat 20

 <210> 36
 <211> 19
 <212> DNA
 <213> Artificial Sequence

RDQL-J6430-Sequence-Listing_ST25.txt

<220>

<223> Reverse Primer

<220>

<221> misc_feature

<222> (1)..(19)

<223> Reverse primer of Probable WRKY transcription factor 40 polynucleotide

<400> 36

gaccgacccc ctatctgag

19

<210> 37

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Forward Primer

<220>

<221> misc_feature

<222> (1)..(20)

<223> Forward primer of Probable WRKY transcription factor 53 polynucleotide

<400> 37

ggacgatggc tatagctgga

20

<210> 38

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Reverse Primer

<220>

<221> misc_feature

<222> (1)..(19)

<223> Reverse primer of Probable WRKY transcription factor 53 polynucleotide

<400> 38

tggatgttg gctccaagt

19

<210> 39

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Forward Primer

<220>

<221> misc_feature

RDQL-J6430-Sequence-Listing_ST25.txt

<222> (1)..(19)
 <223> Forward primer of Dirigent protein 5-like polynucleotide

 <400> 39
 atccgccaag tcttggtcc 19

 <210> 40
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Reverse Primer

 <220>
 <221> misc_feature
 <222> (1)..(20)
 <223> Reverse primer of Dirigent protein 5-like polynucleotide

 <400> 40
 gtgagcaagg cctatttgga 20

 <210> 41
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Forward Primer

 <220>
 <221> misc_feature
 <222> (1)..(21)
 <223> Forward primer of G-type lectin S-receptor-like
 serine/threonine-protein kinase polynucleotide

 <400> 41
 tgcttacaag tgatgcgaat g 21

 <210> 42
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Reverse Primer

 <220>
 <221> misc_feature
 <222> (1)..(21)
 <223> Reverse primer of G-type lectin S-receptor-like
 serine/threonine-protein kinase polynucleotide

 <400> 42
 ttctccttcc aaagaatgca g 21

RDQL-J6430-Sequence-Listing_ST25.txt

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<210> 43
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer

<220>
<221> misc_feature
<222> (1)..(23)
<223> Forward primer of Putative disease resistance protein RGA3
      polynucleotide

<400> 43
tttaggcaaa gagcatttac acc                                23

<210> 44
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer

<220>
<221> misc_feature
<222> (1)..(20)
<223> Reverse primer of Putative disease resistance protein RGA3
      polynucleotide

<400> 44
cgccaatttc aatcagctct                                20

<210> 45
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer

<220>
<221> misc_feature
<222> (1)..(19)
<223> Forward primer of Polyamine oxidase polynucleotide

<400> 45
aagctgggat caggagcat                                19

<210> 46
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer

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RDQL-J6430-Sequence-Listing_ST25.txt

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<220>
<221> misc_feature
<222> (1)..(25)
<223> Reverse primer of Polyamine oxidase polynucleotide

<400> 46
gatagtatcc ttgcaccata agtcc 25

<210> 47
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer

<220>
<221> misc_feature
<222> (1)..(18)
<223> Forward primer of Putative lipoxygenase 5 polynucleotide

<400> 47
agcggtgacg gtgaggaa 18

<210> 48
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer

<220>
<221> misc_feature
<222> (1)..(20)
<223> Reverse primer of Putative lipoxygenase 5 polynucleotide

<400> 48
agctggcttg caatcttctc 20

<210> 49
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer

<220>
<221> misc_feature
<222> (1)..(21)
<223> Forward primer of 12-oxophytodienoate reductase 1-like
polynucleotide

<400> 49

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RDQL-J6430-Sequence-Listing_ST25.txt
aaagatatcc ccggtatttg g 21

<210> 50
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer

<220>
<221> misc_feature
<222> (1)..(22)
<223> Reverse primer of 12-oxophytodienoate reductase 1-like polynucleotide

<400> 50
cagcattcac tattggtttc ca 22