

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
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3033

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 <213> Elaeis guineensis

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<211> 1617

<212> DNA

<213> Elaeis guineensis

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<222> (1)..(1617)

<223> Putative disease resistance protein RGA3 polynucleotide

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<210> 8

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<212> DNA

<213> Elaeis guineensis

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<220>
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 <222> (1)..(1795)
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RDQL-J6430-Sequence-Listing_ST25.txt

aatgtcagat ctcttcagg ctgtattaag ggaggaaatg actgaagcca tggccccct	1740
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<210> 9
 <211> 2510
 <212> DNA
 <213> Elaeis guineensis

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

<400> 9	
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gaaagcttgg gcacttcttt gatccaaaga ttgcctctcc ttccttcctc gagctctcga	180
atcttttcgag gggagcagag caacctcggc ttccaacctg ctctgtttcc gttgacacaa	240
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aaagtgggtga aggtgggtggc agagaagcca gtgagggtta aggttcgggc agcgttgacg	360
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RDQL-J6430-Sequence-Listing_ST25.txt

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tacctcccat ttcttgaccg gatcaatgcc caagatggga ggaaagccta tggcacaaga 1620
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<210> 10
<211> 1137
<212> DNA
<213> Elaeis guineensis

```

```

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

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gtagaagata tccctcttct cactccatac aagatgggag gattcctgct ttcgcatagg 120
gtagtattgg caccattgac aaggcagaga tcctatggat atattccaca acaacatgct 180
attttgtact actcccagag gacttccaaa gggggctttt tgatatctga aggcactgtg 240
gtatcaaaca cgggcatagg gtataaagat atccccggtt tttggactag agagcagggtg 300
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RDQL-J6430-Sequence-Listing_ST25.txt

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gctattgaag	ctggctttga	tggagttgag	atccatgcgg	cattcgggtca	tctactcgag	600
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cgctgccggt	tcgcattgga	agtagttgag	gctgtagtcg	atgaaatcgg	agccagtaga	720
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aatcctgact	tgcccaagag	atttgaattc	aatgctcctc	tcaacaagta	tgataggctt	1080
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<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
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	ttggaagaca	gtggaatatc	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	tggtgcctat	ttacatcagt	ccccaatctg	gtcaatttaa	tggagagaac	480
	attcggctgg	gatctcgtgg	tgacagttac	tatgagtact	taattaaagt	gtggattcag	540
	caaaaatctg	gtcacaatag	ccagctaaag	tatctatatg	agatgtatac	agaagcaatg	600
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RDQL-J6430-Sequence-Listing_ST25.txt

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acatgctttg aaatgtattc tgtgacttct actggtcttt ctctgaaat tgtttatttc 900
catgttgagg gtggttctga agggggacct gatggcggtg acaaaagctc cgtgtatgta 960
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acattgaagt atttatattt gttgtttgga gacaataatg ttcttcctct ggataagttt 1260
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<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

```

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<400> 12
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tttatattca tccagatgcg cttttttgca acacagtctg agtatgcaga tcgcctagct 120
tctgctgtgg agtctgaaag ccagtgcaca agtcagatga gattgttgat tgatcagatt 180
agcatacaac aaggaaaaat tgttgcccta gaagaggcga agaagcttca agatgaagag 240
tatgttcact tgaaggccct agttcaagat cttgaaaaaa aaggctttca gagcttgttg 300
aaccacttag aggtacctgt agcagcagtt gttataatgg cttgtaatcg cccagactat 360
ttacaaagga cggttcaatc tgttttaaaa tatcagactt cagttgcac caaatttcca 420
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cagatcacat atttgcagca cttggatttt acacctgtgc atacggaaag gcctggagaa 540
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aagcataatt tcaatcgagt aatcatatta gaagatgaca tggagattgc cccggatttt 660
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RDQL-J6430-Sequence-Listing_ST25.txt

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cgtcaattta ttctgtccaga agttttaga acttacaatt tcggtgagca tggctctagt	960
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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	
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cgcaatagtc ccaagcatga ggaagagggg cttcttatga aaagagaggt tgggtgttctt	180
gaggcagagc tcaatcgggt ttctgaggag aatagaagac taaatgagaa gattgccatc	240
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ggctacagtg atgtggctaa tggaaatgacc aattggatgg gacgtcagat tgaaagcaac	420
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tttgctcctg cttgccctgt caagaagaag gtgcaaagaa gtgtagagga tagatcgatc	660
ctggttgcaa cttatgaagg cgagcacaaac catggttacc cttctcagct tccagcagcc	720
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RDQL-J6430-Sequence-Listing_ST25.txt

cttgatctca cacgagtggg atcgagcag gaggttgagt caccgagct tccgcggagt	840
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accgccgttt ctgggaacat tctttag	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	
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tatgggcaga aagaaatact tggagccaaa catccaagag gctactatag gtgcacgcac	180
cgcaacactc agggctgccc agcaacaaaa caggtgcaga gatccgatga gaacccgctg	240
gtcttcgatg tcacctacca tgggtctcac acatgcctcc agaggtccca agcagtccca	300
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cagcagcagg accacaacct gcttctaacc ttccaaagag gcctcaaagt aataacccaa	420
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<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

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<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	
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RDQL-J6430-Sequence-Listing_ST25.txt

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gagacatggt cagcaaattg 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	
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gatcggactg gatgggtttg 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 acttgctcgt 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 attttttctca cacacattga gaggcaacag	120
tcttccccac cttcagtcatt tgtgattggg ggaggctttt cagggatcgc agctgcacgt	180
gcattgacga atgcttcatt taagggttatt ttggttagagt cacgcaatcg gcttggtggc	240
cgagtgcata ctgactattc ttttggtgtg cctgttgaca tgggggcata atggctgcat	300
ggtgttttga atgaaaattc tctggcacca tttattcgtg gtctgggcct aagattatac	360
cgcactagtg gtgacaactc tgtgttgtat gaccacgatt tagagagcta tgcactgttt	420
gatatgaatg gttgccaagt ccttcaacag ctggtaatta gagttggaga aatgtttgag	480
agaatttctca aagagacagt gaaagtaagg gatgaacatg ctgaggacat gtctctgctc	540
caagctatatt ctattgtttt gaacagaaat ccagatctaa ggcaagaggg gccggcacat	600
gaagtgttgc agtggatatat atgcagaatg gaggcattgg ttgctgcaga cgtggatact	660
atatctttga aaagctggga tcaggagcat gttctttctg gtggccatgg acttatgggtg	720
caaggatact atcctgttat caaaaccctt gcaaatgata tggatatcaa actgaaccac	780
aggggtgaaaa aaattgtcca gcgttgtaac aaagtaatgg tcaccgtgga ggatggctca	840
aattttgtgg ctgatgctgc tattatcact gttcctcttg gggttctcaa agcaaattgtg	900
atcgaatttg aaccgaagct accagaatgg aaagtctcag caatctctga tcttggtggt	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
ccctccaaa 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 lipoxxygenase 5 polynucleotide

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

RDQL-J6430-Sequence-Listing_ST25.txt

gcgtggctgc gagatgacga gttcgctcgg caggcactcg ccggcattaa ccccgtaac	1320
gtagagagggc ttcaggtggt ccctcctggt agcaagctcg atcccacat atatggtcct	1380
cctgaatctg ccatcaaaga ggagcacatt attggccatc tcggtggcat gtcagtccaa	1440
caggcactgg aggagaacaa gctattcatg ttggattacc atgatgttta cctcccat	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
ctaagcgcgga tgcattcaat cttcaagctg ctcaagcccc atatgctgta cacccttgag	1860
atcaatgctc ttgctcgcca aatcctcatc agtgggtggtg gaggatcga gtctggcttc	1920
acccctggat catgttgcat ggagatgagt gtctctttct atcgggatca ctggcgtttt	1980
gatcgagagg gcctccctgc cgatctcatt agaagaggca tggcaataga ggaccctagc	2040
caaccccatg ggctaaagct tctcatagag gactaccctc acgccaacga tggcctcctc	2100
ctttggtccg ccctccaggc ctgggtccgg acctacgtcc aggcctacta cccgaacccc	2160
cacgtcgtcc aagccgaccc cgagctccaa gcctggtacg ccgaagccgt ccgctggggc	2220
cacgccgaca agagcggcgc cgactgggtg ccccggtcga gctccccgc cgacctgac	2280
tccctgctca ccacctcct ctggctcgcg tcggctcagc acgccgcgct caacttcggg	2340
cagtaccgcg tcggcggcta catccgaac cggccccctc tcatgcgccg gctcgtcccc	2400
gccgagggcg accccgagta cgacaacttc ctcgcc	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 agaggagga aggagaggca	60
gtagaagata tccctcttct cactccatac aagatgggag gattcctgct ttcgcatagg	120
gtagtattgg caccattgac aaggcagaga tcctatggat atattccaca acaacatgct	180
atattgtact actcccagag gacttcaaaa gggggctttt tgatatctga aggcactgtg	240

RDQL-J6430-Sequence-Listing_ST25.txt

```

gtatcaaaca cgggcatagg gtataaagat atccccgga tttggactag agagcagggtg 300
gaagcatgga aaccaatagt gaatgctgta catgagaagg gtggtatttt ctttttacag 360
attgggcaca tgggaaggat ctcaaattat ggtttccagc ctaatggaca agcaccatc 420
tcaagtactg acaagccaat cactcctcag actccagaag atgatttctc cctcctcga 480
cgcttgagca ctgatgaaat tcctcttata gtcaatgatt ttagagttgc tgcaaggaat 540
gctattgaag ctggccttga tggagttgag atccatgcgg cattcgggtca tctactcgag 600
cagttcatga aagacaacat caacgaccga acagatgaat atggtggaag cttgcagaac 660
cgctgccggt tcgcattgga agtagttgag gctgtagtcg atgaaatcgg agccagtaga 720
gttggcatga gattatctct ctttgcagac atcatggaga gtggagactc agaccctgag 780
ggctctgcac tgtacatggc tgaatcactg aacaagtttg gcgttctcta ctgccatgtg 840
attgaaccaa acatggaagt tgtggatgga aagcagcaaa taccacatgt gcatctttcc 900
atgagaaagg ctttcaaagg tacattcatc cttgctgggg gatttgatag agaagaagg 960
aacaaggtaa tcaaagaagg ttatgctgat ctagtggcat atggccgctc attcatagct 1020
aatcctgact tgcccaagag atttgaattc aatgctcctc tcaacaagta tgataggctc 1080
actattttac actatcagta cccggttggt gggtatgtag actaccatt ccttgaatcc 1140
ttaaactaa 1149

```

```

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

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<220>
<221> MISC_FEATURE
<222> (1)..(432)
<223> Translation of ORF 4 in reading frame 3 on reverse strand of
      Mannosyl-oligosaccharide 1,2-alpha-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 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
Page 23

RDQL-J6430-Sequence-Listing_ST25.txt

65		70		75		80
Tyr	Val	His	Leu	Lys	Ala	Leu
			85			Val
Gln	Asp	Leu	Glu	Lys	Lys	Gly
			90			95
Gln	Ser	Leu	Leu	Asn	His	Leu
		100				Glu
Val	Pro	Val	Ala	Ala	Val	Val
			105			110
Met	Ala	Cys	Asn	Arg	Pro	Asp
		115				Tyr
Leu	Gln	Arg	Thr	Val	Gln	Ser
				125		Val
Leu	Lys	Tyr	Gln	Thr	Ser	Val
	130					Ala
Val	Ala	Ser	Lys	Phe	Pro	Leu
			135		140	Phe
Gln	Asp	Gly	Thr	Asn	Pro	Asp
				150		Val
Val	Ala	Leu	Ser	Phe	Lys	
				155		160
Gln	Ile	Thr	Tyr	Leu	Gln	His
				165		Thr
Val	His	Leu	Asp	Phe	Thr	Pro
				170		175
Arg	Pro	Gly	Glu	Leu	Ile	Ala
			180			Tyr
Tyr	Lys	Ile	Ala	Arg	His	Tyr
			185		190	Lys
Trp	Ala	Leu	Asp	Glu	Leu	Phe
		195				Ile
Ile	Lys	His	Asn	Phe	Asn	Arg
				200		Val
Ile	Ala	Pro	Asp	Phe	Phe	Asn
				205		Tyr
Glu	Ala	Thr	Ala	Ser	Ile	Leu
				210		Asp
Met	Glu	Ile	Ala	Pro	Asp	Phe
				215		220
Glu	Ala	Thr	Ala	Ser	Ile	Leu
				225		Asp
Ser	Asp	Ser	Asp	Lys	Thr	Ile
				230		Met
Ala	Tyr	Trp	Ala	Val	His	Asp
				235		Pro
Ser	Ser	Trp	Asn	Asp	Asn	Gly
				240		Gln
Val	Gln	Phe	Val	His	Asp	Pro
				245		250
Thr	Leu	Tyr	Arg	Ser	Asp	Phe
				255		Phe
Pro	Gly	Leu	Gly	Trp	Met	Leu
				260		265
Lys	Ser	Ile	Trp	Asp	Glu	Leu
				270		Ser
Pro	Lys	Trp	Pro	Lys	Ala	Tyr
				275		280
Asp	Asp	Trp	Ile	Arg	Leu	Lys
				285		Glu
Ile	His	Gly	Glu	Arg	Gln	Phe
				290		295
Arg	Pro	Glu	Val	Cys	Arg	Thr
				300		Tyr
Asn	Phe	Gly	Glu	His	Gly	Ser
				305		310
Arg	Pro	Glu	Val	Cys	Arg	Thr
				315		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
Page 25

RDQL-J6430-Sequence-Listing-ST25.txt

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

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

195
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 Met Gln Gly Ser Pro Thr Pro Ser Ala Lys Ser Cys Ser Leu Leu
1 5 10 15
Leu Leu Ser Phe Leu Leu Ala Phe Gln Ile Gly Leu Ala His Thr Lys
20 25 30
Ala Thr Ile Ser Lys Asp Lys Pro Cys Lys Arg Leu Val Leu Tyr Tyr
35 40 45
His Asp Ile Leu Phe Asn Gly Thr Asn Val Ser Asn Ala Thr Ser Ala
50 55 60
Ala Val Ala Asn Gln Thr Ala Leu Gly Asp Tyr Lys Phe Gly Met Phe
65 70 75 80
Val Val Phe Asp Asp Pro Met Thr Glu Asp His His Leu Leu Ser Lys
85 90 95
Pro Val Ala Arg Ala Gln Gly Phe Tyr Phe Tyr Asp Met Lys Lys Glu
100 105 110
Tyr Asn Ala Trp Phe Ala Tyr Thr Leu Val Phe Asn Ser Thr Glu Tyr
115 120 125

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

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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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 95Val 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

Glu Ser Ser Glu Ala Leu Leu Arg Phe Asp Thr Pro Asp Ile Ile Thr
Page 36

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

35

40

45

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

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
 tcggaatct gtaccaagg 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 gccagctaata

20

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

RDQL-J6430-Sequence-Listing_ST25.txt

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<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
tggatgtttg gctccaagt                                     19

<210> 39
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer

<220>
<221> misc_feature

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RDQL-J6430-Sequence-Listing_ST25.txt

<222> (1)..(19)
 <223> Forward primer of Dirigent protein 5-like polynucleotide
 <400> 39
 atccgccaag tcttgttcc 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
 ttctccttc 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
agcgttgacg 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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aaagatatcc ccggtatttg g	RDQL-J6430-Sequence-Listing_ST25.txt	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