SEQUENCE LISTING

<110> Tropic Biosciences UK Limited
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MEIR, Ofir

<120> COMPOSITIONS AND METHODS FOR REDUCING CAFFEINE CONTENT IN COFFEE BEANS

<130> 73882

<150> 1807192.8
<151> 2018-05-01

<160> 86

<170> PatentIn version 3.5

<210> 1
<211> 1137
<212> DNA
<213> Artificial sequence

<220>
<223> MXMT - Monomethylxanthine methyltransferase 1 nucleic acid sequence

<400> 1
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gaattgttgc gggccaactt gcccaacatc aacaagtgca ttaaagttgc ggatttggga 180

tgcgcttctg gaccaaacac acttttaaca gtgcgggaca ttgtgcaaag tattgacaaa 240

gttggccagg aagagaagaa tgaattagaa cgtcccacca ttcagatttt tctgaatgat 300

cttttccaaa atgatttcaa ttcggttttc aagttgctgc caagcttcta ccgcaaactc 360

gagaaagaaa atggacgcaa gataggatcg tgcctaataa gcgcaatgcc tggctctttc 420

tacggcagac tcttccccga ggagtccatg catttttgc actcttgtta cagtgttcat 480

tggttatctc aggttcccag cggtttggtg attgaattgg ggattggtgc aaacaaaggg 540

agtatttact cttccaaagg atgtcgtccg cccgtccaga aggcatattt ggatcaattt 600

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atgctcctta cttgcatttg taaagtagat gaattcgacg aaccgaatcc cctagactta 720

cttgacatgg caataaacga cttgattgtt gagggacttc tggaggaaga aaaattggat 780

agtttcaata ttccattctt tacaccttca gcagaagaag taaagtgcat agttgaggag 840

gaaggttctt gcgaaatttt atatctggag acttttaagg cccattatga tgctgccttc 900

tctattgatg atgattaccc agtaacatcc catgaacaaa ttaaagcaga gtatgtggca 960

tcattaatta gatcagttta cgaacccatc ctcgcaagtc attttggaga agctattatg 1020

cctgacttat tccacaggct tgcgaagcat gcagcaaagg ttctccacat gggcaaaggc 1080

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<211> 378
<212> PRT
<213> Artificial sequence

<220>
<223> MXMT - Monomethylxanthine methyltransferase 1 amino acid sequence

<400> 2

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1 5 10 15

Ser Tyr Ala Lys Asn Ala Ser Tyr Asn Leu Ala Leu Ala Lys Val Lys
20 25 30

Pro Phe Leu Glu Gln Cys Ile Arg Glu Leu Leu Arg Ala Asn Leu Pro
35 40 45

Asn Ile Asn Lys Cys Ile Lys Val Ala Asp Leu Gly Cys Ala Ser Gly
50 55 60

Pro Asn Thr Leu Leu Thr Val Arg Asp Ile Val Gln Ser Ile Asp Lys

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65                  70                  75                  80

Val Gly Gln Glu Glu Lys Asn Glu Leu Glu Arg Pro Thr Ile Gln Ile
                85                  90                  95

Phe Leu Asn Asp Leu Phe Gln Asn Asp Phe Asn Ser Val Phe Lys Leu
            100                 105                 110

Leu Pro Ser Phe Tyr Arg Lys Leu Glu Lys Glu Asn Gly Arg Lys Ile
        115                 120                 125

Gly Ser Cys Leu Ile Ser Ala Met Pro Gly Ser Phe Tyr Gly Arg Leu
    130                 135                 140

Phe Pro Glu Glu Ser Met His Phe Leu His Ser Cys Tyr Ser Val His
145                 150                 155                 160

Trp Leu Ser Gln Val Pro Ser Gly Leu Val Ile Glu Leu Gly Ile Gly
                165                 170                 175

Ala Asn Lys Gly Ser Ile Tyr Ser Ser Lys Gly Cys Arg Pro Pro Val
            180                 185                 190

Gln Lys Ala Tyr Leu Asp Gln Phe Thr Lys Asp Phe Thr Thr Phe Leu
        195                 200                 205

Arg Ile His Ser Lys Glu Leu Phe Ser Arg Gly Arg Met Leu Leu Thr
    210                 215                 220

Cys Ile Cys Lys Val Asp Glu Phe Asp Glu Pro Asn Pro Leu Asp Leu
225                 230                 235                 240

Leu Asp Met Ala Ile Asn Asp Leu Ile Val Glu Gly Leu Leu Glu Glu
                245                 250                 255

Glu Lys Leu Asp Ser Phe Asn Ile Pro Phe Phe Thr Pro Ser Ala Glu
            260                 265                 270
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Glu Val Lys Cys Ile Val Glu Glu Glu Gly Ser Cys Glu Ile Leu Tyr
275 280 285

Leu Glu Thr Phe Lys Ala His Tyr Asp Ala Ala Phe Ser Ile Asp Asp
290 295 300

Asp Tyr Pro Val Thr Ser His Glu Gln Ile Lys Ala Glu Tyr Val Ala
305 310 315 320

Ser Leu Ile Arg Ser Val Tyr Glu Pro Ile Leu Ala Ser His Phe Gly
325 330 335

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

Lys Val Leu His Met Gly Lys Gly Cys Tyr Asn Asn Leu Ile Ile Ser
355 360 365

Leu Ala Lys Lys Pro Glu Lys Ser Asp Val
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<211> 1155
<212> DNA
<213> Artificial sequence

<220>
<223> DXMT - 3,7-dimethylxanthine N-methyltransferase nucleic acid seuence

<400> 3
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aactcatcct acaatctgtt tctcatcagg gtgaaacctg tccttgaaca atgcatacaa 120

gaattgttgc gggccaactt gcccaacatc aacaagtgct ttaaagttgg ggatttggga 180

tgcgcttctg gaccaaacac attttcaaca gttcgggaca ttgtacaaag tattgacaaa 240

gttggccagg aaaagaagaa tgaattagaa cgtcccacca ttcagatttt tctgaatgat 300

cttttccaaa atgatttcaa ttcggttttc aagttgctgc caagcttcta ccgcaatctt 360

gagaaagaaa atggacgcaa aataggatcg tgcctgatag gcgcaatgcc cggctctttc 420

tacagcagac tcttccccga ggagtccatg catttttac actcttgtta ctgtttgcat 480

tggttatctc aggttcccag cggtttggtg actgaattgg ggatcagtgt gaacaaaggg 540

tgcatttact cttccaaagc aagtcgtccg cccatccaga aggcatattt ggatcaattt 600

acgaaagatt ttaccacatt tctgaggatt cattcggaag agttgatttc acgtggccga 660

atgctcctta ctttcatttg taaagaagat gaattcgacc acccgaattc catggacttg 720

cttgagatgt caataaacga cttggttgtt gagggacatc tggaggaaga aaaattggat 780

agtttcaatg ttccaatcta tgcaccttca acagaagaag taaagcgcat agttgaggag 840

gaaggttctt ttgaaatttt atacctggag acttttttatg ccccttatga tgctggcttc 900

tctattgatg atgattacca aggaagatcc cattcccctg tatcctgcga tgaacatgct 960

agagcagcgc atgtggcatc tgtcgttaga tcaatttacg aacccatcct cgcaagtcat 1020

tttggagaag ctattttacc tgacttatcc cacaggattg cgaagaatgc agcaaaggtt 1080

ctccgctcgg gcaaaggctt ctatgatagt gttatcattt ctctcgccaa aaagccggag 1140

aaggcagaca tgtaa 1155

<210> 4
<211> 384
<212> PRT
<213> Artificial sequence

<220>
<223> DXMT - 3,7-dimethylxanthine N-methyltransferase amino acid sequence

<400> 4

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

Ser Tyr Ala Lys Asn Ser Ser Tyr Asn Leu Phe Leu Ile Arg Val Lys
20 25 30

Pro Val Leu Glu Gln Cys Ile Gln Glu Leu Leu Arg Ala Asn Leu Pro

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        35                  40                  45

Asn Ile Asn Lys Cys Phe Lys Val Gly Asp Leu Gly Cys Ala Ser Gly
    50                  55                  60

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

Val Gly Gln Glu Lys Lys Asn Glu Leu Glu Arg Pro Thr Ile Gln Ile
                85                  90                  95

Phe Leu Asn Asp Leu Phe Gln Asn Asp Phe Asn Ser Val Phe Lys Leu
            100                 105                 110

Leu Pro Ser Phe Tyr Arg Asn Leu Glu Lys Glu Asn Gly Arg Lys Ile
        115                 120                 125

Gly Ser Cys Leu Ile Gly Ala Met Pro Gly Ser Phe Tyr Ser Arg Leu
    130                 135                 140

Phe Pro Glu Glu Ser Met His Phe Leu His Ser Cys Tyr Cys Leu His
145                 150                 155                 160

Trp Leu Ser Gln Val Pro Ser Gly Leu Val Thr Glu Leu Gly Ile Ser
                165                 170                 175

Val Asn Lys Gly Cys Ile Tyr Ser Ser Lys Ala Ser Arg Pro Pro Ile
            180                 185                 190

Gln Lys Ala Tyr Leu Asp Gln Phe Thr Lys Asp Phe Thr Thr Phe Leu
        195                 200                 205

Arg Ile His Ser Glu Glu Leu Ile Ser Arg Gly Arg Met Leu Leu Thr
    210                 215                 220

Phe Ile Cys Lys Glu Asp Glu Phe Asp His Pro Asn Ser Met Asp Leu
225                 230                 235                 240
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Leu Glu Met Ser Ile Asn Asp Leu Val Val Glu Gly His Leu Glu Glu
                245                 250                 255


Glu Lys Leu Asp Ser Phe Asn Val Pro Ile Tyr Ala Pro Ser Thr Glu
            260                 265                 270


Glu Val Lys Arg Ile Val Glu Glu Glu Gly Ser Phe Glu Ile Leu Tyr
        275                 280                 285


Leu Glu Thr Phe Tyr Ala Pro Tyr Asp Ala Gly Phe Ser Ile Asp Asp
    290                 295                 300


Asp Tyr Gln Gly Arg Ser His Ser Pro Val Ser Cys Asp Glu His Ala
305                 310                 315                 320


Arg Ala Ala His Val Ala Ser Val Val Arg Ser Ile Tyr Glu Pro Ile
                325                 330                 335


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


Ile Ala Lys Asn Ala Ala Lys Val Leu Arg Ser Gly Lys Gly Phe Tyr
        355                 360                 365


Asp Ser Val Ile Ile Ser Leu Ala Lys Lys Pro Glu Lys Ala Asp Met
    370                 375                 380


<210>  5
<211>  1158
<212>  DNA
<213>  Artificial sequence

<220>
<223>  DXMT - Probable caffeine synthase 4 nucleic acid sequence

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aattcatcct tcaatcaact ggttctcgcc aaggtgaaac ctgtccttga acaatgcgta      120
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cgggaattgt tgcgggccaa cttgcccaac atcaacaagt gcattaaagt tgcagatttg 180

ggatgcgctt ccggaccaaa cacactttta accgttcggg acactgtaca aagtattgac 240

aaagttaggc aagaaatgaa gaatgaatta gaacgtccca ccattcaggt ttttctgact 300

gatcttttcc aaaatgattt caattcggtt ttcatgctgc tgccaagctt ctaccgcaaa 360

cttgagaaag aaaatggacg caaaatagga tcgtgcctaa tagccgcaat gcctggctct 420

ttccacggca gactcttccc cgaggagtcc atgcattttt tacactcttc ttacagtctt 480

cagtttttat cccaggttcc cagcggtttg gtgactgaat tggggatcac tgcgaacaaa 540

aggagcattt actcttccaa agcaagtcct ccgcccgtcc agaaggcata tttggatcaa 600

tttacgaaag attttaccac atttttaagg atgcgttcgg aagagttgct ttcacgtggc 660

cgaatgctcc ttacttgcat ttgtaaagga gatgaatgcg acggcccgaa taccatggac 720

ttacttgaga tggcaataaa cgacttggtt gttgagggac gtctgggggа agaaaaattg 780

gacagtttca atgttccaat ctatacagct tcagtagaag aagtaaagtg catggttgag 840

gaggaaggtt cttttgaaat tttatacttg cagactttta agctccgtta tgatgctggc 900

ttctctattg atgatgattg ccaagtaaga tcccattccc cagaatacag cgatgaacat 960

gctagagcag cgcatgtggc atcattaatt agatcagttt acgaacccat cctagcaagt 1020

cattttggag aagctattat acctgacata ttccacaggt ttgcgacgaa tgcagcaaag 1080

gttatccgct tgggcaaagg cttctataat aatcttatca tttctcttgc caaaaaacca 1140

gagaagtcag acatataa 1158

<210> 6
<211> 385
<212> PRT
<213> Artificial sequence

<220>
<223> DXMT - Probable caffeine synthase 4 amino acid sequence

<400> 6

Met Glu Leu Gln Glu Val Leu His Met Asn Gly Gly Glu Gly Glu Ala
1 5 10 15

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Ser Tyr Ala Lys Asn Ser Ser Phe Asn Gln Leu Val Leu Ala Lys Val
            20                  25                  30

Lys Pro Val Leu Glu Gln Cys Val Arg Glu Leu Leu Arg Ala Asn Leu
        35                  40                  45

Pro Asn Ile Asn Lys Cys Ile Lys Val Ala Asp Leu Gly Cys Ala Ser
    50                  55                  60

Gly Pro Asn Thr Leu Leu Thr Val Arg Asp Thr Val Gln Ser Ile Asp
65                  70                  75                  80

Lys Val Arg Gln Glu Met Lys Asn Glu Leu Glu Arg Pro Thr Ile Gln
                85                  90                  95

Val Phe Leu Thr Asp Leu Phe Gln Asn Asp Phe Asn Ser Val Phe Met
            100                 105                 110

Leu Leu Pro Ser Phe Tyr Arg Lys Leu Glu Lys Glu Asn Gly Arg Lys
        115                 120                 125

Ile Gly Ser Cys Leu Ile Ala Ala Met Pro Gly Ser Phe His Gly Arg
    130                 135                 140

Leu Phe Pro Glu Glu Ser Met His Phe Leu His Ser Ser Tyr Ser Leu
145                 150                 155                 160

Gln Phe Leu Ser Gln Val Pro Ser Gly Leu Val Thr Glu Leu Gly Ile
                165                 170                 175

Thr Ala Asn Lys Arg Ser Ile Tyr Ser Ser Lys Ala Ser Pro Pro Pro
            180                 185                 190

Val Gln Lys Ala Tyr Leu Asp Gln Phe Thr Lys Asp Phe Thr Thr Phe
        195                 200                 205

Leu Arg Met Arg Ser Glu Glu Leu Leu Ser Arg Gly Arg Met Leu Leu
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    210                 215                 220

Thr Cys Ile Cys Lys Gly Asp Glu Cys Asp Gly Pro Asn Thr Met Asp
225                 230                 235                 240

Leu Leu Glu Met Ala Ile Asn Asp Leu Val Val Glu Gly Arg Leu Gly
                245                 250                 255

Glu Glu Lys Leu Asp Ser Phe Asn Val Pro Ile Tyr Thr Ala Ser Val
            260                 265                 270

Glu Glu Val Lys Cys Met Val Glu Glu Glu Gly Ser Phe Glu Ile Leu
        275                 280                 285

Tyr Leu Gln Thr Phe Lys Leu Arg Tyr Asp Ala Gly Phe Ser Ile Asp
    290                 295                 300

Asp Asp Cys Gln Val Arg Ser His Ser Pro Glu Tyr Ser Asp Glu His
305                 310                 315                 320

Ala Arg Ala Ala His Val Ala Ser Leu Ile Arg Ser Val Tyr Glu Pro
                325                 330                 335

Ile Leu Ala Ser His Phe Gly Glu Ala Ile Ile Pro Asp Ile Phe His
            340                 345                 350

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

Tyr Asn Asn Leu Ile Ile Ser Leu Ala Lys Lys Pro Glu Lys Ser Asp
    370                 375                 380

Ile
385
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<210> 7
<211> 1158
<212> DNA

<213> Artificial sequence

<220>
<223> MXMT - Theobromine synthase 2 nucleic acid sequence

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cgagaattgt tgcgggccaa cttgcccaac atcaacaagt gcattaaagt tgcggatttg 180

ggatgcgctt ctggaccaaa cacactttta acagttcggg acattgtgca aagtattgac 240

aaagttggcc aggaagagaa gaatgaatta gaacatccca ccattcaaat ttttctgaat 300

gatcttttcc aaaatgattt caattcagtt ttcaagttgc tgccaagctt ctaccgcaaa 360

ctcgagaaag aaaatggacg caaaatagga tcgtgcctaa taagcgcaat gcctggctct 420

ttctacggca gactcttccc cgaggagtcc atgcattttt tgcactcttg ttacagtgtt 480

cattggttat ctcaggttcc cagcggattg gtgactgaac tggggatcag tgcgaacaaa 540

gggatcattt actcttccaa agcaagtcct ccgcccgtcc agaaggcata tttggaccaa 600

tttacaaaag attttaccac atttctgagg attcattcgg aagagttgct ttcaggtggc 660

cgaatgctcc ttacttgcat ttgtaaagga gatgaatccg atggcctgaa taccatagac 720

ttacttgaga gagcaataaa cgacttggtt gttgagggac ttctggagga agaaaaattg 780

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gaggaaggtt cttttgaaat tttatacctg gagactttta aggtccgtta tgatgctggc 900

ttctctattg atgatgatta ccaagtaaga tccctttttcc aagtatactg cgatgaacat 960

gttaaagcag cgtatgtgac attcttcttt agagcagttt tcgaacccat cctcgcaagt 1020

cattttggag aagctattat gcctgactta ttccacaggt ttgcgaagaa tgcagcaaag 1080

gctctccgct tgggcaacgg cttctataat agtcttatca tttctcttgc caaaaaacca 1140

gagaagtcag acatgtaa 1158

<210> 8
<211> 385
<212> PRT

<213> Artificial sequence

<220>
<223> MXMT - Theobromine synthase 2 amino acid sequence

<400> 8

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Met Glu Leu Gln Glu Val Leu His Met Asn Gly Gly Glu Gly Asp Thr
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Ser Tyr Ala Lys Asn Ser Ser Tyr Asn Gln Leu Val Leu Thr Lys Val
            20                  25                  30


Lys Pro Val Leu Glu Gln Cys Ile Arg Glu Leu Leu Arg Ala Asn Leu
        35                  40                  45


Pro Asn Ile Asn Lys Cys Ile Lys Val Ala Asp Leu Gly Cys Ala Ser
    50                  55                  60


Gly Pro Asn Thr Leu Leu Thr Val Arg Asp Ile Val Gln Ser Ile Asp
65                  70                  75                  80


Lys Val Gly Gln Glu Glu Lys Asn Glu Leu Glu His Pro Thr Ile Gln
                85                  90                  95


Ile Phe Leu Asn Asp Leu Phe Gln Asn Asp Phe Asn Ser Val Phe Lys
            100                 105                 110


Leu Leu Pro Ser Phe Tyr Arg Lys Leu Glu Lys Glu Asn Gly Arg Lys
        115                 120                 125


Ile Gly Ser Cys Leu Ile Ser Ala Met Pro Gly Ser Phe Tyr Gly Arg
    130                 135                 140


Leu Phe Pro Glu Glu Ser Met His Phe Leu His Ser Cys Tyr Ser Val
145                 150                 155                 160


His Trp Leu Ser Gln Val Pro Ser Gly Leu Val Thr Glu Leu Gly Ile
                165                 170                 175
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Ser Ala Asn Lys Gly Ile Ile Tyr Ser Ser Lys Ala Ser Pro Pro Pro
            180                 185                 190

Val Gln Lys Ala Tyr Leu Asp Gln Phe Thr Lys Asp Phe Thr Thr Phe
        195                 200                 205

Leu Arg Ile His Ser Glu Glu Leu Leu Ser Gly Gly Arg Met Leu Leu
    210                 215                 220

Thr Cys Ile Cys Lys Gly Asp Glu Ser Asp Gly Leu Asn Thr Ile Asp
225                 230                 235                 240

Leu Leu Glu Arg Ala Ile Asn Asp Leu Val Val Glu Gly Leu Leu Glu
                245                 250                 255

Glu Glu Lys Leu Asp Ser Phe Asn Leu Pro Leu Tyr Thr Pro Ser Leu
            260                 265                 270

Glu Val Val Lys Cys Ile Val Glu Glu Glu Gly Ser Phe Glu Ile Leu
        275                 280                 285

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

Asp Asp Tyr Gln Val Arg Ser Leu Phe Gln Val Tyr Cys Asp Glu His
305                 310                 315                 320

Val Lys Ala Ala Tyr Val Thr Phe Phe Phe Arg Ala Val Phe Glu Pro
                325                 330                 335

Ile Leu Ala Ser His Phe Gly Glu Ala Ile Met Pro Asp Leu Phe His
            340                 345                 350

Arg Phe Ala Lys Asn Ala Ala Lys Ala Leu Arg Leu Gly Asn Gly Phe
        355                 360                 365

Tyr Asn Ser Leu Ile Ile Ser Leu Ala Lys Lys Pro Glu Lys Ser Asp
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370 375 380

Met
385

<210> 9
<211> 1119
<212> DNA
<213> Artificial sequence

<220>
<223> XMT - 7-methylxanthosine synthase 1 nucleic acid sequence

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cgggaattgt tgcgggccaa cttgcccaac atcaacaagt gcattaaagt tgcggatttg 180

ggatgcgctt ctggaccaaa cacactttta acagttcggg acattgtcca aagtattgac 240

aaagttggcc aggaaaagaa gaatgaatta gaacgtccca ccattcagat ttttctgaat 300

gatcttttcc caaatgattt caattcggtt ttcaagttgc tgccaagctt ctaccgcaaa 360

cttgagaaag aaaatggacg caaaatagga tcgtgcctaa taggggcaat gcccggctct 420

ttctacagca gactcttccc cgaggagtcc atgcattttt tacactcttg ttactgtctt 480

caatggttat ctcaggttcc tagcggtttg gtgactgaat cggggatcag tacgaacaaa 540

gggagcattt actcttccaa agcaagtcgt ctgcccgtcc agaaggcata tttggatcaa 600

tttacgaaag attttaccac atttctaagg attcattcgg aagagttgtt ttcacatggc 660

cgaatgctcc ttacttgcat ttgtaaagga gttgaattag acgcccggaa tgccatagac 720

ttacttgaga tggcaataaa cgacttggtt gttgagggac atctggagga agaaaaattg 780

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gaggaaggtt cttttgaaat tttatacctg gagactttta aggtccttta cgatgctggc 900

ttctctattg acgatgaaca tattaaagca gagtatgttg catcttccgt tagagcagtt 960

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atttctctcg ccaaaaagcc agagaagtca gacgtgtaa 1119

<210> 10
<211> 372
<212> PRT
<213> Artificial sequence

<220>
<223> XMT - 7-methylxanthosine synthase 1 amino acid sequence

<400> 10

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

Ser Tyr Ala Lys Asn Ser Ala Tyr Asn Gln Leu Val Leu Ala Lys Val
20 25 30

Lys Pro Val Leu Glu Gln Cys Val Arg Glu Leu Leu Arg Ala Asn Leu
35 40 45

Pro Asn Ile Asn Lys Cys Ile Lys Val Ala Asp Leu Gly Cys Ala Ser
50 55 60

Gly Pro Asn Thr Leu Leu Thr Val Arg Asp Ile Val Gln Ser Ile Asp
65 70 75 80

Lys Val Gly Gln Glu Lys Lys Asn Glu Leu Glu Arg Pro Thr Ile Gln
85 90 95

Ile Phe Leu Asn Asp Leu Phe Pro Asn Asp Phe Asn Ser Val Phe Lys
100 105 110

Leu Leu Pro Ser Phe Tyr Arg Lys Leu Glu Lys Glu Asn Gly Arg Lys
115 120 125

Ile Gly Ser Cys Leu Ile Gly Ala Met Pro Gly Ser Phe Tyr Ser Arg
130 135 140

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Leu Phe Pro Glu Glu Ser Met His Phe Leu His Ser Cys Tyr Cys Leu
145                 150                 155                 160

Gln Trp Leu Ser Gln Val Pro Ser Gly Leu Val Thr Glu Ser Gly Ile
                165                 170                 175

Ser Thr Asn Lys Gly Ser Ile Tyr Ser Ser Lys Ala Ser Arg Leu Pro
            180                 185                 190

Val Gln Lys Ala Tyr Leu Asp Gln Phe Thr Lys Asp Phe Thr Thr Phe
        195                 200                 205

Leu Arg Ile His Ser Glu Glu Leu Phe Ser His Gly Arg Met Leu Leu
    210                 215                 220

Thr Cys Ile Cys Lys Gly Val Glu Leu Asp Ala Arg Asn Ala Ile Asp
225                 230                 235                 240

Leu Leu Glu Met Ala Ile Asn Asp Leu Val Val Glu Gly His Leu Glu
                245                 250                 255

Glu Glu Lys Leu Asp Ser Phe Asn Leu Pro Val Tyr Ile Pro Ser Ala
            260                 265                 270

Glu Glu Val Lys Cys Ile Val Glu Glu Glu Gly Ser Phe Glu Ile Leu
        275                 280                 285

Tyr Leu Glu Thr Phe Lys Val Leu Tyr Asp Ala Gly Phe Ser Ile Asp
    290                 295                 300

Asp Glu His Ile Lys Ala Glu Tyr Val Ala Ser Ser Val Arg Ala Val
305                 310                 315                 320

Tyr Glu Pro Ile Leu Ala Ser His Phe Gly Glu Ala Ile Ile Pro Asp
                325                 330                 335

Ile Phe His Arg Phe Ala Lys His Ala Ala Lys Val Leu Pro Leu Gly
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340 345 350

Lys Gly Phe Tyr Asn Asn Leu Ile Ile Ser Leu Ala Lys Lys Pro Glu
355 360 365

Lys Ser Asp Val
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<210> 11
<211> 1119
<212> DNA
<213> Artificial sequence

<220>
<223> DXMT - Probable caffeine synthase 3 nucleic acid sequence

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aacttaccct acgacgagaa gtgcattaga gttgctgatt tgggatgctc ttcaggacca 180

aacacactat taacagtttc ggacatcata caaagtattg acaaagttag ccaggaaatg 240

gacaatgaat ttgcactgcc cacgattcag gtttttctga atgatctttt cgaaaatgat 300

ttcaatacgg ttatcaagtc gctgccaagc ttctaccgca aacttgaaaa agaaaatgga 360

cgcaaaatag gatcgtgcct gatagcagca atgcctggct ctttctacgg cagactcttc 420

cccgagcagt ccgtccattt tttacactct tcttacagtc tccattggtt atctcaggtt 480

cccaatggtt tggtgactga atcggggatc agtgcgaata aagggagcat ttactcttcc 540

aaagcaagtc ctccggccat ccagaaggca tatttggatc aatttacgaa agattttacc 600

acatttctca ggatgcattc ggaagagttg gtttcacatg gccgaatcct cctcactttc 660

atgtgtaaag gagatgaatt cgacggccca aatatcttag acttacttga ggtggcaata 720

aacgacttgg ttgtcgaggg aagtctggag gaagaaaaac tggacagttt caatgttcca 780

atctatgcgc cttcagtaga agaagtcagg cacataattg aggaggaacg ttcttttgaa 840

attgtatacc tggagacgtt taagctccgt catgatgctg gcttctccat tgatgataac 900

caagcagccc atgtggcatc attcgttaga gcagcttggg aacctatcct agcaagccat 960

tttggagaag ctattatagc cgacttattc cacaggtttg ccaagaatgc agcaacgcct 1020

ctccgcatgg gcaaaggctt ctttaataat ctcatcattt ctctcgccaa gaaaccacac 1080

aagtcagaga catgtaaata tttgttttta gatatgtag 1119

<210> 12
<211> 387
<212> PRT
<213> Artificial sequence

<220>
<223> DXMT - Probable caffeine synthase 3 amino acid sequence

<400> 12

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

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

Cys Ile Gln Glu Leu Leu Arg Thr Asn Leu Pro Tyr Asp Glu Lys Cys
35 40 45

Ile Arg Val Ala Asp Leu Gly Cys Ser Ser Gly Pro Asn Thr Leu Leu
50 55 60

Thr Val Ser Asp Ile Ile Gln Ser Ile Asp Lys Val Ser Gln Glu Met
65 70 75 80

Asp Asn Glu Phe Ala Leu Pro Thr Ile Gln Val Phe Leu Asn Asp Leu
85 90 95

Phe Glu Asn Asp Phe Asn Thr Val Ile Lys Ser Leu Pro Ser Phe Tyr
100 105 110

Arg Lys Leu Glu Lys Glu Asn Gly Arg Lys Ile Gly Ser Cys Leu Ile
115 120 125

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Ala Ala Met Pro Gly Ser Phe Tyr Gly Arg Leu Phe Pro Glu Gln Ser
    130                 135                 140

Val His Phe Leu His Ser Ser Tyr Ser Leu His Trp Leu Ser Gln Val
145                 150                 155                 160

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

Ile Tyr Ser Ser Lys Ala Ser Pro Pro Ala Ile Gln Lys Ala Tyr Leu
            180                 185                 190

Asp Gln Phe Thr Lys Asp Phe Thr Thr Phe Leu Arg Met His Ser Glu
        195                 200                 205

Glu Leu Val Ser His Gly Arg Ile Leu Leu Thr Phe Met Cys Lys Gly
    210                 215                 220

Asp Glu Phe Asp Gly Pro Asn Ile Leu Asp Leu Leu Glu Val Ala Ile
225                 230                 235                 240

Asn Asp Leu Val Val Glu Gly Ser Leu Glu Glu Glu Lys Leu Asp Ser
                245                 250                 255

Phe Asn Val Pro Ile Tyr Ala Pro Ser Val Glu Glu Val Arg His Ile
            260                 265                 270

Ile Glu Glu Glu Arg Ser Phe Glu Ile Val Tyr Leu Glu Thr Phe Lys
        275                 280                 285

Leu Arg His Asp Ala Gly Phe Ser Ile Asp Asp Asn Gln Leu Gly Ser
    290                 295                 300

His Ser Gln Val Arg Phe Cys Asp Glu His Val Arg Ala Ala His Val
305                 310                 315                 320

Ala Ser Phe Val Arg Ala Ala Trp Glu Pro Ile Leu Ala Ser His Phe
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325 330 335

Gly Glu Ala Ile Ile Ala Asp Leu Phe His Arg Phe Ala Lys Asn Ala
340 345 350

Ala Thr Pro Leu Arg Met Gly Lys Gly Phe Phe Asn Asn Leu Ile Ile
355 360 365

Ser Leu Ala Lys Lys Pro His Lys Ser Glu Thr Cys Lys Tyr Leu Phe
370 375 380

Leu Asp Met
385

<210> 13
<211> 1155
<212> DNA
<213> Coffea arabica

<400> 13
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aactcattct acaatctgtt tctcatcagg gtgaaaccta tccttgaaca atgcatacaa 120

gaattgttgc gggccaactt gcccaacatc aacaagtgca ttaaagttgc ggatttggga 180

tgcgcttctg gaccaaacac acttttaaca gttcgggaca ttgtacaaag tattgacaaa 240

gttggccagg aaaagaagaa tgaattagaa cgtcccacca ttcagatttt tctgaatgat 300

cttttccaaa atgatttcaa ttcggttttc aagtcgctgc caagcttcta ccgcaaactt 360

gagaaagaaa atggacgcaa aataggatca tgcctgatag gcgcaatgcc tggctctttc 420

tacggcagac tcttccccga ggagtccatg catttttac actcttgtta ctgtttgcat 480

tggttatctc aggttcccag cggtttggtg actgaattgg ggatcagtgc gaacaaaggg 540

tgcatttact cttccaaagc aagtcgtccg cccatccaga aggcatattt ggatcaattt 600

acgaaagatt ttaccacatt tcttaggatt cattcggaag agttgatttc acgtggccga 660

atgctcctta cttggatttg caaagaagat gaattcgaga acccgaattc catagactta 720

cttgagatgt caataaacga cttggttatt gagggacatc tggaggaaga aaaattggac 780

agtttcaatg ttccaatcta tgcaccttca acagaagaag taaagtgcat agttgaggag 840

gaaggttctt ttgaaatttt atacctggag acttttaagg tcccttatga tgctggcttc 900

tctattgatg atgattacca aggaagatcc cattccccag tatcctgcga tgaacatgct 960

agagcagcgc atgtggcatc tgtcgttaga tcaattttcg aacccatcgt cgcaagtcat 1020

tttggagaag ctatcatgcc tgacttatcc cacaggattg cgaagaatgc agcaaaggtt 1080

cttcgctccg gcaaaggctt ctatgatagt cttatcattt ctctcgccaa aaagccagag 1140

aagtcagacg tgtaa 1155

<210> 14
<211> 384
<212> PRT
<213> Coffea arabica

<400> 14

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

Ser Tyr Ala Lys Asn Ser Phe Tyr Asn Leu Phe Leu Ile Arg Val Lys
20 25 30

Pro Ile Leu Glu Gln Cys Ile Gln Glu Leu Leu Arg Ala Asn Leu Pro
35 40 45

Asn Ile Asn Lys Cys Ile Lys Val Ala Asp Leu Gly Cys Ala Ser Gly
50 55 60

Pro Asn Thr Leu Leu Thr Val Arg Asp Ile Val Gln Ser Ile Asp Lys
65 70 75 80

Val Gly Gln Glu Lys Lys Asn Glu Leu Glu Arg Pro Thr Ile Gln Ile
85 90 95

Phe Leu Asn Asp Leu Phe Gln Asn Asp Phe Asn Ser Val Phe Lys Ser
100 105 110

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Leu Pro Ser Phe Tyr Arg Lys Leu Glu Lys Glu Asn Gly Arg Lys Ile
        115                 120                 125

Gly Ser Cys Leu Ile Gly Ala Met Pro Gly Ser Phe Tyr Gly Arg Leu
    130                 135                 140

Phe Pro Glu Glu Ser Met His Phe Leu His Ser Cys Tyr Cys Leu His
145                 150                 155                 160

Trp Leu Ser Gln Val Pro Ser Gly Leu Val Thr Glu Leu Gly Ile Ser
                165                 170                 175

Ala Asn Lys Gly Cys Ile Tyr Ser Ser Lys Ala Ser Arg Pro Pro Ile
            180                 185                 190

Gln Lys Ala Tyr Leu Asp Gln Phe Thr Lys Asp Phe Thr Thr Phe Leu
        195                 200                 205

Arg Ile His Ser Glu Glu Leu Ile Ser Arg Gly Arg Met Leu Leu Thr
    210                 215                 220

Trp Ile Cys Lys Glu Asp Glu Phe Glu Asn Pro Asn Ser Ile Asp Leu
225                 230                 235                 240

Leu Glu Met Ser Ile Asn Asp Leu Val Ile Glu Gly His Leu Glu Glu
                245                 250                 255

Glu Lys Leu Asp Ser Phe Asn Val Pro Ile Tyr Ala Pro Ser Thr Glu
            260                 265                 270

Glu Val Lys Cys Ile Val Glu Glu Glu Gly Ser Phe Glu Ile Leu Tyr
        275                 280                 285

Leu Glu Thr Phe Lys Val Pro Tyr Asp Ala Gly Phe Ser Ile Asp Asp
    290                 295                 300

Asp Tyr Gln Gly Arg Ser His Ser Pro Val Ser Cys Asp Glu His Ala
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305 310 315 320

Arg Ala Ala His Val Ala Ser Val Val Arg Ser Ile Phe Glu Pro Ile
325 330 335

Val Ala Ser His Phe Gly Glu Ala Ile Met Pro Asp Leu Ser His Arg
340 345 350

Ile Ala Lys Asn Ala Ala Lys Val Leu Arg Ser Gly Lys Gly Phe Tyr
355 360 365

Asp Ser Leu Ile Ile Ser Leu Ala Lys Lys Pro Glu Lys Ser Asp Val
370 375 380

<210> 15
<211> 1155
<212> DNA
<213> Coffea canephora

<400> 15
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aactcatcct acaatctgtt tctcatcagg gtgaaacctg tccttgaaca atgcatacaa 120

gaattgttgc gggccaactt gcccaacatc aacaagtgct ttaaagttgg ggatttggga 180

tgcgcttctg gaccaaacac attttcaaca gttcgggaca ttgtacaaag tattgacaaa 240

gttggccagg aaaagaagaa tgaattagaa cgtcccacca ttcagatttt tctgaatgat 300

cttttccaaa atgatttcaa ttcggttttc aagttgctgc caagcttcta ccgcaatctt 360

gagaaagaaa atggacgcaa aataggatcg tgcctgatag gcgcaatgcc cggctctttc 420

tacagcagac tcttccccga ggagtccatg catttttac actcttgtta ctgtttgcat 480

tggttatctc aggttcccag cggtttggtg actgaattgg ggatcagtgt gaacaaaggg 540

tgcatttact cttccaaagc aagtcgtccg cccatccaga aggcatattt ggatcaattt 600

acgaaagatt ttaccacatt tcttaggatt cattcggaag agttgatttc acgtggccga 660

atgctcctta ctttcatttg taaagaagat gaattcgacc acccgaattc catggacttg 720

cttgagatgt caataaacga cttggttatt gagggacatc tggaggaaga aaaattggat 780

agcttcaatg ttccaatcta tgcaccttca acagaagaag taaagcgcat agttgaggag 840

gaaggttctt ttgaaatttt atacctggag acttttaatg ccccttatga tgctggcttc 900

tctattgatg atgattacca aggaagatcc cattcccctg tatcctgcga tgaacatgct 960

agagcagcgc atgtggcatc tgtcgttaga tcaatttacg aacccatcct cgcgagtcat 1020

tttggagaag ctattttacc tgacttatcc cacaggattg cgaagaatgc agcaaaggtt 1080

ctccgctcgg gcaaaggctt ctatgatagt gttatcattt ctctcgccaa aaagccggag 1140

aaggcagaca tgtaa 1155

<210> 16
<211> 384
<212> PRT
<213> Coffea canephora

<400> 16

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

Ser Tyr Ala Lys Asn Ser Ser Tyr Asn Leu Phe Leu Ile Arg Val Lys
20 25 30

Pro Val Leu Glu Gln Cys Ile Gln Glu Leu Leu Arg Ala Asn Leu Pro
35 40 45

Asn Ile Asn Lys Cys Phe Lys Val Gly Asp Leu Gly Cys Ala Ser Gly
50 55 60

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

Val Gly Gln Glu Lys Lys Asn Glu Leu Glu Arg Pro Thr Ile Gln Ile
85 90 95

Phe Leu Asn Asp Leu Phe Gln Asn Asp Phe Asn Ser Val Phe Lys Leu
100 105 110

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Leu Pro Ser Phe Tyr Arg Asn Leu Glu Lys Glu Asn Gly Arg Lys Ile
        115                 120                 125

Gly Ser Cys Leu Ile Gly Ala Met Pro Gly Ser Phe Tyr Ser Arg Leu
    130                 135                 140

Phe Pro Glu Glu Ser Met His Phe Leu His Ser Cys Tyr Cys Leu His
145                 150                 155                 160

Trp Leu Ser Gln Val Pro Ser Gly Leu Val Thr Glu Leu Gly Ile Ser
                165                 170                 175

Val Asn Lys Gly Cys Ile Tyr Ser Ser Lys Ala Ser Arg Pro Pro Ile
            180                 185                 190

Gln Lys Ala Tyr Leu Asp Gln Phe Thr Lys Asp Phe Thr Thr Phe Leu
        195                 200                 205

Arg Ile His Ser Glu Glu Leu Ile Ser Arg Gly Arg Met Leu Leu Thr
    210                 215                 220

Phe Ile Cys Lys Glu Asp Glu Phe Asp His Pro Asn Ser Met Asp Leu
225                 230                 235                 240

Leu Glu Met Ser Ile Asn Asp Leu Val Ile Glu Gly His Leu Glu Glu
                245                 250                 255

Glu Lys Leu Asp Ser Phe Asn Val Pro Ile Tyr Ala Pro Ser Thr Glu
            260                 265                 270

Glu Val Lys Arg Ile Val Glu Glu Glu Gly Ser Phe Glu Ile Leu Tyr
        275                 280                 285

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

Asp Tyr Gln Gly Arg Ser His Ser Pro Val Ser Cys Asp Glu His Ala
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305                 310                 315                 320

Arg Ala Ala His Val Ala Ser Val Val Arg Ser Ile Tyr Glu Pro Ile
                325                 330                 335

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

Ile Ala Lys Asn Ala Ala Lys Val Leu Arg Ser Gly Lys Gly Phe Tyr
        355                 360                 365

Asp Ser Val Ile Ile Ser Leu Ala Lys Lys Pro Glu Lys Ala Asp Met
    370                 375                 380
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<210> 17
<211> 1119
<212> DNA
<213> Coffea arabica

<400> 17

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atggagctcc aagaagtcct gcggatgaat ggaggcgaag gcgatacaag ctacgccaag       60

aattcagcct acaatcaact ggttctcgcc aaggtgaaac ctgtccttga acaatgcgta      120

cgggaattgt tgcgggccaa cttgcccaac atcaacaagt gcattaaagt tgcggatttg      180

ggatgcgctt ctggaccaaa cacactttta acagttcggg acattgtcca aagtattgac      240

aaagttggcc aggaaaagaa gaatgaatta gaacgtccca ccattcagat ttttctgaat      300

gatcttttcc caaatgattt caattcggtt ttcaagttgc tgccaagctt ctaccgcaaa      360

cttgagaaag aaaatggacg caaaatagga tcgtgcctaa taggggcaat gcccggctct      420

ttctacagca gactcttccc cgaggagtcc atgcattttt tacactcttg ttactgtctt      480

caatggttat ctcaggttcc tagcggtttg gtgactgaat tggggatcag tacgaacaaa      540

gggagcattt actcttccaa agcaagtcgt ctgcccgtcc agaaggcata tttggatcaa      600

tttacgaaag attttaccac atttctaagg attcattcgg aagagttgtt ttcacatggc      660

cgaatgctcc ttacttgcat ttgtaaagga gttgaattag acgcccggaa tgccatagac      720

ttacttgaga tggcaataaa cgacttggtt gttgagggac atctggagga agaaaaattg      780
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gatagtttca atcttccagt ctatatacct tcagcagaag aagtaaagtg catagttgag 840

gaggaaggtt cttttgaaat tttatacctg gagactttta aggtccttta cgatgctggc 900

ttctctattg acgatgaaca tattaaagca gagtatgttg catcttccgt tagagcagtt 960

tacgaaccca tcctcgcaag tcattttgga gaagctatta tacctgacat attccacagg 1020

tttgcgaagc atgcagcaaa ggttctcccc ttgggcaaag gcttctataa taatcttatc 1080

atttctctcg ccaaaaagcc agagaagtca gacgtgtaa 1119

<210> 18
<211> 372
<212> PRT
<213> Coffea arabica

<400> 18

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

Ser Tyr Ala Lys Asn Ser Ala Tyr Asn Gln Leu Val Leu Ala Lys Val
20 25 30

Lys Pro Val Leu Glu Gln Cys Val Arg Glu Leu Leu Arg Ala Asn Leu
35 40 45

Pro Asn Ile Asn Lys Cys Ile Lys Val Ala Asp Leu Gly Cys Ala Ser
50 55 60

Gly Pro Asn Thr Leu Leu Thr Val Arg Asp Ile Val Gln Ser Ile Asp
65 70 75 80

Lys Val Gly Gln Glu Lys Lys Asn Glu Leu Glu Arg Pro Thr Ile Gln
85 90 95

Ile Phe Leu Asn Asp Leu Phe Pro Asn Asp Phe Asn Ser Val Phe Lys
100 105 110

Leu Leu Pro Ser Phe Tyr Arg Lys Leu Glu Lys Glu Asn Gly Arg Lys

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        115                 120                 125

Ile Gly Ser Cys Leu Ile Gly Ala Met Pro Gly Ser Phe Tyr Ser Arg
    130                 135                 140

Leu Phe Pro Glu Glu Ser Met His Phe Leu His Ser Cys Tyr Cys Leu
145                 150                 155                 160

Gln Trp Leu Ser Gln Val Pro Ser Gly Leu Val Thr Glu Leu Gly Ile
                165                 170                 175

Ser Thr Asn Lys Gly Ser Ile Tyr Ser Ser Lys Ala Ser Arg Leu Pro
            180                 185                 190

Val Gln Lys Ala Tyr Leu Asp Gln Phe Thr Lys Asp Phe Thr Thr Phe
        195                 200                 205

Leu Arg Ile His Ser Glu Glu Leu Phe Ser His Gly Arg Met Leu Leu
    210                 215                 220

Thr Cys Ile Cys Lys Gly Val Glu Leu Asp Ala Arg Asn Ala Ile Asp
225                 230                 235                 240

Leu Leu Glu Met Ala Ile Asn Asp Leu Val Val Glu Gly His Leu Glu
                245                 250                 255

Glu Glu Lys Leu Asp Ser Phe Asn Leu Pro Val Tyr Ile Pro Ser Ala
            260                 265                 270

Glu Glu Val Lys Cys Ile Val Glu Glu Glu Gly Ser Phe Glu Ile Leu
        275                 280                 285

Tyr Leu Glu Thr Phe Lys Val Leu Tyr Asp Ala Gly Phe Ser Ile Asp
    290                 295                 300

Asp Glu His Ile Lys Ala Glu Tyr Val Ala Ser Ser Val Arg Ala Val
305                 310                 315                 320
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Tyr Glu Pro Ile Leu Ala Ser His Phe Gly Glu Ala Ile Ile Pro Asp
325 330 335

Ile Phe His Arg Phe Ala Lys His Ala Ala Lys Val Leu Pro Leu Gly
340 345 350

Lys Gly Phe Tyr Asn Asn Leu Ile Ile Ser Leu Ala Lys Lys Pro Glu
355 360 365

Lys Ser Asp Val
370

<210> 19
<211> 1119
<212> DNA
<213> Coffea canephora

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aattcagcct acaatcaact ggttctcgcc aaggtgaaac ctgtccttga acaatgcgta 120

cgggaattgt tgcgggccaa cttgcccaac atcaacaagt gcattaaagt tgcggatttg 180

ggatgcgctt ctggaccaaa cacactttta acggttcggg acattgtcca aagtattgac 240

aaagttggcc aggaaaagaa gaatgaatta gaacgtccca ccattcagat ttttctgaat 300

gatcttttcc caaatgattt caattcggtt ttcaagttgc tgccaagctt ctaccgcaaa 360

cttgagaaag aaaatggacg caaaatagga tcgtgcctaa taggggcaat gcccggctct 420

ttctacagca gactcttccc cgaggagtcc atgcattttt tacactcttg ttactgtctt 480

caatggttat ctcaggttcc tagcggtttg gtgactgaat tggggatcgg cacgaacaaa 540

gggagcattt actcttccaa agcaagtcgt ctgcccgtcc agaaggcata tttggatcaa 600

tttacgaaag attttaccac atttctaagg attcattcgg aagagttgtt ttcacatggc 660

cgaatgctcc ttacttgcat ttgtaaagga gttgaattag acgcccggaa tgccatagac 720

ttacttgaga tggcaataaa cgacttggtt gttgagggac atctggagga agaaaaattg 780

gatagtttca atcttccagt ctatatacct tcagcagaag aagtaaagtg catagttgag 840

gaggaaggtt cttttgaaat tttatacctg gagactttta aggtccttta cgatgctggc 900

ttctctattg acgatgaaca tattaaagca gagtatgttg catcttccgt tagagcagtt 960

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tttgcgaagc atgcagcaaa ggttctcccc ttgggcaaag gcttctataa taatcttatc 1080

atttctctcg ccaaaaagcc agagaagtca gacatgtaa 1119

<210> 20
<211> 372
<212> PRT
<213> Coffea canephora

<400> 20

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

Ser Tyr Ala Lys Asn Ser Ala Tyr Asn Gln Leu Val Leu Ala Lys Val
20 25 30

Lys Pro Val Leu Glu Gln Cys Val Arg Glu Leu Leu Arg Ala Asn Leu
35 40 45

Pro Asn Ile Asn Lys Cys Ile Lys Val Ala Asp Leu Gly Cys Ala Ser
50 55 60

Gly Pro Asn Thr Leu Leu Thr Val Arg Asp Ile Val Gln Ser Ile Asp
65 70 75 80

Lys Val Gly Gln Glu Lys Lys Asn Glu Leu Glu Arg Pro Thr Ile Gln
85 90 95

Ile Phe Leu Asn Asp Leu Phe Pro Asn Asp Phe Asn Ser Val Phe Lys
100 105 110

Leu Leu Pro Ser Phe Tyr Arg Lys Leu Glu Lys Glu Asn Gly Arg Lys
115 120 125

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Ile Gly Ser Cys Leu Ile Gly Ala Met Pro Gly Ser Phe Tyr Ser Arg
    130                 135                 140

Leu Phe Pro Glu Glu Ser Met His Phe Leu His Ser Cys Tyr Cys Leu
145                 150                 155                 160

Gln Trp Leu Ser Gln Val Pro Ser Gly Leu Val Thr Glu Leu Gly Ile
                165                 170                 175

Gly Thr Asn Lys Gly Ser Ile Tyr Ser Ser Lys Ala Ser Arg Leu Pro
            180                 185                 190

Val Gln Lys Ala Tyr Leu Asp Gln Phe Thr Lys Asp Phe Thr Thr Phe
        195                 200                 205

Leu Arg Ile His Ser Glu Glu Leu Phe Ser His Gly Arg Met Leu Leu
    210                 215                 220

Thr Cys Ile Cys Lys Gly Val Glu Leu Asp Ala Arg Asn Ala Ile Asp
225                 230                 235                 240

Leu Leu Glu Met Ala Ile Asn Asp Leu Val Val Glu Gly His Leu Glu
                245                 250                 255

Glu Glu Lys Leu Asp Ser Phe Asn Leu Pro Val Tyr Ile Pro Ser Ala
            260                 265                 270

Glu Glu Val Lys Cys Ile Val Glu Glu Glu Gly Ser Phe Glu Ile Leu
        275                 280                 285

Tyr Leu Glu Thr Phe Lys Val Leu Tyr Asp Ala Gly Phe Ser Ile Asp
    290                 295                 300

Asp Glu His Ile Lys Ala Glu Tyr Val Ala Ser Ser Val Arg Ala Val
305                 310                 315                 320

Tyr Glu Pro Ile Leu Ala Ser His Phe Gly Glu Ala Ile Ile Pro Asp
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325 330 335

Ile Phe His Arg Phe Ala Lys His Ala Ala Lys Val Leu Pro Leu Gly
340 345 350

Lys Gly Phe Tyr Asn Asn Leu Ile Ile Ser Leu Ala Lys Lys Pro Glu
355 360 365

Lys Ser Asp Met
370

<210> 21
<211> 1137
<212> DNA
<213> Coffea arabica

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gaattgttgc gggccaactt gcccaacatc aacaagtgca ttaaagttgc ggatttggga 180

tgcgcttctg gaccaaacac acttttaaca gtgcgggaca ttgtgcaaag tattgacaaa 240

gttggccagg aagagaagaa tgaattagaa cgtcccacca ttcagatttt tctgaatgat 300

cttttccaaa atgatttcaa ttcggttttc aagttgctgc caagcttcta ccgcaaactc 360

gagaaagaaa atggacgcaa gataggatcg tgcctaataa gcgcaatgcc tggctctttc 420

tacggcagac tcttccccga ggagtccatg catttttgc actcttgtta cagtgttcat 480

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agtatttact cttccaaagg atgtcgtccg cccgtccaga aggcatattt ggatcaattt 600

acgaaagatt ttaccacatt tctaaggatt cattcgaaag agttgttttc acgtggccga 660

atgctcctta cctgcatttg taaagtagat gaattcgacg aaccgaatcc cctagactta 720

cttgacatgg caataaacga cttgattgtt gagggacttc tggaggaaga aaaattggat 780

agtttcaata ttccattctt tacaccttca gcagaagaag taaagtgcat agttgaggag 840

gaaggttctt gcgaaatttt atatctggag acttttaagg cccattatga tgctgccttc 900

tctattgatg atgattaccc agtaagatcc catgaacaaa ttaaagcaga gtatgtggca 960

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cctgacttat tccacaggct tgcgaagcat gcagcaaagg ttctccacat gggcaaaggc 1080

tgctataata atcttatcat ttctctcgcc aaaaagccag agaagtcaga cgtgtaa 1137

<210> 22
<211> 378
<212> PRT
<213> Coffea arabica

<400> 22

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

Ser Tyr Ala Lys Asn Ala Ser Tyr Asn Leu Ala Leu Ala Lys Val Lys
20 25 30

Pro Phe Leu Glu Gln Cys Ile Arg Glu Leu Leu Arg Ala Asn Leu Pro
35 40 45

Asn Ile Asn Lys Cys Ile Lys Val Ala Asp Leu Gly Cys Ala Ser Gly
50 55 60

Pro Asn Thr Leu Leu Thr Val Arg Asp Ile Val Gln Ser Ile Asp Lys
65 70 75 80

Val Gly Gln Glu Glu Lys Asn Glu Leu Glu Arg Pro Thr Ile Gln Ile
85 90 95

Phe Leu Asn Asp Leu Phe Gln Asn Asp Phe Asn Ser Val Phe Lys Leu
100 105 110

Leu Pro Ser Phe Tyr Arg Lys Leu Glu Lys Glu Asn Gly Arg Lys Ile
115 120 125

Gly Ser Cys Leu Ile Ser Ala Met Pro Gly Ser Phe Tyr Gly Arg Leu

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    130                 135                 140

Phe Pro Glu Glu Ser Met His Phe Leu His Ser Cys Tyr Ser Val His
145                 150                 155                 160

Trp Leu Ser Gln Val Pro Ser Gly Leu Val Ile Glu Leu Gly Ile Gly
                165                 170                 175

Ala Asn Lys Gly Ser Ile Tyr Ser Ser Lys Gly Cys Arg Pro Pro Val
            180                 185                 190

Gln Lys Ala Tyr Leu Asp Gln Phe Thr Lys Asp Phe Thr Thr Phe Leu
        195                 200                 205

Arg Ile His Ser Lys Glu Leu Phe Ser Arg Gly Arg Met Leu Leu Thr
    210                 215                 220

Cys Ile Cys Lys Val Asp Glu Phe Asp Glu Pro Asn Pro Leu Asp Leu
225                 230                 235                 240

Leu Asp Met Ala Ile Asn Asp Leu Ile Val Glu Gly Leu Leu Glu Glu
                245                 250                 255

Glu Lys Leu Asp Ser Phe Asn Ile Pro Phe Phe Thr Pro Ser Ala Glu
            260                 265                 270

Glu Val Lys Cys Ile Val Glu Glu Glu Gly Ser Cys Glu Ile Leu Tyr
        275                 280                 285

Leu Glu Thr Phe Lys Ala His Tyr Asp Ala Ala Phe Ser Ile Asp Asp
    290                 295                 300

Asp Tyr Pro Val Arg Ser His Glu Gln Ile Lys Ala Glu Tyr Val Ala
305                 310                 315                 320

Ser Leu Ile Arg Ser Val Tyr Glu Pro Ile Leu Ala Ser His Phe Gly
                325                 330                 335
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Glu Ala Ile Met Pro Asp Leu Phe His Arg Leu Ala Lys His Ala Ala
340 345 350

Lys Val Leu His Met Gly Lys Gly Cys Tyr Asn Asn Leu Ile Ile Ser
355 360 365

Leu Ala Lys Lys Pro Glu Lys Ser Asp Val
370 375

<210> 23
<211> 1155
<212> DNA
<213> Coffea arabica

<400> 23
atggagctcc aagaagtcct gcatatgaat gaaggtgaag gcgatacaag ctacgccaag 60

aatgcatcct acaatctggc tcttgccaag gtgaaacctt tccttgaaca atgcatacga 120

gaattgttgc gggccaactt gcccaacatc aacaagtgca ttaaagttgc ggatttggga 180

tgcgcttctg gaccaaacac acttttaaca gtgcgggaca ttgtgcaaag tattgacaaa 240

gttggccagg aagagaagaa tgaattagaa cgtcccacca ttcagatttt tctgaatgat 300

cttttccaaa atgatttcaa ttcggttttc aagttgctgc caagcttcta ccgcaaactc 360

gagaaagaaa atggacgcaa gataggatcg tgcctaataa gcgcaatgcc tggctctttc 420

tacggcagac tcttccccga ggagtccatg catttttgc actcttgtta cagtgttcat 480

tggttatctc aggttcccag cggtttggtg attgaattgg ggattggtgc aaacaaaggg 540

agtatttact cttccaaagc aagtcgtccg cccgtccaga aggcatattt ggatcaattt 600

acgaaagatt ttaccacatt tctaaggatt cattcgaaag agttgttttc acgtggccga 660

atgctcctta cttgcatttg taaagtagat gaatacgacg aaccgaatcc cctagactta 720

cttgacatgg caataaacga cttgattgtt gagggacatc tggaggaaga aaaattggct 780

agtttcaatc ttccattctt tacaccttca gcagaagaag taaagtgcat agttgaggag 840

gaaggttctt ttgaaatttt atacctggag acttttaagg cccattatga tgctggcttc 900

tctattgatg atgattaccc agtaagatcc catttccaag tatacggcga tgaacatatt 960

aaagcagagt atgtggcatc attaattaga tcagtttacg aacccatcct cgcaagtcat 1020

tttggagaag ctattatgcc tgacttattc cacaggcttg cgaagcatgc agcaaaggtt 1080

ctccacttgg gcaaaggctg ctataataat cttatcattt ctctcgccaa aaagccagag 1140

aagtcagacg tgtaa 1155

<210> 24
<211> 384
<212> PRT
<213> Coffea arabica

<400> 24

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

Ser Tyr Ala Lys Asn Ala Ser Tyr Asn Leu Ala Leu Ala Lys Val Lys
20 25 30

Pro Phe Leu Glu Gln Cys Ile Arg Glu Leu Leu Arg Ala Asn Leu Pro
35 40 45

Asn Ile Asn Lys Cys Ile Lys Val Ala Asp Leu Gly Cys Ala Ser Gly
50 55 60

Pro Asn Thr Leu Leu Thr Val Arg Asp Ile Val Gln Ser Ile Asp Lys
65 70 75 80

Val Gly Gln Glu Glu Lys Asn Glu Leu Glu Arg Pro Thr Ile Gln Ile
85 90 95

Phe Leu Asn Asp Leu Phe Gln Asn Asp Phe Asn Ser Val Phe Lys Leu
100 105 110

Leu Pro Ser Phe Tyr Arg Lys Leu Glu Lys Glu Asn Gly Arg Lys Ile
115 120 125

Gly Ser Cys Leu Ile Ser Ala Met Pro Gly Ser Phe Tyr Gly Arg Leu

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    130                 135                 140

Phe Pro Glu Glu Ser Met His Phe Leu His Ser Cys Tyr Ser Val His
145                 150                 155                 160

Trp Leu Ser Gln Val Pro Ser Gly Leu Val Ile Glu Leu Gly Ile Gly
                165                 170                 175

Ala Asn Lys Gly Ser Ile Tyr Ser Ser Lys Ala Ser Arg Pro Pro Val
            180                 185                 190

Gln Lys Ala Tyr Leu Asp Gln Phe Thr Lys Asp Phe Thr Thr Phe Leu
        195                 200                 205

Arg Ile His Ser Lys Glu Leu Phe Ser Arg Gly Arg Met Leu Leu Thr
    210                 215                 220

Cys Ile Cys Lys Val Asp Glu Tyr Asp Glu Pro Asn Pro Leu Asp Leu
225                 230                 235                 240

Leu Asp Met Ala Ile Asn Asp Leu Ile Val Glu Gly His Leu Glu Glu
                245                 250                 255

Glu Lys Leu Ala Ser Phe Asn Leu Pro Phe Phe Thr Pro Ser Ala Glu
            260                 265                 270

Glu Val Lys Cys Ile Val Glu Glu Glu Gly Ser Phe Glu Ile Leu Tyr
        275                 280                 285

Leu Glu Thr Phe Lys Ala His Tyr Asp Ala Gly Phe Ser Ile Asp Asp
    290                 295                 300

Asp Tyr Pro Val Arg Ser His Phe Gln Val Tyr Gly Asp Glu His Ile
305                 310                 315                 320

Lys Ala Glu Tyr Val Ala Ser Leu Ile Arg Ser Val Tyr Glu Pro Ile
                325                 330                 335
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Leu Ala Ser His Phe Gly Glu Ala Ile Met Pro Asp Leu Phe His Arg
340 345 350

Leu Ala Lys His Ala Ala Lys Val Leu His Leu Gly Lys Gly Cys Tyr
355 360 365

Asn Asn Leu Ile Ile Ser Leu Ala Lys Lys Pro Glu Lys Ser Asp Val
370 375 380

<210> 25
<211> 1024
<212> DNA
<213> Artificial sequence

<220>
<223> XMT Cc09_g06970 - partial nucleic acid sequence

<400> 25
atggagctcc aagaagtcct gcggatgaat ggaggcgaag gcgatacaag ctacgccaag 60

aattcagcct acaatgtctg tctgtctctc tatctctctt taacacacac acacacagag 120

tagtagtaaa tcatgctatg atacgtcgat ctctaactta gtatgtcttt tttccccct 180

taacatttgt attttggagt ggtatgtgta gcaactggtt ctcgccaagg tgaaacctgt 240

ccttgaacaa tgcgtacggg aattgttgcg ggccaacttg cccaacatca acaagtgcat 300

taaagttgcg gatttgggat gcgcttctgg accaaacaca cttttaacag ttcgggacat 360

tgtccaaagt attgacaaag ttggccagga aaagaagaat gaattagaac gtcccaccat 420

tcagattttt ctgaatgatc ttttcccaaa tgatttcaat tcggttttca agttgctgcc 480

aagcttctac cgcaaacttg agaaagaaaa tggacgcaaa ataggatcgt gcctaatagg 540

ggcaatgccc ggctctttct acagcagact cttccccgag gagtccatgc atttttaca 600

ctcttgttac tgtcttcaat ggttatctca ggtctttgag ttaatccctt ttatcttttt 660

aatttttctt gtagcaaaaa tagttcatga ttttcattca acacattagt aactatgcac 720

ggaaatttct ttaataattc tcaagatatc cacaggaatc caagaaagag atttctgaag 780

aaactaataa catattttat tcaagtcgtg gctcatgatt tatattccca catgcaacac 840

taacaaaatg atccaactat ataagttacc agctctggac gtgcaggttc ctagcggttt 900

ggtgactgaa tcggggatca gtacgaacaa agggagcatt tactcttcca aagcaagtcg 960

tctgcccgtc cagaaggcat atttggatca atttacgaaa gattttacca catttctaag 1020

gatt 1024

<210> 26
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> XMT Cc09_g06970 target sequence

<400> 26
ccaaggtgaa acctgtcctt gaa 23

<210> 27
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> XMT Cc09_g06970 target sequence

<400> 27
caagtgcatt aaagttgcgg 20

<210> 28
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> XMT Cc09_g06970 target sequence

<400> 28
ccaaatgatt tcaattcggt ttt 23

<210> 29
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> XMT Cc09_g06970 target sequence

<400> 29
aaagaaaatg gacgcaaaat agg 23

<210> 30
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> XMT Cc09_g06970 target sequence

<400> 30
tgcctaatag gggcaatgcc cgg 23

<210> 31
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> XMT Cc09_g06970 target sequence

<400> 31
cccgaggagt ccatgcattt ttt 23

<210> 32
<211> 1400
<212> DNA
<213> Artificial sequence

<220>
<223> MXMT Cc09_g06960 - partial nucleic acid sequence

<400> 32
tcattcgtgt ctggttccca ttggctgtgc gctttctttc tgacccattg acagactttt 60

ctacgcacgt aactagctgg ttagcatacg catctatgaa attttcgcta tttaagcccg 120

aaattttgca caattaatca ttaacagaca ccttctttag ccgtcgcaat tcgattgtcc 180

tgtatatgaa tggagctcca agaagtcctg catatgaatg gaggcgaagg cgatacaagc 240

tacgccaaga attcatcgta caatgtctgt ctgtctatct ctctctttaa cacacacaca 300

cacacagagt agtagtaaat tatgctatga tacgttgatc tctgacttag tatgtctttt 360

ttcgcccctt aacatttgta ttttggagtg gtatgtgtag caactggttc tcaccaaggt 420

gaaacctgtc cttgaacaat gcatacgaga attgttgcgg gccaacttgc ccaacatcaa 480

caagtgcatt aaagttgcgg atttgggatg cgcttctgga ccaaacacac ttttaacagt 540

tcgggacatt gtgcaaagta ttgacaaagt tggccaggaa gagaagaatg aattagaaca 600

tcccaccatt caaatttttc tgaatgatct tttccaaaat gatttcaatt cagttttcaa 660

gttgctgcca agcttctacc gcaaactcga gaaagaaaat ggacgcaaaa taggatcgtg 720

cctaataagc gcaatgcctg gctctttcta cggcagactc ttccccgagg agtccatgca 780

ttttttgcac tcttgttaca gtgttcattg gttatctcag gtctttgagt taatcccttt 840

tatctttta ctttttcttg tagcaaaaat agttcatgat tttcattcaa cacattagta 900

actatgcatg gaaatttctt taataattct aaagacatcc acaggaatcc aagaaagaga 960

tttctgaaga aactaataac atattttatt taagtcgtgg ctcatgattt atattcccac 1020

atgcaacact aacaaaatga tccaactata taagttacca gttctagacg tgcaggttcc 1080

cagcggattg gtgactgaac tggggatcag tgcgaacaaa gggatcattt actcttccaa 1140

agcaagtcct ccgcccgtcc agaaggcata tttggaccaa tttacaaaag attttaccac 1200

atttctgagg attcattcgg aagagttgct ttcaggtggc cgaatgctcc ttacttgcat 1260

ttgtaaagga gatgaatccg atggcctgaa taccatagac ttacttgaga gagcaataaa 1320

cgacttggtt gttgaggtta tcatttctct gtctctttga taatcagatg ctcattgctt 1380

gttatctgaa ataaactaga 1400

<210> 33
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> MXMT Cc09_g06960 target sequence

<400> 33
ccaaggtgaa acctgtcctt gaa 23

<210> 34
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> MXMT Cc09_g06960 target sequence

<400> 34
caacaagtgc attaaagttg cgg 23

<210> 35
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> MXMT Cc09_g06960 target sequence

<400> 35
aaagaaaatg gacgcaaaat agg 23

<210> 36
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> MXMT Cc09_g06960 target sequence

<400> 36
cccgaggagt ccatgcattt ttt 23

<210> 37
<211> 1105
<212> DNA
<213> Artificial sequence

<220>
<223> MXMT Cc00_g24720 - partial nucleic acid sequence

<400> 37
gtgcgctttc tttctgacga attgacagac ttttctacgc acggaggtag ctggctagca 60

tacgcatcta tgaaattttc gctacttaag cccgaaattt tgcacaatta atcattaaca 120

gacaccttct ttagcagtcg caattcgatt gtcctgcata tgaatggagc tccaagaagt 180

cctgcatatg aatgaaggtg aaggcgatac aagctacgcc aagaatgcat cctacaatgt 240

ctgtctgtct ctctatctct ctttaacaca cacacacaca gagaatagtg gtaaatcatg 300

ctatgatacg tcgatctcta acttcacatt tgtattttgg actggtatgt gtaacagctg 360

gctcttgcca aggtgaaacc tttccttgaa caatgcatac gagaattgtt gcgggccaac 420

ttgcccaaca tcaacaagtg cattaaagtt gcggatttgg gatgcgcttc tggaccaaac 480

acacttttaa cagtgcggga cattgtgcaa agtattgaca aagttggcca ggaagagaag 540

aatgaattag aacgtcccac cattcagatt tttctgaatg atcttttcca aaatgatttc 600

aattcggttt tcaagttgct gccaagcttc taccgcaaac tcgagaaaga aaatggacgc 660

aagataggat cgtgcctaat aagcgcaatg cctggctctt tctacggcag actcttcccc 720

gaggagtcca tgcatttttt gcactcttgt tacagtgttc attggttatc tcaggtcttt 780

gagttaatcc cttttatctt tttacttttt cttgtagcaa aaatggttcg tgattttcat 840

tcaacacatt agtaactatg catggaaatt tctttaataa ttctaaagat atccacagga 900

atccaagaaa gagatttctg aagaaactaa taacatattt tatctaagtc gtggctcatg 960

atttacattc ccacatgcaa cactaacaaa atgatccaac tatataagtt accagttctg 1020

gacgtgcagg ttcccagcgg tttggtgatt gaattgggga ttggtgcaaa caaagggagt 1080

atttactctt ccaaaggatg tcgtc 1105

<210> 38
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> MXMT Cc00_g24720 target sequence

<400> 38
cctttccttg aacaatgcat acg 23

<210> 39
<211> 23
<212> DNA

<213> Artificial sequence

<220>
<223> MXMT Cc00_g24720 target sequence

<400> 39
caacaagtgc attaaagttg cgg 23

<210> 40
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> MXMT Cc00_g24720 target sequence

<400> 40
aaagaaaatg gacgcaagat agg 23

<210> 41
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> MXMT Cc00_g24720 target sequence

<400> 41
cccgaggagt ccatgcattt ttt 23

<210> 42
<211> 1315
<212> DNA
<213> Artificial sequence

<220>
<223> DXMT Cc09_g06950 - partial nucleic acid sequence

<400> 42
tttatcccaa ttgtgtgtgg ttcccattgg ctgtgctctt tctctctgac caattgacag 60

atttttctac gcacgtagtt agccggttag catacgcatc taagaaattt tcgccattta 120

agtccgaaat ttcgcacagt taatcattaa cagacacctt ccttagcagt cccaattcga 180

tttatgtaca agtcctgcat atgaatggag ctccaagaag tcctgcatat gaatggaggc 240

gaaggcgaag caagctacgc caagaattca tccttcaatg tctgtctatc tgtctatctc 300

tctctttaac acacacacac acacacacag agtagtagta aatcatgcta tgatacgtcg 360

atctctaact tagtatgtct tttttcgccc cttaacattt gtattttgga gtggtatgtg 420

tagcaactgg ttctcgccaa ggtgaaacct gtccttgaac aatgcgtacg ggaattgttg 480

cgggccaact tgcccaacat caacaagtgc attaaagttg cagatttggg atgcgcttcc 540

ggaccaaaca cacttttaac cgttcgggac actgtacaaa gtattgacaa agttaggcaa 600

gaaatgaaga atgaattaga acgtcccacc attcaggttt ttctgactga tcttttccaa 660

aatgatttca attcggtttt catgctgctg ccaagcttct accgcaaact tgagaaagaa 720

aatggacgca aaataggatc gtgcctaata gccgcaatgc ctggctcttt ccacggcaga 780

ctcttccccg aggagtccat gcatttttta cactcttctt acagtcttca gtttttatcc 840

caggtctttg aattactccc ttttatcttt ttacttttc ttgtagcaaa aatagttcat 900

gattttcatt caacacatta gttactatgc atggaaattt ctttaataat tctcaagata 960

tccacaggaa tccaagaaag agatttctaa agggaaccag ctttagactg caggttccca 1020

gcggtttggt gactgaattg gggatcactg cgaacaaaag gagcatttac tcttccaaag 1080

caagtcctcc gcccgtccag aaggcatatt tggatcaatt tacgaaagat tttaccacat 1140

ttttaaggat gcgttcggaa gagttgcttt cacgtggccg aatgctcctt acttgcattt 1200

gtaaaggaga tgaatgcgac ggcccgaata ccatggactt acttgagatg gcaataaacg 1260

acttggttgt tgaggttaat catttctctg tctctttgat gatcagatgc tcatt 1315

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

<220>
<223> DXMT Cc09_g06950 target sequence

<400> 43
ccaaggtgaa acctgtcctt gaa 23

<210> 44

<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> DXMT Cc09_g06950 target sequence

<400> 44
aaagaaaatg gacgcaaaat agg 23

<210> 45
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> DXMT Cc09_g06950 target sequence

<400> 45
cccgaggagt ccatgcattt ttt 23

<210> 46
<211> 1270
<212> DNA
<213> Artificial sequence

<220>
<223> DXMT Cc01_g00720 - partial nucleic acid sequence

<400> 46
aaaacaaacg aaagtgactt cattatctct aacctccgat ttttatcatt agtggcttgt 60

tcccattggc tgtgcgcttc ctttctgact aattgataga ctttctacgc acgtaggtag 120

gcagctagca tacgcatcta tgaaattttc gctatttaag cccgaaattt cgcacaatta 180

atcattaaca gataccttct ttagcagtcc caattcgatt tatgcacaag tcctgcgtat 240

gaatggagct ccaagaagtc ctgcatatga atggaggcga aggcgataca agctacgcca 300

agaactcatc ctacaatgtc tgtctgtctc tctatctctc tctttaacac acacacacac 360

acacacagag tagtagtaaa tcatgctatg atacgtcgat ctctaactta gtatgtcttt 420

tttccccctt aacatttgta ttttggagtg gtatgtgttg cagctgtttc tcatcagggt 480

gaaacctgtc cttgaacaat gcatacaaga attgttgcgg gccaacttgc ccaacatcaa 540

caagtgcttt aaagttgggg atttgggatg cgcttctgga ccaaacacat tttcaacagt 600

tcgggacatt gtacaaagta ttgacaaagt tggccaggaa aagaagaatg aattagaacg 660

tcccaccatt cagatttttc tgaatgatct tttccaaaat gatttcaatt cggttttcaa 720

gttgctgcca agcttctacc gcaatcttga gaaagaaaat ggacgcaaaa taggatcgtg 780

cctgataggc gcaatgcccg gctctttcta cagcagactc ttccccgagg agtccatgca 840

ttttttacac tcttgttact gtttgcattg gttatctcag gtctttgagt taatcccttc 900

tatcttgttt actttttctt gtagcaaaaa taagttcacg atttttattc aacacattag 960

taactatgca tggaaatttc tttaataatt ctcaagatat ccacaggaat ccaagaaaga 1020

gatttctgac gaaactaata acacatttta tttaattcgt ggctcatgat ttatattccc 1080

acatgcaaca ctaacaaaat gatccaacta tataagttac cagctctaga cgtgcaggtt 1140

cccagcggtt tggtgactga attggggatc agtgtgaaca aagggtgcat ttactcttcc 1200

aaagcaagtc gtccgcccat ccagaaggca tatttggatc aatttacgaa agattttacc 1260

acatttctga 1270

<210> 47
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> DXMT Cc01_g00720 target sequence

<400> 47
aaagaaaatg gacgcaaaat agg 23

<210> 48
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> DXMT Cc01_g00720 target sequence

<400> 48
cccgaggagt ccatgcattt ttt 23

<210> 49
<211> 1319
<212> DNA
<213> Artificial sequence

<220>
<223> DXMT Cc02_g09350 - partial nucleic acid sequence

<400> 49
gagtatgtaa atatgtgatt gaaaaaaagt actcagatta tgtttaacaa atttgccaaa 60

aaaggcaata catgctgatt atattcgaac attccacttt tttggaccgg aaagagaagg 120

gatatgggca tttattgagg atcgtttgga ggatgagcag taatggcatc tctgaaagct 180

gtccaatact gacacttgga ttgattattt gttgaagatg atgattgatg atgatgatga 240

tgataccgat acttggacac ttggattgat gatgatgagg aaaggataaa tactcctata 300

caagattgtc gaaaattcga ttaagtaaga gatcagaaat ggaactccaa cgagtcctgc 360

acatgagtgg aggcgaaggc gatacaagct acgccaaaaa ttcatcctac caagtctgtc 420

tatccctctt tgacaaacac acacgcacgc gcccgcagtc acaggagtgg taacacaaga 480

ctgtgatacg ttgatctcta acatagcgta ccctttttt ggctttaact ttttttttt 540

ttttttgag tggtgtatgt agaagttggt actgacctag gtgaagcctg tacttgaaca 600

atgcatacaa gaattgttgc ggaccaactt accctacgac gagaagtgca ttagagttgc 660

tgatttggga tgctcttcag gaccaaacac actattaaca gtttcggaca tcatacaaag 720

tattgacaaa gttagccagg aaatggacaa tgaatttgca ctgcccacga ttcaggtttt 780

tctgaatgat cttttcgaaa atgatttcaa tacggttatc aagtcgctgc caagcttcta 840

ccgcaaactt gaaaaagaaa atggacgcaa aataggatcg tgcctgatag cagcaatgcc 900

tggctctttc tacggcagac tcttccccga gcagtccgtc catttttac actcttctta 960

cagtctccat tggttatctc aggtttttga atcaatccct ctaatcattt tccattttct 1020

tgcagcaaag atagttcatg catgattttc attcaacaca ttagtaacta tgcatggaag 1080

gcttctttaa caattctcaa gacatcccca agaacccaac ccaagaaaag atttctcaag 1140

aaatcaacaa ccttttttt cttttttttt tggtgtggtc gcggctcatg atttgtagta 1200

ttcccacatg caattgaccc taacaaaatg ctccaacaat gtaacaagtt accagcttga 1260

gacgcgtcac gttgacaggt tcccaatggt ttggtgactg aatcggggat cagtgcgaa 1319

<210> 50
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> DXMT Cc02_g09350 target sequence

<400> 50
aaagaaaatg gacgcaaaat agg 23

<210> 51
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> sgRNA sequence

<400> 51
aaaaccgaat tgaaatcatt 20

<210> 52
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> sgRNA sequence

<400> 52
tgcctaatag gggcaatgcc 20

<210> 53
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> sgRNA sequence

<400> 53

ttcaaggaca ggtttcacct 20

<210> 54
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> sgRNA sequence

<400> 54
caacaagtgc attaaagttg 20

<210> 55
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> sgRNA sequence

<400> 55
aaagaaaatg gacgcaaaat 20

<210> 56
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> sgRNA sequence

<400> 56
aaaaaatgca tggactcctc 20

<210> 57
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> sgRNA sequence

<400> 57
cgtatgcatt gttcaaggaa 20

<210> 58
<211> 20
<212> DNA
<213> Artificial sequence

<220>
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<400> 59
tttgcacaat taatcattaa ggg 23

<210> 60
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caagaagtcc tgcggatgaa tgg 23

<210> 61
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acttgtacat aaatcaaatt ggg 23

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<210> 66
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<400> 66
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<210> 67
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<400> 67
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<210> 68
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<400> 68
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<210> 69
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<400> 69
aaaataggat cgtgcctgat agg 23

<210> 70
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<220>
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<400> 70
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<210> 71
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<400> 71
cctcggggaa gagtctgccg tgg 23

<210> 72
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<400> 72
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<210> 73
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<210> 74
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<400> 74
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<210> 75
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<400> 75
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<210> 76
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<400> 76
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<210> 77
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<400> 77
agcggattgg tgactgaact ggg 23

<210> 78
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<220>
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<400> 78

tcggaagagt tgctttcagg tgg 23

<210> 79
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<212> DNA
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<400> 79
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ctacgcacgt aactagctgg ttagcatacg catctatgaa attttcgcta tttaagcccg 120

aaattttgca caattaatca ttaacagaca ccttctttag ccgtcgcaat tcgattgtcc 180

tgtatatgaa tggagctcca agaagtcctg catatgaatg gaggcgaagg cgatacaagc 240

tacgccaaga attcatcgta caatgtctgt ctgtctatct ctctctttaa cacacacaca 300

cacacagagt agtagtaaat tatgctatga tacgttgatc tctgacttag tatgtctttt 360

ttcgcccctt aacatttgta ttttggagtg gtatgtgtag caactggttc tcaccaaggg 420

aaacctgtcc ttgaacaatg catacgagaa ttgttgcggg ccaacttgcc caacatcaac 480

aagtgcatta aagttgcgga tttgggatgc gcttctggac caaacacact tttaacagtt 540

cgggacattg tgcaaagtat tgacaaagtt ggccaggaag agaagaatga attagaacat 600

cccaccattc aaatttttct gaatgatctt ttccaaaatg atttcaattc agttttcaag 660

ttgctgccaa gcttctaccg caaactcgag aaagaaaatg gacgcaaaat aggatcgtgc 720

ctaataagcg caatgcctgg ctctttctac ggcagactct tccccgagga gtccatgcat 780

tttttgcact cttgttacag tgttcattgg ttatctcagg tctttgagtt aatccctttt 840

atctttttac tttttcttgt agcaaaaata gttcatgatt ttcattcaac acattagtaa 900

ctatgcatgg aaatttcttt aataattcta aagacatcca caggaatcca agaaagagat 960

ttctgaagaa actaataaca tattttattt aagtcgtggc tcatgattta tattcccaca 1020

tgcaacacta acaaaatgat ccaactatat aagttaccag ttctagacgt gcaggttccc 1080

agcggattgg tgactgaact ggggatcagt gcgaacaaag ggatcattta ctcttccaaa 1140

gcaagtcctc cgcccgtcca gaaggcatat ttggaccaat ttacaaaaga ttttaccaca 1200

tttctgagga ttcattcgga agagttgctt tcaggtggcc gaatgctcct tacttgcatt 1260

tgtaaaggag atgaatccga tggcctgaat accatagact tacttgagag agcaataaac 1320

gacttggttg ttgaggttat catttctctg tctctttgat aatcagatgc tcattgcttg 1380

ttatctgaaa taaactaga 1399

<210> 80
<211> 1399
<212> DNA
<213> Artificial sequence

<220>
<223> XMT/MXMT/DXMT mutant seq 2023-6

<400> 80
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ctacgcacgt aactagctgg ttagcatacg catctatgaa attttcgcta tttaagcccg 120

aaattttgca caattaatca ttaacagaca ccttctttag ccgtcgcaat tcgattgtcc 180

tgtatatgaa tggagctcca agaagtcctg catatgaatg gaggcgaagg cgatacaagc 240

tacgccaaga attcatcgta caatgtctgt ctgtctatct ctctctttaa cacacacaca 300

cacacagagt agtagtaaat tatgctatga tacgttgatc tctgacttag tatgtctttt 360

ttcgcccctt aacatttgta ttttggagtg gtatgtgtag caactggttc tcaccaaggg 420

aaacctgtcc ttgaacaatg catacgagaa ttgttgcggg ccaacttgcc caacatcaac 480

aagtgcatta aagttgcgga tttgggatgc gcttctggac caaacacact tttaacagtt 540

cgggacattg tgcaaagtat tgacaaagtt ggccaggaag agaagaatga attagaacat 600

cccaccattc aaatttttct gaatgatctt ttccaaaatg atttcaattc agttttcaag 660

ttgctgccaa gcttctaccg caaactcgag aaagaaaatg gacgcaaaat aggatcgtgc 720

ctaataagcg caatgcctgg ctctttctac ggcagactct tccccgagga gtccatgcat 780

tttttgcact cttgttacag tgttcattgg ttatctcagg tctttgagtt aatccctttt 840

atctttttac tttttcttgt agcaaaaata gttcatgatt ttcattcaac acattagtaa 900

ctatgcatgg aaatttcttt aataattcta aagacatcca caggaatcca agaaagagat 960

ttctgaagaa actaataaca tattttattt aagtcgtggc tcatgattta tattcccaca 1020

tgcaacacta acaaaatgat ccaactatat aagttaccag ttctagacgt gcaggttccc 1080

agcggattgg tgactgaact ggggatcagt gcgaacaaag ggatcattta ctcttccaaa 1140

gcaagtcctc cgcccgtcca gaaggcatat ttggaccaat ttacaaaaga ttttaccaca 1200

tttctgagga ttcattcgga agagttgctt tcaggtggcc gaatgctcct tacttgcatt 1260

tgtaaaggag atgaatccga tggcctgaat accatagact tacttgagag agcaataaac 1320

gacttggttg ttgaggttat catttctctg tctctttgat aatcagatgc tcattgcttg 1380

ttatctgaaa taaactaga 1399

<210> 81
<211> 1022
<212> DNA
<213> Artificial sequence

<220>
<223> XMT mutant seq 2023-2

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aattcagcct acaatgtctg tctgtctctc tatctctctt taacacacac acacagagta 120

gtagtaaatc atgctatgat acgtcgatct ctaacttagt atgtcttttt tccccccttа 180

acatttgtat tttggagtgg tatgtgtagc aactggttct cgccaaggtg aaacctgtcc 240

ttgaacaatg cgtacgggaa ttgttgcggg ccaacttgcc caacatcaac aagtgcatta 300

aagttgcgga tttgggatgc gcttctggac caaacacact tttaacagtt cgggacattg 360

tccaaagtat tgacaaagtt ggccaggaaa agaagaatga attagaacgt cccaccattc 420

agatttttct gaatgatctt ttcccaaatg atttcaattc ggttttcaag ttgctgccaa 480

gcttctaccg caaacttgag aaagaaaatg gacgcaaaat aggatcgtgc ctaatagggg 540

caatgcccgg ctctttctac agcagactct tccccgagga gtccatgcat tttttacact 600

cttgttactg tcttcaatgg ttatctcagg tctttgagtt aatccctttt atctttttaa 660

ttttttcttgt agcaaaaata gttcatgatt ttcattcaac acattagtaa ctatgcacgg 720

aaatttcttt aataattctc aagatatcca caggaatcca agaaagagat ttctgaagaa 780

actaataaca tattttattc aagtcgtggc tcatgattta tattcccaca tgcaacacta 840

acaaaatgat ccaactatat aagttaccag ctctggacgt gcaggttcct agcggtttgg 900

tgactgaatc ggggatcagt acgaacaaag ggagcattta ctcttccaaa gcaagtcgtc 960

tgcccgtcca gaaggcatat ttggatcaat ttacgaaaga ttttaccaca tttctaagga 1020

tt 1022

<210> 82
<211> 1025
<212> DNA
<213> Artificial sequence

<220>
<223> XMT mutant seq 2023-3

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aattcagcct acaatgtctg tctgtctctc tatctctctt taacacacac acacacagag 120

tagtagtaaa tcatgctatg atacgtcgat ctctaactta gtatgtcttt tttccccccct 180

taacatttgt attttggagt ggtatgtgta gcaactggtt ctcgccaagg atgaaacctg 240

tccttgaaca atgcgtacgg gaattgttgc gggccaactt gcccaacatc aacaagtgca 300

ttaaagttgc ggatttggga tgcgcttctg gaccaaacac acttttaaca gttcgggaca 360

ttgtccaaag tattgacaaa gttggccagg aaaagaagaa tgaattagaa cgtcccacca 420

ttcagatttt tctgaatgat cttttcccaa atgatttcaa ttcggttttc aagttgctgc 480

caagcttcta ccgcaaactt gagaaagaaa atggacgcaa aataggatcg tgcctaatag 540

gggcaatgcc cggctctttc tacagcagac tcttccccga ggagtccatg catttttac 600

actcttgtta ctgtcttcaa tggttatctc aggtctttga gttaatccct tttatctttt 660

taatttttct tgtagcaaaa atagttcatg attttcattc aacacattag taactatgca 720

cggaaatttc tttaataatt ctcaagatat ccacaggaat ccaagaaaga gatttctgaa 780

gaaactaata acatatttta ttcaagtcgt ggctcatgat ttatattccc acatgcaaca 840

ctaacaaaat gatccaacta tataagttac cagctctgga cgtgcaggtt cctagcggtt 900

tggtgactga atcggggatc agtacgaaca aagggagcat ttactcttcc aaagcaagtc 960

gtctgcccgt ccagaaggca tatttggatc aatttacgaa agattttacc acatttctaa 1020

ggatt 1025

<210> 83
<211> 1025
<212> DNA
<213> Artificial sequence

<220>
<223> XMT mutant seq 2023-4

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aattcagcct acaatgtctg tctgtctctc tatctctctt taacacacac acacacagag 120

tagtagtaaa tcatgctatg atacgtcgat ctctaactta gtatgtcttt tttccccccct 180

taacatttgt attttggagt ggtatgtgta gcaactggtt ctcgccaagg atgaaacctg 240

tccttgaaca atgcgtacgg gaattgttgc gggccaactt gcccaacatc aacaagtgca 300

ttaaagttgc ggatttggga tgcgcttctg gaccaaacac acttttaaca gttcgggaca 360

ttgtccaaag tattgacaaa gttggccagg aaaagaagaa tgaattagaa cgtcccacca 420

ttcagatttt tctgaatgat cttttcccaa atgatttcaa ttcggttttc aagttgctgc 480

caagcttcta ccgcaaactt gagaaagaaa atggacgcaa aataggatcg tgcctaatag 540

gggcaatgcc cggctctttc tacagcagac tcttccccga ggagtccatg catttttac 600

actcttgtta ctgtcttcaa tggttatctc aggtctttga gttaatccct tttatctttt 660

taatttttct tgtagcaaaa atagttcatg attttcattc aacacattag taactatgca 720

cggaaatttc tttaataatt ctcaagatat ccacaggaat ccaagaaaga gatttctgaa 780

gaaactaata acatatttta ttcaagtcgt ggctcatgat ttatattccc acatgcaaca 840

ctaacaaaat gatccaacta tataagttac cagctctgga cgtgcaggtt cctagcggtt 900

tggtgactga atcggggatc agtacgaaca aagggagcat ttactcttcc aaagcaagtc 960

gtctgcccgt ccagaaggca tatttggatc aatttacgaa agattttacc acatttctaa 1020

ggatt 1025

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gtagtaaatc atgctatgat acgtcgatct ctaacttagt atgtcttttt tccccccctta 180

acatttgtat tttggagtgg tatgtgtagc aactggttct cgccaaggtg aaacctgtcc 240

ttgaacaatg cgtacgggaa ttgttgcggg ccaacttgcc caacatcaac aagtgcatta 300

aagttgcgga tttgggatgc gcttctggac caaacacact tttaacagtt cgggacattg 360

tccaaagtat tgacaaagtt ggccaggaaa agaagaatga attagaacgt cccaccattc 420

agatttttct gaatgatctt ttcccaaatg atttcaattc ggttttcaag ttgctgccaa 480

gcttctaccg caaacttgag aaagaaaatg gacgcaaaat aggatcgtgc ctaatagggg 540

caatgcccgg ctctttctac agcagactct tccccgagga gtccatgcat tttttacact 600

cttgttactg tcttcaatgg ttatctcagg tctttgagtt aatccctttt atctttttaa 660

ttttcttgt agcaaaaata gttcatgatt ttcattcaac acattagtaa ctatgcacgg 720

aaatttcttt aataattctc aagatatcca caggaatcca agaaagagat ttctgaagaa 780

actaataaca tattttattc aagtcgtggc tcatgattta tattcccaca tgcaacacta 840

acaaaatgat ccaactatat aagttaccag ctctggacgt gcaggttcct agcggtttgg 900

tgactgaatc ggggatcagt acgaacaaag ggagcattta ctcttccaaa gcaagtcgtc 960

tgcccgtcca gaaggcatat ttggatcaat ttacgaaaga ttttaccaca tttctaagga 1020

tt 1022

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cggttagcat acgcatctaa gaaattttcg ccatttaagt ccgaaatttc gcacagttaa 120

tcattaacag acaccttcct tagcagtccc aattcgattt atgtacaagt cctgcatatg 180

aatggagctc caagaagtcc tgcatatgaa tggaggcgaa ggcgaagcaa gctacgccaa 240

gaattcatcc ttcaatgtct gtctatctgt ctatctctct ctttaacaca cacacacaca 300

cacacagagt agtagtaaat catgctatga tacgtcgatc tctaacttag tatgtctttt 360

ttcgcccctt aacatttgta ttttggagtg gtatgtgtag caactggttc tcgccaagga 420

ataggatcgt gcctaatagc cgcaatgcct ggctctttcc acggcagact cttccccgag 480

gagtccatgc atttttttaca ctcttcttac agtcttcagt ttttatccca ggtctttgaa 540

ttactccctt ttatcttttt acttttttctt gtagcaaaaa tagttcatga ttttcattca 600

acacattagt tactatgcat ggaaatttct ttaataattc tcaagatatc cacaggaatc 660

caagaaagag atttctaaag ggaaccagct ttagactgca ggttcccagc ggtttggtga 720

ctgaattggg gatcactgcg aacaaaagga gcatttactc ttccaaagca agtcctccgc 780

ccgtccagaa ggcatatttg gatcaattta cgaaagattt taccacattt ttaaggatgc 840

gttcggaaga gttgctttca cgtggccgaa tgctccttac ttgcatttgt aaag 894

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acacacacac acagagtagt agtaaatcat gctatgatac gtcgatctct aacttagtat 180

gtctttttc ccccttaac atttgtattt tggagtggta tgtgtagcaa ctggttctcg 240

ccaaggtggg ataccttcta gttaacagtc acaccattca tgacatatcc atggaatagg 300

atcgtgccta ataggggcaa tgcccggctc tttctacagc agactcttcc ccgaggagtc 360

catgcatttt ttacactctt gttactgtct tcaatggtta tctcaggtct ttgagttaat 420

ccctttatc tttttaattt ttcttgtagc aaaaatagtt catgattttc attcaacaca 480

ttagtaacta tgcacggaaa tttctttaat aattctcaag atatccacag gaatccaaga 540

aagagatttc tgaagaaact aataacatat tttattcaag tcgtggctca tgatttatat 600

tcccacatgc aacactaaca aa 622