## SEQUENCE LISTING

SEQ ID NO: 1
6S 5′ genomic donor sequence

GCTCTTCGCCGCCGCCACTCCTGCTCGAGCGCGCCCGCGCGTGCGCCGCCAGCGCCTTGGCCTTTTCG
CCGCGCTCGTGCGCGTCGCTGATGTCCATCACCAGGTCCATGAGGTCTGCCTTGCGCCGGCTGAGCCA
CTGCTTCGTCCGGGCGGCCAAGAGGAGCATGAGGGAGGACTCCTGGTCCAGGGTCCTGACGTGGTCGC
GGCTCTGGGAGCGGGCCAGCATCATCTGGCTCTGCCGCACCGAGGCCGCCTCCAACTGGTCCTCCAGC
AGCCGCAGTCGCCGCCGACCCTGGCAGAGGAAGACAGGTGAGGGGGGTATGAATTGTACAGAACAACC
ACGAGCCTTGTCTAGGCAGAATCCCTACCAGTCATGGCTTTACCTGGATGACGGCCTGCGAACAGCTG
TCCAGCGACCCTCGCTGCCGCCGCTTCTCCCGCACGCTTCTTTCCAGCACCGTGATGGCGCGAGCCAG
CGCCGCACGCTGGCGCTGCGCTTCGCCGATCTGAGGACAGTCGGGGAACTCTGATCAGTCTAAACCCC
CTTGCGCGTTAGTGTTGCCATCCTTTGCAGACCGGTGAGAGCCGACTTGTTGTGCGCCACCCCCCACA
CCACCTCCTCCCAGACCAATTCTGTCACCTTTTTGGCGAAGGCATCGGCCTCGGCCTGCAGAGAGGAC
AGCAGTGCCCAGCCGCTGGGGGTTGGCGGATGCACGCTCAGGTACC

SEQ ID NO: 2
6S 3′ genomic donor sequence

GAGCTCCTTGTTTTCCAGAAGGAGTTGCTCCTTGAGCCTTTCATTCTCAGCCTCGATAACCTCCAAAG
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CCAGACTTGTTGCTCACTGGGAAAAGGACCATCAGCTCCAAAAAACTTGCCGCTCAAACCGCGTACCT
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AATTGCCTCAGAATGTGGAATCATCTGCCCCCTGTGCGAGCCCATGCCAGGCATGTCGCGGGCGAGGA
CACCCGCCACTCGTACAGCAGACCATTATGCTACCTCACAATAGTTCATAACAGTGACCATATTTCTC
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GGTCAACCGGCATGGGGCTACCGAAATCCCCGACCGGATCCCACCACCCCCGCGATGGGAAGAATCTC
TCCCCGGGATGTGGGCCCACCACCAGCACAACCTGCTGGCCCAGGCGAGCGTCAAACCATACCACACA
AATATCCTTGGCATCGGCCCTGAATTCCTTCTGCCGCTCTGCTACCCGGTGCTTCTGTCCGAAGCAGG
GGTTGCTAGGGATCGCTCCGAGTCCGCAAACCCTTGTCGCGTGGCGGGGCTTGTTCGAGCTTGAAGAG
C

SEQ ID NO: 3
*S. cereviseae* invertase protein sequence

MLLQAFLFLLAGFAAKISASMTNETSDRPLVHFTPNKGWMNDPNGLWYDEKDAKWHLYFQYNPNDTVW
GTPLFWGHATSDDLTNWEDQPIAIAPKRNDSGAFSGSMVVDYNNTSGFFNDTIDPRQRCVAIWTYNTP
ESEEQYISYSLDGGYTFTEYQKNPVLAANSTQFRDPKVFWYEPSQKWIMTAAKSQDYKIEIYSSDDLK
SWKLESAFANEGFLGYQYECPGLIEVPTEQDPSKSYWVMFISINPGAPAGGSFNQYFVGSFNGTHFEA
FDNQSRVVDFGKDYYALQTFFNTDPTYGSALGIAWASNWEYSAFVPTNPWRSSMSLVRKFSLNTEYQA
NPETELINLKAEPILNISNAGPWSRFATNTTLTKANSYNVDLSNSTGTLEFELVYAVNTTQTISKSVF
ADLSLWFKGLEDPEEYLRMGFEVSASSFFLDRGNSKVKFVKENPYFTNRMSVNNQPFKSENDLSYYKV
YGLLDQNILELYFNDGDVVSTNTYFMTTGNALGSVNMTTGVDNLFYIDKFQVREVK

SEQ ID NO: 4
S. cereviseae invertase protein coding sequence codon optimized for expression in P. moriformis (UTEX 1435)

ATGctgctgcaggccttcctgttcctgctggccggcttcgccgccaagatcagcgcctccatgacgaa
cgagacgtccgaccgccccctggtgcacttcacccccaacaagggctggatgaacgaccccaacggcc
tgtggtacgacgagaaggacgccaagtggcacctgtacttccagtacaacccgaacgacaccgtctgg
gggacgcccttgttctggggccacgccacgtccgacgacctgaccaactgggaggaccagcccatcgc
catcgccccgaagcgcaacgactccggcgccttctccggctccatggtggtggactacaacaacacct
ccggcttcttcaacgacaccatcgacccgcgccagcgctgcgtggccatctggacctacaacaccccg
gagtccgaggagcagtacatctcctacagcctggacggcggctacaccttcaccgagtaccagaagaa

ccccgtgctggccgccaactccacccagttccgcgacccgaaggtcttctggtacgagccctcccaga
agtggatcatgaccgcggccaagtcccaggactacaagatcgagatctactcctccgacgacctgaag
tcctggaagctggagtccgcgttcgccaacgagggcttcctcggctaccagtacgagtgccccggcct
gatcgaggtccccaccgagcaggaccccagcaagtcctactgggtgatgttcatctccatcaaccccg
gcgccccggccggcggctccttcaaccagtacttcgtcggcagcttcaacggcacccacttcgaggcc
ttcgacaaccagtcccgcgtggtggacttcggcaaggactactacgccctgcagaccttcttcaacac
cgacccgacctacgggagcgccctgggcatcgcgtgggcctccaactgggagtactccgccttcgtgc
ccaccaaccccctggcgctcctccatgtccctcgtgcgcaagttctccctcaacaccgagtaccaggcc
aacccggagacggagctgatcaacctgaaggccgagccgatcctgaacatcagcaacgccggcccctg
gagccggttcgccaccaacaccacgttgacgaaggccaacagctacaacgtcgacctgtccaacagca
ccggcaccctggagttcgagctggtgtacgccgtcaacaccacccagacgatctccaagtccgtgttc
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tcaccaaccgcatgagcgtgaacaaccagcccttcaagagcgagaacgacctgtcctactacaaggtg
tacggcttgctggaccagaacatcctggagctgtacttcaacgacggcgacgtcgtgtccaccaacac
ctacttcatgaccaccgggaacgccctgggctccgtgaacatgacgacgggggtggacaacctgttct
acatcgacaagttccaggtgcgcgaggtcaagTGA

SEQ ID NO: 5
*Chlamydomonas reinhardtii* TUB2 (B-tub) promoter/5′ UTR

CTTTCTTGCGCTATGACACTTCCAGCAAAAGGTAGGGCGGGCTGCGAGACGGCTTCCCGGCGCTGCAT
GCAACACCGATGATGCTTCGACCCCCCGAAGCTCCTTCGGGGCTGCATGGGCGCTCCGATGCCGCTCC
AGGGCGAGCGCTGTTTAAATAGCCAGGCCCCCGATTGCAAAGACATTATAGCGAGCTACCAAAGCCAT
ATTCAAACACCTAGATCACTACCACTTCTACACAGGCCACTCGAGCTTGTGATCGCACTCCGCTAAGG
GGGCGCCTCTTCCTCTTCGTTTCAGTCACAACCCGCAAAC

SEQ ID NO: 6
*Chlorella vulgaris* nitrate reductase 3′UTR

GCAGCAGCAGCTCGGATAGTATCGACACACTCTGGACGCTGGTCGTGTGATGGACTGTTGCCGCCACA
CTTGCTGCCTTGACCTGTGAATATCCCTGCCGCTTTTATCAAACAGCCTCAGTGTGTTTGATCTTGTG
TGTACGCGCTTTTGCGAGTTGCTAGCTGCTTGTGCTATTTGCGAATACCACCCCCAGCATCCCCTTCC
CTCGTTTCATATCGCTTGCATCCCAACCGCAACTTATCTACGCTGTCCTGCTATCCCTCAGCGCTGCT
CCTGCTCCTGCTCACTGCCCCTCGCACAGCCTTGGTTTGGGCTCCGCCTGTATTCTCCTGGTACTGCA
ACCTGTAAACCAGCACTGCAATGCTGATGCACGGGAAGTAGTGGGATGGGAACACAAATGGAAAGCTT

SEQ ID NO: 7
Nucleotide sequence of the codon-optimized expression cassette of *S. cerevisiae suc2* gene with *C. reinhardtii* β-tubulin promoter/5′UTR and *C. vulgaris* nitrate reductase 3′ UTR

CTTTCTTGCGCTATGACACTTCCAGCAAAAGGTAGGGCGGGCTGCGAGACGGCTTCCCGGCGCTGCAT
GCAACACCGATGATGCTTCGACCCCCCGAAGCTCCTTCGGGGCTGCATGGGCGCTCCGATGCCGCTCC
AGGGCGAGCGCTGTTTAAATAGCCAGGCCCCCGATTGCAAAGACATTATAGCGAGCTACCAAAGCCAT
ATTCAAACACCTAGATCACTACCACTTCTACACAGGCCACTCGAGCTTGTGATCGCACTCCGCTAAGG
GGGCGCCTCTTCCTCTTCGTTTCAGTCACAACCCGCAAACGGCGCGCCATGCTGCTGCAGGCCTTCCT
GTTCCTGCTGGCCGGCTTCGCCGCCAAGATCAGCGCCTCCATGACGAACGAGACGTCCGACCGCCCCC
TGGTGCACTTCACCCCCAACAAGGGCTGGATGAACGACCCCAACGGCCTGTGGTACGACGAGAAGGAC
GCCAAGTGGCACCTGTACTTCCAGTACAACCCGAACGACACCGTCTGGGGGACGCCCTTGTTCTGGGG
CCACGCCACGTCCGACGACCTGACCAACTGGGAGGACCAGCCCATCGCCATCGCCCCGAAGCGCAACG
ACTCCGGCGCCTTCTCCGGCTCCATGGTGGTGGACTACAACAACACCTCCGGCTTCTTCAACGACACC
ATCGACCCGCGCCAGCGCTGCGTGGCCATCTGGACCTACAACACCCCGGAGTCCGAGGAGCAGTACAT
CTCCTACAGCCTGGACGGCGGCTACACCTTCACCGAGTACCAGAAGAACCCCGTGCTGGCCGCCAACT
CCACCCAGTTCCGCGACCCGAAGGTCTTCTGGTACGAGCCCTCCCAGAAGTGGATCATGACCGCGGCC

AAGTCCCAGGACTACAAGATCGAGATCTACTCCTCCGACGACCTGAAGTCCTGGAAGCTGGAGTCCGC
GTTCGCCAACGAGGGCTTCCTCGGCTACCAGTACGAGTGCCCCGGCCTGATCGAGGTCCCCACCGAGC
AGGACCCCAGCAAGTCCTACTGGGTGATGTTCATCTCCATCAACCCCGGCGCCCCGGCCGGCGGCTCC
TTCAACCAGTACTTCGTCGGCAGCTTCAACGGCACCCACTTCGAGGCCTTCGACAACCAGTCCCGCGT
GGTGGACTTCGGCAAGGACTACTACGCCCTGCAGACCTTCTTCAACACCGACCCGACCTACGGGAGCG
CCCTGGGCATCGCGTGGGCCTCCAACTGGGAGTACTCCGCCTTCGTGCCCACCAACCCCTGGCGCTCC
TCCATGTCCCTCGTGCGCAAGTTCTCCCTCAACACCGAGTACCAGGCCAACCCGGAGACGGAGCTGAT
CAACCTGAAGGCCGAGCCGATCCTGAACATCAGCAACGCCGGCCCCTGGAGCCGGTTCGCCACCAACA
CCACGTTGACGAAGGCCAACAGCTACAACGTCGACCTGTCCAACAGCACCGGCACCCTGGAGTTCGAG
CTGGTGTACGCCGTCAACACCACCCAGACGATCTCCAAGTCCGTGTTCGCGGACCTCTCCCTCTGGTT
CAAGGGCCTGGAGGACCCCGAGGAGTACCTCCGCATGGGCTTCGAGGTGTCCGCGTCCTCCTTCTTCC
TGGACCGCGGGAACAGCAAGGTGAAGTTCGTGAAGGAGAACCCCTACTTCACCAACCGCATGAGCGTG
AACAACCAGCCCTTCAAGAGCGAGAACGACCTGTCCTACTACAAGGTGTACGGCTTGCTGGACCAGAA
CATCCTGGAGCTGTACTTCAACGACGGCGACGTCGTGTCCACCAACACCTACTTCATGACCACCGGGA
ACGCCCTGGGCTCCGTGAACATGACGACGGGGGTGGACAACCTGTTCTACATCGACAAGTTCCAGGTG
CGCGAGGTCAAGTGACAATTGGCAGCAGCAGCTCGGATAGTATCGACACACTCTGGACGCTGGTCGTG
TGATGGACTGTTGCCGCCACACTTGCTGCCTTGACCTGTGAATATCCCTGCCGCTTTTATCAAACAGC
CTCAGTGTGTTTGATCTTGTGTGTACGCGCTTTTGCGAGTTGCTAGCTGCTTGTGCTATTTGCGAATA
CCACCCCCAGCATCCCCTTCCCTCGTTTCATATCGCTTGCATCCCAACCGCAACTTATCTACGCTGTC
CTGCTATCCCTCAGCGCTGCTCCTGCTCCTGCTCACTGCCCCTCGCACAGCCTTGGTTTGGGCTCCGC
CTGTATTCTCCTGGTACTGCAACCTGTAAACCAGCACTGCAATGCTGATGCACGGGAAGTAGTGGGAT
GGGAACACAAATGGAGGATCC

SEQ ID NO: 8
*Prototheca moriformis* (UTEX 1435) Amt03 promoter

GGCCGACAGGACGCGCGTCAAAGGTGCTGGTCGTGTATGCCCTGGCCGGCAGGTCGTTGCTGCTGCTG
GTTAGTGATTCCGCAACCCTGATTTTGGCGTCTTATTTTGGCGTGGCAAACGCTGGCGCCCGCGAGCC
GGGCCGGCGGCGATGCGGTGCCCCACGGCTGCCGGAATCCAAGGGAGGCAAGAGCGCCCGGGTCAGTT
GAAGGGCTTTACGCGCAAGGTACAGCCGCTCCTGCAAGGCTGCGTGGTGGAATTGGACGTGCAGGTCC
TGCTGAAGTTCCTCCACCGCCTCACCAGCGGACAAAGCACCGGTGTATCAGGTCCGTGTCATCCACTC
TAAAGAGCTCGACTACGACCTACTGATGGCCCTAGATTCTTCATCAAAAACGCCTGAGACACTTGCCC
AGGATTGAAACTCCCTGAAGGGACCACCAGGGGCCCTGAGTTGTTCCTTCCCCCCGTGGCGAGCTGCC
AGCCAGGCTGTACCTGTGATCGAGGCTGGCGGGAAAATAGGCTTCGTGTGCTCAGGTCATGGGAGGTG
CAGGACAGCTCATGAAACGCCAACAATCGCACAATTCATGTCAAGCTAATCAGCTATTTCCTCTTCAC
GAGCTGTAATTGTCCCAAAATTCTGGTCTACCGGGGGTGATCCTTCGTGTACGGGCCCTTCCCTCAAC
CCTAGGTATGCGCGCATGCGGTCGCCGCGCAACTCGCGCGAGGGCCGAGGGTTTGGGACGGGCCGTCC
CGAAATGCAGTTGCACCCGGATGCGTGGCACCTTTTTTGCGATAATTTATGCAATGGACTGCTCTGCA
AAATTCTGGCTCTGTCGCCAACCCTAGGATCAGCGGCGTAGGATTTCGTAATCATTCGTCCTGATGGG
GAGCTACCGACTACCCTAATATCAGCCCGACTGCCTGACGCCAGCGTCCACTTTTGTGCACACATTCC
ATTCGTGCCCAAGACATTTCATTGTGGTGCGAAGCGTCCCCAGTTACGCTCACCTGTTTCCCGACCTC
CTTACTGTTCTGTCGACAGAGCGGGCCCACAGGCCGGTCGCAGCC

SEQ ID NO: 9
*Chlorella protothecoides* (UTEX 250) stearoyl ACP desaturase transit peptide cDNA sequence codon optimized for expression in P. moriformis.

ACTAGTATGGCCACCGCATCCACTTTCTCGGCGTTCAATGCCCGCTGCGGCGACCTGCGTCGCTCGGC
GGGCTCCGGGCCCCGGCGCCCAGCGAGGCCCCTCCCCGTGCGCGGGCGCGCC

SEQ ID NO: 10

*Cuphea wrightii* FatB2 thioesterase nucleic acid sequence; Gen Bank Accession No. U56104

ATGGTGGTGGCCGCCGCCGCCAGCAGCGCCTTCTTCCCCGTGCCCGCCCCCCGCCCCACCCCCAAGCC
CGGCAAGTTCGGCAACTGGCCCAGCAGCCTGAGCCAGCCCTTCAAGCCCAAGAGCAACCCCAACGGCC
GCTTCCAGGTGAAGGCCAACGTGAGCCCCCACGGGCGCGCCCCCAAGGCCAACGGCAGCGCCGTGAGC
CTGAAGTCCGGCAGCCTGAACACCCTGGAGGACCCCCCCCAGCAGCCCCCCCCCCCCGCACCTTCCTGAA
CCAGCTGCCCGACTGGAGCCGCCTGCGCACCGCCATCACCACCGTGTTCGTGGCCGCCGAGAAGCAGT
TCACCCGCCTGGACCGCAAGAGCAAGCGCCCCGACATGCTGGTGGACTGGTTCGGCAGCGAGACCATC
GTGCAGGACGGCCTGGTGTTCCGCGAGCGCTTCAGCATCCGCAGCTACGAGATCGGCGCCGACCGCAC
CGCCAGCATCGAGACCCTGATGAACCACCTGCAGGACACCAGCCTGAACCACTGCAAGAGCGTGGGCC
TGCTGAACGACGGCTTCGGCCGCACCCCCGAGATGTGCACCCGCGACCTGATCTGGGTGCTGACCAAG
ATGCAGATCGTGGTGAACCGCTACCCCACCTGGGGCGACACCGTGGAGATCAACAGCTGGTTCAGCCA
GAGCGGCAAGATCGGCATGGGCCGCGAGTGGCTGATCAGCGACTGCAACACCGGCGAGATCCTGGTGC
GCGCCACCAGCGCCTGGGCCATGATGAACCAGAAGACCCGCCGCTTCAGCAAGCTGCCCTGCGAGGTG
CGCCAGGAGATCGCCCCCCACTTCGTGGACGCCCCCCCCGTGATCGAGGACAACGACCGCAAGCTGCA
CAAGTTCGACGTGAAGACCGGCGACAGCATCTGCAAGGGCCTGACCCCCGGCTGGAACGACTTCGACG
TGAACCAGCACGTGAGCAACGTGAAGTACATCGGCTGGATTCTGGAGAGCATGCCCACCGAGGTGCTG
GAGACCCAGGAGCTGTGCAGCCTGACCCTGGAGTACCGCCGCGAGTGCGGCCGCGAGAGCGTGGTGGA
GAGCGTGACCAGCATGAACCCCAGCAAGGTGGGCGACCGCAGCCAGTACCAGCACCTGCTGCGCCTGG
AGGACGGCGCCGACATCATGAAGGGCCGCACCGAGTGGCGCCCCAAGAACGCCGGCACCAACCGCGCC
ATCAGCACCTGA

SEQ ID NO: 11
*Cuphea wrightii* FatB2 thioesterase amino acid sequence; Gen Bank Accession No. U56104

MVVAAAASSAFFPVPAPRPTPKPGKFGNWPSSLSQPFKPKSNPNGRFQVKANVSPHPKANGSAVSLKS
GSLNTLEDPPSSPPPRTFLNQLPDWSRLRTAITTVFVAAEKQFTRLDRKSKRPDMLVDWFGSETIVQD
GLVFRERFSIRSYEIGADRTASIETLMNHLQDTSLNHCKSVGLLNDGFGRTPEMCTRDLIWVLTKMQI
VVNRYPTWGDTVEINSWFSQSGKIGMGREWLISDCNTGEILVRATSAWAMMNQKTRRFSKLPCEVRQE
IAPHFVDAPPVIEDNDRKLHKFDVKTGDSICKGLTPGWNDFDVNQHVSNVKYIGWILESMPTEVLETQ
ELCSLTLEYRRECGRESVVESVTSMNPSKVGDRSQYQHLLRLEDGADIMKGRTEWRPKNAGTNRAIST

SEQ ID NO: 12
Codon-optimized coding region of *Cocus nucifera* C12:0-preferring LPAAT from pSZ2046

ATGGACGCCTCCGGCGCCTCCTCCTTCCTGCGCGGCCGCTGCCTGGAGTCCTGCTTCAAGGCCTCCTT
CGGCTACGTAATGTCCCAGCCCAAGGACGCCGCCGGCCAGCCCTCCCGCCGCCCCGCCGACGCCGACG
ACTTCGTGGACGACGACCGCTGGATCACCGTGATCCTGTCCGTGGTGCGCATCGCCGCCTGCTTCCTG
TCCATGATGGTGACCACCATCGTGTGGAACATGATCATGCTGATCCTGCTGCCCTGGCCCTACGCCCG
CATCCGCCAGGGCAACCTGTACGGCCACGTGACCGGCCGCATGCTGATGTGGATTCTGGGCAACCCCA
TCACCATCGAGGGCTCCGAGTTCTCCAACACCCGCGCCATCTACATCTGCAACCACGCCTCCCTGGTG
GACATCTTCCTGATCATGTGGCTGATCCCCAAGGGCACCGTGACCATCGCCAAGAAGGAGATCATCTG
GTATCCCCTGTTCGGCCAGCTGTACGTGCTGGCCAACCACCAGCGCATCGACCGCTCCAACCCCTCCG
CCGCCATCGAGTCCATCAAGGAGGTGGCCCGCGCCGTGGTGAAGAAGAACCTGTCCCTGATCATCTTC
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CCAGACCCGCCTGCCCATCGTGCCGATGGTGCTGACCGGCACCCACCTGGCCTGGCGCAAGAACTCCC
TGCGCGTGCGCCCCGCCCCCATCACCGTGAAGTACTTCTCCCCCATCAAGACCGACGACTGGGAGGAG
GAGAAGATCAACCACTACGTGGAGATGATCCACGCCCTGTACGTGGACCACCTGCCCGAGTCCCAGAA
GCCCCTGGTGTCCAAGGGCCGCGACGCCTCCGGCCGCTCCAACTCCTGA

SEQ ID NO: 13
pLoop 5’ genomic donor sequence

gctcttcgctaacggaggtctgtcaccaaatggaccccgtctattgcgggaaaccacggcgatggcac
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ggccccgatcaagagccaggacatccaaactacccacagcatcaacgccccggcctatactcgaaccc
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SEQ ID NO: 14
pLoop 3' genomic donor sequence

gagctcagcggcgacggtcctgctaccgtacgacgttgggcacgcccatgaaagtttgtataccgagc
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gatggaaaatccgaacctcgtgcaagaactgagcaaacctcgttacatggatgcacagtcgccagtcc
aatgaacattgaagtgagcgaactgttcgcttcggtggcagtactactcaaagaatgagctgctgtta
aaaatgcactctcgttctctcaagtgagtggcagatgagtgctcacgccttgcacttcgctgcccgtg
tcatgccctgcgccccaaaatttgaaaaaagggatgagattattgggcaatggacgacgtcgtcgctc
cgggagtcaggaccggcggaaaataagaggcaacacactccgcttcttagctcttcc

SEQ ID NO: 15
NeoR expression cassette including *C. reinhardtii* β-tubulin promoter/5'UTR and *C. vulgaris* nitrate reductase 3' UTR

ctttcttgcgctatgacacttccagcaaaaggtagggcgggctgcgagacggcttcccggcgctgcat
gcaacaccgatgatgcttcgacccccgaagctccttcggggctgcatgggcgctccgatgccgctcc
agggcgagcgctgtttaaatagccaggcccccgattgcaaagacattatagcgagctaccaaagccat
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*gcctccacgccggctcccccgccgcctgggtggagcgcctgttcggctacgactgggcccagcagacc*
*atcggctgctccgacgccgccgtgttccgcctgtccgcccagggccgccccgtgctgttcgtgaagac*
*cgacctgtccggcgccctgaacgagctgcaggacgaggccgcccgcctgtcctggctggccaccaccg*
*gcgtgccctgcgccgccgtgctggacgtggtgaccgaggccggccgcgactggctgctgctgggcgag*
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*agcgcgcccgcacccgcatggaggccggcctggtggaccaggacgacctggacgaggagcaccagggc*
*ctggcccccgccgagctgttcgcccgcctgaaggcccgcatgcccgacggcgaggacctggtggtgac*
*ccacggcgacgcctgcctgcccaacatcatggtggagaacggccgcttctccggcttcatcgactgcg*
*gccgcctgggcgtggccgaccgctaccaggacatcgccctggccacccgcgacatcgccgaggagctg*
*ggcggcgagtgggccgaccgcttcctggtgctgtacggcatcgccgcccccgactcccagcgcatcgc*
*cttctaccgcctgctggacgagttcttcTGA*caattggcagcagcagctcggatagtatcgacacact
ctggacgctggtcgtgtgatggactgttgccgccacacttgctgccttgacctgtgaatatccctgcc
gcttttatcaaacagcctcagtgtgtttgatcttgtgtgtacgcgcttttgcgagttgctagctgctt
gtgctatttgcgaataccacccccagcatccccttccctcgtttcatatcgcttgcatcccaaccgca
acttatctacgctgtcctgctatccctcagcgctgctcctgctcctgctcactgcccctcgcacagcc
ttggtttgggctccgcctgtattctcctggtactgcaacctgtaaaccagcactgcaatgctgatgca
cgggaagtagtgggatgggaacacaaatggaggatcc

SEQ ID NO: 16
*Cocos nucifera* 1-acyl-sn-glycerol-3-phosphate acyltransferase (LPAAT)

MDASGASSFLRGRCLESCFKASFGYVMSQPKDAAGQPSRRPADADDFVDDDRWITVILSV
VRIAACFLSMMVTTIVWNMIMLILLPWPYARIRQGNLYGHVTGRMLMWILGNPITIEGSE

FSNTRAIYICNHASLVDIFLIMWLIPKGTVTIAKKEIIWYPLFGQLYVLANHQRIDRSNP
SAAIESIKEVARAVVKKNLSLIIFPEGTRSKTGRLLPFKKGFIHIALQTRLPIVPMVLTG
THLAWRKNSLRVRPAPITVKYFSPIKTDDWEEEKINHYVEMIHALYVDHLPESQKPLVSK
GRDASGRSNS

SEQ ID NO: 17
pSZ1500

GGGCTGGTCTGAATCCTTCAGGCGGGTGTTACCCGAGAAAGAAAGGGTGCCGATTTCAAAGCAGACCC
ATGTGCCGGGCCCTGTGGCCTGTGTTGGCGCCTATGTAGTCACCCCCCCTCACCCAATTGTCGCCAGT
TTGCGCACTCCATAAACTCAAAACAGCAGCTTCTGAGCTGCGCTGTTCAAGAACACCTCTGGGGTTTG
CTCACCCGCGAGGTCGACGCCCAGCATGGCTATCAAGACGAACAGGCAGCCTGTGGAGAAGCCTCCGT
TCACGATCGGGACGCTGCGCAAGGCCATCCCCGCGCACTGTTTCGAGCGCTCGGCGCTTCGTAGCAGC
ATGTACCTGGCCTTTGACATCGCGGTCATGTCCCTGCTCTACGTCGCGTCGACGTACATCGACCCTGC
ACCGGTGCCTACGTGGGTCAAGTACGGCATCATGTGGCCGCTCTACTGGTTCTTCCAGGTGTGTTTGA
GGGTTTTGGTTGCCCGTATTGAGGTCCTGGTGGCGCGCATGGAGGAGAAGGCGCCTGTCCCGCTGACC
CCCCCGGCTACCCTCCCGGCACCTTCCAGGGCGCCTTCGGCACGGGTGTCTGGGTGTGCGCGCACGAG
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CCCCGAAGCTCCTTCGGGGCTGCATGGGCGCTCCGATGCCGCTCCAGGGCGAGCGCTGTTTAAATAGC
CAGGCCCCCGATTGCAAAGACATTATAGCGAGCTACCAAAGCCATATTCAAACACCTAGATCACTACC
ACTTCTACACAGGCCACTCGAGCTTGTGATCGCACTCCGCTAAGGGGGCGCCTCTTCCTCTTCGTTTC
AGTCACAACCCGCAAACTCTAGAATATCAATGCTGCTGCAGGCCTTCCTGTTCCTGCTGGCCGGCTTC
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CAAGGGCTGGATGAACGACCCCAACGGCCTGTGGTACGACGAGAAGGACGCCAAGTGGCACCTGTACT
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CTGACCAACTGGGAGGACCAGCCCATCGCCATCGCCCCGAAGCGCAACGACTCCGGCGCCTTCTCCGG
CTCCATGGTGGTGGACTACAACAACACCTCCGGCTTCTTCAACGACACCATCGACCCGCGCCAGCGCT
GCGTGGCCATCTGGACCTACAACACCCCGGAGTCCGAGGAGCAGTACATCTCCTACAGCCTGGACGGC
GGCTACACCTTCACCGAGTACCAGAAGAACCCCGTGCTGGCCGCCAACTCCACCCAGTTCCGCGACCC
GAAGGTCTTCTGGTACGAGCCCTCCCAGAAGTGGATCATGACCGCGGCCAAGTCCCAGGACTACAAGA
TCGAGATCTACTCCTCCGACGACCTGAAGTCCTGGAAGCTGGAGTCCGCGTTCGCCAACGAGGGCTTC
CTCGGCTACCAGTACGAGTGCCCCGGCCTGATCGAGGTCCCCACCGAGCAGGACCCCAGCAAGTCCTA
CTGGGTGATGTTCATCTCCATCAACCCCGGCGCCCCGGCCGGCGGCTCCTTCAACCAGTACTTCGTCG
GCAGCTTCAACGGCACCCACTTCGAGGCCTTCGACAACCAGTCCCGCGTGGTGGACTTCGGCAAGGAC
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CCGAGATCATCGACACCCACGAGCTGCAGGCCATCACCCTGGACTACCGCCGCGAGTGCCAGCGCGAC
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CGACACCCACGTGCTGCACCACCTCTTCAGCACCATCCCGCACTACCACGCCGAGGAGGCCTCCGCCG
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GACTGGCGCGACTGCCGCTACGTCGTCCCGGACGCGCCCGAGGACGACTCCGCGCTCTGGTTCCACAA
GTGAGTGAGTGA

SEQ ID NO: 18
5′ FADc genomic region donor DNA

GGGCTGGTCTGAATCCTTCAGGCGGGTGTTACCCGAGAAAGAAAGGGTGCCGATTTCAAAGCAGACCC
ATGTGCCGGGCCCTGTGGCCTGTGTTGGCGCCTATGTAGTCACCCCCCCTCACCCAATTGTCGCCAGT
TTGCGCACTCCATAAACTCAAAACAGCAGCTTCTGAGCTGCGCTGTTCAAGAACACCTCTGGGGTTTG
CTCACCCGCGAGGTCGACGCCCAGCATGGCTATCAAGACGAACAGGCAGCCTGTGGAGAAGCCTCCGT
TCACGATCGGGACGCTGCGCAAGGCCATCCCCGCGCACTGTTTCGAGCGCTCGGCGCTTCGTAGCAGC
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ACCGGTGCCTACGTGGGTCAAGTACGGCATCATGTGGCCGCTCTACTGGTTCTTCCAGGTGTGTTTGA
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TGCGGCCACCAGGCCTTTTCCTCCAGCCAGGCCATCAACGACGGCGTGGGCCTGGTGTTCCACAGCCT
GCTGCTGGTGCCCTACTACTCCTGGAAGCACTCGCACCG

SEQ ID NO: 19
3′ FADc genomic region donor DNA

CCGCCACCACTCCAACACGGGGTGCCTGGACAAGGACGAGGTGTTTGTGCCGCCGCACCGCGCAGTGG
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SEQ ID NO: 20
5′ donor DNA sequence of *Prototheca moriformis* FATA1 knockout homologous recombination targeting construct

GCTCTTCGGAGTCACTGTGCCACTGAGTTCGACTGGTAGCTGAATGGAGTCGCTGCTCCACTAAACGA
ATTGTCAGCACCGCCAGCCGGCCGAGGACCCGAGTCATAGCGAGGGTAGTAGCGCGCCATGGCACCGA
CCAGCCTGCTTGCCAGTACTGGCGTCTCTTCCGCTTCTCTGTGGTCCTCTGCGCGCTCCAGCGCGTGC
GCTTTTCCGGTGGATCATGCGGTCCGTGGCGCACCGCAGCGGCCGCTGCCCATGCAGCGCCGCTGCTT
CCGAACAGTGGCGGTCAGGGCCGCACCCGCGGTAGCCGTCCGTCCGGAACCCGCCCAAGAGTTTTGGG
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GTCCGGGGCTGACCGGCCGTCGCATTCAACGTAATCAATCGCATGATGATCAGAGGACACGAAGTCTT
GGTGGCGGTGGCCAGAAACACTGTCCATTGCAAGGGCATAGGGATGCGTTCCTTCACCTCTCATTTCT
CATTTCTGAATCCCTCCCTGCTCACTCTTTCTCCTCCTCCTTCCCGTTCACGCAGCATTCGGGGTACC

SEQ ID NO: 21
3′ donor DNA sequence of *Prototheca moriformis* FATA1 knockout homologous recombination targeting construct

GACAGGGTGGTTGGCTGGATGGGGAAACGCTGGTCGCGGGATTCGATCCTGCTGCTTATATCCTCCCT
GGAAGCACACCCACGACTCTGAAGAAGAAAACGTGCACACACACAACCCAACCGGCCGAATATTTGCT
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CCTTGTGCGCAGTGCTCCTGTACCCTTTACCGCTCCTTCCATTCTGCGAGGCCCCCTATTGAATGTAT
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SEQ ID NO: 22
*Chlorella protothecoides* actin promoter/5'UTR

agtttaggtccagcgtccgtgggggggggacgggctgggagcttgggccgggaagggcaagacgatgca
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*ccacaaggagaacttcgcctacgagcactgggacgacatcctggacatctgcaaccagtacgacgtcg*
*ccctgtccatcggcgacggcctgcgccccggctccatctacgacgccaacgacacggcccagttcgcc*
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*acctggccaagcagcacccccacgcccaggcgtgggacgacgcgctgtccaaggcgcgcttcgagttcc*
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aaccagcactgcaatgctgatgcacgggaagtagtgggatgggaacacaaatggaggatcc

SEQ ID NO: 24
PmKASII (Prototheca moriformis KASII) comprising a *C. protothecoides* S106 stearoyl-ACP desaturase transit peptide

ATGgccaccgcatccactttctcggcgttcaatgcccgctgcggcgacctgcgtcgctcggcgggctc
cgggccccggcgcccagcgaggcccctccccgtgcgcgggcgcgccgccgccgccgccgacgccaacc
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tcggcggccacaactcctgcgtgatcttccgcaagtacgacgagatggactacaaggaccacgacggc
gactacaaggaccacgacatcgactacaaggacgacgacgacaagTGA

SEQ ID NO: 25

PmKASII (Prototheca moriformis KASII) comprising a *C. protothecoides* S106 stearoylACP desaturase transit peptide

MATASTFSAFNARCGDLRRSAGSGPRRPARPLPVRGRAAAAADANPARPERRVVITGQGVVTSLGQTI
EQFYSSLLEGVSGISQIQKFDTTGYTTTIAGEIKSLQLDPYVPKRWAKRVDDVIKYVYIAGKQALESA
GLPIEAAGLAGAGLDPALCGVLIGTAMAGMTSFAAGVEALTRGGVRKMNPFCIPFSISNMGGAMLAMD
IGFMGPNYSISTACATGNYCILGAADHIRRGDANVMLAGGADAAIIPSGIGGFIACKALSKRNDEPER
ASRPWDADRDGFVMGEGAGVLVLEELEHAKRRGATILAELVGGAATSDAHHMTEPDPQGRGVRLCLER
ALERARLAPERVGYVNAHGTSTPAGDVAEYRAIRAVIPQDSLRINSTKSMIGHLLGGAGAVEAVAAIQ
ALRTGWLHPNLNLENPAPGVDPVVLVGPRKERAEDLDVVLSNSFGFGGHNSCVIFRKYDEMDYKDHDG
DYKDHDIDYKDDDDK

SEQ ID NO: 26
Codon-optimized Prototheca moriformis (UTEX 1435) FAD2 protein-coding sequence

ATGgccatcaagaccaaccgccagcccgtggagaagccccccttcaccatcggcaccctgcgcaaggc
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tgatgtccctgctgtacgtggcctccacctacatcgaccccgcccccgtgcccacctgggtgaagtac
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SEQ ID NO: 27
Amino acid sequence of Prototheca moriformis FAD2

MAIKTNRQPVEKPPFTIGTLRKAIPAHCFERSALRSSMYLAFDIAVMSLLYVASTYIDPAPVPTWVKY
GVMWPLYWFFQGAFGTGVWVCAHECGHQAFSSSQAINDGVGLVFHSLLLVPYYSWKHSHRRHHSNTGC
LDKDEVFVPPHRAVAHEGLEWEEWLPIRMGKVLVTLTLGWPLYLMFNVASRPYPRFANHFDPWSPIFS
KRERIEVVISDLALVAVLSGLSVLGRTMGWAWLVKTYVVPYLIVNMWLVLITLLQHTHPALPHYFEKD
WDWLRGAMATVDRSMGPPFMDNILHHISDTHVLHHLFSTIPHYHAEEASAAIRPILGKYYQSDSRWVG
RALWEDWRDCRYVVPDAPEDDSALWFHK

SEQ ID NO: 28
Codon-optimized coding region of Brassica napus C18:0-preferring thioesterase from pSZ1358

ACTAGTATGCTGAAGCTGTCCTGCAACGTGACCAACAACCTGCACACCTTCTCCTTCTTCTCCGACTC
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GACACCCGCCGCCTGCAGCGCGTGACCGACGAGGTGCGCGACGAGTACCTGGTGTTCTGCCCCCGCGA
GCCCCGCCTGGCCTTCCCCGAGGAGAACAACTCCTCCCTGAAGAAGATCCCCAAGCTGGAGGACCCCG
CCCAGTACTCCATGCTGGAGCTGAAGCCCCGCCGCGCCGACCTGGACATGAACCAGCACGTGAACAAC
GTGACCTACATCGGCTGGGTGCTGGAGTCCATCCCCCAGGAGATCATCGACACCCACGAGCTGCAGGT
GATCACCCTGGACTACCGCCGCGAGTGCCAGCAGGACGACATCGTGGACTCCCTGACCACCTCCGAGA
TCCCCGACGACCCCATCTCCAAGTTCACCGGCACCAACGGCTCCGCCATGTCCTCCATCCAGGGCCAC
AACGAGTCCCAGTTCCTGCACATGCTGCGCCTGTCCGAGAACGGCCAGGAGATCAACCGCGGCCGCAC
CCAGTGGCGCAAGAAGTCCTCCCGCATGGACTACAAGGACCACGACGGCGACTACAAGGACCACGACA
TCGACTACAAGGACGACGACGACAAGTGAATCGAT

SEQ ID NO: 29
Amino acid sequence of Brassica napus C18:0-preferring thioesterase
(Accession No. CAA52070.1)

MLKLSCNVTNNLHTFSFFSDSSLFIPVNRRTIAVSSSQLRKPALDPLRAVISADQGSISPVNSCTPAD
RLRAGRLMEDGYSYKEKFIVRSYEVGINKTATVETIANLLQEVACNHVQKCGFSTDGFATTLTMRKLH
LIWVTARMHIEIYKYPAWSDVVEIETWCQSEGRIGTRRDWILRDSATNEVIGRATSKWVMMNQDTRRL
QRVTDEVRDEYLVFCPREPRLAFPEENNSSLKKIPKLEDPAQYSMLELKPRRADLDMNQHVNNVTYIG
WVLESIPQEIIDTHELQVITLDYRRECQQDDIVDSLTTSEIPDDPISKFTGTNGSAMSSIQGHNESQF
LHMLRLSENGQEINRGRTQWRKKSSR

SEQ ID NO: 30
*Prototheca moriformis* FATA1 allele 1 5' homology donor region

GGAGTCACTGTGCCACTGAGTTCGACTGGTAGCTGAATGGAGTCGCTGCTCCACTAAACGAATTGTCA
GCACCGCCAGCCGGCCGAGGACCCGAGTCATAGCGAGGGTAGTAGCGCGCCATGGCACCGACCAGCCT
GCTTGCCAGTACTGGCGTCTCTTCCGCTTCTCTGTGGTCCTCTGCGCGCTCCAGCGCGTGCGCTTTTC
CGGTGGATCATGCGGTCCGTGGCGCACCGCAGCGGCCGCTGCCCATGCAGCGCCGCTGCTTCCGAACA
GTGGCGGTCAGGGCCGCACCCGCGGTAGCCGTCCGTCCGGAACCCGCCCAAGAGTTTTGGGAGCAGCT
TGAGCCCTGCAAGATGGCGGAGGACAAGCGCATCTTCCTGGAGGAGCACCGGTGCGTGGAGGTCCGGG
GCTGACCGGCCGTCGCATTCAACGTAATCAATCGCATGATGATCAGAGGACACGAAGTCTTGGTGGCG
GTGGCCAGAAACACTGTCCATTGCAAGGGCATAGGGATGCGTTCCTTCACCTCTCATTTCTCATTTCT
GAATCCCTCCCTGCTCACTCTTTCTCCTCCTCCTTCCCGTTCACGCAGCATTCGG

SEQ ID NO: 31
*Prototheca moriformis* FATA1 allele 1 3' homology donor region

GACAGGGTGGTTGGCTGGATGGGGAAACGCTGGTCGCGGGATTCGATCCTGCTGCTTATATCCTCCCT
GGAAGCACACCCACGACTCTGAAGAAGAAAACGTGCACACACACAACCCAACCGGCCGAATATTTGCT
TCCTTATCCCGGGTCCAAGAGAGACTGCGATGCCCCCCTCAATCAGCATCCTCCTCCCTGCCGCTTCA
ATCTTCCCTGCTTGCCTGCGCCCGCGGTGCGCCGTCTGCCCGCCCAGTCAGTCACTCCTGCACAGGCC
CCTTGTGCGCAGTGCTCCTGTACCCTTTACCGCTCCTTCCATTCTGCGAGGCCCCCTATTGAATGTAT
TCGTTGCCTGTGTGGCCAAGCGGGCTGCTGGGCGCGCCGCCGTCGGGCAGTGCTCGGCGACTTTGGCG
GAAGCCGATTGTTCTTCTGTAAGCCACGCGCTTGCTGCTTTGGGAAGAGAAGGGGGGGGGTACTGAAT
GGATGAGGAGGAGAAGGAGGGGTATTGGTATTATCTGAGTTGGGT

SEQ ID NO: 32
*Prototheca moriformis* FATA1 allele 2 5' homology donor region

AATGGAGTCGCTGCTCCACTAATCGAATTGTCAGCACCGCCAGCCGGCCGAGGACCCGAGTCATAGCG
AGGGTAGTAGCGCGCCATGGCACCGACCAGCCTGCTTGCCCGTACTGGCGTCTCTTCCGCTTCTCTGT
GCTCCTCTACGCGCTCCGGCGCGTGCGCTTTTCCGGTGGATCATGCGGTCCGTGGCGCACCGCAGCGG
CCGCTGCCCATGCAGCGCCGCTGCTTCCGAACAGTGGCTGTCAGGGCCGCACCCGCAGTAGCCGTCCG

TCCGGAACCCGCCCAAGAGTTTTGGGAGCAGCTTGAGCCCTGCAAGATGGCGGAGGACAAGCGCATCT
TCCTGGAGGAGCACCGGTGCGCGGAGGTCCGGGGCTGACCGGCCGTCGCATTCAACGTAATCAATCGC
ATGATGATCACAGGACGCGACGTCTTGGTGGCGGTGGCCAGGGACACTGCCCATTGCACAGGCATAGG
AATGCGTTCCTTCTCATTTCTCAGTTTTCTGAGCCCCTCCCTCTTCACTCTTTCTCCTCCTCCTCCCC
TCTCACGCAGCATTCGTGG

SEQ ID NO: 33
*Prototheca moriformis* FATA1 allele 2 3' homology donor region

CACTAGTATCGATTTCGAACAGAGGAGAGGGTGGCTGGTAGTTGCGGGATGGCTGGTCGCCCGTCGAT
CCTGCTGCTGCTATTGTCTCCTCCTGCACAAGCCCACCCACGACTCCGAAGAAGAAGAAGAAAACGCG
CACACACACAACCCAACCGGCCGAATATTTGCTTCCTTATCCCGGGTCCAAGAGAGACGGCGATGCCC
CCCTCAATCAGCCTCCTCCTCCCTGCCGCTCCAATCTTCCCTGCTTGCATGCGCCCGCGAGAGGCTGT
CTGCGCGCCCCGTCAGTCACTCCCCGTGCAGACGCCTCGTGCTCGGTGCTCCTGTATCCTTTACCGCT
CCTTTCATTCTGCGAGGCCCCCTGTTGAATGTATTCGTTGCCTGTGTGGCCAAGCGCGCTGCTGGGCG
CGCCGCCGTCGGGCGGTGCTCGGCGACTCTGGCGGAAGCCGGTTGTTCTTCTGTAAGCCACGCGCTTG
CTGCTTTTGGAAAAGAGGGGGGTTTACTGAATGGAGGAGGAGCAGGATAATTGGTAGTATCTGAGTTG
TTG

SEQ ID NO: 34
SAD2 hairpin C

actagtGCGCTGGACGCGGCAGTGGGTGGCCGAGGAGAACCGGCACGGCGACCTGCTGAACAAGTACT
GTTGGCTGACGGGGCGCGTCAACATGCGGGCCGTGGAGGTGACCATCAACAACCTGATCAAGAGCGGC
ATGAACCCGCAGACGGACAACAACCCTTACTTGGGCTTCGTCTACACCTCCTTCCAGGAGCGCGCGAC
CAAGTACAGCCACGGCAACACCGCGCGCCTTGCGGCCGAGCAGTGTGTTTGAGGGTTTTGGTTGCCCG
TATCGAGGTCCTGGTGGCGCGCATGGGGGAGAAGGCGCCTGTCCCGCTGACCCCCCCGGCTACCCTCC
CGGCACCTTCCAGGGCGCGTACGggatccTGCTCGGCCGCAAGGCGCGCGGTGTTGCCGTGGCTGTAC
TTGGTCGCGCGCTCCTGGAAGGAGGTGTAGACGAAGCCCAAGTAAGGGTTGTTGTCCGTCTGCGGGTT
CATGCCGCTCTTGATCAGGTTGTTGATGGTCACCTCCACGGCCCGCATGTTGACGCGCCCCGTCAGCC
AACAGTACTTGTTCAGCAGGTCGCCGTGCCGGTTCTCCTCGGCCACCCACTGCCGCGTCCAGCGCaag
ctt

SEQ ID NO: 35
*Prototheca moriformis* FAD-D omega 3 desaturase

MSIQFALRAAYIKGTCQRLSGRGAALGLSRDWTPGWTLPRCWPASAAATAPPRARHQERAIHLTSGRR
RHSALASDADERALPSNAPGLVMASQANYFRVRLLPEQEEGELESWSPNVRHTTLLCKPRAMLSKLQM
RVMVGDRVIVTAIDPVNMTVHAPPFDPLPATRFLVAGEAADMDITVVLNKADLVPEEESAALAQEVAS
WGPVVLTSTLTGRGLQELERQLGSTTAVLAGPSGAGKSSIINALARAARERPSDASVSNVPEEQVVGE
DGRALANPPPFTLADIRNAIPKDCFRKSAAKSLAYLGDLSITGMAVLAYKINSPWLWPLYWFAQGTMF
WALFVVGHDCGHQSFSTSKRLNDALAWLGALAAGTWTWALGVLPMLNLYLAPYVWLLVTYLHHHGPSD
PREEMPWYRGREWSYMRGGLTTIDRDYGLFNKVHHDIGTHVVHH

SEQ ID NO: 36

MFWALFVVGHDCGHQSFSTSKRLNDAVGLFVHSIIGVPYHGWRISHRTHHNNHGHVENDESWYPPTES
GLKAMTDMGRQGRFHFPSMLFVYPFYLFWRSPGKTGSHFSPATDLFALWEAPLIRTSNACQLAWLGAL
AAGTWALGVLPMLNLYLAPYVISVAWLDLVTYLHHHGPSDPREEMPWYRGREWSYMRGGLTTIDRDYG
LFNKVHHDIGTHVVHHLFPQIPHYNLCRATKAAKKVLGPYYREPERCPLGLLPVHLLAPLLRSLGQDH
FVDDAGSVLFYRRAEGINPWIQKLLPWLGGARRGADAQRDAAQ

SEQ ID NO: 37
Camelina sativa omega-3 FAD7-2

MANLVLSECGIRPLPRIYTTPRSNFVSNNNKPIFKFRPFTSYKTSSSPLACSRDGFGKNWSLNVSVPL
TTTTPIVDESPLKEEEEEKQRFDPGAPPPFNLADIRAAIPKHCWVKNPWKSMSYVLRDVAIVFALAAG
ASYLNNWIVWPLYWLAQGTMFWALFVLGHDCGHGSFSNNPRLNNVVGHLLHSSILVPYHGWRISHRTH
HQNHGHVENDESWHPMSEKIYQSLDKPTRFFRFTLPLVMLAYPFYLWARSPGKKGSHYHPESDLFLPK
EKTDVLTSTACWTAMAALLICLNFVVGPVQMLKLYGIPYWINVMWLDFVTYLHHHGHEDKLPWYRGKE
WSYLRGGLTTLDRDYGVINNIHHDIGTHVIHHLFPQIPHYHLVEATEAVKPVLGKYYREPDKSGPLPL
HLLGILAKSIKEDHYVSDEGDVVYYKADPNMYGEIKVGAD

SEQ ID NO: 38
Prototheca moriformis delta 12 desaturase allele 2

MAIKTNRQPVEKPPFTIGTLRKAIPAHCFERSALRSSMYLAFDIAVMSLLYVASTYIDPAPVPTWVKY
GIMWPLYWFFQGAFGTGVWVCAHECGHQAFSSSQAINDGVGLVFHSLLLVPYYSWKHSHRRHHSNTGC
LDKDEVFVPPHRAVAHEGLEWEEWLPIRMGKVLVTLTLGWPLYLMFNVASRPYPRFANHFDPWSPIFS
KRERIEVVISDLALVAVLSGLSVLGRTMGWAWLVKTYVVPYMIVNMWLVLITLLQHTHPALPHYFEKD
WDWLRGAMATVDRSMGPPFMDSILHHISDTHVLHHLFSTIPHYHAEEASAAIRPILGKYYQSDSRWVG
RALWEDWRDCRYVVPDAPEDDSALWFHK

SEQ ID NO: 39
Camelina sativa omega-3 FAD7-1

MANLVLSECGIRPLPRIYTTPRSNFVSNNNKPIFKFRPLTSYKTSSPLFCSRDGFGRNWSLNVSVPLA
TTTPIVDESPLEEEEEEEKQRFDPGAPPPFNLADIRAAIPKHCWVKNPWKSMSYVLRDVAIVFALAAG
AAYLNNWIVWPLYWLAQGTMFWALFVLGHDCGHGSFSNNPRLNNVVGHLLHSSILVPYHGWRISHRTH
HQNHGHVENDESWHPMSEKIYQSLDKPTRFFRFTLPLVMLAYPFYLWARSPGKKGSHYHPESDLFLPK
EKTDVLTSTACWTAMAALLICLNFVVGPVQMLKLYGIPYWINVMWLDFVTYLHHHGHEDKLPWYRGKE
WSYLRGGLTTLDRDYGVINNIHHDIGTHVIHHLFPQIPHYHLVEATEAVKPVLGKYYREPDKSGPLPL
HLLGILAKSIKEDHYVSDEGDVVYYKADPNMYGEIKVGAD

SEQ ID NO: 40
PmFATA-hpB

actagtCATTCGGGGCAACGAGGTGGGCCCCTCGCAGCGGCTGACGATCACGGCGGTGGCCAACATCC
TGCAGGAGGCGGCGGGCAACCACGCGGTGGCCATGTGGGGCCGGAGCGTGTGTTTGAGGGTTTTGGTT
GCCCGTATTGAGGTCCTGGTGGCGCGCATGGGGGAGAAGGCGCCTGTCCCGCTGACCCCCCCGGCTAC
CCTCCCGGCACCTTCCAGGGCGCGTACGggatccGCTCCGGCCCCACATGGCCACCGCGTGGTTGCCC
GCCGCCTCCTGCAGGATGTTGGCCACCGCCGTGATCGTCAGCCGCTGCGAGGGGCCCACCTCGTTGCC
CCGAATGaagctt

SEQ ID NO: 41
PmFATA-hpC

actagtGGAGGGTTTCGCGACGGACCCGGAGCTGCAGGAGGCGGGTCTCATCTTTGTGATGACGCGCA
TGCAGATCCAGATGTACCGCTACCCGCGCTGGGGCGACCTGATGCAGGTGGAGACCTGGTTCCAGAGT
GTGTTTGAGGGTTTTGGTTGCCCGTATTGAGGTCCTGGTGGCGCGCATGGGGGAGAAGGCGCCTGTCC
CGCTGACCCCCCCGGCTACCCTCCCGGCACCTTCCAGGGCGCGTACGggatccTCTGGAACCAGGTCT
CCACCTGCATCAGGTCGCCCCAGCGCGGGTAGCGGTACATCTGGATCTGCATGCGCGTCATCACAAAG
ATGAGACCCGCCTCCTGCAGCTCCGGGTCCGTCGCGAAACCCTCCaagctt

SEQ ID NO: 42
PmFATA-hpD

actagtCGGCGGGCAAGCTGGGCGCGCAGCGCGAGTGGGTGCTGCGCGACAAGCTGACCGGCGAGGCG
CTGGGCGCGGCCACCTCGAGCTGGGTCATGATCAACATCCGCACGCGCCGGCCGTGCCGCATGCCGGG
TGTGTTTGAGGGTTTTGGTTGCCCGTATCGAGGTCCTGGTGGCGCGCATGGGGGAGAAGGCGCCTGTC

CCGCTGACCCCCCCGGCTACCCTCCCGGCACCTTCCAGGGCGCGTACGgatccCCGGCATGCGGCAC
GGCCGGCGCGTGCGGATGTTGATCATGACCCAGCTCGAGGTGGCCGCGCCCAGCGCCTCGCCGGTCAG
CTTGTCGCGCAGCACCCACTCGCGCTGCGCGCCCAGCTTGCCCGCCGaagctt

SEQ ID NO: 43
PmFATA-hpE

actagtGTCCGCGTCAAGTCGGCCTTCTTCGCGCGCGAGCCGCCGCGCCTGGCGCTGCCGCCCGCGGT
CACGCGTGCCAAGCTGCCCAACATCGCGACGCCGGCGCCGCTGCGCGGGCACCGCCAGGTCGCGCGCC
GCACCGACATGGACATGAACGGGCACGTGAACAACGTGGCCTACCTGGCCTGGTGCCTGGAGTGTGTT
TGAGGGTTTTGGTTGCCCGTATTGAGGTCCTGGTGGCGCGCATGGGGGAGAAGGCGCCTGTCCCGCTG
ACCCCCCCGGCTACCCTCCCGGCACCTTCCAGGGCGCGTACGgatccTCCAGGCACCAGGCCAGGTA
GGCCACGTTGTTCACGTGCCCGTTCATGTCCATGTCGGTGCGGCGCGCGACCTGGCGGTGCCCGCGCA
GCGGCGCCGGCGTCGCGATGTTGGGCAGCTTGGCACGCGTGACCGCGGGCGGCAGCGCCAGGCGCGGC
GGCTCGCGCGCGAAGAAGGCCGACTTGACGCGGACaagctt

SEQ ID NO: 44
PmFATA-hpF

actagtCCGTGCCCGAGCACGTCTTCAGCGACTACCACCTCTACCAGATGGAGATCGACTTCAAGGCC
GAGTGCCACGCGGGCGACGTCATCTCCTCCCAGGCCGAGCAGATCCCGCCCCAGGAGGCGCTCACGCA
CAACGGCGCCGGCCGCAACCCCTCCTGCTTCGTCCATAGCATTCTGCGCGCCGAGACCGAGCGTGTGT
TTGAGGGTTTTGGTTGCCCGTATCGAGGTCCTGGTGGCGCGCATGGGGGAGAAGGCGCCTGTCCCGCT
GACCCCCCCGGCTACCCTCCCGGCACCTTCCAGGGCGCGTACGgatccGCTCGGTCTCGGCGCGCAG
AATGCTATGGACGAAGCAGGAGGGGTTGCGGCCGGCGCCGTTGTGCGTGAGCGCCTCCTGGGGCGGGA
TCTGCTCGGCCTGGGAGGAGATGACGTCGCCCGCGTGGCACTCGGCCTTGAAGTCGATCTCCATCTGG
TAGAGGTGGTAGTCGCTGAAGACGTGCTCGGGCACGGaagctt

SEQ ID NO: 45
PmFATA-hpG

actagtTCGTCCGCGCGCGAACCACATGGTCGGCCCCCATCGACGCGCCCGCCGCCAAGCCGCCCAAG
GCGAGCCACTGAGGACAGGGTGGTTGGCTGGATGGGGAAACGCTGGTCGCGGGATTCGATCCTGCTGC
TTATATCCTCGTGTGTTTGAGGGTTTTGGTTGCCCGTATTGAGGTCCTGGTGGCGCGCATGGGGGAGA
AGGCGCCTGTCCCGCTGACCCCCCCGGCTACCCTCCCGGCACCTTCCAGGGCGCGTACGgatccGAG
GATATAAGCAGCAGGATCGAATCCCGCGACCAGCGTTTCCCCATCCAGCCAACCACCCTGTCCTCAGT
GGCTCGCCTTGGGCGGCTTGGCGGCGGGCGCGTCGATGGGGGCCGACCATGTGGTTCGCGCGCGGACG
Aaagctt

SEQ ID NO: 46
Codon-optimized *Cuphea wrightii* KASAI

ATGGCCGCCGCCGCCAGCATGGTGGCCAGCCCCTTCTGCACCTGGCTGGTGGCCAGCTGCATGAGCAC
CAGCTTCGACAACGACCCCCGCAGCCCCAGCGTGAAGCGCTTCCCCCGCCGCAAGCGCGTGCTGAGCC
AGCGCGGCAGCACCTACGTATTCCAGTGCCTGGTGGCCAGCTGCATCGACCCCTGCGACCAGTACCGC
AGCAGCGCCAGCCTGAGCTTCCTGGGCGACAACGGCTTCGCCAGCCTGTTCGGCAGCAAGCCCTTCAT
GAGCAACCGCGGCCACCGCCGCCTGCGCCGCGCCAGCCACAGCGGCGAGGCCATGGCCGTGGCCCTGC
AGCCCGCCCAGGAGGCCGGCACCAAGAAGAAGCCCGTGATCAAGCAGCGCCGCGTGGTGGTGACCGGC
ATGGGCGTGGTGACCCCCCTGGGCCACGAGCCCGACGTGTTCTACAACAACCTGCTGGACGGCGTGAG
CGGCATCAGCGAGATCGAGACCTTCGACTGCACCCAGTTCCCCACCCGCATCGCCGGCGAGATCAAGA
GCTTCAGCACCGACGGCTGGGTGGCCCCCAAGCTGAGCAAGCGCATGGACAAGTTCATGCTGTACCTG
CTGACCGCCGGCAAGAAGGCCCTGGCCGACGGCGGCATCACCGACGAGGTGATGAAGGAGCTGGACAA
GCGCAAGTGCGGCGTGCTGATCGGCAGCGGCATGGGCGGCATGAAGGTGTTCAACGACGCCATCGAGG
CCCTGCGCGTGAGCTACAAGAAGATGAACCCCTTCTGCGTGCCCTTCGCCACCACCAACATGGGCAGC
GCCATGCTGGCCATGGACCTGGGCTGGATGGGCCCCAACTACAGCATCAGCACCGCCTGCGCCACCAG

CAACTTCTGCATCCTGAACGCCGCCAACCACATCATCCGCGGCGAGGCCGACATGATGCTGTGCGGCG
GCAGCGACGCCGTGATCATCCCCATCGGCCTGGGCGGCTTCGTGGCCTGCCGCGCCCTGAGCCAGCGC
AACAGCGACCCCACCAAGGCCAGCCGCCCCTGGGACAGCAACCGCGACGGCTTCGTGATGGGCGAGGG
CGCCGGCGTGCTGCTGCTGGAGGAGCTGGAGCACGCCAAGAAGCGCGGCGCCACCATCTACGCCGAGT
TCCTGGGCGGCAGCTTCACCTGCGACGCCTACCACATGACCGAGCCCCACCCCGAGGGCGCCGGCGTG
ATCCTGTGCATCGAGAAGGCCCTGGCCCAGGCCGGCGTGAGCAAGGAGGACGTGAACTACATCAACGC
CCACGCCACCAGCACCAGCGCCGGCGACATCAAGGAGTACCAGGCCCTGGCCCGCTGCTTCGGCCAGA
ACAGCGAGCTGCGCGTGAACAGCACCAAGAGCATGATCGGCCACCTGCTGGGCGCCGCCGGCGGCGTG
GAGGCCGTGACCGTGGTGCAGGCCATCCGCACCGGCTGGATTCACCCCAACCTGAACCTGGAGGACCC
CGACAAGGCCGTGGACGCCAAGCTGCTGGTGGGCCCCAAGAAGGAGCGCCTGAACGTGAAGGTGGGCC
TGAGCAACAGCTTCGGCTTCGGCGGCCACAACAGCAGCATCCTGTTCGCCCCCTGCAACGTGTGA

SEQ ID NO: 47
Codon-optimized *Cuphea wrightii* KASAI with P.moriformis SAD transit peptide

ATGGGCCGCGGTGTCTCCCTTCCCCGGCCCAGGGTCGCGGTGCGCGCCCAGTCGGCGAGTCAGGTTTT
GGAGAGCTGTATTCCAGTGCCTGGTGGCCAGCTGCATCGACCCCTGCGACCAGTACCGCAGCAGCGCC
AGCCTGAGCTTCCTGGGCGACAACGGCTTCGCCAGCCTGTTCGGCAGCAAGCCCTTCATGAGCAACCG
CGGCCACCGCCGCCTGCGCCGCGCCAGCCACAGCGGCGAGGCCATGGCCGTGGCCCTGCAGCCCGCCC
AGGAGGCCGGCACCAAGAAGAAGCCCGTGATCAAGCAGCGCCGCGTGGTGGTGACCGGCATGGGCGTG
GTGACCCCCCTGGGCCACGAGCCCGACGTGTTCTACAACAACCTGCTGGACGGCGTGAGCGGCATCAG
CGAGATCGAGACCTTCGACTGCACCCAGTTCCCCACCCGCATCGCCGGCGAGATCAAGAGCTTCAGCA
CCGACGGCTGGGTGGCCCCCAAGCTGAGCAAGCGCATGGACAAGTTCATGCTGTACCTGCTGACCGCC
GGCAAGAAGGCCCTGGCCGACGGCGGCATCACCGACGAGGTGATGAAGGAGCTGGACAAGCGCAAGTG
CGGCGTGCTGATCGGCAGCGGCATGGGCGGCATGAAGGTGTTCAACGACGCCATCGAGGCCCTGCGCG
TGAGCTACAAGAAGATGAACCCCTTCTGCGTGCCCTTCGCCACCACCAACATGGGCAGCGCCATGCTG
GCCATGGACCTGGGCTGGATGGGCCCCAACTACAGCATCAGCACCGCCTGCGCCACCAGCAACTTCTG
CATCCTGAACGCCGCCAACCACATCATCCGCGGCGAGGCCGACATGATGCTGTGCGGCGGCAGCGACG
CCGTGATCATCCCCATCGGCCTGGGCGGCTTCGTGGCCTGCCGCGCCCTGAGCCAGCGCAACAGCGAC
CCCACCAAGGCCAGCCGCCCCTGGGACAGCAACCGCGACGGCTTCGTGATGGGCGAGGGCGCCGGCGT
GCTGCTGCTGGAGGAGCTGGAGCACGCCAAGAAGCGCGGCGCCACCATCTACGCCGAGTTCCTGGGCG
GCAGCTTCACCTGCGACGCCTACCACATGACCGAGCCCCACCCCGAGGGCGCCGGCGTGATCCTGTGC
ATCGAGAAGGCCCTGGCCCAGGCCGGCGTGAGCAAGGAGGACGTGAACTACATCAACGCCCACGCCAC
CAGCACCAGCGCCGGCGACATCAAGGAGTACCAGGCCCTGGCCCGCTGCTTCGGCCAGAACAGCGAGC
TGCGCGTGAACAGCACCAAGAGCATGATCGGCCACCTGCTGGGCGCCGCCGGCGGCGTGGAGGCCGTG
ACCGTGGTGCAGGCCATCCGCACCGGCTGGATTCACCCCAACCTGAACCTGGAGGACCCCGACAAGGC
CGTGGACGCCAAGCTGCTGGTGGGCCCCAAGAAGGAGCGCCTGAACGTGAAGGTGGGCCTGAGCAACA
GCTTCGGCTTCGGCGGCCACAACAGCAGCATCCTGTTCGCCCCCTGCAACGTGTGA

SEQ ID NO: 48
Codon-optimized *Cuphea pulcherrima* KASIV

ATGCCCGCGGCCAGCTCGCTGCTGGCGTCCCCCCTGTGCACCTGGCTGCTGGCCGCGTGCATGAGCAC
CTCGTTCCACCCCTCCGACCCCCTGCCCCCCAGCATCTCGTCCCCCCGCCGCCGCCTGAGCCGCCGCC
GCATCCTGTCGCAGTGCGCCCCCCTGCCCTCCGCGAGCTCGGCCCTGCGCGGCTCCAGCTTCCACACC
CTGGTGACCTCGTATCTGGCGTGCTTCGAGCCCTGCCACGACTATTATACCAGCGCCTCCCTGTTCGG
CTCGCGCCCCATCCGCACCACCCGCCGCCACCGCCGCCTGAACCGCGCGAGCCCCTCGCGCGAGGCGA
TGGCGGTCGCCCTGCAGCCCGAGCAGGAGGTGACCACCAAGAAGAAGCCCTCCATCAAGCAGCGCCGC
GTCGTGGTCACCGGCATGGGCGTGGTCACCCCCCTGGGCCACGACCCCGACGTGTTCTATAACAACCT
GCTGGACGGCACCAGCGGCATCTCGGAGATCGAGACCTTCGACTGCGCGCAGTTCCCCACCCGCATCG
CCGGCGAGATCAAGTCCTTCAGCACCGACGGCTGGGTCGCGCCCAAGCTGTCGAAGCGCATGGACAAG
TTCATGCTGTATATGCTGACCGCCGGCAAGAAGGCGCTGACCGACGGCGGCATCACCGAGGACGTGAT
GAAGGAGCTGGACAAGCGCAAGTGCGGCGTCCTGATCGGCTCCGCGATGGGCGGCATGAAGGTGTTCA
ACGACGCGATCGAGGCCCTGCGCATCAGCTATAAGAAGATGAACCCCTTCTGCGTGCCCTTCGCGACC

ACCAACATGGGCTCGGCCATGCTGGCGATGGACCTGGGCTGGATGGGCCCCAACTATTCCATCAGCAC
CGCCTGCGCGACCTCGAACTTCTGCATCATGAACGCGGCCAACCACATCATCCGCGGCGAGGCGGACG
TCATGCTGTGCGGCGGCTCCGACGCCGTGATCATCCCCATCGGCATGGGCGGCTTCGTCGCGTGCCGC
GCCCTGAGCCAGCGCAACTCGGACCCCACCAAGGCGTCCCGCCCCTGGGACAGCAACCGCGACGGCTT
CGTGATGGGCGAGGGCGCCGGCGTCCTGCTGCTGGAGGAGCTGGAGCACGCGAAGAAGCGCGGCGCCA
CCATCTATGCGGAGTTCCTGGGCGGCTCGTTCACCTGCGACGCCTATCACATGACCGAGCCCCACCCC
GACGGCGCCGGCGTGATCCTGTGCATCGAGAAGGCGCTGGCCCAGTCCGGCGTCAGCCGCGAGGACGT
GAACTATATCAACGCGCACGCCACCTCGACCCCCGCGGGCGACATCAAGGAGTATCAGGCCCTGATCC
ACTGCTTCGGCCAGAACCGCGAGCTGAAGGTCAACTCCACCAAGAGCATGATCGGCCACCTGCTGGGC
GCGGCGGGCGGCGTGGAGGCGGTCTCGGTGGTCCAGGCCATCCGCACCGGCTGGATCCACCCCAACAT
CAACCTGGAGAACCCCGACGAGGGCGTGGACACCAAGCTGCTGGTGGGCCCCAAGAAGGAGCGCCTGA
ACGTCAAGGTGGGCCTGTCCAACAGCTTCGGCTTCGGCGGCCACAACTCGTCCATCCTGTTCGCGCCC
TATATCTGA

SEQ ID NO: 49
Codon-optimized *Cuphea hookeriana* KASIV

ATGGTGGCCGCCGCCGCCTCCAGCGCCTTCTTCCCCGTGCCCGCCCCCGGCGCCTCCCCCAAGCCCGG
CAAGTTCGGCAACTGGCCCTCCAGCCTGAGCCCCTCCTTCAAGCCCAAGTCCATCCCCAACGGCGGCT
TCCAGGTGAAGGCCAACGACAGCGCCCACCCCAAGGCCAACGGCTCCGCCGTGAGCCTGAAGAGCGGC
AGCCTGAACACCCAGGAGGACACCTCCTCCAGCCCCCCCCCCCGCACCTTCCTGCACCAGCTGCCCGA
CTGGAGCCGCCTGCTGACCGCCATCACCACCGTGTTCGTGAAGTCCAAGCGCCCCGACATGCACGACC
GCAAGTCCAAGCGCCCCGACATGCTGGTGGACAGCTTCGGCCTGGAGTCCACCGTGCAGGACGGCCTG
GTGTTCCGCCAGTCCTTCTCCATCCGCTCCTACGAGATCGGCACCGACCGCACCGCCAGCATCGAGAC
CCTGATGAACCACCTGCAGGAGACCTCCCTGAACCACTGCAAGAGCACCGGCATCCTGCTGGACGGCT
TCGGCCGCACCCTGGAGATGTGCAAGCGCGACCTGATCTGGGTGGTGATCAAGATGCAGATCAAGGTG
AACCGCTACCCCGCCTGGGGCGACACCGTGGAGATCAACACCCGCTTCAGCCGCCTGGGCAAGATCGG
CATGGGCCGCGACTGGCTGATCTCCGACTGCAACACCGGCGAGATCCTGGTGCGCGCCACCAGCGCCT
ACGCCATGATGAACCAGAAGACCCGCCGCCTGTCCAAGCTGCCCTACGAGGTGCACCAGGAGATCGTG
CCCCTGTTCGTGGACAGCCCCGTGATCGAGGACTCCGACCTGAAGGTGCACAAGTTCAAGGTGAAGAC
CGGCGACAGCATCCAGAAGGGCCTGACCCCCGGCTGGAACGACCTGGACGTGAACCAGCACGTGTCCA
ACGTGAAGTACATCGGCTGGATCCTGGAGAGCATGCCCACCGAGGTGCTGGAGACCCAGGAGCTGTGC
TCCCTGGCCCTGGAGTACCGCCGCGAGTGCGGCCGCGACTCCGTGCTGGAGAGCGTGACCGCCATGGA
CCCCAGCAAGGTGGGCGTGCGCTCCCAGTACCAGCACCTGCTGCGCCTGGAGGACGGCACCGCCATCG
TGAACGGCGCCACCGAGTGGCGCCCCAAGAACGCCGGCGCCAACGGCGCCATCTCCACCGGCAAGACC
AGCAACGGCAACTCCGTGTCCATGTGA

SEQ ID NO: 50
*Prototheca moriformis* (UTEX 1435) KAS1 allele 1 5’ donor sequence

gctcttcctcaccgcgtgaattgctgtcccaaacgtaagcatcatcgtggctcggtcacgcgatcctg
gatccggggatcctagaccgctggtggagagcgctgccgtcggattggtggcaagtaagattgcgcag
gttggcgaagggagagaccaaaaccggaggctggaagcgggcacaacatcgtattattgcgtatagta
gagcagtggcagtcgcatttcgaggtccgcaacggatctcgcaagctcgctacgctcacagtaggaga
aaggggaccactgcccctgccagaatggtcgcgaccctctccctcgccggccccgcctgcaacacgca
gtgcgtatccggcaagcgggctgtcgccttcaaccgcccccatgttggcgtccgggctcgatcaggtg
cgctgaggggggtttggtgtgcccgcgcctctgggcccgtgtcggccgtgcggacgtggggccctggg
cagtggatcagcagggtttgcgtgcaaatgcctataccggcgattgaatagcgatgaacgggatacgg
ttgcgctcactccatgcccatgcgaccccgtttctgtccgccagccgtggtcgcccgggctgcgaagc
gggaccccacccagcgcattgtgatcaccggaatgggcgtgggtacc

SEQ ID NO: 51
*Prototheca moriformis* (UTEX 1435) KAS1 allele 1 3’ donor sequence

gagctccacctgcatccgcctggcgctcgaggacgccggcgtctcgcccgacgaggtcaactacgtca
acgcgcacgccacctccaccctggtgggcgacaaggccgaggtgcgcgcggtcaagtcggtctttggc
gacatgaagggcatcaagatgaacgccaccaagtccatgatcgggcactgcctgggcgccgccggcgg
catggaggccgtcgccacgctcatggccatccgcaccggctgggtgcaccccaccatcaaccacgaca
accccatcgccgaggtcgacggcctggacgtcgtcgccaacgccaaggcccagcacaaaatcaacgtc
gccatctccaactccttcggcttcggcgggcacaactccgtcgtcgcctttgcgcccttccgcgagta
ggcggagcgagcgcgcttggctgaggagggaggcggggtgcgagccctttggctgcgcgcgatactct
ccccgcacgagcagactccacgcgcctgaatctacttgtcaacgagcaaccgtgtgttttgtccgtgg
ccattcttattatttctccgactgtggccgtactctgtttggctgtgcaagcaccgaagagcc

SEQ ID NO: 52
*Prototheca moriformis* (UTEX 1435) KAS1 allele 2 5’ donor sequence

gctcttcgcgcaagctcgctacgctcacagtaggagataggggaccactgcccctgccagaatggtcg
cgaccctgtccctcgccggccccgcctgcaacacgcagtgcgtatccagcaagcgggttgtcgccttc
aaccgccccccatgttggcgtccgggctcgatcaggtgcgctgaggggggtttggtgggcccgcgcctc
tgggcccgtgtcggccgtgcggacgtggggcccggggtagtggatcagcaggggttgcatgcaaatgc
ctataccggcgattgaatagcgatgaacgggatacggttgcgctcactccatgcccatgcgaccccgt
ttctgtccgccagccgtggtcgcccgagctgcgaagcgggaccccacccagcgcattgtgatcaccgg
aatgggcgtggcctccgtgtttggcaacgatgtcgagacctttacgacaagcttctggaaggaacga
gcggcgtggacctgatttccaggtgcgtaggtccttggatgaatgcgtctaggttgcgaggtgactgg
ccaggaagcagcaggcttggggtttggtgttctgatttctggtaatttgaggtttcattataagattc
tgtacggtcttgtttcggggtacc

SEQ ID NO: 53
*Prototheca moriformis* (UTEX 1435) KAS1 allele 2 3’ donor sequence

gagctccacctgcatccgcctggcgctcgaggacgccggcgtctcgcccgacgaggtcaactacgtca
acgcgcacgccacctccaccctggtgggcgacaaggccgaggtgcgcgcggtcaagtcggtctttggc
gacatgaagggcatcaagatgaacgccaccaagtccatgatcgggcactgcctgggcgccgccggcgg
catggaggccgtcgccacgctcatggccatccgcaccggctgggtgcaccccaccatcaaccacgaca
accccatcgccgaggtcgacggcctggacgtcgtcgccaacgccaaggcccagcacaaaatcaacgtc
gccatctccaactccttcggcttcggcgggcacaactccgtcgtcgcctttgcgcccttccgcgagta
ggcggagcgagcgcgcttggctgaggagggaggcggggtgcgagccctttggctgcgcgcgatactct
ccccgcacgagcagactccacgcgcctgaatctacttgtcaacgagcaaccgtgtgttttgtccgtgg
ccattcttattatttctccgactgtggccgtactctgtttggctgtgcaagcaccgaagagcc

SEQ ID NO: 54
*Prototheca moriformis* (UTEX 1435) KASI-hairpin B

actagtcaTGGTCGCCCGGGCTGCGAAGCGGGACCCCACCCAGCGCATTGTGATCACCGGAATGGGCG
TGGCCTCCGTGTTTGGCAACGATGTCGAGACCTTTTACAgtgtgtttgagggttttggttgcccgtat
tgaggtcctggtggcgcgcatggaggagaaggcgcctgtcccgctgacccccccggctaccctcccgg
caccttccagggcgcgtacgggatccTGTAAAAGGTCTCGACATCGTTGCCAAACACGGAGGCCACGC
CCATTCCGGTGATCACAATGCGCTGGGTGGGGTCCCGCTTCGCAGCCCGGGCGACCAaagctt

SEQ ID NO: 55
*Prototheca moriformis* (UTEX 1435) KASI-hairpin C

actagtcaTTGACATCTCCGAGTTCCCGACCAAGTTTGCGGCGCAGATCACCGGCTTCTCCGTGGAGG
ACTGCGTGGACAAGAAGAACGCGCGGCGGTACGACGACGCGCTGTCGTACGCGATGGTGGCCTCCAAG
AAGGCCCTGCGCCAGGCGGGACTGGAGAAGGACAAGTGCCCCGAGGGCTACGGAGgtgtgtttgaggg
ttttggttgcccgtattgaggtcctggtggcgcgcatggaggagaaggcgcctgtcccgctgaccccc
ccggctaccctcccggcaccttccagggcgcgtacgggatccCTCCGTAGCCCTCGGGGCACTTGTCC
TTCTCCAGTCCCGCCTGGCGCAGGGCCTTCTTGGAGGCCACCATCGCGTACGACAGCGCGTCGTCGTA

CCGCCGCGCGTTCTTCTTGTCCACGCAGTCCTCCACGGAGAAGCCGGTGATCTGCGCCGCAAACTTGG
TCGGGAACTCGGAGATGTCAAaagctt

SEQ ID NO: 56
*Prototheca moriformis* (UTEX 1435) KASI-hairpin D

actagtcaTGGGCGTGAGCACCTGCATCCGCCTGGCGCTCGAGGACGCCGGCGTCTCGCCCGACGAGG
TCAACTACGTCAACGCGCACGCCACCTCCACCCTGGTGGGCGACAAGGCCGAGGTGCGCGCGGTCAAG
TCGGTCTTTGGCGACATGAAGGGCATCAAGATgtgtgtttgagggttttggttgcccgtattgaggtc
ctggtggcgcgcatggaggagaaggcgcctgtcccgctgacccccccggctaccctcccggcaccttc
cagggcgcgtacgggatccATCTTGATGCCCTTCATGTCGCCAAAGACCGACTTGACCGCGCGCACCT
CGGCCTTGTCGCCCACCAGGGTGGAGGTGGCGTGCGCGTTGACGTAGTTGACCTCGTCGGGCGAGACG
CCGGCGTCCTCGAGCGCCAGGCGGATGCAGGTGCTCACGCCCAaagctt

SEQ ID NO: 57
*Prototheca moriformis* (UTEX 1435) KASI-hairpin E

actagtcaCAACCATCAACCACGACAACCCCATCGCCGAGGTCGACGGCCTGGACGTCGTCGCCAACG
CCAAGGCCCAGCACAAAATCAACGTCGCCATCTCCAACTCCTTCGgtgtgtttgagggttttggttgc
ccgtattgaggtcctggtggcgcgcatggaggagaaggcgcctgtcccgctgacccccccggctaccc
tcccggcaccttccagggcgcgtacgggatccCGAAGGAGTTGGAGATGGCGACGTTGATTTTGTGCT
GGGCCTTGGCGTTGGCGACGACGTCCAGGCCGTCGACCTCGGCGATGGGGTTGTCGTGGTTGATGGTa
agctt

SEQ ID NO: 58
Codon optimized *M. polymorpha* FAE3 (GenBank Accession No. AAP74370)

**ATG**gactcccgcgcccagaaccgcgacggcggcgaggacgtgaagcaggagctgctgtccgccggcga
cgacggcaaggtgccctgccccaccgtggccatcggcatccgccagcgcctgcccgacttcctgcagt
ccgtgaacatgaagtacgtgaagctgggctaccactacctgatcacccacgccatgttcctgctgacc
ctgcccgccttcttcctggtggccgccgagatcggccgcctgggccacgagcgcatctaccgcgagct
gtggacccacctgcacctgaacctggtgtccatcatggcctgctcctccgccctggtggccggcgcca
ccctgtacttcatgtcccgcccccgccccgtgtacctggtggagttcgcctgctaccgccccgacgag
cgcctgaaggtgtccaaggacttcttcctggacatgtcccgccgcaccggcctgttctcctcctcctc
catggacttccagaccaagatcacccagcgctccggcctgggcgacgagacctacctgccccccgcca
tcctggcctccccccccaacccctgcatgcgcgaggcccgcgaggaggccgccatggtgatgttcggc
gccctggacgagctgttcgagcagaccggcgtgaagcccaaggagatcggcgtgctggtggtgaactg
ctccctgttcaaccccacccccctccatgtccgccatgatcgtgaaccactaccacatgcgcggcaaca
tcaagtccctgaacctgggcggcatgggctgctccgccggcctgatctccatcgacctggcccgcgac
ctgctgcaggtgcacggcaacacctacgccgtggtggtgtccaccgagaacatcaccctgaactggta
cttcggcgacgaccgctccaagctgatgtccaactgcatcttccgcatgggcggcgccgccgtgctgc
tgtccaacaagcgccgcgagcgccgccgcgccaagtacgagctgctgcacaccgtgcgcacccacaag
ggcgccgacgacaagtgcttccgctgcgtgtaccaggaggaggactccaccggctccctgggcgtgtc
cctgtcccgcgagctgatggccgtggccggcaacgccctgaaggccaacatcaccaccctgggccccc
tggtgctgcccctgtccgagcagatcctgttcttcgcctccctggtggcccgcaagttcctgaacatg
aagatgaagccctacatccccgacttcaagctggccttcgagcacttctgcatccacgccggcggccg
cgccgtgctggacgagctggagaagaacctggacctgaccgagtggcacatggagccctcccgcatga
ccctgtaccgcttcggcaacacctcctcctcctccctgtggtacgagctggcctacaccgaggcccag
ggccgcgtgaagcgcggcgaccgcctgtggcagatcgccttcggctccggcttcaagtgcaactccgc
cgtgtggcgcgcgctgcgcaccgtgaagccccccgtgaacaacgcctggtccgacgtgatcgaccgct
tccccgtgaagctgccccagttc**TGA**

SEQ ID NO: 59
*M. polymorpha* FAE3 (GenBank Accession No. AAP74370)

MDSRAQNRDGGEDVKQELLSAGDDGKVPCPTVAIGIRQRLPDFLQSVNMKYVKLGYHYLITHAMFLLT
LPAFFLVAAEIGRLGHERIYRELWTHLHLNLVSIMACSSALVAGATLYFMSRPRPVYLVEFACYRPDE
RLKVSKDFFLDMSRRTGLFSSSSMDFQTKITQRSGLGDETYLPPAILASPPNPCMREAREEAAMVMFG
ALDELFEQTGVKPKEIGVLVVNCSLFNPTPSMSAMIVNHYHMRGNIKSLNLGGMGCSAGLISIDLARD
LLQVHGNTYAVVVSTENITLNWYFGDDRSKLMSNCIFRMGGAAVLLSNKRRERRRAKYELLHTVRTHK
GADDKCFRCVYQEEDSTGSLGVSLSRELMAVAGNALKANITTLGPLVLPLSEQILFFASLVARKFLNM
KMKPYIPDFKLAFEHFCIHAGGRAVLDELEKNLDLTEWHMEPSRMTLYRFGNTSSSSLWYELAYTEAQ
GRVKRGDRLWQIAFGSGFKCNSAVWRALRTVKPPVNNAWSDVIDRFPVKLPQF

SEQ ID NO: 60
*Trypanosoma brucei* ELO3 (GenBank Accession No. AAX70673)

***ATG****ctgatgaacttcggcggctcctacgacgcctacatcaacaacttccagggcaccttcctggccga*
*gtggatgctggaccacccctccgtgccctacatcgccggcgtgatgtacctgatcctggtgctgtacg*
*tgcccaagtccatcatggcctcccagccccccctgaacctgcgcgccgccaacatcgtgtggaacctg*
*ttcctgaccctgttctccatgtgcggcgcctactacaccgtgccctacctggtgaaggccttcatgaa*
*ccccgagatcgtgatggccgcctccggcatcaagctggacgccaacacctcccccatcatcacccact*
*ccggcttctacaccaccacctgcgccctggccgactccttctacttcaacggcgacgtgggcttctgg*
*gtggccctgttcgccctgtccaagatccccgagatgatcgacaccgccttcctggtgttccagaagaa*
*gcccgtgatcttcctgcactggtaccaccacctgaccgtgatgctgttctgctggttcgcctacgtgc*
*agaagatctcctccggcctgtggttcgcctccatgaactactccgtgcactccatcatgtacctgtac*
*tacttcgtgtgcgcctgcggccaccgccgcctggtgcgccccttcgccccatcatcaccttcgtgca*
*gatcttccagatggtggtgggcaccatcgtggtgtgctacacctacaccgtgaagcacgtgctgggcc*
*gctcctgcaccgtgaccgacttctccctgcacaccggcctggtgatgtacgtgtcctacctgctgctg*
*ttctcccagctgttctaccgctcctacctgtccccccgcgacaaggcctccatcccccacgtggccgc*
*cgagatcaagaagaaggag****TGA***

SEQ ID NO: 61
*Trypanosoma brucei* ELO3 (GenBank Accession No. AAX70673)

MYPTHRDLILNNYSDIYRSPTCHYHTWHTLIHTPINELLFPNLPRECDFGYDIPYFRGQIDVFDGWSM
IHFTSSNWCIPITVCLCYIMMIAGLKKYMGPRDGGRAPIQAKNYIIAWNLFLSFFSFAGVYYTVPYHL
FDPENGLFAQGFYSTVCNNGAYYGNGNVGFFVWLFIYSKIFELVDTFFLLIRKNPVIFLHWYHHLTVL
LYCWHAYSVRIGTGIWFATMNYSVHSVMYLYFAMTQYGPSTKKFAKKFSKFITTIQILQMVVGIIVTF
AAMLYVTFDVPCYTSLANSVLGLMMYASYFVLFVQLYVSHYVSPKHVKQE

SEQ ID NO: 62
Codon optimized *Saccharomyces cerevisiae* ELO1 (GenBank Accession No. P39540)

***ATG****gtgtccgactggaagaacttctgcctggagaaggcctcccgcttccgccccaccatcgaccgccc*
*cttcttcaacatctacctgtgggactacttcaaccgcgccgtgggctgggccaccgccggccgcttcc*
*agcccaaggacttcgagttcaccgtgggcaagcagcccctgtccgagccccgccccgtgctgctgttc*
*atcgccatgtactacgtggtgatcttcggcggccgctccctggtgaagtcctgcaagcccctgaagct*
*gcgcttcatctcccaggtgcacaacctgatgctgacctccgtgtccttcctgtggctgatcctgatgg*
*tggagcagatgctgcccatcgtgtaccgccacggcctgtacttcgccgtgtgcaacgtggagtcctgg*
*acccagcccatggagaccctgtactacctgaactacatgaccaagttcgtggagttcgccgacaccgt*
*gctgatggtgctgaagcaccgcaagctgaccttcctgcacacctaccaccacggcgccaccgccctgc*
*tgtgctacaaccagctggtgggctacaccgccgtgacctgggtgcccgtgaccctgaacctggccgtg*
*cacgtgctgatgtactggtactacttcctgtccgcctccggcatccgcgtgtggtggaaggcctgggt*
*gacccgcctgcagatcgtgcagttcatgctggacctgatcgtggtgtactacgtgctgtaccagaaga*
*tcgtggccgcctacttcaagaacgcctgcacccccagtgcgaggactgcctgggctccatgaccgcc*
*atcgccgccggcgccgccatcctgacctcctacctgttcctgttcatctccttctacatcgaggtgta*
*caagcgcggctccgcctccggcaagaagaagatcaacaagaacaac****TGA***

SEQ ID NO: 63
*Saccharomyces cerevisiae* ELO1 (GenBank Accession No. P39540)

MVSDWKNFCLEKASRFRPTIDRPFFNIYLWDYFNRAVGWATAGRFQPKDFEFTVGKQPLSEPRPVLLF
IAMYYVVIFGGRSLVKSCKPLKLRFISQVHNLMLTSVSFLWLILMVEQMLPIVYRHGLYFAVCNVESW
TQPMETLYYLNYMTKFVEFADTVLMVLKHRKLTFLHTYHHGATALLCYNQLVGYTAVTWVPVTLNLAV
HVLMYWYYFLSASGIRVWWKAWVTRLQIVQFMLDLIVVYYVLYQKIVAAYFKNACTPQCEDCLGSMTA
IAAGAAILTSYLFLFISFYIEVYKRGSASGKKKINKNN

SEQ ID NO: 64
Codon optimized *Brassica napus* acyl-ACP thioesterase (GenBank Accession No. CAA52070) with 3X FLAG Tag

ATGctgaagctgtcctgcaacgtgaccaacaacctgcacaccttctccttcttctccgactcctccct
gttcatccccgtgaaccgccgcaccatcgccgtgtcctccgggcgcgcctcccagctgcgcaagcccg
ccctggacccccctgcgcgccgtgatctccgccgaccagggctccatctcccccgtgaactcctgcacc
cccgccgaccgcctgcgcgccggccgcctgatggaggacggctactcctacaaggagaagttcatcgt
gcgctcctacgaggtgggcatcaacaagaccgccaccgtggagaccatcgccaacctgctgcaggagg
tggcctgcaaccacgtgcagaagtgcggcttctccaccgacggcttcgccaccaccctgaccatgcgc
aagctgcacctgatctgggtgaccgcccgcatgcacatcgagatctacaagtaccccgcctggtccga
cgtggtggagatcgagacctggtgccagtccgagggccgcatcggcacccgccgcgactggatcctgc
gcgactccgccaccaacgaggtgatcggccgcgccacctccaagtgggtgatgatgaaccaggacacc
cgccgcctgcagcgcgtgaccgacgaggtgcgcgacgagtacctggtgttctgcccccgcgagccccg
cctggccttccccgaggagaacaactcctccctgaagaagatccccaagctggaggaccccgcccagt
actccatgctggagctgaagccccgccgcgccgacctggacatgaaccagcacgtgaacaacgtgacc
tacatcggctgggtgctggagtccatcccccaggagatcatcgacacccacgagctgcaggtgatcac
cctggactaccgccgcgagtgccagcaggacgacatcgtggactccctgaccacctccgagatccccg
acgaccccatctccaagttcaccggcaccaacggctccgccatgtcctccatccagggccacaacgag
tcccagttcctgcacatgctgcgcctgtccgagaacggccaggagatcaaccgcggccgcacccagtg
gcgcaagaagtcctcccgcATGGACTACAAGGACCACGACGGCGACTACAAGGACCACGACATCGACT
ACAAGGACGACGACGACAAGTGA

SEQ ID NO: 65
*Brassica napus* acyl-ACP thioesterase (Genbank Accession No. CAA52070) with 3X FLAG Tag (bold)

MLKLSCNVTNNLHTFSFFSDSSLFIPVNRRTIAVSS**GRA** SQLRKPALDPLRAVISADQGSISPVNSCT
PADRLRAGRLMEDGYSYKEKFIVRSYEVGINKTATVETIANLLQEVACNHVQKCGFSTDGFATTLTMR
KLHLIWVTARMHIEIYKYPAWSDVVEIETWCQSEGRIGTRRDWILRDSATNEVIGRATSKWVMMNQDT
RRLQRVTDEVRDEYLVFCPREPRLAFPEENNSSLKKIPKLEDPAQYSMLELKPRRADLDMNQHVNNVT
YIGWVLESIPQEIIDTHELQVITLDYRRECQQDDIVDSLTTSEIPDDPISKFTGTNGSAMSSIQGHNE
SQFLHMLRLSENGQEINRGRTQWRKKSSR**MDYKDHDGDYKDHDIDYKDDDDK**

SEQ ID NO: 66
Codon optimized *Brassica napus* acyl-ACP thioesterase (GenBank Accession No. CAA52070), with UTEX 250 stearoyl-ACP desaturase (SAD) chloroplast transit peptide and 3X FLAG Tag

ATGgccaccgcatccactttctcggcgttcaatgcccgctgcggcgacctgcgtcgctcggcgggctc
cgggccccggcgcccagcgaggcccctccccgtgcgcgggcgcgcctcccagctgcgcaagcccgccc
tggacccccctgcgcgccgtgatctccgccgaccagggctccatctcccccgtgaactcctgcacccccc
gccgaccgcctgcgcgccggccgcctgatggaggacggctactcctacaaggagaagttcatcgtgcg
ctcctacgaggtgggcatcaacaagaccgccaccgtggagaccatcgccaacctgctgcaggaggtgg
cctgcaaccacgtgcagaagtgcggcttctccaccgacggcttcgccaccaccctgaccatgcgcaag
ctgcacctgatctgggtgaccgcccgcatgcacatcgagatctacaagtaccccgcctggtccgacgt

ggtggagatcgagacctggtgccagtccgagggccgcatcggcacccgccgcgactggatcctgcgcg
actccgccaccaacgaggtgatcggccgcgccacctccaagtgggtgatgatgaaccaggacacccgc
cgcctgcagcgcgtgaccgacgaggtgcgcgacgagtacctggtgttctgcccccgcgagccccgcct
ggccttccccgaggagaacaactcctccctgaagaagatccccaagctggaggaccccgcccagtact
ccatgctggagctgaagccccgccgcgccgacctggacatgaaccagcacgtgaacaacgtgacctac
atcggctgggtgctggagtccatcccccaggagatcatcgacacccacgagctgcaggtgatcaccct
ggactaccgccgcgagtgccagcaggacgacatcgtggactccctgaccacctccgagatccccgacg
accccatctccaagttcaccggcaccaacggctccgccatgtcctccatccagggccacaacgagtcc
cagttcctgcacatgctgcgcctgtccgagaacggccaggagatcaaccgcggccgcacccagtggcg
caagaagtcctcccgcATGGACTACAAGGACCACGACGGCGACTACAAGGACCACGACATCGACTACA
AGGACGACGACGACAAGTGA

SEQ ID NO: 67
*Brassica napus* acyl-ACP thioesterase (GenBank Accession No. CAA52070) with UTEX 250 stearoyl-ACP desaturase (SAD) chloroplast transit peptide and 3X FLAG® Tag

MATASTFSAFNARCGDLRRSAGSGPRRPARPLPVR**GRA** SQLRKPALDPLRAVISADQGSISPVNSCTP
ADRLRAGRLMEDGYSYKEKFIVRSYEVGINKTATVETIANLLQEVACNHVQKCGFSTDGFATTLTMRK
LHLIWVTARMHIEIYKYPAWSDVVEIETWCQSEGRIGTRRDWILRDSATNEVIGRATSKWVMMNQDTR
RLQRVTDEVRDEYLVFCPREPRLAFPEENNSSLKKIPKLEDPAQYSMLELKPRRADLDMNQHVNNVTY
IGWVLESIPQEIIDTHELQVITLDYRRECQQDDIVDSLTTSEIPDDPISKFTGTNGSAMSSIQGHNES
QFLHMLRLSENGQEINRGRTQWRKKSSR**MDYKDHDGDYKDHDIDYKDDDDK**

SEQ ID NO: 68
Codon optimized *C. tinctorius* FATA (GenBank Accession No. AAA33019) with UTEX 250 stearoyl-ACP desaturase (SAD) chloroplast transit peptide and 3X FLAG® Tag

***ATG****gccaccgcatccactttctcggcgttcaatgcccgctgcggcgacctgcgtcgctcggcgggctc*
*cgggccccggcgcccagcgaggcccctccccgtgcgcg**ggcgcgcc**gccaccggcgagcagccctccg*
*gcgtggcctccctgcgcgaggccgacaaggagaagtccctgggcaaccgcctgcgcctgggctccctg*
*accgaggacggcctgtcctacaaggagaagttcgtgatccgctgctacgaggtgggcatcaacaagac*
*cgccaccatcgagaccatcgccaacctgctgcaggaggtgggcggcaaccacgcccagggcgtgggct*
*tctccaccgacggcttcgccaccaccaccaccatgcgcaagctgcacctgatctgggtgaccgcccgc*
*atgcacatcgagatctaccgctaccccgcctggtccgacgtgatcgagatcgagacctgggtgcaggg*
*cgagggcaaggtgggcacccgccgcgactggatcctgaaggactacgccaacggcgaggtgatcggcc*
*gcgccacctccaagtgggtgatgatgaacgaggacacccgccgcctgcagaaggtgtccgacgacgtg*
*cgcgaggagtacctggtgttctgcccccgcaccctgcgcctggccttccccgaggagaacaacaactc*
*catgaagaagatccccaagctggaggaccccgccgagtactcccgcctgggcctggtgccccgccgct*
*ccgacctggacatgaacaagcacgtgaacaacgtgacctacatcggctgggccctggagtccatcccc*
*cccgagatcatcgacacccacgagctgcaggccatcaccctggactaccgccgcgagtgccagcgcga*
*cgacatcgtggactccctgacctcccgcgagcccctgggcaacgccgccggcgtgaagttcaaggaga*
*tcaacggctccgtgtcccccaagaaggacgagcaggacctgtcccgcttcatgcacctgctgcgctcc*
*gccggctccggcctggagatcaaccgctgccgcaccgagtggcgcaagaagcccgccaagcgc**ATGGA***
***CTACAAGGACCACGACGGCGACTACAAGGACCACGACATCGACTACAAGGACGACGACGACAAG****TGA***

SEQ ID NO: 69
*C. tinctorius* FATA (GenBank Accession No. AAA33019) with UTEX 250 stearoyl-ACP desaturase (SAD) chloroplast transit peptide

MATASTFSAFNARCGDLRRSAGSGPRRPARPLPVR**GRA** ATGEQPSGVASLREADKEKSLGNRLRLGSL
TEDGLSYKEKFVIRCYEVGINKTATIETIANLLQEVGGNHAQGVGFSTDGFATTTTMRKLHLIWVTAR
MHIEIYRYPAWSDVIEIETWVQGEGKVGTRRDWILKDYANGEVIGRATSKWVMMNEDTRRLQKVSDDV
REEYLVFCPRTLRLAFPEENNNSMKKIPKLEDPAEYSRLGLVPRRSDLDMNKHVNNVTYIGWALESIP

PEIIDTHELQAITLDYRRECQRDDIVDSLTSREPLGNAAGVKFKEINGSVSPKKDEQDLSRFMHLLRS
AGSGLEINRCRTEWRKKPAKR**MDYKDHDGDYKDHDIDYKDDDDK**

SEQ ID NO: 70
Codon optimized *R. communis* FATA (Genbank Accession No. ABS30422)
with a 3xFLAG epitope tag

***ATG****ctgaaggtgccctgctgcaacgccaccgaccccatccagtccctgtcctcccagtgccgcttcct*
*gacccacttcaacaaccgcccctacttcacccgccgccccctccatccccaccttcttctcctccaaga*
*actcctccgcctccctgcaggccgtggtgtccgacatctcctccgtggagtccgccgcctgcgactcc*
*ctggccaaccgcctgcgcctgggcaagctgaccgaggacggcttctcctacaaggagaagttcatcgt*
*ggggcgcgcccgctcctacgaggtgggcatcaacaagaccgccaccgtggagaccatcgccaacctgc*
*tgcaggaggtgggctgcaaccacgcccagtccgtgggcttctccaccgacggcttcgccaccaccacc*
*tccatgcgcaagatgcacctgatctgggtgaccgcccgcatgcacatcgagatctacaagtaccccgc*
*ctggtccgacgtggtggaggtggagacctggtgccagtccgagggccgcatcggcacccgccgcgact*
*ggatcctgaccgactacgccaccggccagatcatcggccgcgccacctccaagtgggtgatgatgaac*
*caggacacccgccgcctgcagaaggtgaccgacgacgtgcgcgaggagtacctggtgttctgcccccg*
*cgagctgcgcctggccttccccgaggagaacaaccgctcctccaagaagatctccaagctggaggacc*
*ccgcccagtactccaagctgggcctggtgccccgccgcgccgacctggacatgaaccagcacgtgaac*
*aacgtgacctacatcggctgggtgctggagtccatcccccaggagatcatcgacacccacgagctgca*
*gaccatcaccctggactaccgccgcgagtgccagcacgacgacatcgtggactccctgacctccgtgg*
*agccctccgagaacctggaggccgtgtccgagctgcgcggcaccaacggctccgccaccaccaccgcc*
*ggcgacgaggactgccgcaacttcctgcacctgctgcgcctgtccggcgacggcctggagatcaaccg*
*cggccgcaccgagtggcgcaagaagtccgcccgc**ATGGACTACAAGGACCACGACGGCGACTACAAGG***
***ACCACGACATCGACTACAAGGACGACGACGACAAG****TGA***

SEQ ID NO: 71
*R. communis* FATA (Genbank Accession No. ABS30422) with a 3xFLAG®
epitope tag

MLKVPCCNATDPIQSLSSQCRFLTHFNNRPYFTRRPSIPTFFSSKNSSASLQAVVSDISSVESAACDS
LANRLRLGKLTEDGFSYKEKFIV***GRA*** RSYEVGINKTATVETIANLLQEVGCNHAQSVGFSTDGFATTT
SMRKMHLIWVTARMHIEIYKYPAWSDVVEVETWCQSEGRIGTRRDWILTDYATGQIIGRATSKWVMMN
QDTRRLQKVTDDVREEYLVFCPRELRLAFPEENNRSSKKISKLEDPAQYSKLGLVPRRADLDMNQHVN
NVTYIGWVLESIPQEIIDTHELQTITLDYRRECQHDDIVDSLTSVEPSENLEAVSELRGTNGSATTTA
GDEDCRNFLHLLRLSGDGLEINRGRTEWRKKSAR**MDYKDHDGDYKDHDIDYKDDDDK**

SEQ ID NO: 72
Codon optimized *G. mangostana* FATA1 (GenBank Accession No. AAB51523)
with 3X FLAG® epitope tag

***ATG****ctgaagctgtcctcctcccgctccccctggcccgcatccccacccgcccccgccccaactccat*
*ccccccccgcatcatcgtggtgtcctcctcctcctccaaggtgaaccccctgaagaccgaggccgtgg*
*tgtcctccggcctggccgaccgcctgcgcctgggctccctgaccgaggacggcctgtcctacaaggag*
*aagttcatcgtgcgctgctacgaggtgggcatcaacaagaccgccaccgtggagaccatcgccaacct*
*gctgcaggaggtgggctgcaaccacgcccagtccgtgggctactccaccggcggcttctccaccaccc*
*ccaccatgcgcaagctgcgcctgatctgggtgaccgcccgcatgcacatcgagatctacaagtacccc*
*gcctggtccgacgtggtggagatcgagtcctggggccagggcgagggcaagatcggcacccgccgcga*
*ctggatcctgcgcgactacgccaccggccaggtgatcggccgcgccacctccaagtgggtgatgatga*
*accaggacacccgccgcctgcagaaggtggacgtggacgtgcgcgacgagtacctggtgcactgcccc*
*cgcgagctgcgcctggccttccccgaggagaacaactcctccctgaagaagatctccaagctggagga*
*cccctcccagtactccaagctgggcctggtgccccgccgcgccgacctggacatgaaccagcacgtga*
*acaacgtgacctacatcggctgggtgctggagtccatgccccaggagatcatcgacacccacgagctg*
*cagaccatcaccctggactaccgccgcgagtgccagcacgacgacgtggtggactccctgacctcccc*
*cgagccctccgaggacgccgaggccgtgttcaaccacaacggcaccaacggctccgccaacgtgtccg*

*ccaacgaccacggctgccgcaacttcctgcacctgctgcgcctgtccggcaacggcctggagatcaac*
*cgcggccgcaccgagtggcgcaagaagcccacccgcATGGACTACAAGGACCACGACGGCGACTACAA*
*GGACCACGACATCGACTACAAGGACGACGACGACAAG**TGA***

SEQ ID NO: 73
*G. mangostana* FATA1 (GenBank Accession No. AAB51523) with 3X FLAG® epitope tag

MLKLSSSRSPLARIPTRPRPNSIPPRIIVVSSSSSKVNPLKTEAVVSSGLADRLRLGSLTEDGLSYKE
KFIVRCYEVGINKTATVETIANLLQEVGCNHAQSVGYSTGGFSTTPTMRKLRLIWVTARMHIEIYKYP
AWSDVVEIESWGQGEGKIGTRRDWILRDYATGQVIGRATSKWVMMNQDTRRLQKVDVDVRDEYLVHCP
RELRLAFPEENNSSLKKISKLEDPSQYSKLGLVPRRADLDMNQHVNNVTYIGWVLESMPQEIIDTHEL
QTITLDYRRECQHDDVVDSLTSPEPSEDAEAVFNHNGTNGSANVSANDHGCRNFLHLLRLSGNGLEIN
RGRTEWRKKPTR**MDYKDHDGDYKDHDIDYKDDDDK**

SEQ ID NO: 74
Codon optimized *Theobroma cacao* FATA1 with 3X FLAG® epitope tag

***ATG****ctgaagctgtcctcctgcaacgtgaccgaccagcgccaggccctggcccagtgccgcttcctggc*
*ccccccgccccctctccttccgctggcgcacccccgtggtggtgtcctgctcccctcctcccgcc*
*ccaacctgtcccccctgcaggtggtgctgtccggccagcagcaggccggcatggagctggtggagtcc*
*ggctccggctccctggccgaccgcctgcgcctgggctccctgaccgaggacggcctgtcctacaagga*
*gaagttcatcgtgcgctgctacgaggtgggcatcaacaagaccgccaccgtggagaccatcgccaacc*
*tgctgcaggaggtgggctgcaaccacgcccagtccgtgggctactccaccgacggcttcgccaccacc*
*cgcaccatgcgcaagctgcacctgatctgggtgaccgcccgcatgcacatcgagatctacaagtaccc*
*cgcctggtccgacgtgatcgagatcgagacctggtgccagtccgagggccgcatcggcacccgccgcg*
*actggatcctgaaggacttcggcaccggcgaggtgatcggccgcgccacctccaagtgggtgatgatg*
*aaccaggacacccgccgcctgcagaaggtgtccgacgacgtgcgcgaggagtacctggtgttctgccc*
*ccgcgagctgcgcctggccttccccgaggagaacaacaactccctgaagaagatcgccaagctggacg*
*actccttccagtactcccgcctgggcctgatgccccgccgccgacctggacatgaaccagcacgtg*
*aacaacgtgacctacatcggctgggtgctggagtccatgccccaggagatcatcgacacccacgagct*
*gcagaccatcaccctggactaccgccgcgagtgccagcaggacgacgtggtggactccctgacctccc*
*ccgagcaggtggagggcaccgagaaggtgtccgccatccacggcaccaacggctccgccgccgcccgc*
*gaggacaagcaggactgccgccagttcctgcacctgctgcgcctgtcctccgacggccaggagatcaa*
*ccgcggccgcaccgagtggcgcaagaagcccgcccgcATGGACTACAAGGACCACGACGGCGACTACA*
*AGGACCACGACATCGACTACAAGGACGACGACGACAAG**TGA***

SEQ ID NO: 75
*Theobroma cacao* FATA1 with 3X FLAG® epitope tag

MLKLSSCNVTDQRQALAQCRFLAPPAPFSFRWRTPVVVSCSPSSRPNLSPLQVVLSGQQQAGMELVES
GSGSLADRLRLGSLTEDGLSYKEKFIVRCYEVGINKTATVETIANLLQEVGCNHAQSVGYSTDGFATT
RTMRKLHLIWVTARMHIEIYKYPAWSDVIEIETWCQSEGRIGTRRDWILKDFGTGEVIGRATSKWVMM
NQDTRRLQKVSDDVREEYLVFCPRELRLAFPEENNNSLKKIAKLDDSFQYSRLGLMPRRADLDMNQHV
NNVTYIGWVLESMPQEIIDTHELQTITLDYRRECQQDDVVDSLTSPEQVEGTEKVSAIHGTNGSAAAR
EDKQDCRQF**LHLLRLSSDGQEINRGRTEWRKKPARMDYKDHDGDYKDHDIDYKDDDDK**

SEQ ID NO: 76
23S rRNA for UTEX 1439, UTEX 1441, UTEX 1435, UTEX 1437 Prototheca moriformis

TGTTGAAGAATGAGCCGGCGACTTAAAATAAATGGCAGGCTAAGAGAATTAATAACTCGAAACCTAAG
CGAAAGCAAGTCTTAATAGGGCGCTAATTTAACAAAACATTAAATAAAATCTAAAGTCATTTATTTTA
GACCCGAACCTGAGTGATCTAACCATGGTCAGGATGAAACTTGGGTGACACCAAGTGGAAGTCCGAAC
CGACCGATGTTGAAAAATCGGCGGATGAACTGTGGTTAGTGGTGAAATACCAGTCGAACTCAGAGCTA

GCTGGTTCTCCCCGAAATGCGTTGAGGCGCAGCAATATATCTCGTCTATCTAGGGGTAAAGCACTGTT
TCGGTGCGGGCTATGAAAATGGTACCAAATCGTGGCAAACTCTGAATACTAGAAATGACGATATATTA
GTGAGACTATGGGGGATAAGCTCCATAGTCGAGAGGGAAACAGCCCAGACCACCAGTTAAGGCCCCAA
AATGATAATGAAGTGGTAAAGGAGGTGAAAATGCAAATACAACCAGGAGGTTGGCTTAGAAGCAGCCA
TCCTTTAAAGAGTGCGTAATAGCTCACTG

SEQ ID NO: 77
Cu PSR23 LPAAT2-1

MAIAAAAVIFLFGLIFFASGLIINLFQALCFVLIRPLSKNAYRRINRVFAELLLSELLCLFDWWAGAK
LKLFTDPETFRLMGKEHALVIINHMTELDWMVGWVMGQHFGCLGSIISVAKKSTKFLPVLGWSMWFSE
YLYLERSWAKDKSTLKSHIERLIDYPLPFWLVIFVEGTRFTRTKLLAAQQYAVSSGLPVPRNVLIPRT
KGFVSCVSHMRSFVPAVYDVTVAFPKTSPPPTLLNLFEGQSIMLHVHIKRHAMKDLPESDDAVAEWCR
DKFVEKDALLDKHNAEDTFSGQEVCHSGSRQLKSLLVVISWVVVTTFGALKFLQWSSWKGKAFSAIGL
GIVTLLMHVLILSSQAERSNPAEVAQAKLKTGLSISKKVTDKEN

SEQ ID NO: 78
CuPSR23 LPAAT3-1

MAIAAAAVIVPLSLLFFVSGLIVNLVQAVCFVLIRPLSKNTYRRINRVVAELLWLELVWLIDWWAGVK
IKVFTDHETFHLMGKEHALVICNHKSDIDWLVGWVLGQRSGCLGSTLAVMKKSSKFLPVLGWSMWFSE
YLFLERSWAKDEITLKSGLNRLKDYPLPFWLALFVEGTRFTRAKLLAAQQYAASSGLPVPRNVLIPRT
KGFVSSVSHMRSFVPAIYDVTVAIPKTSPPPTLIRMFKGQSSVLHVHLKRHLMKDLPESDDAVAQWCR
DIFVEKDALLDKHNAEDTFSGQELQETGRPIKSLLVVISWAVLEVFGAVKFLQWSSLLSSWKGLAFSG
IGLGVITLLMHILILFSQSERSTPAKVAPAKPKNEGESSKTEMEKEK

SEQ ID NO: 79
Amino acid sequence for CuPSR23 LPPATx

MEIPPHCLCSPSPAPSQLYYKKKKHAILQTQTPYRYRVSPTCFAPPRLRKQHPYPLPVLCYPKLLHFS
QPRYPLVRSHLAEAGVAYRPGYELLGKIRGVCFYAVTAAVALLLFQCMLLLHPFVLLFDPFPRKAHHT
IAKLWSICSVSLFYKIHIKGLENLPPPHSPAVYVSNHQSFLDIYTLLTLGRTFKFISKTEIFLYPIIG
WAMYMLGTIPLKRLDSRSQLDTLKRCMDLIKKGASVFFFPEGTRSKDGKLGAFKKGAFSIAAKSKVPV
VPITLIGTGKIMPPGSELTVNPGTVQVIIHKPIEGSDAEAMCNEARATISHSLDD

SEQ ID NO: 80
cDNA sequence for CuPSR23 LPAATx coding region

ATGGAGATCCCGCCTCACTGTCTCTGTTCGCCTTCGCCTGCGCCTTCGCAATTGTATTACAAGAAGAA
GAAGCATGCCATTCTCCAAACTCAAACTCCCTATAGATATAGAGTTTCCCCGACATGCTTTGCCCCCC
CCCGATTGAGGAAGCAGCATCCTTACCCTCTCCCTGTCCTCTGCTATCCAAAACTCCTCCACTTCAGC
CAGCCTAGGTACCCTCTGGTTAGATCTCATTTGGCTGAAGCTGGTGTTGCTTATCGTCCAGGATACGA
ATTATTAGGAAAAATAAGGGGAGTGTGTTTCTATGCTGTCACTGCTGCCGTTGCCTTGCTTCTATTTC
AGTGCATGCTCCTCCTCCATCCCTTTGTGCTCCTCTTCGATCCATTTCCAAGAAAGGCTCACCATACC
ATCGCCAAACTCTGGTCTATCTGCTCTGTTTCTCTTTTTTACAAGATTCACATCAAGGGTTTGGAAAA
TCTTCCCCCACCCCACTCTCCTGCCGTCTATGTCTCTAATCATCAGAGTTTTCTCGACATCTATACTC
TCCTCACTCTCGGTAGAACCTTCAAGTTCATCAGCAAGACTGAGATCTTTCTCTATCCAATTATCGGT
TGGGCCATGTATATGTTGGGTACCATTCCTCTCAAGCGGTTGGACAGCAGAAGCCAATTGGACACTCT
TAAGCGATGTATGGATCTCATCAAGAAGGGAGCATCCGTCTTTTTCTTCCCAGAGGGAACACGAAGTA
AAGATGGGAAACTGGGTGCTTTCAAGAAAGGTGCATTCAGCATCGCAGCAAAAAGCAAGGTTCCTGTT
GTGCCGATCACCCTTATTGGAACTGGCAAGATTATGCCACCTGGGAGCGAACTTACTGTCAATCCAGG
AACTGTGCAAGTAATCATACATAAACCTATCGAAGGAAGTGATGCAGAAGCAATGTGCAATGAAGCTA
GAGCCACGATTTCTCACTCACTTGATGATTAA

SEQ ID NO: 81

cDNA sequence for CuPSR23 LPAAT 2-1 coding region

ATGGCGATTGCAGCGGCAGCTGTCATCTTCCTCTTCGGCCTTATCTTCTTCGCCTCCGGCCTCATAAT
CAATCTCTTCCAGGCGCTTTGCTTTGTCCTTATTCGGCCTCTTTCGAAAAACGCCTACMGGAGAATAA
ACAGAGTTTTTGCAGAATTGTTGTTGTCGGAGCTTTTATGCCTATTCGATTGGTGGGCTGGTGCTAAG
CTCAAATTATTTACCGACCCTGAAACCTTTCGCCTTATGGGCAAGGAACATGCTCTTGTCATAATTAA
TCACATGACTGAACTTGACTGGATGGTTGGATGGGTTATGGGTCAGCATTTTGGTTGCCTTGGGAGCA
TAATATCTGTTGCGAAGAAATCAACAAAATTTCTTCCGGTATTGGGGTGGTCAATGTGGTTTTCAGAG
TACCTATATCTTGAGAGAAGCTGGGCCAAGGATAAAAGTACATTAAAGTCACATATCGAGAGGCTGAT
AGACTACCCCCTGCCCTTCTGGTTGGTAATTTTTGTGGAAGGAACTCGGTTTACTCGGACAAAACTCT
TGGCAGCCCAGCAGTATGCTGTCTCATCTGGGCTACCAGTGCCGAGAAATGTTTTGATCCCACGTACT
AAGGGTTTTGTTTCATGTGTAAGTCACATGCGATCATTTGTTCCAGCAGTATATGATGTCACAGTGGC
ATTCCCTAAGACTTCACCTCCACCAACGTTGCTAAATCTTTTCGAGGGTCAGTCCATAATGCTTCACG
TTCACATCAAGCGACATGCAATGAAAGATTTACCAGAATCCGATGATGCAGTAGCAGAGTGGTGTAGA
GACAAATTTGTGGAAAAGGATGCTTTGTTGGACAAGCATAATGCTGAGGACACTTTCAGTGGTCAAGA
AGTTTGTCATAGCGGCAGCCGCCAGTTAAAGTCTCTTCTGGTGGTAATATCTTGGGTGGTTGTAACAA
CATTTGGGGCTCTAAAGTTCCTTCAGTGGTCATCATGGAAGGGGAAAGCATTTTCAGCTATCGGGCTG
GGCATCGTCACTCTACTTATGCACGTATTGATTCTATCCTCACAAGCAGAGCGGTCTAACCCTGCGGA
GGTGGCACAGGCAAAGCTAAAGACCGGGTTGTCGATCTCAAAGAAGGTAACGGACAAGGAAAACTAG

SEQ ID NO: 82
cDNA sequence for CuPSR23 LPAAx 3-1 coding region

ATGGCGATTGCTGCGGCAGCTGTCATCGTCCCGCTCAGCCTCCTCTTCTTCGTCTCCGGCCTCATCGT
CAATCTCGTACAGGCAGTTTGCTTTGTACTGATTAGGCCTCTGTCGAAAAACACTTACAGAAGAATAA
ACAGAGTGGTTGCAGAATTGTTGTGGTTGGAGTTGGTATGGCTGATTGATTGGTGGGCTGGTGTCAAG
ATAAAAGTATTCACGGATCATGAAACCTTTCACCTTATGGGCAAAGAACATGCTCTTGTCATTTGTAA
TCACAAGAGTGACATAGACTGGCTGGTTGGGTGGGTTCTGGGACAGCGGTCAGGTTGCCTTGGAAGCA
CATTAGCTGTTATGAAGAAATCATCAAAGTTTCTCCCGGTATTAGGGTGGTCAATGTGGTTCTCAGAG
TATCTATTCCTTGAAAGAAGCTGGGCCAAGGATGAAATTACATTAAAGTCAGGTTTGAATAGGCTGAA
AGACTATCCCTTACCCTTCTGGTTGGCACTTTTTGTGGAAGGAACTCGGTTCACTCGAGCAAAACTCT
TGGCAGCCCAGCAGTATGCTGCCTCTTCGGGGCTACCTGTGCCGAGAAATGTTCTGATCCCGCGTACT
AAGGGTTTTGTTTCTTCTGTGAGTCACATGCGATCATTTGTTCCAGCCATATATGATGTTACAGTGGC
AATCCCAAAGACGTCACCTCCACCAACATTGATAAGAATGTTCAAGGGACAGTCCTCAGTGCTTCACG
TCCACCTCAAGCGACACCTAATGAAAGATTTACCTGAATCAGATGATGCTGTTGCTCAGTGGTGCAGA
GATATATTCGTCGAGAAGGATGCTTTGTTGGATAAGCATAATGCTGAGGACACTTTCAGTGGCCAAGA
ACTTCAAGAAACTGGCCGCCCAATAAAGTCTCTTCTGGTTGTAATCTCTTGGGCGGTGTTGGAGGTAT
TTGGAGCTGTGAAGTTTCTTCAATGGTCATCGCTGTTATCATCATGGAAGGGACTTGCATTTTCGGGA
ATAGGACTGGGTGTCATCACGCTACTCATGCACATACTGATTTTATTCTCACAATCCGAGCGGTCTAC
CCCTGCAAAAGTGGCACCAGCAAAGCCAAAGAATGAGGGAGAGTCCTCCAAGACGGAAATGGAAAAGG
AAAAGTAG

SEQ ID NO: 83
cDNA sequence for CuPSR23 LPAATx coding region codon optimized for Prototheca moriformis

ATGgagatccccccccactgcctgtgctccccctcccccgcccccctcccagctgtactacaagaagaa
gaagcacgccatcctgcagacccagacccccctaccgctaccgcgtgtcccccacctgcttcgcccccc
cccgcctgcgcaagcagcacccctaccccctgcccgtgctgtgctaccccaagctgctgcacttctcc
cagccccgctaccccctggtgcgctcccacctggccgaggccggcgtggcctaccgccccggctacga
gctgctgggcaagatccgcggcgtgtgcttctacgccgtgaccgccgccgtggccctgctgctgttcc
agtgcatgctgctgctgcacccctttcgtgctgctgttcgacccctttcccccgcaaggcccaccacacc
atcgccaagctgtggtccatctgctccgtgtccctgttctacaagatccacatcaagggcctggagaa
cctgcccccccccccactcccccgccgtgtacgtgtccaaccaccagtccttcctggacatctacaccc
tgctgaccctgggccgcaccttcaagttcatctccaagaccgagatcttcctgtaccccatcatcggc

tgggccatgtacatgctgggcaccatccccctgaagcgcctggactcccgctcccagctggacaccct
gaagcgctgcatggacctgatcaagaagggcgcctccgtgttcttcttccccgagggcacccgctcca
aggacggcaagctgggcgccttcaagaagggcgccttctccatcgccgccaagtccaaggtgcccgtg
gtgcccatcaccctgatcggcaccggcaagatcatgccccccggctccgagctgaccgtgaaccccgg
caccgtgcaggtgatcatccacaagcccatcgagggctccgacgccgaggccatgtgcaacgaggccc
gcgccaccatctcccactccctggacgacTGA

SEQ ID NO: 84
cDNA sequence for CuPSR23 LPAAT 2-1 coding region codon optimized
for Prototheca moriformis

ATGgcgatcgcggccgcggcggtgatcttcctgttcggcctgatcttcttcgcctccggcctgatcat
caacctgttccaggcgctgtgcttcgtcctgatccgcccccctgtccaagaacgcctaccgccgcatca
accgcgtgttcgcggagctgctgctgtccgagctgctgtgcctgttcgactggtgggcgggcgcgaag
ctgaagctgttcaccgaccccgagacgttccgcctgatgggcaaggagcacgccctggtcatcatcaa
ccacatgaccgagctggactggatggtgggctgggtgatgggccagcacttcggctgcctgggctcca
tcatctccgtcgccaagaagtccacgaagttcctgcccgtgctgggctggtccatgtggttctccgag
tacctgtacctggagcgctcctgggccaaggacaagtccaccctgaagtcccacatcgagcgcctgat
cgactacccccctgcccttctggctggtcatcttcgtcgagggcacccgcttcacgcgcacgaagctgc
tggcggcccagcagtacgcggtctcctccggcctgcccgtcccccgcaacgtcctgatcccccgcacg
aagggcttcgtctcctgcgtgtcccacatgcgctccttcgtccccgcggtgtacgacgtcacggtggc
gttccccaagacgtccccccccccccacgctgctgaacctgttcgagggccagtccatcatgctgcacg
tgcacatcaagcgccacgccatgaaggacctgcccgagtccgacgacgccgtcgcggagtggtgccgc
gacaagttcgtcgagaaggacgccctgctggacaagcacaacgcggaggacacgttctccggccagga
ggtgtgccactccggctcccgccagctgaagtccctgctggtcgtgatctcctgggtcgtggtgacga
cgttcggcgccctgaagttcctgcagtggtcctcctggaagggcaaggcgttctccgccatcggcctg
ggcatcgtcaccctgctgatgcacgtgctgatcctgtcctcccaggccgagcgctccaaccccgccga
ggtggcccaggccaagctgaagaccggcctgtccatctccaagaaggtgacggacaaggagaacTGA

SEQ ID NO: 85
cDNA sequence for CuPSR23 LPAAx 3-1 coding region codon optimized
for Prototheca moriformis

ATGgccatcgcggcggccgcggtgatcgtgcccctgtccctgctgttcttcgtgtccggcctgatcgt
caacctggtgcaggccgtctgcttcgtcctgatccgcccccctgtccaagaacacgtaccgccgcatca
accgcgtggtcgcggagctgctgtggctggagctggtgtggctgatcgactggtgggcgggcgtgaag
atcaaggtcttcacggaccacgagacgttccacctgatgggcaaggagcacgccctggtcatctgcaa
ccacaagtccgacatcgactggctggtcggctgggtcctgggccagcgctccggctgcctgggctcca
ccctggcggtcatgaagaagtcctccaagttcctgcccgtcctgggctggtccatgtggttctccgag
tacctgttcctggagcgctcctgggccaaggacgagatcacgctgaagtccggcctgaaccgcctgaa
ggactacccccctgcccttctggctggcgctgttcgtggagggcacgcgcttcacccgcgcgaagctgc
tggcggcgcagcagtacgccgcgtcctccggcctgcccgtgccccgcaacgtgctgatcccccgcacg
aagggcttcgtgtcctccgtgtcccacatgcgctccttcgtgcccgcgatctacgacgtcaccgtggc
catccccaagacgtccccccccccccacgctgatccgcatgttcaagggccagtcctccgtgctgcacg
tgcacctgaagcgccacctgatgaaggacctgcccgagtccgacgacgccgtcgcgcagtggtgccgc
gacatcttcgtggagaaggacgcgctgctggacaagcacaacgccgaggacaccttctccggccagga
gctgcaggagaccggccgccccatcaagtccctgctggtcgtcatctcctgggccgtcctggaggtgt
tcggcgccgtcaagttcctgcagtggtcctccctgctgtcctcctggaagggcctggcgttctccggc
atcggcctgggcgtgatcaccctgctgatgcacatcctgatcctgttctcccagtccgagcgctccac
ccccgccaaggtggcccccgcgaagcccaagaacgagggcgagtcctccaagaccgagatggagaagg
agaagTGA

SEQ ID NO: 86
Nucleic acid sequence encoding 14:0-ACP thioesterase, Cuphea
palustris (Cpal FATB2, accession AAC49180) containing an extended

heterologous transit peptide from C. protothecoides and a 41 amino acid N-terminal extension derived from the native Cpal FATB2 sequence in construct D1481 [pSZ2479]

GCGCACCCCAAGGCGAACGGCAGCGCGGTGTCGCTGAAGTCGGGCTCCCTGGAGACCCAGGAGGACAA
GACGAGCAGCTCGTCCCCCCCCCCCCCGCACGTTCATCAACCAGCTGCCCGTGTGGAGCATGCTGCTGT
CGGCGGTGACCACGGTCTTCGGCGTGGCCGAGAAGCAGTGGCCCATGCTGGACCGCAAGTCCAAGCGC
CCCGACATGCTGGTCGAGCCCCTGGGCGTGGACCGCATCGTCTACGACGGCGTGAGCTTCCGCCAGTC
GTTCTCCATCCGCAGCTACGAGATCGGCGCCGACCGCACCGCCTCGATCGAGACGCTGATGAACATGT
TCCAGGAGACCTCCCTGAACCACTGCAAGATCATCGGCCTGCTGAACGACGGCTTCGGCCGCACGCCC
GAGATGTGCAAGCGCGACCTGATCTGGGTCGTGACCAAGATGCAGATCGAGGTGAACCGCTACCCCAC
GTGGGGCGACACCATCGAGGTCAACACGTGGGTGAGCGCCTCGGGCAAGCACGGCATGGGCCGCGACT
GGCTGATCTCCGACTGCCACACCGGCGAGATCCTGATCCGCGCGACGAGCGTCTGGGCGATGATGAAC
CAGAAGACCCGCCGCCTGTCGAAGATCCCCTACGAGGTGCGCCAGGAGATCGAGCCCCAGTTCGTCGA
CTCCGCCCCCGTGATCGTGGACGACCGCAAGTTCCACAAGCTGGACCTGAAGACGGGCGACAGCATCT
GCAACGGCCTGACCCCCCGCTGGACGGACCTGGACGTGAACCAGCACGTCAACAACGTGAAGTACATC
GGCTGGATCCTGCAGTCGGTCCCCACCGAGGTGTTCGAGACGCAGGAGCTGTGCGGCCTGACCCTGGA
GTACCGCCGCGAGTGCGGCCGCGACTCCGTGCTGGAGAGCGTCACGGCCATGGACCCCTCGAAGGAGG
GCGACCGCTCCCTGTACCAGCACCTGCTGCGCCTGGAGGACGGCGCGGACATCGTGAAGGGCCGCACC
GAGTGGCGCCCCAAGAACGCCGGCGCCAAGGGCGCCATCCTGACGGGCAAGACCAGCAACGGCAACTC
GATCTCCTGA

SEQ ID NO: 87
Amino acid sequence of 14:0-ACP thioesterase, Cuphea palustris (Cpal FATB2, accession AAC49180) containing an extended heterologous transit peptide from C. protothecoides and a 41 amino acid N-terminal extension derived from the native Cpal FATB2 sequence encoded by construct D1481 [pSZ2479]

AHPKANGSAVSLKSGSLETQEDKTSSSSPPPRTFINQLPVWSMLLSAVTTVFGVAEKQWP
MLDRKSKRPDMLVEPLGVDRIVYDGVSFRQSFSIRSYEIGADRTASIETLMNMFQETSLN
HCKIIGLLNDGFGRTPEMCKRDLIWVVTKMQIEVNRYPTWGDTIEVNTWVSASGKHGMGR
DWLISDCHTGEILIRATSVWAMMNQKTRRLSKIPYEVRQEIEPQFVDSAPVIVDDRKFHK
LDLKTGDSICNGLTPRWTDLDVNQHVNNVKYIGWILQSVPTEVFETQELCGLTLEYRREC
GRDSVLESVTAMDPSKEGDRSLYQHLLRLEDGADIVKGRTEWRPKNAGAKGAILTGKTSN
GNSIS

SEQ ID No: 88
Nucleic acid sequence encoding 14:0-ACP thioesterase, Cuphea palustris (Cpal FATB2, accession AAC49180) containing an extended heterologous transit peptide from C. protothecoides, a 41 amino acid N-terminal extension derived from the native Cpal FATB2 sequence, and a C-terminal FLAG epitope tag in construct D1482 [pSZ2480]

GCGCACCCCAAGGCGAACGGCAGCGCGGTGTCGCTGAAGTCGGGCTCCCTGGAGACCCAGGAGGACAA
GACGAGCAGCTCGTCCCCCCCCCCCCCGCACGTTCATCAACCAGCTGCCCGTGTGGAGCATGCTGCTGT
CGGCGGTGACCACGGTCTTCGGCGTGGCCGAGAAGCAGTGGCCCATGCTGGACCGCAAGTCCAAGCGC
CCCGACATGCTGGTCGAGCCCCTGGGCGTGGACCGCATCGTCTACGACGGCGTGAGCTTCCGCCAGTC
GTTCTCCATCCGCAGCTACGAGATCGGCGCCGACCGCACCGCCTCGATCGAGACGCTGATGAACATGT
TCCAGGAGACCTCCCTGAACCACTGCAAGATCATCGGCCTGCTGAACGACGGCTTCGGCCGCACGCCC
GAGATGTGCAAGCGCGACCTGATCTGGGTCGTGACCAAGATGCAGATCGAGGTGAACCGCTACCCCAC
GTGGGGCGACACCATCGAGGTCAACACGTGGGTGAGCGCCTCGGGCAAGCACGGCATGGGCCGCGACT
GGCTGATCTCCGACTGCCACACCGGCGAGATCCTGATCCGCGCGACGAGCGTCTGGGCGATGATGAAC
CAGAAGACCCGCCGCCTGTCGAAGATCCCCTACGAGGTGCGCCAGGAGATCGAGCCCCAGTTCGTCGA

CTCCGCCCCCGTGATCGTGGACGACCGCAAGTTCCACAAGCTGGACCTGAAGACGGGCGACAGCATCT
GCAACGGCCTGACCCCCCGCTGGACGGACCTGGACGTGAACCAGCACGTCAACAACGTGAAGTACATC
GGCTGGATCCTGCAGTCGGTCCCCACCGAGGTGTTCGAGACGCAGGAGCTGTGCGGCCTGACCCTGGA
GTACCGCCGCGAGTGCGGCCGCGACTCCGTGCTGGAGAGCGTCACGGCCATGGACCCCTCGAAGGAGG
GCGACCGCTCCCTGTACCAGCACCTGCTGCGCCTGGAGGACGGCGCGGACATCGTGAAGGGCCGCACC
GAGTGGCGCCCCAAGAACGCCGGCGCCAAGGGCGCCATCCTGACGGGCAAGACCAGCAACGGCAACTC
GATCTCCatggactacaaggaccacgacggcgactacaaggaccacgacatcgactacaaggacgacg
acgacaagtga

SEQ ID NO: 89
Amino acid sequence of 14:0-ACP thioesterase, Cuphea palustris (Cpal FATB2, accession AAC49180) containing an extended heterologous transit peptide from C. protothecoides, a 41 amino acid N-terminal extension derived from the native Cpal FATB2 sequence, and a C-terminal FLAG epitope tag encoded by construct D1482 [pSZ2480]

AHPKANGSAVSLKSGSLETQEDKTSSSSPPPRTFINQLPVWSMLLSAVTTVFGVAEKQWP
MLDRKSKRPDMLVEPLGVDRIVYDGVSFRQSFSIRSYEIGADRTASIETLMNMFQETSLN
HCKIIGLLNDGFGRTPEMCKRDLIWVVTKMQIEVNRYPTWGDTIEVNTWVSASGKHGMGR
DWLISDCHTGEILIRATSVWAMMNQKTRRLSKIPYEVRQEIEPQFVDSAPVIVDDRKFHK
LDLKTGDSICNGLTPRWTDLDVNQHVNNVKYIGWILQSVPTEVFETQELCGLTLEYRREC
GRDSVLESVTAMDPSKEGDRSLYQHLLRLEDGADIVKGRTEWRPKNAGAKGAILTGKTSN
GNSISMDYKDHDGDYKDHDIDYKDDDDK

SEQ ID NO: 154
Cuphea hyssopifolia FATB3 coding region, codon optimized for Prototheca moriformis

gtggccgccgaggcctcctccgccctgttctccgtgcgcacccccggcacctcccccaagcccggcaa
gttcggcaactggcccacctccctgtccgtgcccttcaagtccaagtccaaccacaacggcggcttcc
aggtgaaggccaacgcctccgcccgccccaaggccaacggctccgccgtgtccctgaagtccggctcc
ctggacacccaggaggacacctcctcctcctcctcccccccccgcaccttcatcaaccagctgcccga
ctggtccatgctgctgtccgccatcaccaccgtgttcgtggccgccgagaagcagtggaccatgctgg
accgcaagtccaagcgccccgacatgctgatggacccccttcggcgtggaccgcgtggtgcaggacggc
gccgtgttccgccagtccttctccatccgctcctacgagatcggcgccgaccgcaccgcctccatcga
gaccctgatgaacatcttccaggagacctccctgaaccactgcaagtccatcggcctgctgaacgacg
gcttcggccgcacccccgagatgtgcaagcgcgacctgatctgggtggtgaccaagatgcacgtggag
gtgaaccgctaccccacctggggcgacaccatcgaggtgaacacctgggtgtccgagtccggcaagac
cggcatgggccgcgactggctgatctccgactgccacaccggcgagatcctgatccgcgccacctcca
tgtgcgccatgatgaaccagaagacccgccgcttctccaagttcccctacgaggtgcgccaggagctg
gccccccacttcgtggactccgcccccgtgatcgaggactaccagaagctgcacaagctggacgtgaa
gaccggcgactccatctgcaacggcctgaccccccgctggaacgacctggacgtgaaccagcacgtga
acaacgtgaagtacatcggctggatcctggagtccgtgcccaccgaggtgttcgagacccaggagctg
tgcggcctgaccctggagtaccgccgcgagtgcggccgcgactccgtgctggagtccgtgaccgccat
ggacccctccaaggagggcgaccgctccctgtaccagcacctgctgcgcctggaggacggcgccgaca
tcgccaagggccgcaccaagtggcgccccaagaacgccggcaccaacggcgccatctccaccggcaag
acctccaacggcaactccatctccatggactacaaggaccacgacggcgactacaaggaccacgacat
cgactacaaggacgacgacgacaag

SEQ ID NO: 155
Cuphea hyssopifolia FATB1 coding region, codon optimized for Prototheca moriformis

gccaccgcctccaccttctccgccttcaacgcccgctgcggcgacctgcgccgctccgccggctccgg
cccccgccgccccgcccgcccctgcccgtgcgcgccgccatcaacgcctccgcccaccccaaggcca

acggctccgccgtgaacctgaagtccggctccctggagacccaggaggacacctcctcctcctccccc
ccccccccgcaccttcatcaagcagctgcccgactggggcatgctgctgtccaagatcaccaccgtgtt
cggcgccgccgagcgccagtggaagcgccccggcatgctggtggagcccttcggcgtggaccgcatct
tccaggacggcgtgttcttccgccagtccttctccatccgctcctacgagatcggcgccgaccgcacc
gcctccatcgagaccctgatgaacatcttccaggagacctccctgaaccactgcaagtccatcggcct
gctgaacgacggcttcggccgcacccccgagatgtgcaagcgcgacctgatctgggtggtgaccaaga
tccaggtggaggtgaaccgctaccccacctggggcgacaccatcgaggtgaacacctgggtgtccgag
tccggcaagaacggcatgggccgcgactggctgatctccgactgccgcaccggcgagatcctgatccg
cgccacctccgtgtgggccatgatgaaccgcaagacccgccgcctgtccaagttcccctacgaggtgc
gccaggagatcgccccccacttcgtggactccgcccccgtgatcgaggacgacaagaagctgcacaag
ctggacgtgaagaccggcgactccatccgcaagggcctgacccccgctggaacgacctggacgtgaa
ccagcacgtgaacaacgtgaagtacatcggctggatcctgaagtccgtgcccgccgaggtgttcgaga
cccaggagctgtgcggcgtgaccctggagtaccgccgcgagtgcggccgcgactccgtgctggagtcc
gtgaccgccatggacaccgccaaggagggcgaccgctccctgtaccagcacctgctgcgcctggagga
cggcgccgacatcaccatcggccgcaccgagtggcgccccaagaacgccggcgccaacggcgccatct
ccaccggcaagacctccaacgagaactccgtgtccatggactacaaggaccacgacggcgactacaag
gaccacgacatcgactacaaggacgacgacgacaag

SEQ ID NO: 156
Garcinia mangostana FATA1 CDS

MLKLSSSRSPLARIPTRPRPNSIPPRIIVVSSSSSKVNPLKTEAVVSSGLADRLRLGSLTEDGLSYKEKF
IVRCYEVGINKTATVETIANLLQEVGCNHAQSVGYSTGGFSTTPTMRKLRLIWVTARMHIEIYKYPAWSD
VVEIESWGQGEGKIGTRRDWILRDYATGQVIGRATSKWVMMNQDTRRLQKVDVDVRDEYLVHCPRELRLA
FPEENNSSLKKISKLEDPSQYSKLGLVPRRADLDMNQHVNNVTYIGWVLESMPQEIIDTHELQTITLDYR
RECQHDDVVDSLTSPEPSEDAEAVFNHNGTNGSANVSANDHGCRNFLHLLRLSGNGLEINRGRTEWRKKP
TR

SEQ ID NO: 157
Brassic napus LPAAT CDS

MAMAAAVIVPLGILFFISGLVVNLLQAVCYVLVRPMSKNTYRKINRVVAETLWLELVWIVDWWAGVKIQV
FADDETFNRMGKEHALVVCNHRSDIDWLVGWILAQRSGCLGSALAVMKKSSKFLPVIGWSMWFSEYLFLE
RNWAKDESTLQSGLQRLNDFPRPFWLALFVEGTRFTEAKLKAAQEYAASSELPVPRNVLIPRTKGFVSAV
SNMRSFVPAIYDMTVAIPKTSPPPTMLRLFKGQPSVVHVHIKCHSMKDLPEPEDEIAQWCRDQFVAKDAL
LDKHIAADTFPGQKEQNIGRPIKSLAVVVSWACLLTLGAMKFLHWSNLFSSWKGIALSAFGLGIITLCMQ
ILIRSSQSERSTPAKVAPAKPKDNHQSGPSSQTEVEEKQK

SEQ ID NO: 158
Cuphea hookeriana FATB2 CDS

MVAAAAASSAFFPVPAPGASPKPGKFGNWPSSLSPSFKPKSIPNGGFQVKANDSAHPKANGSAVSLKSGSL
NTQEDTSSSPPPRTFLHQLPDWSRLLTAITTVFVKSKRPDMHDRKSKRPDMLVDSFGLESTVQDGLVFRQ
SFSIRSYEIGTDRTASIETLMNHLQETSLNHCKSTGILLDGFGRTLEMCKRDLIWVVIKMQIKVNRYPAW
GDTVEINTRFSRLGKIGMGRDWLISDCNTGEILVRATSAYAMMNQKTRRLSKLPYEVHQEIVPLFVDSPV
IEDSDLKVHKFKVKTGDSIQKGLTPGWNDLDVNQHVSNVKYIGWILESMPTEVLETQELCSLALEYRREC
GRDSVLESVTAMDPSKVGVRSQYQHLLRLEDGTAIVNGATEWRPKNAGANGAISTGKTSNGNSVS

SEQ ID NO: 159
Cuphea wrightii KASA1 CDS with P moriformis SAD transit peptide
(underlined)

MASAAFTMSACPAMTGRAPGARRSGRPVATRLRYVFQCLVASCIDPCDQYRSSASLSFLGDNGFASLF
GSKPFMSNRGHRRLRRASHSGEAMAVALQPAQEAGTKKKPVIKQRRVVVTGMGVVTPLGHEPDVFYNN
LLDGVSGISEIETFDCTQFPTRIAGEIKSFSTDGWVAPKLSKRMDKFMLYLLTAGKKALADGGITDEV
MKELDKRKCGVLIGSGMGGMKVFNDAIEALRVSYKKMNPFCVPFATTNMGSAMLAMDLGWMGPNYSIS
TACATSNFCILNAANHIIRGEADMMLCGGSDAVIIPIGLGGFVACRALSQRNSDPTKASRPWDSNRDG

FVMGEGAGVLLLEELEHAKKRGATIYAEFLGGSFTCDAYHMTEPHPEGAGVILCIEKALAQAGVSKED
VNYINAHATSTSAGDIKEYQALARCFGQNSELRVNSTKSMIGHLLGAAGGVEAVTVVQAIRTGWIHPN
LNLEDPDKAVDAKLLVGPKKERLNVKVGLSNSFGFGGHNSSILFAPCNV

SEQ ID NO: 160
Native Protheca moriformis KASII amino acid sequence (native transit peptide is underlined)

MQTAHQRPPTEGHCFGARLPTASRRAVRRAWSRIARAAAAADANPARPERRVVITGQGVVTSLGQTIE
QFYSSLLEGVSGISQIQKFDTTGYTTTIAGEIKSLQLDPYVPKRWAKRVDDVIKYVYIAGKQALESAG
LPIEAAGLAGAGLDPALCGVLIGTAMAGMTSFAAGVEALTRGGVRKMNPFCIPFSISNMGGAMLAMDI
GFMGPNYSISTACATGNYCILGAADHIRRGDANVMLAGGADAAIIPSGIGGFIACKALSKRNDEPERA
SRPWDADRDGFVMGEGAGVLVLEELEHAKRRGATILAELVGGAATSDAHHMTEPDPQGRGVRLCLERA
LERARLAPERVGYVNAHGTSTPAGDVAEYRAIRAVIPQDSLRINSTKSMIGHLLGGAGAVEAVAAIQA
LRTGWLHPNLNLENPAPGVDPVVLVGPRKERAEDLDVVLSNSFGFGGHNSCVIFRKYDE

SEQ ID NO: 161
Mature native Protheca moriformis KASII amino acid sequence (native transit peptide is underlined)

AAAAADANPARPERRVVITGQGVVTSLGQTIEQFYSSLLEGVSGISQIQKFDTTGYTTTIAGEIKSLQ
LDPYVPKRWAKRVDDVIKYVYIAGKQALESAGLPIEAAGLAGAGLDPALCGVLIGTAMAGMTSFAAGV
EALTRGGVRKMNPFCIPFSISNMGGAMLAMDIGFMGPNYSISTACATGNYCILGAADHIRRGDANVML
AGGADAAIIPSGIGGFIACKALSKRNDEPERASRPWDADRDGFVMGEGAGVLVLEELEHAKRRGATIL
AELVGGAATSDAHHMTEPDPQGRGVRLCLERALERARLAPERVGYVNAHGTSTPAGDVAEYRAIRAVI
PQDSLRINSTKSMIGHLLGGAGAVEAVAAIQALRTGWLHPNLNLENPAPGVDPVVLVGPRKERAEDLD
VVLSNSFGFGGHNSCVIFRKYDE

SEQ ID NO: 162
CcFATB2-UcFATB2 chimeric FATB

PDWSMLFAVITTIFSAAEKQWTNLEWKPKPNPPQLLDDHFGPHGLVFRRTFAIRSYEVGP
DRSTSIVAVMNHLQEAALNHAKSVGILGDGFGTTLEMSKRDLIWVVRRTHVAVERYPTWG
DTVEVECWIGASGNNGMRRDFLVRDCKTGEILTRCTSLSVLMNTRTRRLSTIPDEVRGEI
GPAFIDNVAVKDDEIKKLQKLNDSTADYIQGGLTPRWNDLDVNQHVNNLKYVAWVFETVP
DSIFESHHISSFTLEYRRECTRDSVLRSLTTVSGGSSEAGLVCDHLLQLEGGSEVLRART
EWRPKLTDSFRGISVIPAEPRV

SEQ ID NO: 163
Cuphea hyssopifolia FATB1

MVATNAAAFSAYTFFLTSPTHGYSSKRLADTQNGYPGTSLKSKSTPPPAAAAARNGALPLLASICKCP
KKADGSMQLDSSLVFGFQFYIRSYEVGADQTVSIQTVLNYLQEAAINHVQSAGYFGDSFGATPEMTKR
NLIWVITKMQVLVDRYPAWGDVVQVDTWTCSSGKNSMQRDWFVRDLKTGDIITRASSVWVLMNRLTRK
LSKIPEAVLEEAKLFVMNTAPTVDDNRKLPKLDGSSADYVLSGLTPRWSDLDMNQHVNNVKYIAWILE
SVPQSIPETHKLSAITVEYRRECGKNSVLQSLTNVSGDGITCGNSIIECHHLLQLETGPEILLARTEW
ISKEPGFRGAPIQAEKVYNNK*

SEQ ID NO: 164
Cuphea hyssopifolia FATB3

MVAAEASSALFSVRTPGTSPKPGKFGNWPTSLSVPFKSKSNHNGGFQVKANASARPKANGSAVSLKSG
SLDTQEDTSSSSSPPRTFINQLPDWSMLLSAITTVFVAAEKQWTMLDRKSKRPDMLMDPFGVDRVVQD
GAVFRQSFSIRSYEIGADRTASIETLMNIFQETSLNHCKSIGLLNDGFGRTPEMCKRDLIWVVTKMHV
EVNRYPTWGDTIEVNTWVSESGKTGMGRDWLISDCHTGEILIRATSMCAMMNQKTRRFSKFPYEVRQE

LAPHFVDSAPVIEDYQKLHKLDVKTGDSICNGLTPRWNDLDVNQHVNNVKYIGWILESVPTEVFETQE
LCGLTLEYRRECGRDSVLESVTAMDPSKEGDRSLYQHLLRLEDGADIAKGRTKWRPKNAGTNGAISTG
KTSNGNSIS*