

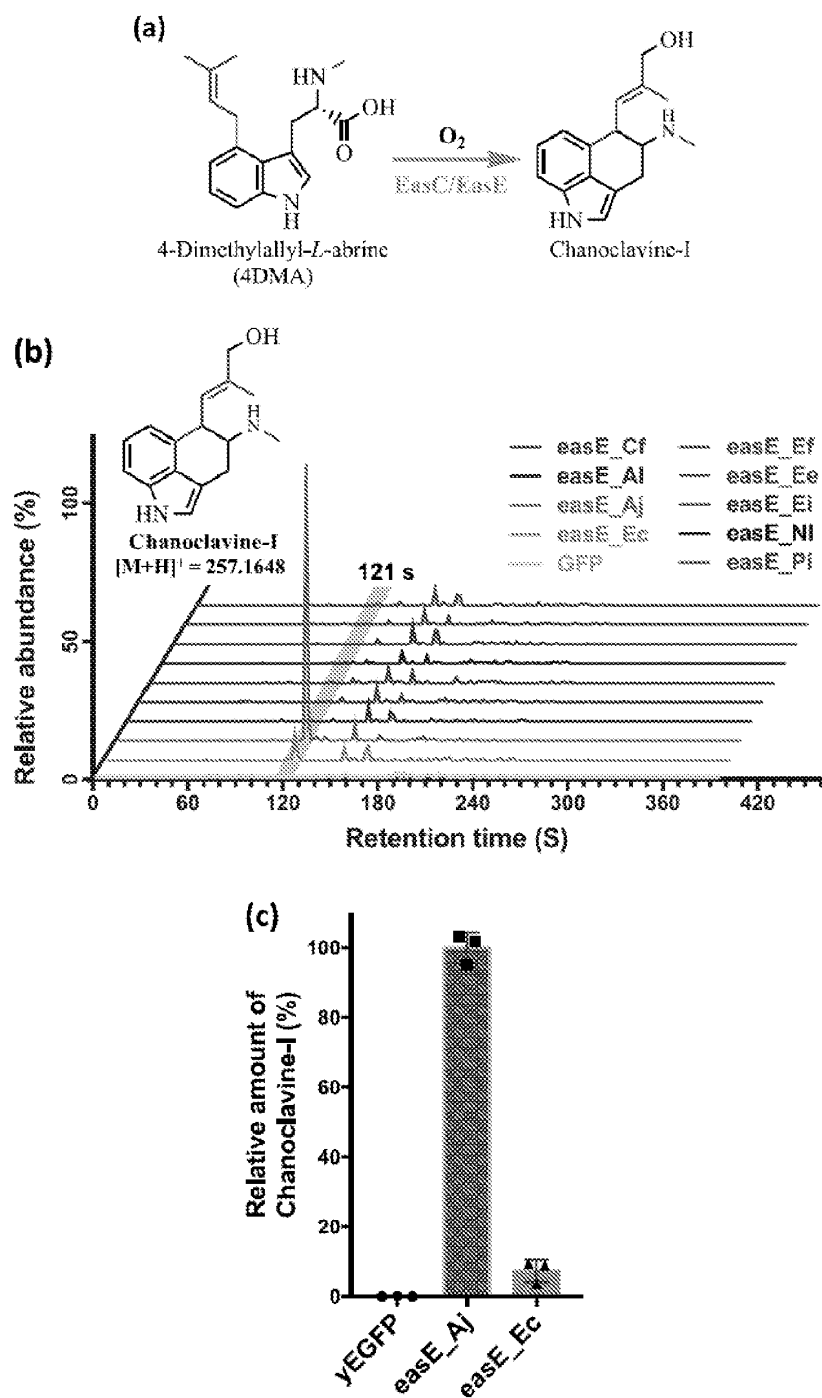
FIG. 2

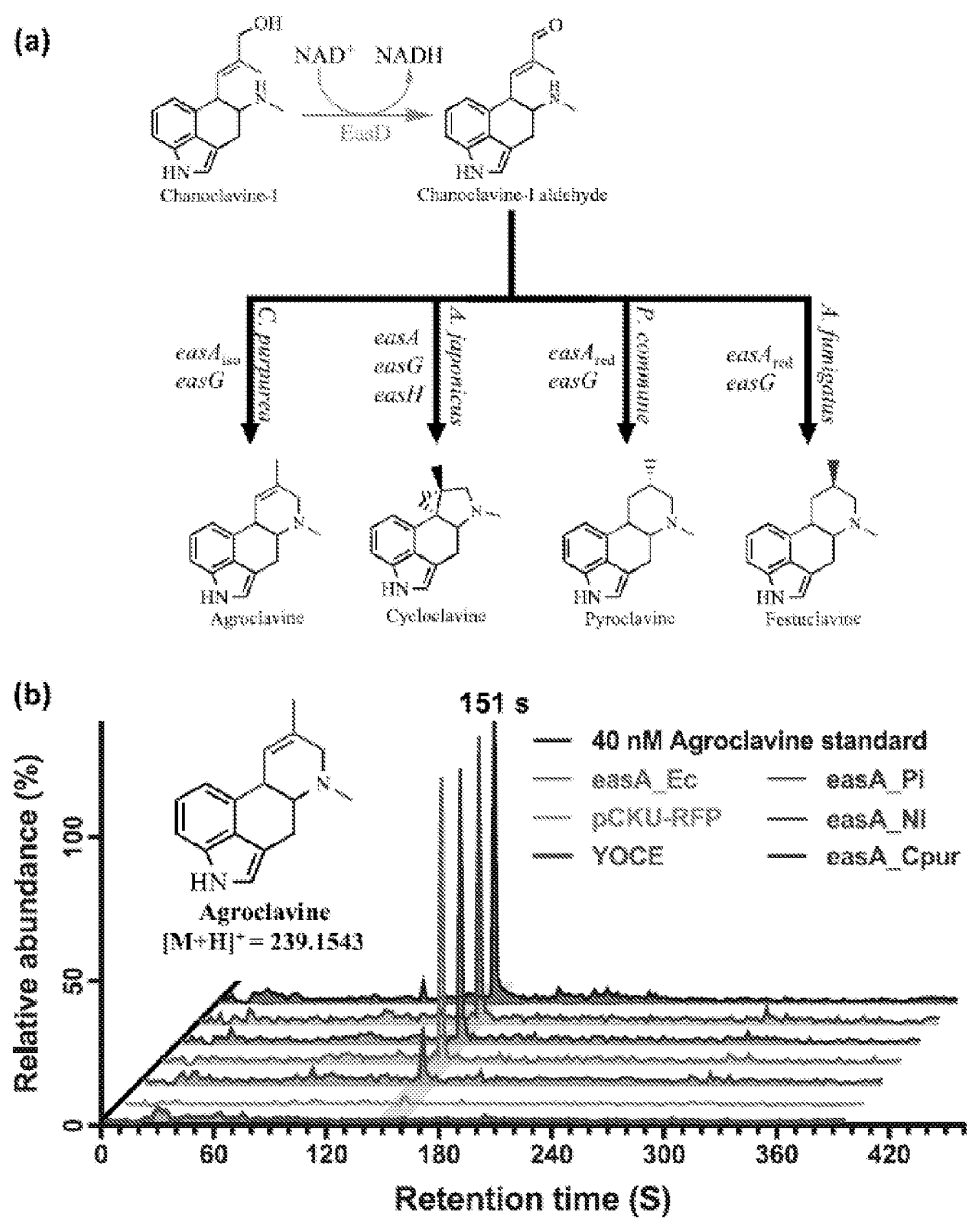
FIG. 3

FIG. 4

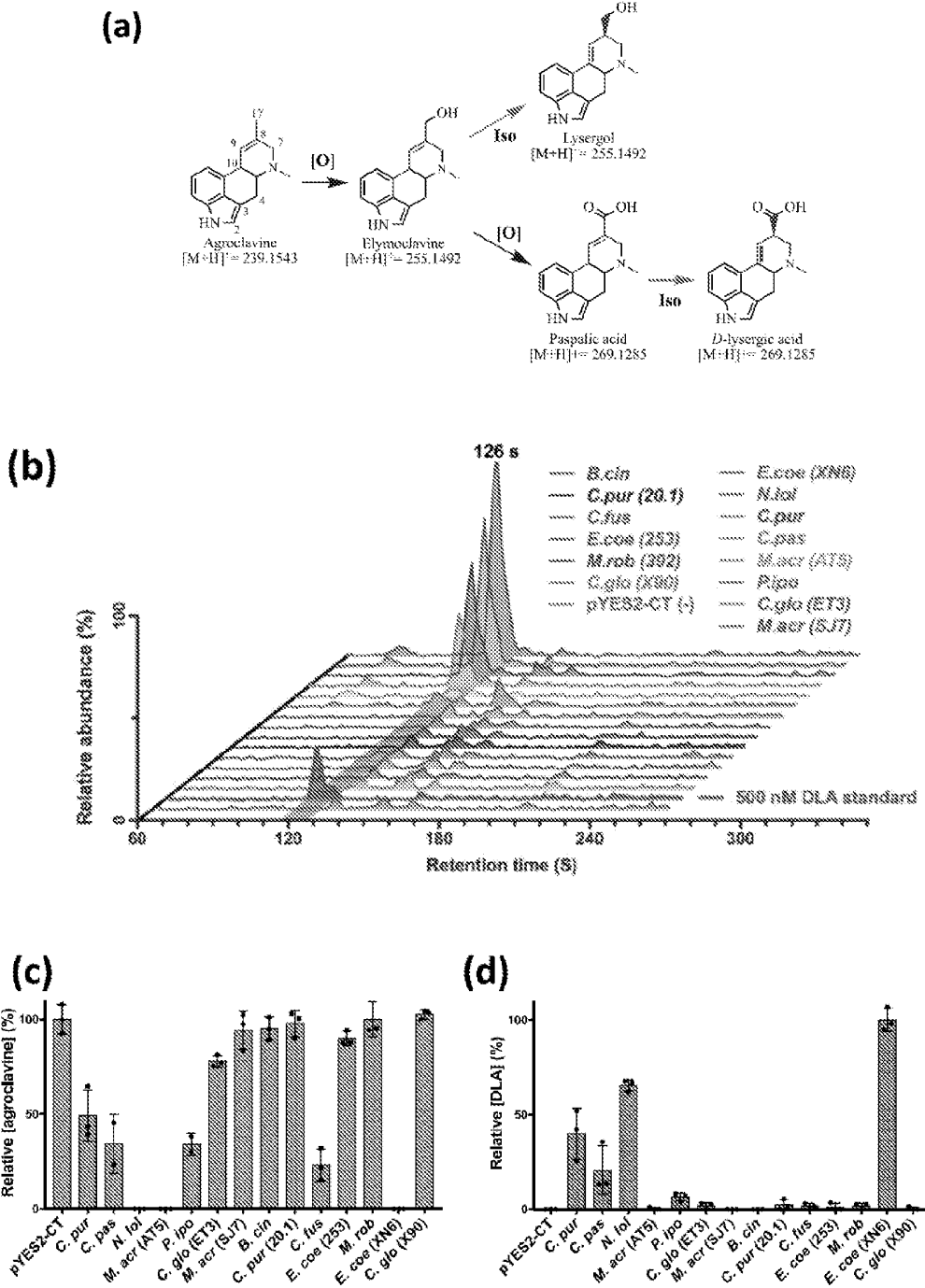


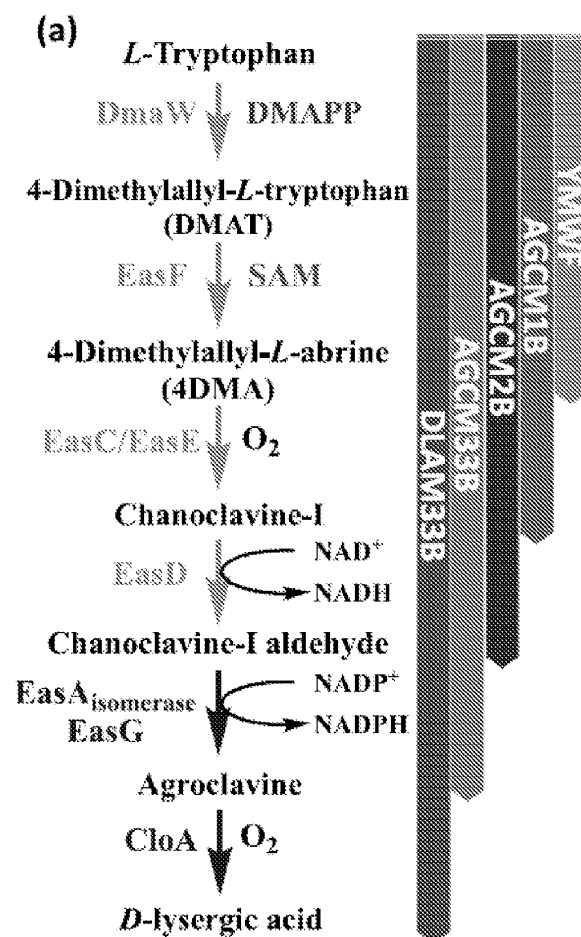
FIG. 5

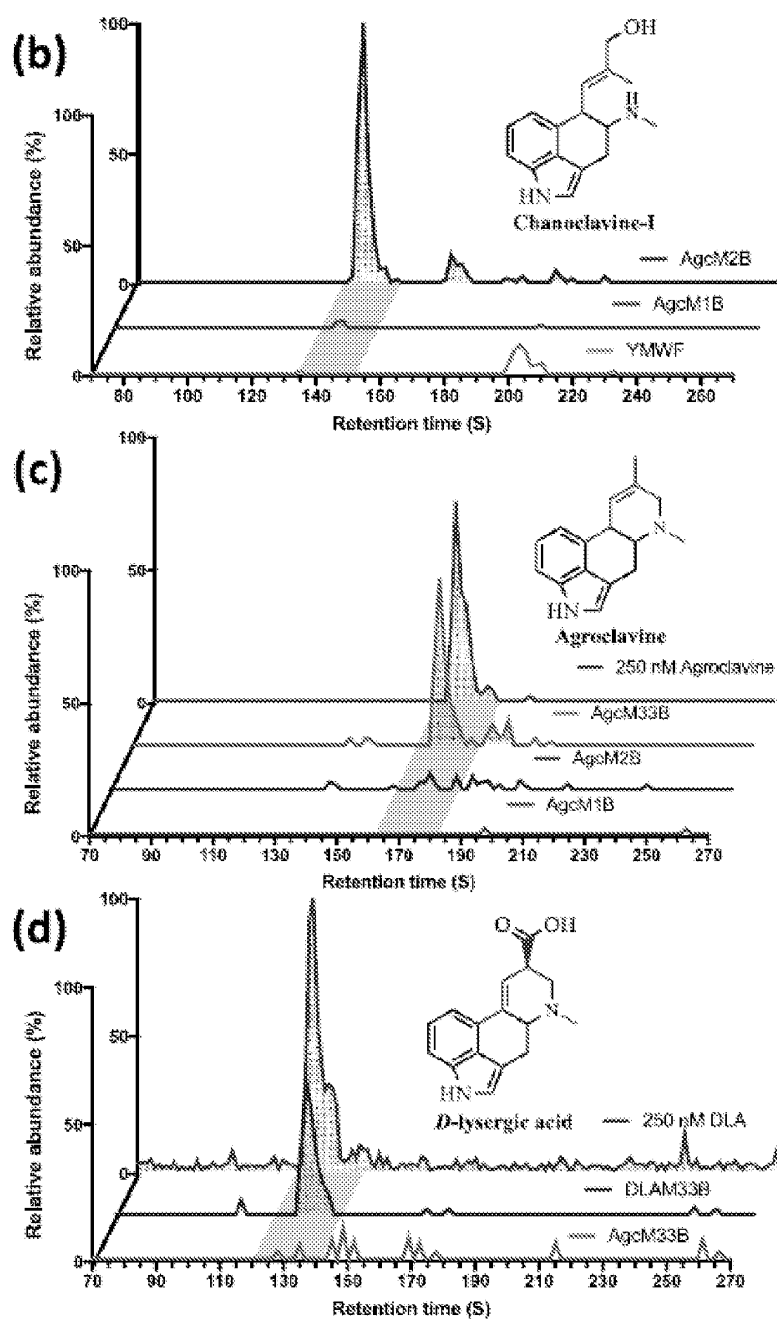
FIG. 5 (cont'd)

FIG. 6

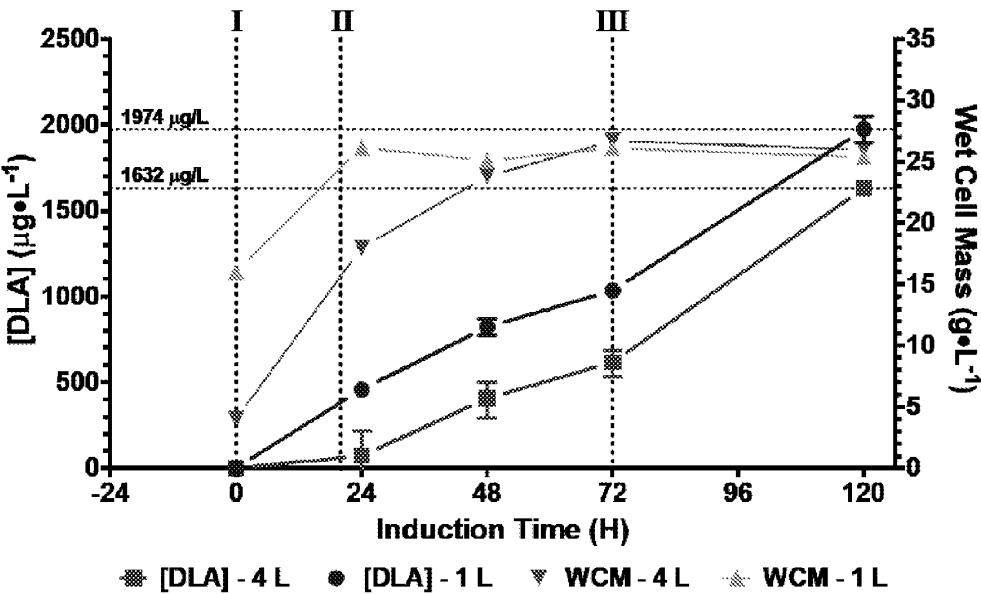
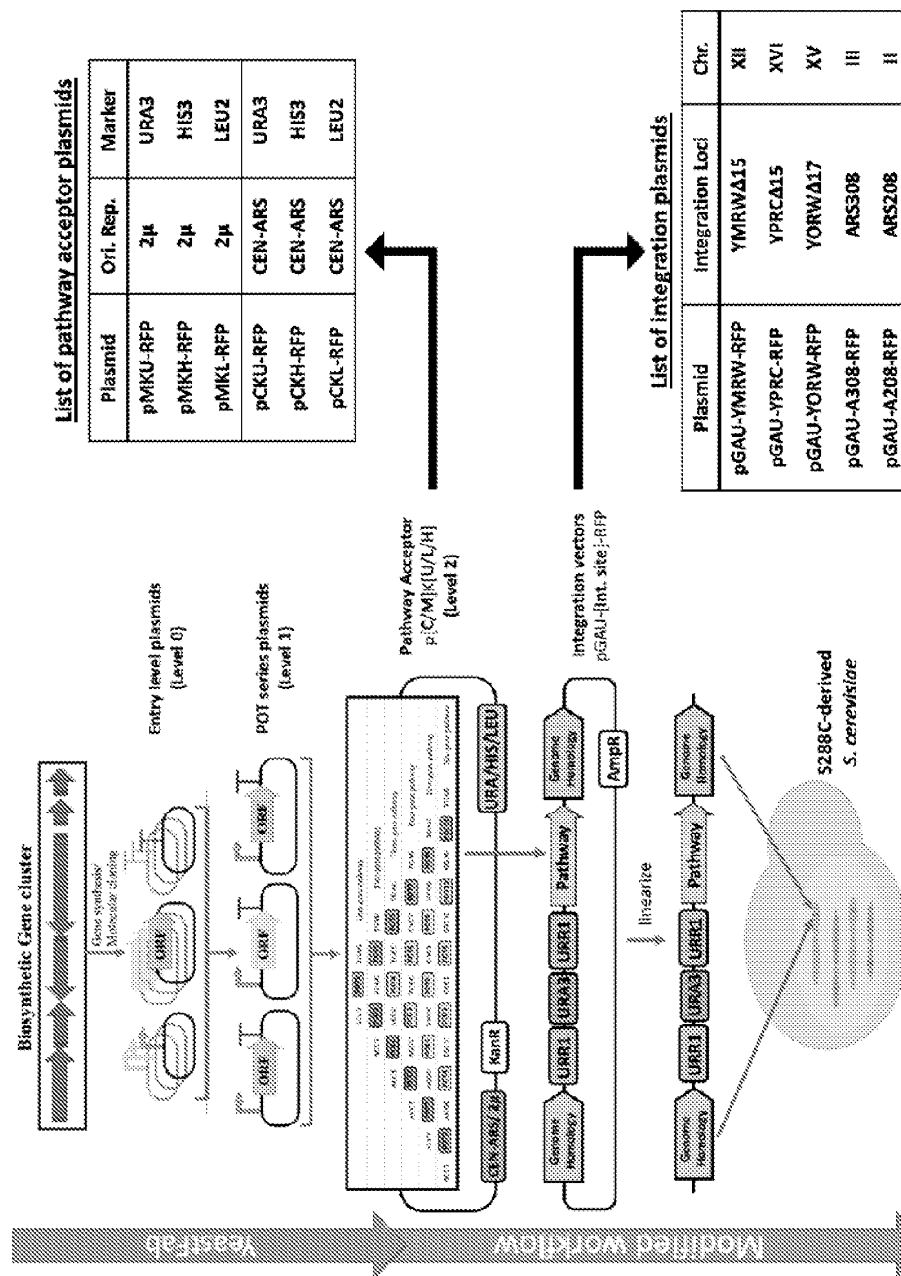


FIG. 7



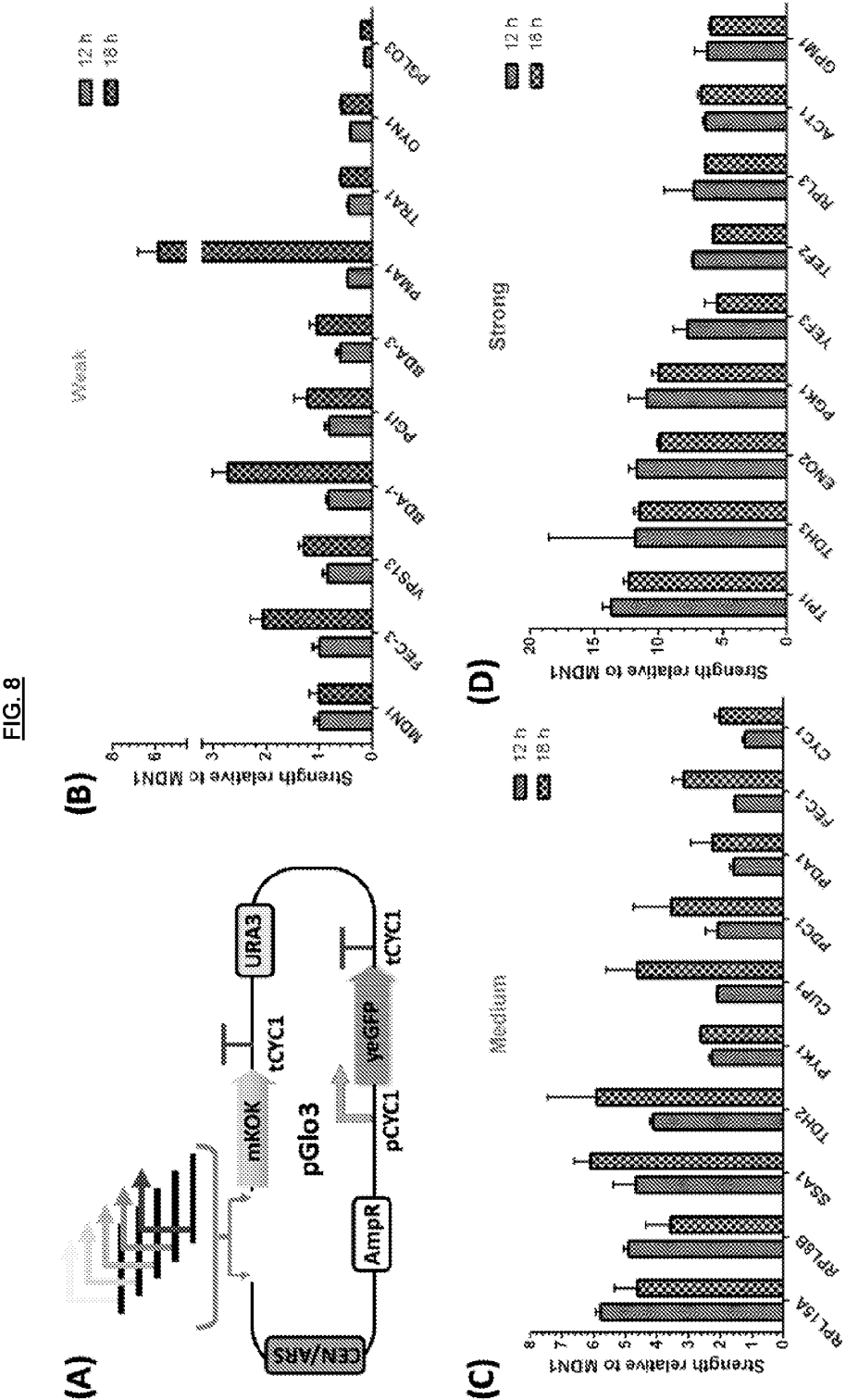


FIG. 8

FIG. 9

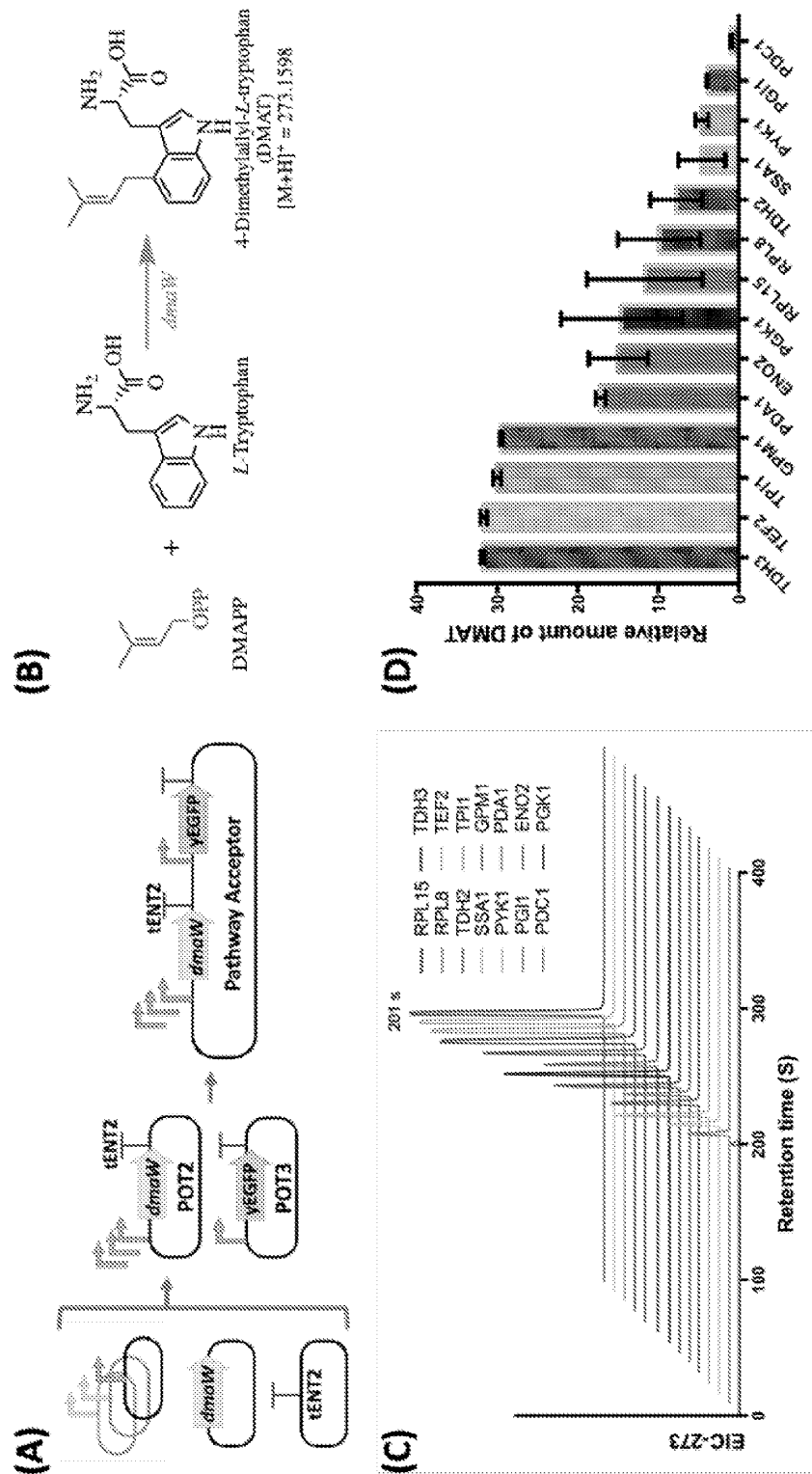


FIG. 10

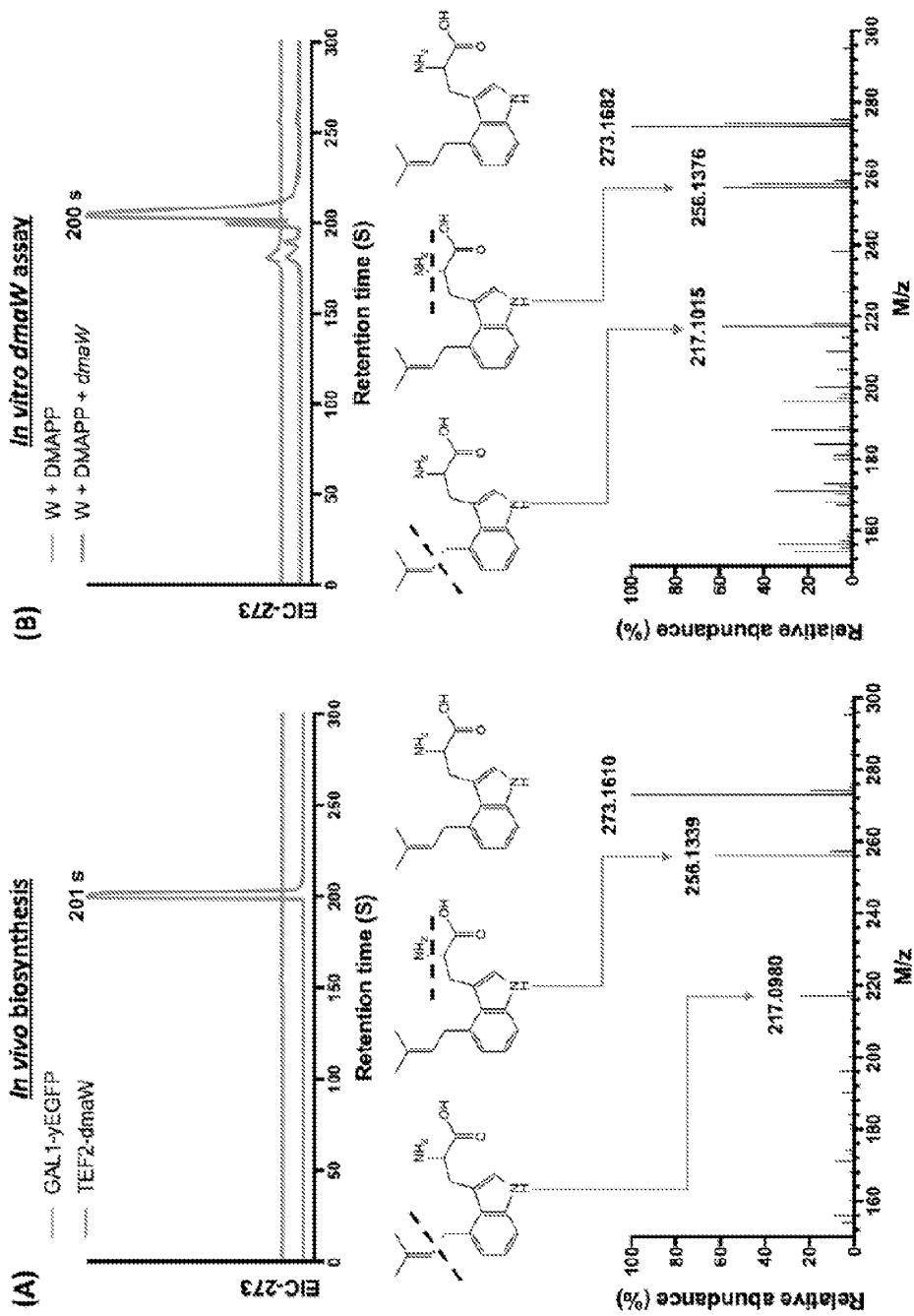


FIG. 11

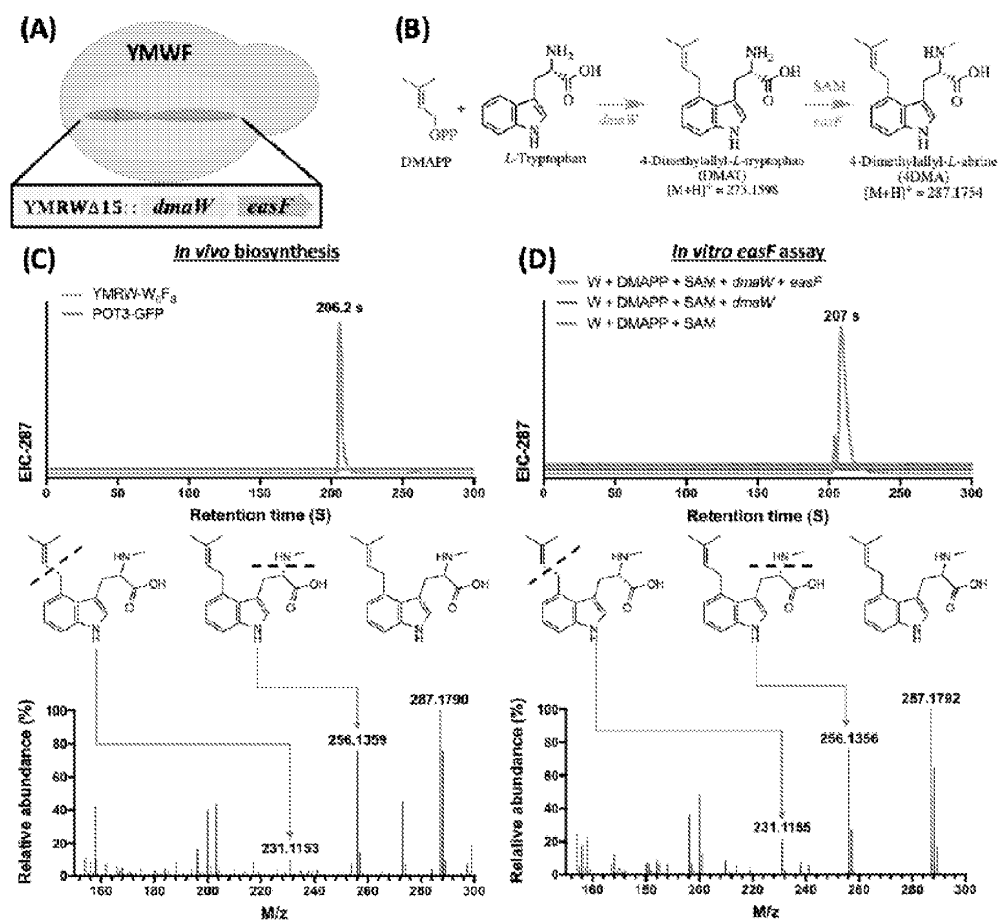


FIG. 12

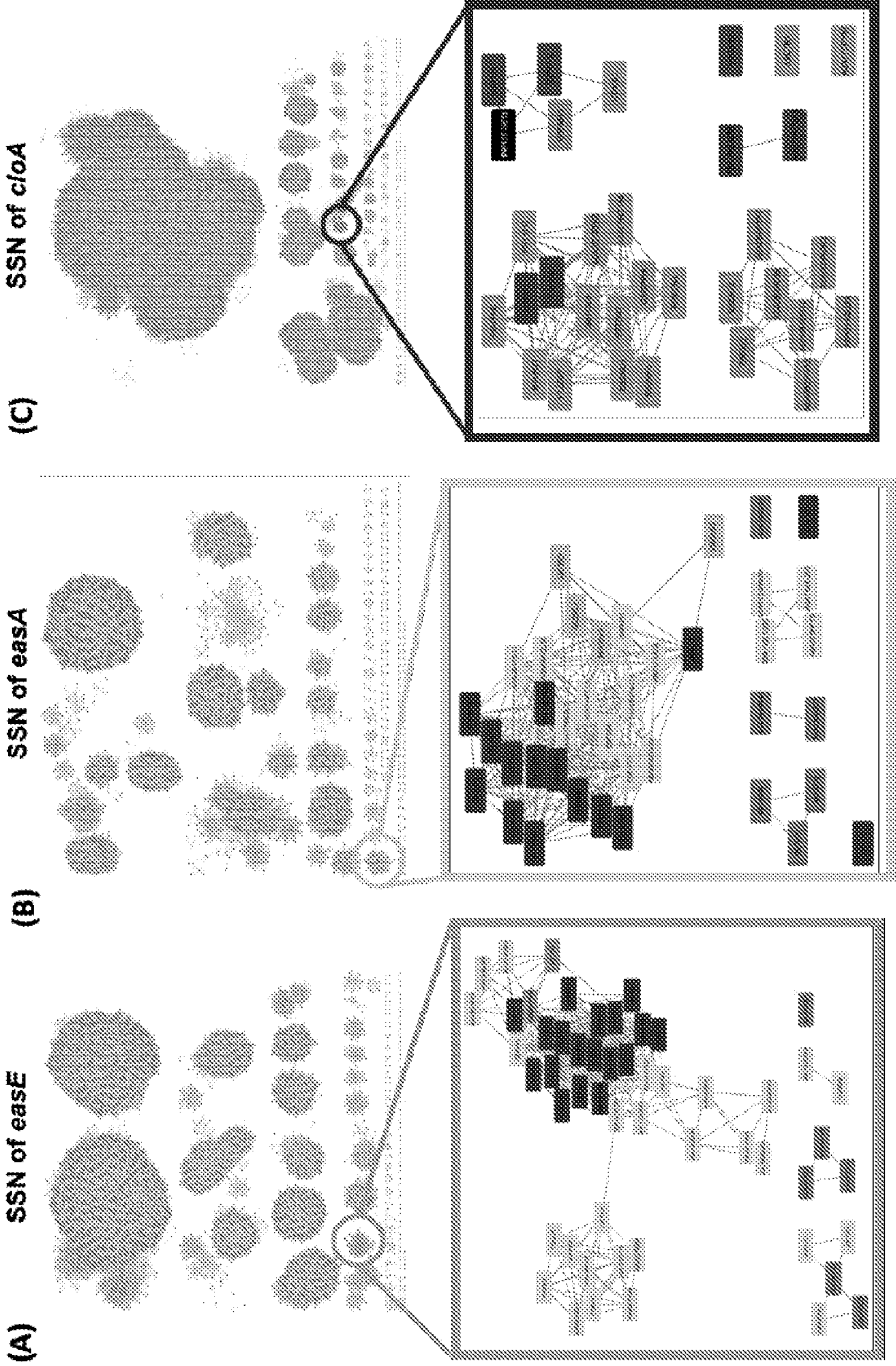


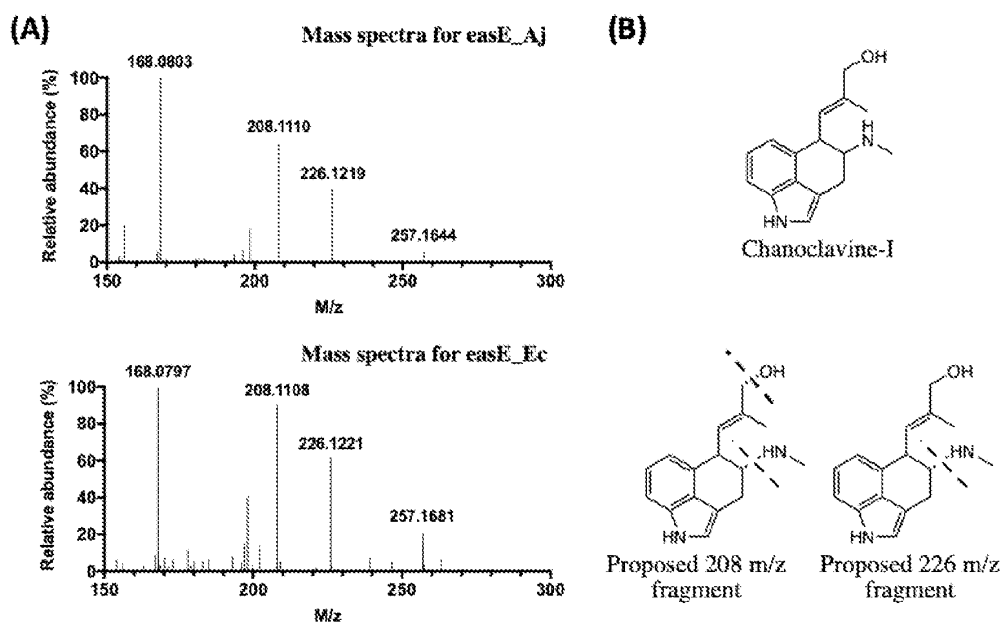
FIG. 13

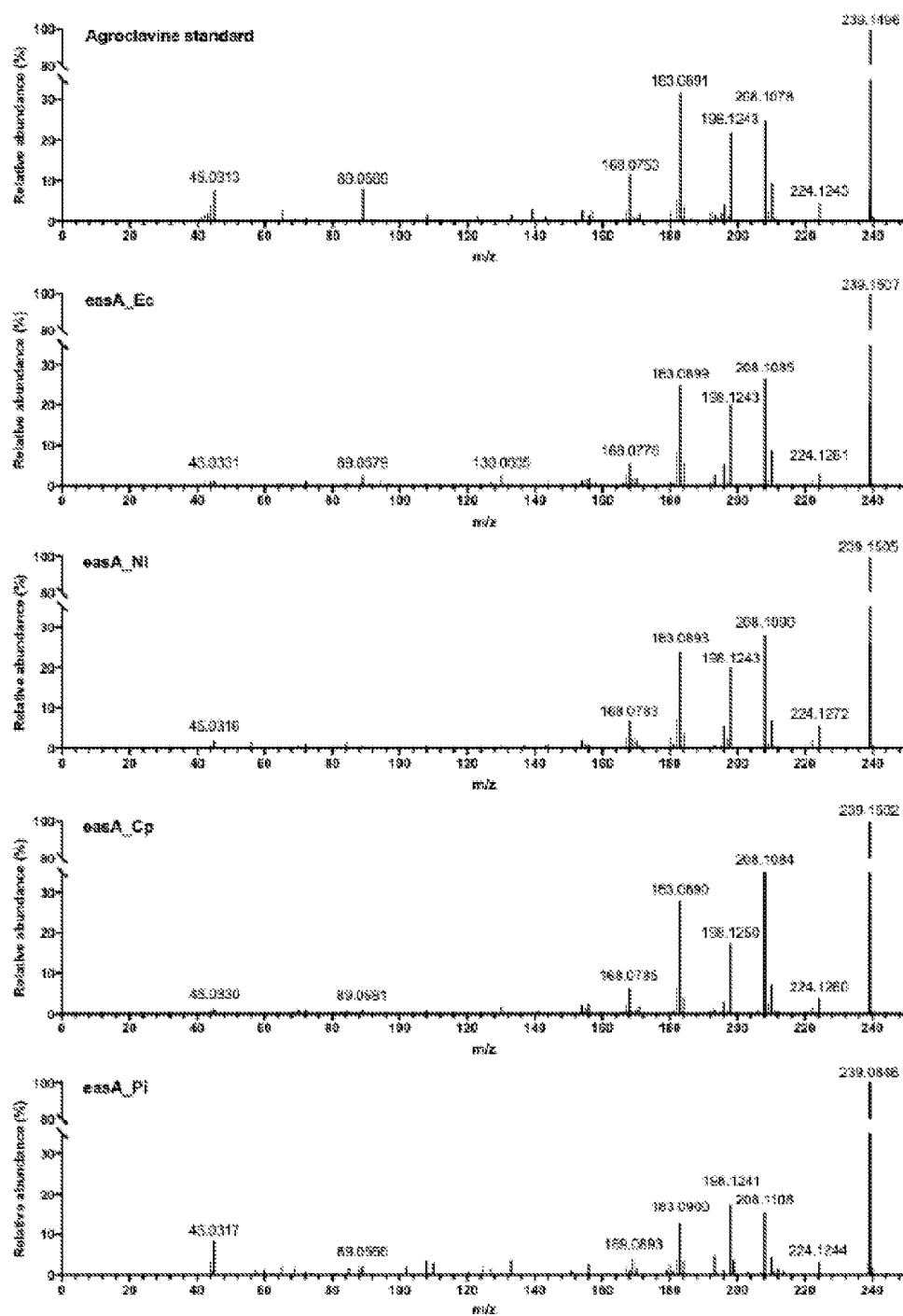
FIG. 14

FIG. 15

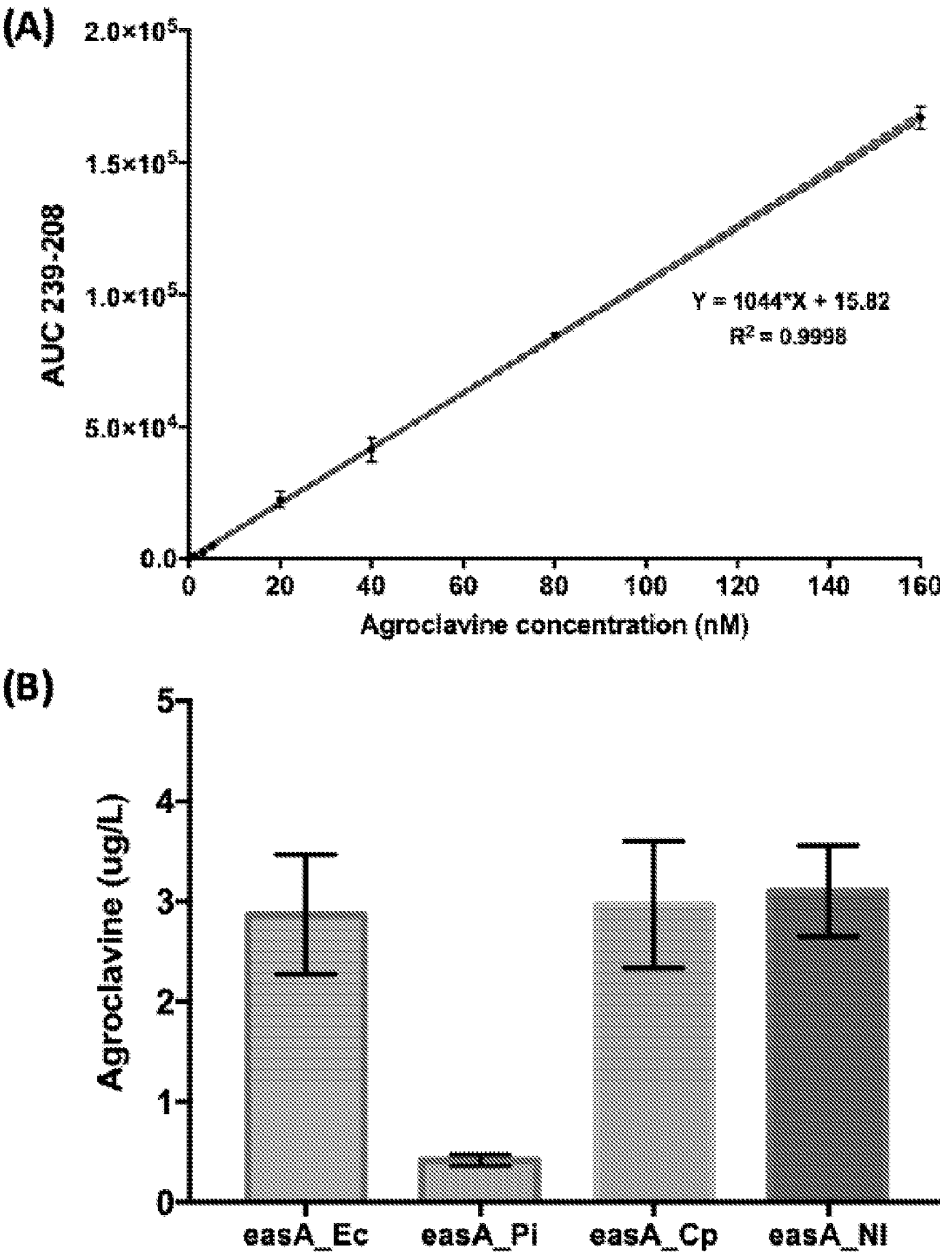


FIG. 16

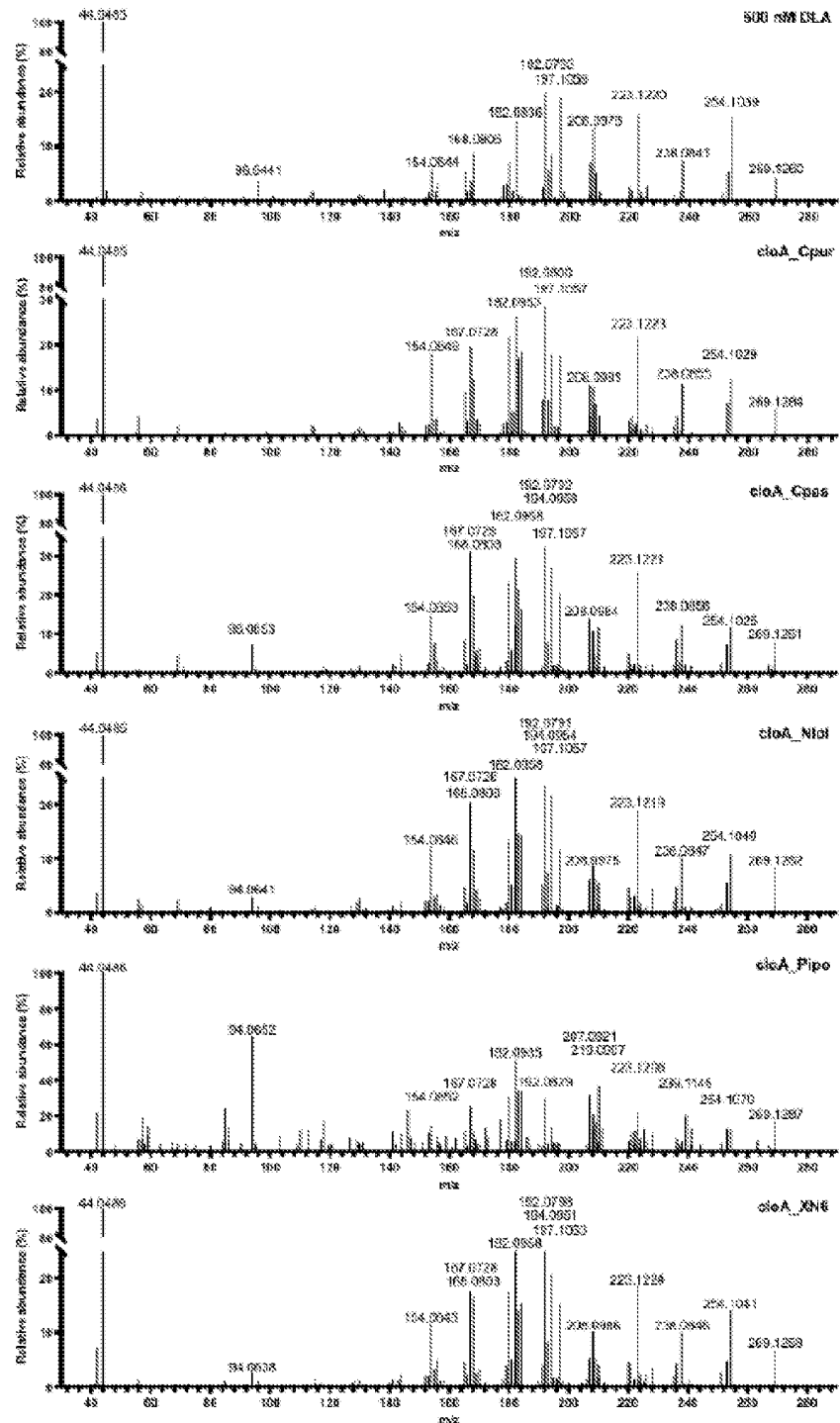


FIG. 17

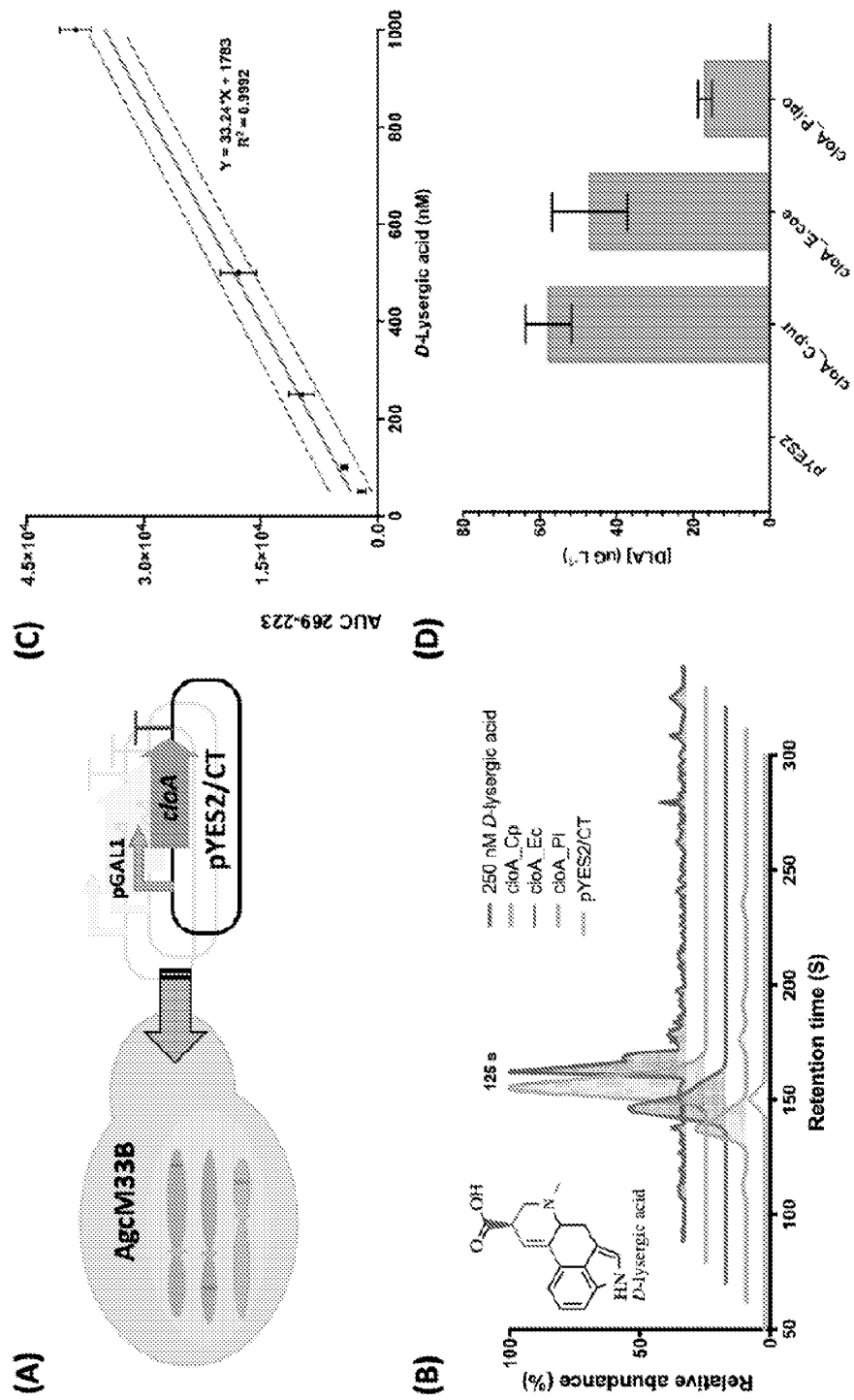


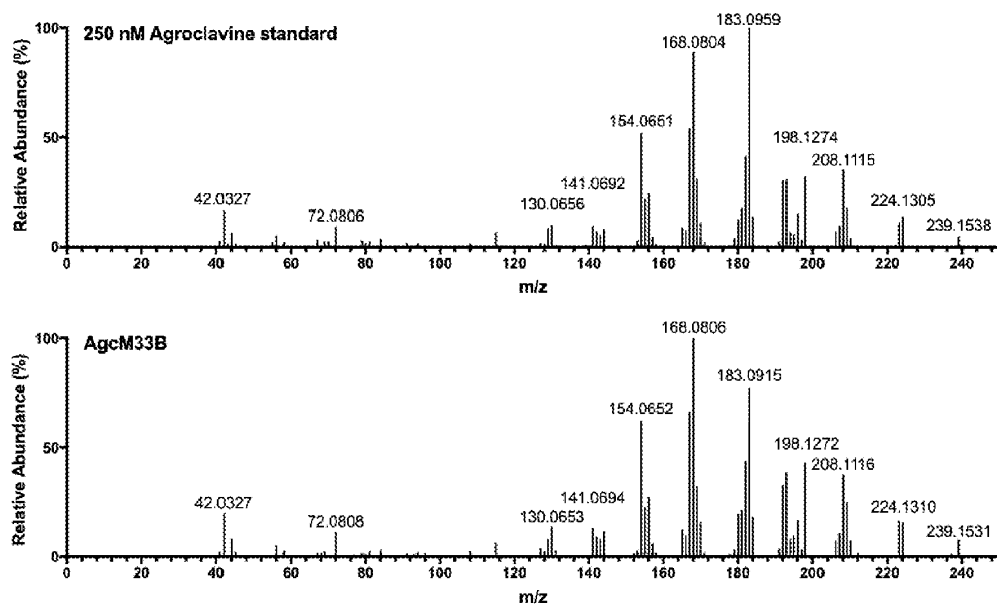
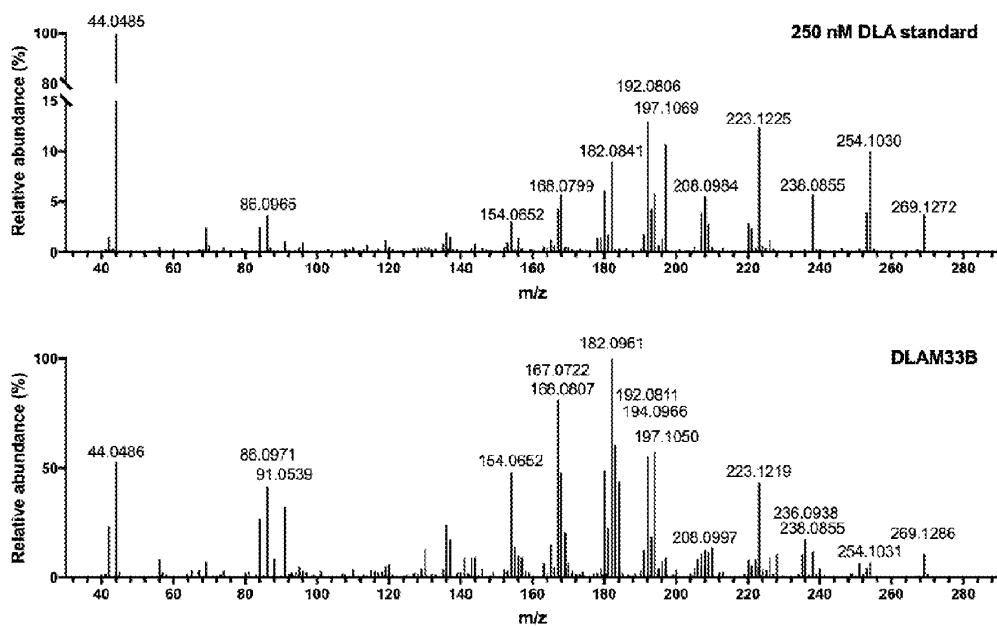
FIG. 19**FIG. 20**

FIG. 21

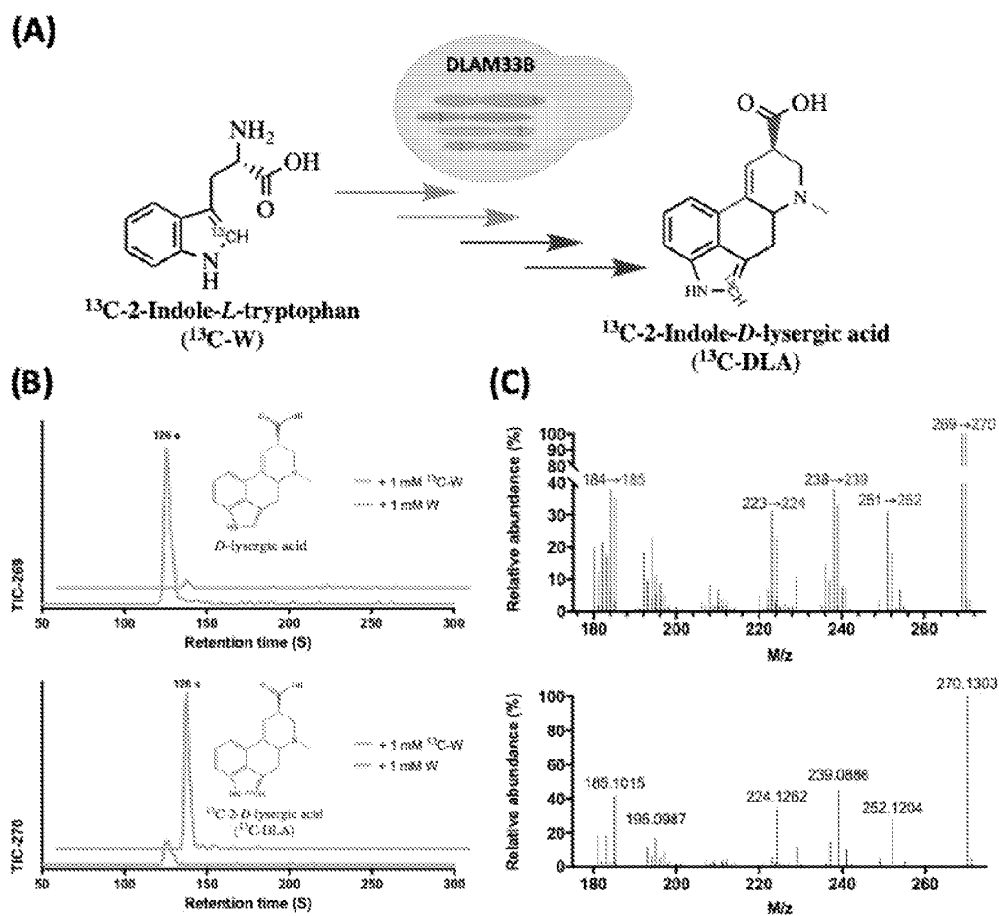


FIG. 22

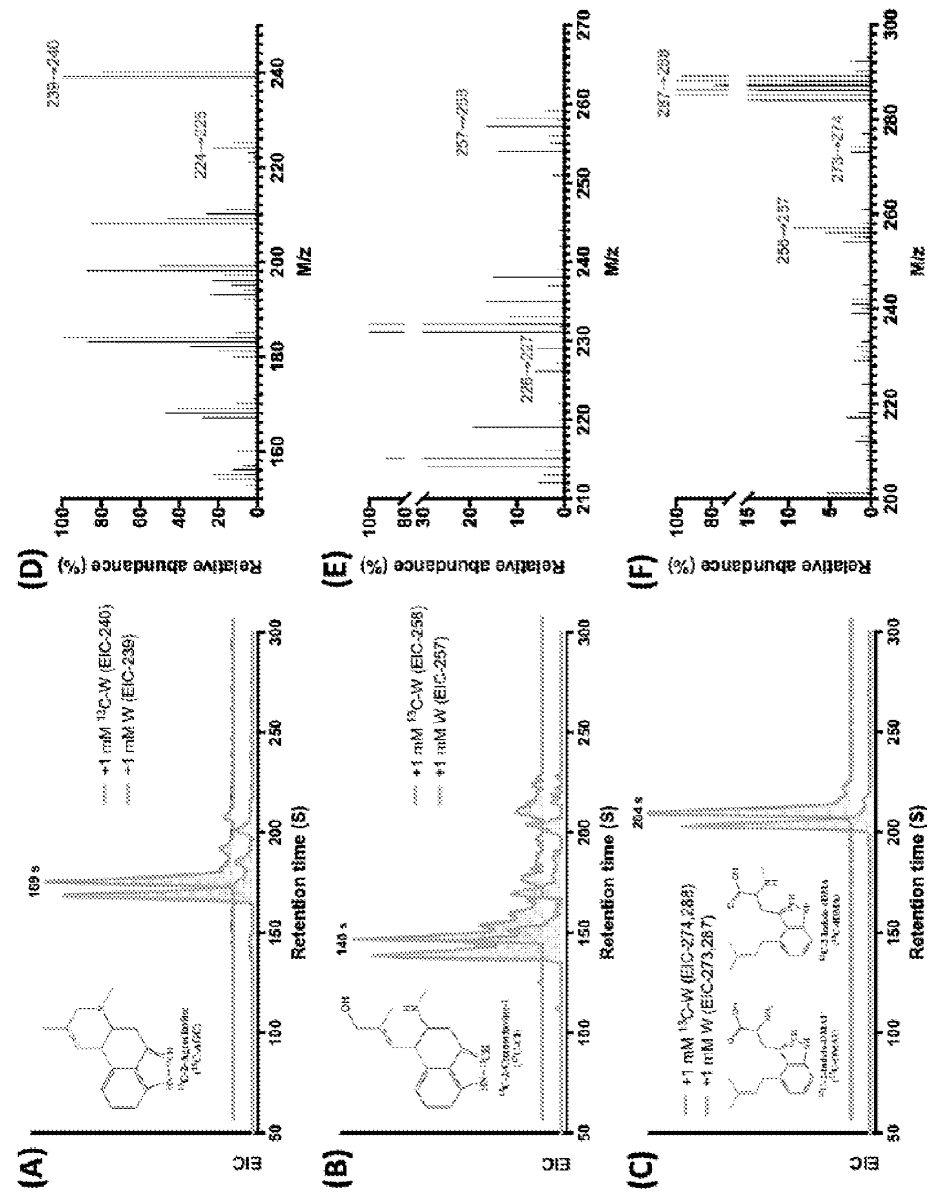


FIG. 23

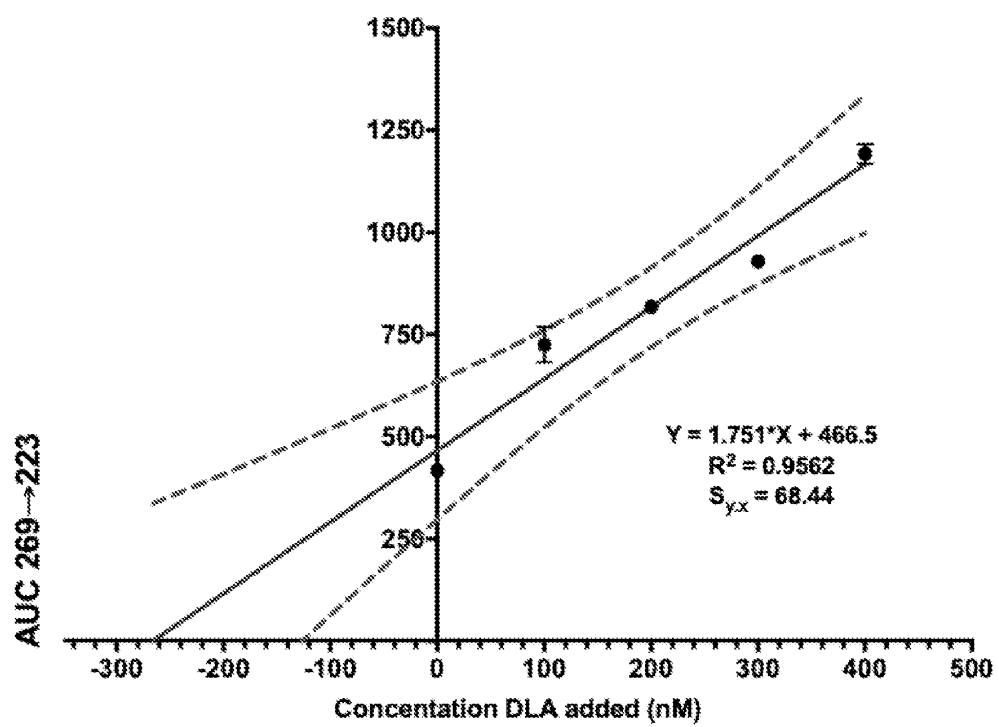


FIG. 24

Promoter Name	Nucleotide Sequence	SEQ ID NO:
MDN1	CTTCCCATACTAAAGCTTTCTCTTGATATATAGTCAAACCTGAATGTATACTGA AACACATATTCAAAGCATTGATTTTAAATGCACTTGAACCGTTATTCATTTC TTTTCTACTCATCATTTATTGTGCGCCCTTACGAGGTATTTTTCTTTTTGGA GTGAAAAATTTTAAAGAAGCGATGAGCTAAGGTCTATTTAGCTTTATGAAAA GAAAAACATTATATCACTTACTGCTTTACTTTAGACATTCCTCTCCAAAGTGAT TATTTTAAACATTCAAAGTACCTCTGAGTTAATTTGACATCGAATTCTACTCT TATTATTTAAGGTACCTCTACTTTACGCGGTACACATTATTTTAAACCGTT ATAATCTGCTGAGA	73
VP813	CTGACACTATTGACAACGTTAAGTCGAAAATTCAAGACAAGGAAGGTATTCC TCCAGACCAGCAAAGATTGATTTTGGCCGGTAAGCAACTAGAAAGATGGTAGA ACGCTGTGCGACTACAATATTCAAAAGGAGTCCACTCTTCACCTTGCTTGA GGTTGAGGGGGTAACTGATCAGTCTCGCAATATTTTCATTATGTCATAT ATATATGTTTACTCTCCTTTTTCTTTTTGGTTTTTTTTTTTTTGATAAATAC TCCATAGAACACTAAATAAATTGTTCAACTGTGTTATTGTCTTTATTCTATGTT GGTTTCAAGAGCTTGGATTTTGAATCGTCTTATACTATGACGTTCACTATT TTCGCGAAGCGGGTAAATACCATTAGCTATTTTGATAGAAAAGGGATTTTTATT AGGGAATATAAACCACCTTTATAGTGTCTATCATGTTTCAATCTCCAGTAA ACGCACATAAGCCGACCAATTGAGTCAACCTTTTAACTCTATTTAATTGATA CGGATAGAATATTGTGACTACCAAAAGGGAAAAAGGCAGAAAAAAGGAAAA TTAAGAACAG	74
PGH1	AAAAAGTCTTTCTTCATAATCAATGCTTTCTTTTACTTAATATTTTACTTGCA TTCAGTGAATTTTAAATACATATTCCCTCTAGTCTTGCAAAATCGATTTAGAATC AAGATACCAGCCTAAAA	75
PMA1	GTATTCTGATAAATCTAAAGAGAAATTACTAAAAAAGAAAAAAGAAAGGA ACGGGGGTGTAATAATTTGTAGTTCATTATTGCAATTATATATCTATATCTAT ATATGTATATAACATTAAACATGTGCATGTACACACGTAATCGCGCGTGTACA TGCTATATGTGTTACTTGAACATACTGTTTTGACGTGTATGTTTATTTATCT CTCTTCTGATTCTCCACCCCTTCCTTACTCAACCGGGTAAATGTGCGCATCAT GACTCCCGACAATAATCCCCTCTGGTATAGCGAGAAGCAACTTTAGCTTCTT AACGGCAAGAACTTTTTATGTTTGTGCGACCTGTATCTTCACAAAAGTTGGA TACAGCAATAAGAAAGGAAACCACATTTGTGCCA	76
TRA1	CACCTTCAATAGGGCAAAACAGAAGGACGAGCTGCATCACTTTTAGCGGCCAC TAATCAACTCCTTCAGATAGATCGCCAGAACGCAAAATAAGTGAAATTTGAAG ATCAACTTGAATCAAAAAGCCAAAACCTAAGAATTGTACGCTACTCTGCCAGA CAATATTTTACGGACACGCGCATTTCAAGACAAAGCCATAATTCATGCCTTT TCAACTAGCATCTGGACGCGCTGAGATCATAGGAACAAACAAAACGCACG AAAATAGCTAAGCGACGTATCGAATAOCAAATCAGTCTGCATTIATTGTACC CTCAAATTACAAATTCAACCAACAATTGTTCAAAAGACCACCTTGAATCTTG TGTTTCCCTAATTTGGTAAGTGATCACGTGGTCAGACAGTTTTCCAGGTCAAAAC TGAAAAAAGCTCAAGAACCATTTTTCTTTAATAGCCTTTTTAGTTGTATT CTAATAACAACACCAACAATAATCGGAGGTATCACACGTAATTACATAAAG AAGATTAATTCAGAGAAGATCTATCACACGATATCTCCATAGTTACAAAGA ATACCGCATTTTGCCG	77
DYN1	AATCAGTCGGAAATGTTCTTGACATAAGATATCAGCAGGCACGCTCTTCCC TACAGCGCCATCTCCACAACAACAATCTTTAGGTGATAATCTGGCAGTTTG TTTGTACGTTTCATCTGCTCATAACTAGGAATGGTAGAAAGGCTTCTAGCGA ATGGAGTAGGCAATCTGGGAAGATTCTTTTCATCTAAAGTGCCAGGTGATTC AGGAAGATTGCTACTTGAGGGCGATCCCTGCCAAACTATGTTACTTTCTGTTT CCACAATTGCCACCTTTTCTGCTTAAATAATAGTGTATTCATGAAAAAGCGTT ACTATTGGAGATTTTGGACCTATTGACTTAAGTTTGGCTGTAACTTTTGAGG GATGCTTATCATGTCTTTTGTGCTCTTAACGTAAAGCTATAACTACTTAAATCA GATCATCCCGAATTGATGCGCGGAAGGTGCGATTGTACGGATTCTAATAAAT AAGCTAATGAAAGGTAAACAAACATTACATATAAAAAATTAACAGAAAGCAT AGAACATAGAAGGGCAATAATACTCGTTCAGAGCTTAAATTGGAAAGTACG TCAAAACGTTTTTTAGGC	78

FIG. 24 (cont'd)

RPL15A	TCGACACTTACTTAATATGTTTTGCCGCCCTTCATAAGAGGGTGTTTTCTAAAATTTA TTGGGCAAGAATGAGATGGACTCGCACCCTACATGACGTTTAAATATTTAGTGTTA AGGTTTCAGAACATGCACCAGGTGCGACATGTGTTGCGATTATCATGACAATGTCTC TATCCGAGATGCATTTGTAGTATCAATTGATGCGTATTATGACATGATTTACATAGC ATACATCGTCAAAACATGATATTATATCTTTTTTTGATAAAATGACGGATTTAAAGC TGTCGAATATATTTTCTGAAATTTCTTGGAGCTGACGCAAAATTTTCAAAGGTGCTA AAATTTTCAAGATTCTCACTTTTGCTTGGTAACAAAGAATGATGGCATTGCATTT TTACCACCGGTACATTTAACTGCTATTTCTCACGTTTCTTTCCCTATCCTTAAGTAAT TCTTTTACAATCTAAGAAAACCACGATCAAACAAATAAATCAGCA	79
RPL8B	GGCAAAAGAGGGATAGCTTCACTGCCAATCACTACACTCTGTTCTGAAGGAGGGGAA TTACTGTTGTCTCATAAAAAAACACCTTTGAAACACTTTCACTCATAGAGAAGCCA AGAACTCTGATGAGTTCTTTATTTGTTGCCGCTAACTTTATCTTATCTTCTCCATTGT ATAAATTACTATTCTTTTACTTGCTGTTTCCATCCCAATGAAGATCCGATACATCT TAGACACCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT CGACAACATAAAGAATTATCGCATTTTTTTTGAATACATCATACTATACGATAGAACG CATTGAAACTTTTCCCATCTCAAAATCCAGGGACAATAGTATGGGATCGATATTATT ATCAAGACATAAGTATTGTGATGCGCACGTTGAAATTCACTATTTTTTTTTTTATAT CTGTTTTCAATACAGTGAACACGATAACTGAAAGAAAAG	80
SSA1	CACATTTTACTTGAGAAAAGTAATTAATTATCTTCTTTTCCAGAACGTTCCATCG GCCGCCAAAAGGGAGAGAAAAGAACCCAAAAAGAGGGGGGCCATTTAGATTAGCTG ATCGTTTCGAGGACTTCAAGGTTATATAAGGGGTGGATTGATGTATCTTCGAGAAG GGATTGAGTTGTAGTTTGTGTTTCCCAATTCTTACTTAAAGTTGTTTATTTTCTCTATT GTAAGATAAGCACATCAAAAGAAAAGTAATCAAGTATTACAAGAAACAAAAATTC AAGTAAATAACAGATAAT	81
TDH2	TAATTCATAAGTATGTCATGAAATACGTTGTGAAGAGCATCCAGAAAATAATGAAA AGAAACAACGAAACTGGGTGCGCCTGTTGTTCTTTTCTTTTACCACGTGATCTGCGG CATTTACAGGAAGTCGCGCGTTTTGCGCAGTTGTTGCAACGCAGCTACGGCTAACCA AAGCCTAGTGGAACCTCGACTGATGTGTTAAGGCCATAAACTGGTGGTGACAGCTGA AGTGAACATTTCAATCCAATCATGTCATGGCTGTCAAAAGACCTTGCGGACCGCA CGTACGAACACATACGTATGCTAATATGTGTTTTGATAGTACCCAGTGATCGCAGA CCTGCAATTTTTTTGTAGGTTTGAAGAATATATAAAGGTTGCACTCATTCAGATA GTTTTTTCTTGTGTGCTATTCAATTTATTTATTTGTTGTTTAAATGTTAAAAAACCC AAGAAGTATGTTTCAAATTAATTCATCACACAAACAAACAAAAACAAA	82
PYK1	ACAGATTGGGAGATTTTCATAGTAGAATTCAGCATGATAGCTACGTAAATGTGTTT CGCACCGTCACAAAGTGTTTTCTACTGTTCTTTCTTCTTTCGTTCAATTCAGTTGAGTT GAGTGAGTGCTTTGTTCAATGGATCTTAGCTAAAATGCATATTTTTCTCTTGGTAA ATGAATGCTTGTGATGCTTCCAAAGTGATTTCCTTTCCCTTCCCATATGATGCTAGGT ACCTTTAGTGCTTCTCTAAAAAAGGCTCGCCATCAAAACGATATTTCGTT GGCTTTTTTTCTGAATTATAAATACTCTTTGGTAACTTTTCATTTCCAAGAACCTCT TTTTTCCAGTTATATCATGGTCCCTTTCAAAGTTATTTCTTACTCTTTTTCATATTTCA TTCTTTTTCACTCTTGGTTTTTATTCTTAACTTGTTTATTATTCTCTCTTGTTCAT TTACAAGACACCAATCAAAACAAATAAAACATCATCACA	83
CUP1	GCCTTGTTACTAGTTAGAAAAAGACATTTTTGCTGTCACTGCTCAAGAGATTCT TTTGCTGGCATTTCTTCTAGAAAGCAAAAGAGCGATGCGTCTTTTCCGCTGAACCGT TCCAGCAAAAAAGACTACCAACGCAATATGGATTGTCAGAAATCATATAAAAGAGA AGCAAAATAACTCCTTGTCTGTATCAATTGCATTAATAATATCTTCTGTTAGTGCAA TATCATATAGAAATCATC	84
PDC1	TTATGTATGCTCTTCTGACTTTTCGTGTGATGAGGCTCGTGAAAAAATGAATAATT TATGAATTTGAGAACAATTTGTGTTGTTACGGTATTTTACTATGGAATAATCAATC AATTGAGGATTTTATGCAAATATCGTTTGAATATTTTTCCGACCTTTGAGTACTTTT CTTCATAATTGCATAATATTGTCGCTGCCCTTTTTCTGTTAGACGGTGCTTGATC TACTTGCTATCGTTCAACACCACCTTATTTTCTAACTATTTTTTTTAACTCATTTG AATCAGCTTATGGTGATGGCACATTTTGCATAAACCTAGCTGCTCCTCGTTGAACAT AGGAAAAAAATATATAAACAAGGCTTTTCACTCTCCTTGAATCAGATTTGGG TTTGTTCCCTTTATTTTCAATTTCTTGTATATTTCTTTCTCAATTATTTTCTAC TCATAACCTCACGCAAAATAACACAGTCAATCAATCAAA	85

Fig. 24 (cont'd)

PDA1	GTATTCTGATAAATCTAAAGAGAAATTAATAAAAAAGAAAAAAGAACGG GGGTGTAATAATTTGTAGTTCAATTAATGCAATTATATATCTATATCTATATGTAT ATAACATTAAACATGTGCATGTACACACGTAATCGCGCGTGTACATGTCTATATGTGT TACTTGAACATACTGTTTTGACGTGTATGTTATTTATCTCTCTTCTGATTCTCCCA CCCCCTTCCTTACTCAACCGGGTAAATGTGCGCATCATGACTCCCGACAATAATCCCCCT CTGGTATAGCGAGAAGCAACTTTAGCTTCTTAACGGCAAGAACTTTTTATGTTTGT CGCACCTGTATCTTCACAAAAGTTGGATACAGCAATAAGAAAGGAAACCACATTTG TGCCA	86
CYC1	AATTTTTTTGGAAAACCAAGAAATGAATTATATTTCCGTGTGAGACGACATCGTCG AATATGATTCAGGGTAACAGTATTGATGTAATCAATTCCTACCTGAATCTAAAAAT CCCCGGAGCAAGATCAAGATGTTTTACCGGATCTTTCCGGTCTCTTTGGCCGGGTT TACGGACGATGGCAGAAGACCAAAAGCGCCAGTTCAATTTGGCGACCGTTGGTTGGTG GATCAAGCCCCACGCGTAGGCAATCCTCGAGCAGATCCGCCAGGCGTGTATATATAG CGTGGATGGCCAGGCAACTTTAGTGCTGACACATACAGGCATATATATATGTGTGC GACGACACATGATCATATGGCATGTCATGTGCTCTGTATGTATATAAAACTCTTGTIT TCTTCTTTCTCTAAATATTTCTTTCTTATACATTAGGACCTTTGCAGCATAAAATTAC TATACTTCTATAGACACACAAACACAAATACACACACTAAATTAATA	87
TPH1	ATTTAACTGTGAGGACCTTAATACATTCAGACACTTCTGCGGTATCACCCCTACTTA TTCCCTTCGAGATTATATCTAGGAACCCATCAGGTTGGTGGAAGATTACCCGTTCTA AGACTTTTCAOCTTCCTCTATTTGATGTTACACCTGGACACCCCTTTTCTGGCATCCA GTTTTTAAATCTTCAGTGGCATGTGAGATTCTCCGAAATTAATTAAGCAATCACACA ATTCTCTCGGATACCACCTCGGTTGAACTGACAGGTGGTTTGTACGCATGCTAAT GCAAAGGAGCCTATATACCTTTGGCTCGGCTGCTGTAAACAGGGAATATAAAGGGCA GCATAATTTAGGAGTTTAGTGAACTTGCAACATTTACTATTTTCCCTTCTTACGTAA ATATTTTCTTTTAAATTTCTAAATCAATCTTTTCAATTTTGTGTATTCTTTTCTT GCTTAAATCTATAACTACAAAAACACATACATAAACTAAAA	88
TDH3	ACAGTTTATTCCTGGCATCCACTAAATATAATGGAGCCCGCTTTTAAAGCTGGCATC CAGAAAAAAGAAATCCCAGCACCAAAATATTGTTTTCTTCACCAACCATCAGTT CATAGGTCCATTCTCTTAGCGCAACTACAGAGAACAGGGGCACAAACAGGCACAAA AACGGGCACAACTCAATGGAGTGATGCAACCTGCCTGGAGTAAATGATGACACA AGGCAATTGACCCACGCATGTATCTATCTCATTTTCTTACACCTTCTATTACCTTCTG CTCTCTCTGATTTGAAAAAGCTGAAAAAAGGTTGAAACCAGTTCCCTGAAATT ATTCCCTACTTGACTAATAAGTATATAAAGACGGTAAAGTATTGATTGTAATTTCTGT AAATCTATTTCTTAACTTCTTAAATTTCTACTTTTATAGTTAGTCTTTTTTTAGTTTT AAAAACCAAGAACTTAGTTTCGAATAAACACACATAAACAAACAAA	89
ENO2	CGACGTGCACCAACTTGGCGAAAGTGGAATCCCGTTCCAAAACCTGGCATCCACTAA TTGATACATCTACACACCGCACGCTTTTTTCTGAAGCCCACTTTTCGTGGACTTTGC CATATGCAAAATTCATGAAGTGTGATACCAAGTCAGCATACACCTCACTAGGGTAG TTTCTTTGGTTGTATTGATCAATTTGGTTTCATCGTGGTTCATTAATTTTTTTCTCCATT GCTTTCTGGCTTTGATCTTACTATCATTTTGGATTTTGTGCGAAGGTTGTAGAATTGTA TGTGACAAGTGGCACCAAGCATATATAAAAAAAGCATTATCTTCCCTACCAGA GTTGATTGTTAAAAACGTATTTATAGCAAACGCAATTGTAATTAATCTTATTTTGT ATCTTTTCTTCCCTTGTCTCAATCTTTTATTTTATTTTATTTTCTTTCTTTAGTTTCT TTCATAACACCAAGCAACTAATACTATAACATACAATAATA	90
PGK1	TGTTTGCAAAAAGAACAAAACCTGAAAAAACCAGACACGCTCGACTTCCTGTCTTC CTATTGATTGCAGCTTCCAATTTCTGTCACACAACAAGGTCTAGCGACGGCTCACA GGTTTTGTAAACAAGCAATCGAAGTTCTGGAATGGCGGGAAAGGGTTTAGTACCAC ATGCTATGATGCCCACTGTGATCTCCAGAGCAAAGTTCGTTTCGATCGTACTGTTACT CTCTCTCTTCAAACAGAAATGTCCGAATCGTGTGACAACAACAGCCTGTTCTCACA CACTCTTTTCTTCTAACCAGGGGGTGGTTTGTAGTTAGTAGAACCTCGTGAACTTA CATTTACATATATATAAACTTGCATAAAATGGTCAATGCAAGAAATACATATTTGGT CTTTTCTAATTCGTAGTTTTTCAAGTTCTTAGATGCTTCTTTTCTCTTTTTTACAGA TCATCAAGGAAGTAATTATCTACTTTTTACAACAAATATAAAACA	91

FIG. 24 (cont'd)

YEF3	ATTAACCAAAACAACTTACAATCATTGTTTCGCCCTTCCATACTTACTGCCACTCGCA AAAGGGCCCAACCAGGGCAATTACGTATCAAAAAATCATGACAGGCTGGGTAATA AATATTCGTGAAGAAAAGAAGAAATTAACCAAAAGAAACGAAAGCAAAAAAAG AAAAGACTCCGTTTAATCACTTTCAACCGCGGTTTATCCGGCCCCACCCATGCATAA CCCTAAATFATTAGATCACTTAGCACGTGAAAAAGAAACGTTTTTAATGTTTTTTT TTTTTTTTCTTTTTCTTTTTTGGCTTGGTGAAAAATTTTTTCGCTTCTCGAGTATAAT TATCTCATCTCATCTTTTCATATAAGATAAGAAAGTTTTATAAAAAACCTTTTGCATCAA AATTTTGTAGAATATCTCTTTTTCTTACGCTCTCTTTCTTTCCCTTAATTGTTTTCTAAA GAACCGTGTATTTTTCTAGTTCGAATCCATCGATAACATTAAAAAG	92
TEF2	GGCGCCATAACCAAGGTATCTATAGACCGCAATCAGCAAACTACCTCCGTACAT TCATGTTGCACCCACACATTTATACACCCAGACCGCGACAAATTACCCATAAGGTT GTTTGTGACGGCGTCGTACAAGAGAACGTGGGAACTTTTTAGGCTCACCAAAAAAG AAAGAAAAAATACGAGTTGCTGACAGAAAGCCTCAAGAAAAAATAATCTTCTTC GACTATGCTGGAGGCAGAGATGATCGAGCCGGTAGTTAACTATATATAGCTAAAT GGTCCATCACCTTCTTTTTCTGGTGTGCGCTCCTTCTAGTGCTATTTCTGGCTTTTCT ATTTTTTTTTTCCATTTTCTTTCTCTCTTTCTAATATATAAATCTCTTGCATTTTCT ATTTTTCTCTCTATCTATTTCTACTTGTATTTTCCCTTCAAGGTTTTTTTTTAAGGAGTA CTTGTTTTTAGAAATATACGGTCAACGAACATAAATTAACATAAC	93
RPL3	CCGGACAGTAATATAGTAATCGTTTTGTACGTTTTTCAAGAAAGCGACGCACAACCTG TTTTCCATTTTTTTTTTTTTTTTTTTCAGTGATCATCGTCCATGAAAAAATTTTTTCATT TGTCTCTTTTCGTGCTTCTCTGATATATAAAATACGATTTAATTTAGTTGTCTTTGTCAA TCCTCATCTTTCTTACTCATTATTTTCATTTCCGTTTTTGTCTCTCTAGAACAACACA GTTACTACAACAATCAATC	94
ACT1	TAACCTACATTCTTCTTATCGGATCCTCAAAACCCCTTAAAAACATATGCCTCACCC TAACATATTTTCCAATTAACCCCTCAATATTTCTCTGTACCCCGGCTCTATTTTCCAT TTTTCTCTTTACCCGCCACGCGTTTTTTTTCTTTCAAATTTTTTCTTCTCTCTTTTT CTTCCACGCTCTCTTGCATAAATAAATAAACCGTTTTTGAAACCAAACTCGCCTCTCT CTCTCCFTTTGAAATATTTTTGGGTTTTGTTTGATCCTTTCTTCCCAATCTCTCTTGT TTAATATATATTCAATTTATATCAGCTCTCTTTTTATCTTCTCTTTTTTCTCTCTCTT GTATTCTTCTTCCCTTTCTACTCAAACCAAGAAGAAAAAGAAAGGTCAATCTTT GTTAAAGAATAAGGATCTTCTACTACATCAGCTTTTAGATTTTTTACGCTTACTGCTTT TTTTTCCCAAGATCGAAAATTTACTGAATTAACA	95
GPM1	GTGATGTCTAAGTAACCTTTATGGTATATTTCTTAATGTGGAAAGATACTAGCGCGC GCACCCACACACAAGCTTCGTCTTTTCTTGAAGAAAAGAGGAAGCTCGCTAAATGG GATTCACATTTCCGTTCCCTGCCAGCTGATGGAAAAAGGTTAGTGGAACGATGAAG AATAAAAAGAGAGATCCACTGAGGTGAAATTTACGCTGACAGCGAGTTTCATGATC GTGATGAACAATGGTAACGAGTTGTGGCTGTTGCCAGGGAGGGTGGTTCTCAACTT TTAATGTATGGCCAAATCGCTACTTGGGTTTGTATATAACAAAGAAGAAATAATG AACTGATTCTCTTCTCTCTTCTTGTCTTTCTTAATCTGTGTGTAATTACCTTCTTTG TAATTTTTTTTTGTAATTATCTTCTTAATAATCCAAACAAACACACATATTACAATA	96
FEC-3	CCTCCTTGAAACTGAAATTTTAGCATGTGATTAAATTAACCTGTAATATTCTAATCAA GCTTATAAAAGAACGATCTACCGACTGTTTCGAGAGGGCCAAAAAAGCATCGAA AAAA	97
FEC-1	CCTCCTTGAAACTGAAATTTTAGCATGTGATTAAATTAACCTGTAATATTCTAATCAA GCTTATAAAAGAGCACTGTTGGGCGTGAGTGGAGGCGCCGGAAGAAAGCATCGAA AAAA	98
BDA-1	GCTCAACGGCACAGAGGGGCGGGGGCGGTGTTAATTAACCTGTAATATTCTAATCA AGCTTATAAAAGAGCACTGTTGGGCGTGAGTGGAGGCGCCGGAAGAAAGCATCGA AAAA	99
BDA-3	GCTCAACGGCACAGAGGGGCGGGGGCGGTGTTAATTAACCTGTAATATTCTAATCA AGCTTATAAAAGAACGATCTACCGACTGTTTCGAGAGGGCCAAAAAAGCATCGA AAAA	100

FIG. 25

Terminator name	Nucleotide Sequence	SEQ ID NO:
APL2	CTATAAACGTCGGTTGTAGTGAACCTTAAGTATTATACCATACATATATA CCCTTCGTATTAAATTTTTCCTTTTTATTGTTGGGCTGTGTGTATATAATT TATGTACAAGAATGGATATATCAAAAAATCCTTAAAAGATGTAAATCA AAAACATCAATCAACACAGCTTATTTTGTAGAGCTTTGTTTTGACATA ACTTTTCAAGCTTGTGATTTTTCTAAAACAATTTTATCCCTTTCACCA TCTAAATATTTCTCATCTGTTTGATAAAACAGGAGGCACGATTTTCATTT CATCTCGTTGCTTATCACAAGTGGGAAAACTTTCATTCCATTTGCCTT AGCACAACTCTGCCATTGCTTGAACAAAATTTGCACATTTTGTATGTT TCCGTCTTCAAGTTCTTGGCAGCCTGTGT	101
ATG10	GGAAAGCTTTTTAAAACACTATGCAATCATCTATGTAAATATATATATA TATATATATTATACCGCGGTAGTAAGCAGTATTTTTTCTATCAGTCT ATATTTTGTCTTTTCTTGTCTGTTTCTCATGTTACCTTCTTAGCA TTACCATAATGCGAATCTTCTGATGATGTGTCGGATAACCCAATAGAA TCAGTCGTCGTCGCACCTAGCGAAGCAGTTTCAATGGAATCTTCTTCTT CAAGAATTGTTGGTATACCACCAAACGTTCTTTGCGCGCTGAACAG ATTTAAATTGCATTTCTTTCTCTGCTTCATTTTCGTTGTCTGAAATA GATGACTTGGTCTTTGTCTTTTGAAGAGCCATTCTTTCTCCAAATTCCTC ATCATCATCGTTATTGTATGAGAAGTCACTCAGGTCCGATGTTCTTCTT GCTCTATTTCTCTTCTTCCAACCAGGCCTTCTAAACCA	102
BNA4	AGCCAGTTTATTCTTGCCATCCGTGTACGCTAGGAGAGGATTATTTAAA ATAAGTGATATATACATATATATATATATATATATATATAATACACT AATTATTTTATGTGATGTTGATCACCAGGAAACGGTAAACGGCTCTGTTC GCGCTTTCTTTGTTTACATTTTGTGAAGTATTGTCAAGATAATATCCA TATGGTTGAACTTTTTATATGGCTAGTTAAATACTCTATTTATTGCACC AAAAAATCATCTTAGTGGACTTTTTGGAGCAAAAAAACAGCAGGTA GTTATATAAGATGACTACACAATAAGGTATGAAAAAACCAGATGACGA TGAAAGAGTAGAATATAATCTCTTTACCAATAGATCCACCATGATGGC AAATTTTGAAGAATGGATCAAAATGGC	103
BUD32	TATAAATGCTAGCGTACTGCCTGTATATCGCTGCACATAATATGTATCT ATAATTTATATTAACGTACATAACTTTTAGGTATGTTACCATCAAAGCG TGTCCGAGTTATTGAGATTTTGACAAATTCAGACAAATCATTTTGAAG AACCATATATATAAATATATAAAGAAAAGAAAGGTAAACCAAAGACA GCAAAACAATCGAAAAGTGGACAACCAGCAATGGTAGATTCAATTCACC GTATTGCATCGGCGTTGGATAACGGCCAAAGTAATAACGAGGGAAGCTG CCGCGGTAGCCACCTCTAAGCTGGGTGAATCCTCTATACTTATTATTC TCAAAACATCAATCCTCAACAGTTAGTCACCTTGTTAAATCTAGGAAC TCTAGAGAAGTTAGAGATGCAATGAAGAGAATAATATCTATAATGGCT TCCGATGATGACTC	104
CBR1	GATAAGGAACTGTAACAGAGTGCCATATATATATATATAGATTGGAAC ATATATAATATATACGCTATTTAGTTTAGTCACCTAAACGCACCGTTTC CATATTTCTGTCTGGACGATTTTCTGACTCGATAATACGTATAAGATCGG TACTAATAGTAACAAAAGTAAAGGTAATACTTGCTTCACTGTACAAA GGAGCATAGAACGTGGGGCAATTTACAAGCGATGTGACGTCAGTCCC AGTCAAGAAGGCATTAAGTGCTCTTTTACGCGATCCAGGAAACAGTCA TTGTGCCGACTGTAAGGCGCAACTACATCCACGCTGGGCTTCCTGGTC ACTTGGTGTTTTCATTTGCATTAATGTGCTGGTATACATAGATCATTG GGAACGCACATTCGAAAGT	105

FIG. 25 (cont'd)

CYC1	ACAGGCCCCCTTTTCCTTTGTTCGATATCATGTAATTAGTTATGTCACGCTTACAT TCACGCCCTCCTCCACATCCGCTCTAACCGAAAAGGAAGGAGTTAGACAACC TGAAGTCTAGGTCCCTATTTATTTTTTTTAAATAGTTATGTTAGTATTAAGAACG TTATTTATATTTCAAATTTTTCTTTTTTTCTGTACAAACGCGTGTACGCATGTA ACATTATACTGAAAACCTTGCTTGAGAAGGTTTTGGGACGCTCGAAGGCTTTA ATTTGCAAGCTTCGCAGTTTACACTCTCATCGTCGCTCTCATCATCGCTTCCGT TGTGTGTTTTCCCTTAGTAGCGTCTGCTTCCAGAGAGTATTTATCTCTTATTACCTC TAAAGGTTCTGCTTGATTTCTGACTTTGTTGCGCTCATGTGCATATTTTTCTTGG TTCTTTTGGGACAAAATATGCGTAAAGGACTTTTTGTTGTTCCCTCACATTCCA	106
EBS1	TATTGTTTCGTTTTTATCATAGTTTTTCAAATCTTCATATGAATACTAGGTAGA AATTTGGCTTATCAGTACGAATGAATTACAGTTTGACTGATTTGTACACGAGA ATTGACGTATAACTTCTTTTGAAAGTCTTTGAAATTACATGGTAGTACATACAT ATATATATATATATATATATGTTATATTATTTGTTAATTAAATATTATTATGCGT ATTTTCCTTTTTCTTTATTAGTATAGTATTAATGACAGTAATAATAATAATA GTAACAATATCTCTTTTTTTTTTTCAGTGAGCTTTATTTTTTTTTTCATTGCTCTT CTTTTGGCCTCTTTGTTTTTTTTCTTGATTTCTCCAGTTTCATCTGTTTTTCTT TGGATCAGATACAAAATCTGGTTTTGAACCGCTCATA	107
EFM1	ATTTAGCTTTGATCTGTAGCCTAAGTATAAAATCTACGTATGTATATATTTAC ATGCAATTTTTCTTTTTCCAATTCAGTTAATGTTCTTCATCAITTTGATAATAG GCCAATGATATTATCTACTATCTTCTCTTTTGAGGAGAAGCTGCTTTCACTTC CTCGTTGCTTTTTCTCTTCGTATAAAATACATGAATTTTCGACTTGTCCAGCATTTT TTATCAATACAATGCATGTGCCCATGAAGTTCACCTCCGACAAAATCTTTAACA AAATATGTCGTTATTTGTGTCATGAATTTCAGTAGGGTTTGAAATATTTCGGGT ATGGCGTTCTTCTTATCCAGAATAACAATTTTGATGTTTGCTGATAATGTTATT GGACGAAGCTGGATGGGCCTATTT	108
ENT2	TACTGTCTATATATACTTTTTGTTCATGGGTACACATACATGTACGACATATA TATATATATATATATATATATAGCGAGTTTACATTGATGTAGAGCAGTAACTG GAAGAAATAAAAAATTTAACTTAATACTAGGGGGTCCGTCTTCTCGTGGGTAC TTCTTTTACAGTTTCAACTTCTGCTGACTTGTATGCCTTCTTGCCGCTTCTTCG GAAAAGTTGACAGCGGGCTTTACTTTAACGGCAAATCGCAGTAAGTAAGCAA GTAACGAACCTCGCACTTCAGCAAAAATAAAAAAGAACAAATCGATTAGAAAATTC AAATTTACCGGTGACTCTTTAACCCCTGCCGAATATTATAAGCAAACTATGAT AACACTCTTATTATACCTGTGCGTAATATGTAACGCAATAGTGTTAATAAGGG CTGATTGATAGCG	109
HBT1	ACACTTCTCGATTAAACAAATTCAGTATTCTTTGAAATCTATTTTTCTTCTCA ATTGAATTTGAATAACTGTCTACGGGACTCCTCCTATCTACAACATAACAACAA ATTTTAAACCACCTTATTACCACCTTTCCTCTTTCATTTATTTTTGTCTTTTATGTIG TCAATTTACTAGTATTTTTTTTTTTTTTCATTTACGTTCAAGGTTTTTATACTCAT TTAACTTGTCTTAGGTTATTTATATATATACCTATATATTTATATATATATATAT ATATGTATGTATATATTATTATCACCAATGAGAAATAATAGCTAATTTGATTT TTGATTTATTTAAATATTGGTTTGTCTTTCTGCAACATCTCGTTTGGTACGAT ATTAGTAAAAACGATGTAATTATCAACACGTGCATTACCCA	110
LSC2	TCTCGAGAAAAACAAAAGAGTTAATAATAAAGTATATATGCTTTTTTACTATT AATAAAGTTTCTTATTTTCCCTACATGTATACATACATATAAATATACTCTTTT GGAAAAAATTTCTTTTTTTTTTTTTTAAATTTTTTATATTTTCCATCTTTTGATG TAATATAGAGGTTATATAATGAAAGAAATATAAGAGGTCATAAAAAATCATT AAAAAAATGCGAGTTTCAGGAACATATTATCGTTTACGTAATCAGTGCGTTATT GGCGGATTAGTACCGATCACACCTTTGTTTCATCGATGTGGATGCAGTTTGCTTT GCTGCGACGGCTGCAGGAGTCTCCCTTTTATTATGTAGTGAATAACCTGTTA AAAGAATCACCGTTCCGTATCCTAAAGTTAGCAATTCCTGTTAGATGGTAGCC TGCAGTGCAACCCAGGAAAAAATTGACGGAAGCTAACAGATAGTTCTTGGGC TTGATGACAAAACGACCAA	111

FIG. 25 (cont'd)

PRX1	AAATAAGCTTTGAAATAAACGACTTTACTATATACAGGTATATGAAGTATCTC TAACTAAAACCTTTTATCTATCTTTCAATCTTATATATCTCATCTCGTACGAAGG GCCGCTCATTGGATCATTTTTCTTTACATACCGTAAAGGAATGGCGTTAAAAAT ATATATATGAAAAATGCATGTAATAAACTCTCTGCAGAAAACCTTAATGTCAAAG GTCCCGTATACAGATTATATTGGCTCTGCGTATACGCATTCTCGTCATGOTGAA GGATAATCGAGATTCTGACCAAGACCAAGATTTTAGTTCTGCTCACATGAAAA GACAACCGGAGCAGCAACAGTTGCAACAGCACCAAGTCCCAAGTAAGAAACA ACGAATATCTCACCATGATGACAGTCATCAAATCAACCATAGACCAGTTACCT CATGTACACATTGTAGACAGCACAAAATCAAATGCGATG	112
RPL15A	TAAGCTGGTTGATGGAAAATATAATTTTATTGGGCAAACTTTTGTATTCTGAT GTGTTTTATACTATTATCTTTTAAATTAATGATTCTATATACAAACCTGTATATT TTTTCTTTAACCAATTTTTTTTTTATAGACCTAGAGCTGTACTTTTATTCTGCT ATCAAGCAAAACCCCTACCCCTCTCTCAATCCTCCCTCAGGCAGAACCTTATC TACCTGTATCAAGGAGCGGACGAGGGAGTCTAATTGTTCTACGTATACCAAT GCTAGCAGCTTACATAGGTGGTGGCACTACCATAATACTTATATATAATATCTT TACGCTCAAGTAAATTTCTCCGCGCATAAATTAACACCATGTTCTTTTTAGTC GCACCTTATTTCTGTATTTTTTCTTTTCTTTTCTTCCCGTTTTTCC	113
RPL41B	GCGGATTGAGAGCAAAATCGTTAAGTTCAGGTCAAGTAAAAATGATTTCGAAA ACTAATTTCTCTTATACAATCCTTTGATTGGACCGTCATCCTTTCGAATATAAG ATTTTGTAAAGAATATTTTAGACAGAGATCTACTTTATATTTAATATCTAGATA TTACATAATTTCTCTCTAATAAAAATATCATTATAAAAATAAAAATGAAGCGA TTTGATTTTGTGTTGTCAACTTAGTTTCCGCTATGCCTCTTGGGTAATGCTATT ATTGAATCGAAGGGCTTTATTATATTACCCTTAGCTTATTCTGAGGTTTCTGT GGCGTGCAAGTGATGAACCGGGCGGGTTTTAAGGATAAAATCAAAAAGTGA AAAAATGAACGGAAAAATGGAATACCTGTGAAATGGAGAATGATAATGAATCT TTCGTGCGTGCTTGAAAGATTTTCGGCT	114
RPP2B	ATAAACAATTTTCTGTTTTCTCTTATTACAAAATCTGGTGTAATCCTCGA TTCATTGTGATTTAAAAATAATTAATTACTGTATAAGATTCTATATAGACAAT TAATTGAAAATAGTATTACTTTTAACTCGCTTAGGATTTTTTATTTTTTCT CTCTTTTCCGGAGAATTGCCAAATGTTTTACGGCCTCTTCCAATAATAGCTTC ATTTCTTCCAACGCACTACTAGTTTCCATTGTAAAGTGCGGAAGTACTCGCTG ATATCATCATCTTCAGAAAGCTTCTTAAATGGAAGTTGTTAAAGAATTTATAGAA TTTGTGTTGGCTCAGAATATCTGATAATTTACTTTTCGCTATTGAGAGCCTGA CATTTTCAGTATTAATCTTTTCTTAAATTACTATACTCGCTTAGAAGCTTTGAGA TCATTTTCCACTTCAACTTCCTCTTCGTCTGCTACTTCCATCTGCGGCAGCTTCA ACACATCT	115
RPS20	AACTAAGCTGGTTCTAACTGGAAATAATTTCCATTAGATTCCCTTTTTCTCGT CCATTAAACCAAAATATATTATTGAATTCAGCGGTTCCTTTTTCTCATTTTCGC ATATAGCTGCATATTAGAATCAGCCCACTCTAGGTAAACACAGTTCCTCGAT ATACCTCTGTCTTACTATCAGTGGTTAAACCTTATGCAAAATATAATATATAT ATATATATATATATATATCTCATACTTTTGTGATTCTTGTGTAATTATTGGAA AAGACAAAACAAGCAAGCGTTTCTATTTCATATTTACAAGTATTTTATGAC AAACTATTTCTTAATTTTCCACCGCGCGCTTGAATAAGGCAATGTCATTGTC CTGCATAATATATTGTTTGCCTGCACGTTTGATAAGTCCCTTAGATTTTAGTAA AGACTCATTAGCGGTGGTTCATCTTC	116
TRM82	TCGTGAAATAAAAAAGGTAGTAAGTACATCTTTATACTAATATAAAAAAGAT ACGTACCGATTTGTGTTAATAATCATTGTTAGTACATCTTTATACCTCTGTTTCT AOCTGAAGCGCGCAATTGAATAGCAGTTCTTTTTAAATTTGCCAGATACAATA GGATTAACTCATTTGATACATTTTGTAGTCTATTTGTGTCGTTCTGGAAACAG TTTTGTAAGCACGCCCTTAATGTGCGCTCGGTGTCCTTTCAAGTAAAGGACCC ATAACCTTCTGAAAGAATTCCAAATCCACTATAATTTGTAATGAGCCATCAT AGAAAGATTACCAACATAAGGCTTAAATGCCTCAAAGAGGTATCTGGCTATAA AAATCTGCGTTTCAATTAATCTTATGGATGAGCTGAGGCCCAATTCTAAAG CACTCACTGTGAACACG	117

FIG. 25 (cont'd)

VPS1	GTTTTCCTCATCTATACCGGTCGACTCAAGCTTGGTTTTGAGTATTCTCCCTA ATATTTACTGCAAATCTTATATATTGTTCTTGTATACGTGGAAGCTAGTCTATA AATTATGCTTTTGAAGAATTTTCCTATCTCGCATTACGATCCTAGTATCTTTTGTG CAATATGAAGAAGGTCAACATGAGGATGGGAATGATAATTGATAGCATATAA TATTATTCTTTTGTCAATACTAGTGTTTAGGATATTCTACTAATACCTAATACC TCAATGGTCCAATACTAAATAAGGTACTATTTCATTGTATTGATTGATTCTGCAT TTATCTTTCTCTTGAACCGTAAATATCATTTTCATAAGTCACATGATAAAAAACA TATTTAAAAATTTTAAAAAAATTAATTTTCAAAATAAATTTATTATATTTTTTTA ATTACATAATCATAAAAAATAAATGTTTCATGATTTCGGAACGT	118
YIP5	AAATATGCGCACGCTCTATACACACAATACTTTTTATGACTAGTATCATTGTATA CTCTTATTATGTAGGGTTATACATGAGTGTTTATACGTTTCTGTGTGTACATA TATATCCATATATGTTAATGCTAAATGCAAGTTTTGTGATGCTATTTCATTAGAG ATGCCTTTGTCTAAAAATCAATGCTTTTATAGTCATCATAOGTTATGTCGTA TGGTTTTATCCTTAAATTTTAAGGAGATTTTGGATGAAATGTTTATGTCAGCTC TGGTAAAGCCTTTTGAAGAAAGTACATTATCATTTTTTGGGAAATTAGTGGAA GAAGAAGAATGCTTTTTCTTAATGCATGGTAAACAAGGTGTGAGCAAAACCAA CTTATCAATATGCTTAATCAACTTGCCTGAGCCTGTACCCCTCAATGACATCATC CGGTATGGCAAT	119
YPR1	TGAGCGCGCTACATTACAGTTAATGCCTCCAGCAACCTGTAGTGCTTCTTTAAA CCGATCCGATACAGCTGAAACAAACATGATTTTACTAATTTTCATATAATATA TACACATATATCGAATGATAATGCAAAATATAATTTAATGAAATTGGAAATAC TCGGAAAAATTTATCATTATCCTTTTCTTCTTTTGAACGTAAACTTCGGACCGTC GTCATCGTCTGTCGTCGCCATCACCGTTATTAGAAGCCCCAAAAGAGCCACGTG ATCTACTAGTTGCGCTTCTACTGTGTCTACTTTGCTTGGAACATTCCTCTGACA AGTTTGGCCGTAAAGTTCATTTCTTTCACCCACAAAAAGATTACGATTATTTTCTC TGTGATTTAGTCTATCGCTTTTATCATCAATATCACCCAGATCATCTTCATCAG TAATAAAAAATTTTGTTTTTTTTATGTTGTTGAACGCTGGCTGCACTACCTGAACA	120
YPT31	GAGATATTTTGCAGCAGTTGCGCACITGTCATGTGAATGACTCTTCTCCCTTTA ATTCTGTGCTAATTTTTTACAATTTTCTGCTGACATATAGTTTATATACATATAG AACGCATATAGGAAATTTGAAGTAAACAGAAATACACAAGTAGAGGCCGGTATG TACGACATTTTGTCTACTACTCTTTAAAAATCATCGTCTTCTTCTGCTCTTCATGCTC TTCTTCTTTTTCACCAIATCCTACATCATCTTTAGAGCCTGTGCTAGGTTCCCTTC TTGICTAATTCTTCTGAGTCTTTTATAGTCAATTACTTTGCCGCGTGTCTTCTC TTCCGGATGTGATGATATTAGAGGTATCAATTTCTGCCAAATCGTCTCTTCTT CTTCTCCCTCAATTTCCCATCAATGCGTCTAACTTGGCATCGTCCATATCAGA	121

FIG. 26

Source Organism	Gene Name	UniProt ID
<i>Aspergillus fumigatus</i>	<i>dmaW</i>	Q50EL0
<i>Aspergillus fumigatus</i>	<i>easF</i>	Q4WZ60
<i>Claviceps purpurea</i>	<i>easC</i>	M1WA44
<i>Aspergillus fumigatus</i>	<i>easD</i>	Q4WZ66
<i>Claviceps purpurea</i>	<i>easG</i>	M1WEN5
<i>Aspergillus japonicus</i>	<i>easE</i>	-
<i>Aspergillus indologenus</i>		GenBank: PY133859.1
<i>Neotyphodium lolii</i>		S5TDB9
<i>Epichloe funkii</i>		R9W1Q5
<i>Periglandula ipomoeae</i>		G9FM46
<i>Epichloe elymi</i>		K0HDR9
<i>Epichloe inebrians</i>		I7DFY5
<i>Claviceps fusiformis</i>		A8C7R9
<i>Aspergillus lentulus</i>		A0A0S7DKV5
<i>Epichloe coenophiala</i>		R9W261
<i>Neotyphodium lolii</i>		S5TCI4
<i>Periglandula ipomoeae</i>		G9FM51
<i>Epichloe coenophiala</i>		R9W1H0
<i>Claviceps purpurea</i>		M1W0Y0
<i>Botrytis cinerea</i>	<i>cloA</i>	M7UEF9
<i>Claviceps fusiformis</i>		A8C7R4
<i>Claviceps paspali</i>		G8GV80
<i>Claviceps purpurea</i>		M1WEN7
<i>Claviceps purpurea 20.1</i>		M1VZB1
<i>Claviceps purpurea 20.1</i>		M1W6N5
<i>Colletotrichum gloeosporioides</i>		T0KET3
<i>Colletotrichum gloeosporioides</i>		T0KX90
<i>Epichloe coenophiala</i>		R9W253
<i>Epichloe coenophiala</i>		R9VXN6
<i>Neotyphodium lolii</i>		S5SWI2
<i>Metarhizium acridum</i>		E9EAT5
<i>Metarhizium acridum</i>		E9DSJ7
<i>Metarhizium robertsii</i>		E9F0X7
<i>Metarhizium robertsii</i>		E9F392
<i>Periglandula ipomoeae</i>		G9FM49
<i>Saccharomyces cerevisiae</i>	FAD1	P38913
<i>Saccharomyces cerevisiae</i>	PDI1	P17967

FIG. 27

<i>easE</i> source	Calculated [M+H] ⁺ (m/z)	Observed [M+H] ⁺ (m/z)	Mass error δ (ppm)	Retention time (s)	Molecular formula [M]
<i>A. japonicus</i>	257.1648	257.1644	-1.56	120.6	C ₁₆ H ₂₀ N ₂ O
<i>E. coenophalia</i>	257.1648	257.1681	12.83	120.6	

FIG. 28

Construct	Calculated [M+H] ⁺ (m/z)	Observed [M+H] ⁺ (m/z)	Mass error δ (ppm)	Retention time (s)	Molecular formula [M]
<i>Agroclavine standard</i>	239.1543	239.1496	-19.65	150.8	C ₁₆ H ₁₈ N ₂
<i>easA_Pi</i>	239.1543	239.1486	-23.83	151.3	
<i>easA_Nl</i>	239.1543	239.1505	-15.89	151.4	
<i>easA_Cpur</i>	239.1543	239.1502	-17.14	151.5	
<i>easA_Ec</i>	239.1543	239.1507	-15.05	151.3	

FIG. 29

Construct	Calculated [M+H] ⁺ (m/z)	Observed [M+H] ⁺ (m/z)	Mass error, δ (ppm)	Retention time (s)	Molecular formula [M]
500 nM DLA	269.1285	269.1260	-9.29	126.3	C ₁₆ H ₁₅ N ₂ O ₂
<i>cloA_Cpur</i>	269.1285	269.1284	-0.37	128.1	
<i>cloA_Cpas</i>	269.1285	269.1261	-8.92	128.0	
<i>cloA_Nlol</i>	269.1285	269.1262	-8.55	128.2	
<i>cloA_Pipo</i>	269.1285	269.1287	0.74	128.1	
<i>cloA_XN6</i>	269.1285	269.1268	-6.32	128.2	

FIG. 30

Detected compounds	Calculated [M+H] ⁺ (m/z)	Observed [M+H] ⁺ (m/z)	Mass error δ (ppm)	Molecular formula [M]
DMAT	273.1598	273.1632	12.45	C ₁₆ H ₂₆ N ₂ O ₂
¹³ C-DMAT	274.1631	274.1623	-2.92	C ₁₅ ¹³ C H ₂₆ N ₂ O ₂
4DMA	287.1754	287.1749	-1.74	C ₁₇ H ₂₂ N ₂ O ₂
¹³ C-4DMA	288.1788	288.1784	-1.39	C ₁₆ ¹³ C H ₂₂ N ₂ O ₂
Chanoclavine-I	257.1648	257.1636	-4.67	C ₁₆ H ₂₆ N ₂ O
¹³ C-Chanoclavine-I	258.1682	258.1668	-5.42	C ₁₅ ¹³ C H ₂₆ N ₂ O
Agroclavine	239.1543	239.1527	-6.69	C ₁₆ H ₁₈ N ₂
¹³ C-Agroclavine	240.1576	240.1572	-1.67	C ₁₅ ¹³ C H ₁₈ N ₂

FIG. 31

<u>DLAM33B</u>	[DLA] (nM)	[DLA] (μg/L)
Mean	<u>266.42</u>	<u>71.48</u>
<u>95% Confidence Interval</u>		
Upper limit	377.53	101.30
Lower limit	155.31	41.67

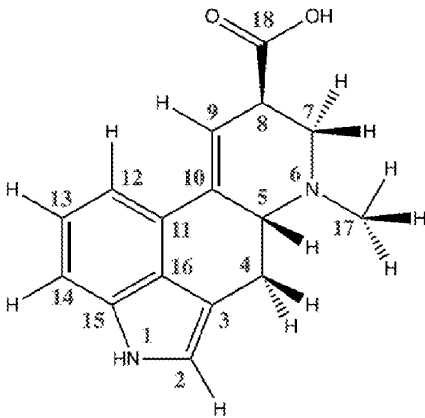
FIG. 32

Strain	Genotype
YMWf	Chr. XIII: YMRWΔ15:: PTEF2- <i>dmaW</i> -TENT2/PGPM1- <i>easF</i> -TPRX1/PGAL1-yEGFP-TcBR1
YMC17	Chr. XIII: YMRWΔ15:: PTEF2- <i>dmaW</i> -TENT2/PGPM1- <i>easF</i> -TPRX1/PGAL10- <i>easC</i> -TYIP5/PCUP1-mKOK-TcBR1
YOCE	Chr. XIII: YMRWΔ15:: PTEF2- <i>dmaW</i> -TENT2/PGPM1- <i>easF</i> -TPRX1/PGAL1-yEGFP-TcBR1 Chr. XV: YORWΔ22::PGAL10- <i>easC</i> -TYIP5/PGAL1- <i>easE</i> _Aj-TRPS20
AgcM1B	Chr. XIII: YMRWΔ15:: PTDH2- <i>dmaW</i> -TENT2/PGPM1- <i>easF</i> -TPRX1/ PTEF2- <i>easE</i> _Aj-TRPS20/ PpGK1- <i>easC</i> -TYIP5/ PCUP1-mKOK-TcBR1
AgcM2B	Chr. XIII: YMRWΔ15:: PTDH2- <i>dmaW</i> -TENT2/PGPM1- <i>easF</i> -TPRX1/ PTEF2- <i>easE</i> _Aj-TRPS20/ PpGK1- <i>easC</i> -TYIP5/ PCUP1-mKOK-TcBR1 Chr. III: ARS308:: PRPL3-PDII1-TYPS1/ PPDA1- <i>easD</i> -TYPR1/ PACT1-FAD1-TEFM2/ PRPL15- <i>easC</i> -TYIP5/ PTPH1- <i>dmaW</i> -TENT2
AgcM33B	Chr. XIII: YMRWΔ15:: PTDH2- <i>dmaW</i> -TENT2/PGPM1- <i>easF</i> -TPRX1/ PTEF2- <i>easE</i> _Aj-TRPS20/ PpGK1- <i>easC</i> -TYIP5/ PCUP1-mKOK-TcBR1 Chr. III: ARS308:: PRPL3-PDII1-TYPS1/ PPDA1- <i>easD</i> -TYPR1/ PACT1-FAD1-TEFM2/ PRPL15- <i>easC</i> -TYIP5/ PTPH1- <i>dmaW</i> -TENT2 Chr. XVI: YPRCΔ15:: PRPL8B- <i>easG</i> -TAFL2/ PSSA1- <i>easA</i> _Ec-TYPT31/ PTEF2- <i>easF</i> -TPRX1/ PTDH2- <i>easC</i> -TYIP5/PTDH3- <i>easD</i> -TYPR1
DLAM33B	Chr. XIII: YMRWΔ15:: PTDH2- <i>dmaW</i> -TENT2/PGPM1- <i>easF</i> -TPRX1/ PTEF2- <i>easE</i> _Aj-TRPS20/ PpGK1- <i>easC</i> -TYIP5/ PCUP1-mKOK-TcBR1 Chr. III: ARS308:: PRPL3-PDII1-TYPS1/ PPDA1- <i>easD</i> -TYPR1/ PACT1-FAD1-TEFM2/ PRPL15- <i>easC</i> -TYIP5/ PTPH1- <i>dmaW</i> -TENT2 Chr. XVI: YPRCΔ15:: PRPL8B- <i>easG</i> -TAFL2/ PSSA1- <i>easA</i> _Ec-TYPT31/ PTEF2- <i>easF</i> -TPRX1/ PTDH2- <i>easC</i> -TYIP5/ PTDH3- <i>easD</i> -TYPR1 Chr. II: ARS208:: PGAL1- <i>cloA</i> _Cpur-TRPL41B

FIG. 33

Component	Mass (for 1 L solution)	Molarity
NaCl (mw: 58.4 g/mol)	80 g	1.37 M
KCl (mw: 74.551 g/mol)	2 g	0.027 M
Na ₂ HPO ₄ (mw: 141.96 g/mol)	14.4 g	0.1 M
KH ₂ PO ₄ (mw: 136.086 g/mol)	2.45 g	0.018 M

FIG. 34



Position	¹ H-NMR (Standard)	¹ H-NMR (Sample)
2	7.194 – 7.197	7.210 – 7.358 ^α
4	2.964 – 3.008	2.913 – 2.984
5	4.006 – 4.040	3.455 – 4.099 ^β
7	3.349 – 3.395	3.455 – 4.099 ^β
8	4.030 – 4.040	3.455 – 4.099 ^β
12	7.225 – 7.227	7.210 – 7.358 ^α
13	7.110 – 7.142	7.112 – 7.129
14	7.209 – 7.213	7.210 – 7.358 ^α
17	2.143	2.108

^{α-β}: Broad indistinguishable peaks, chemical shifts with the same symbol overlap.

FIG. 35

<u>DLAM33B</u>	[DLA] (μM)		[DLA] (μg/L)	
Fermenter Scale	4 L	1 L	4 L	1 L
Mean	6.08	7.36	1631.52	1974.04
95 % Confidence Interval				
Lower limit	5.92	6.64	1587.87	1782.20
Upper limit	6.20	8.07	1663.43	2165.88

FIG. 36

Source Organism	Gene name	UniProt ID	Nucleotide sequence	NT length	SEQ ID NO:
<i>Aspergillus fumigatus</i>	<i>dmhV</i>	Q50EL0	ATGAAGCAGCCAAATGCCCTCCAGCAGAGCCATACAGAGTATATCCAGAGCCTTAGATTCGATATGAAGATCAAAAATTTGGTGGCAATCTACAGCCCCAATGTTGCTAAGATGTTAGAAACCGCCAACTATACCTACACCTTGCTCAATACCAATCTGATCACTTACAAGGAAATGTTGTTATCCCATCATTAGGTTGCTACCTACAAATTCGGTCCAAAGTGGTTAAAGTATTTTGACCAAGATATGGTACTCCCTTCGAAATTTGCTCTAACTCAATAGTAAGATACACTTCGAACCAATCAATACCGGTACTGATAAGGACCCCTTCAACACACATGCAATATGGAAATCCTTACAACACTGTTGCCATTTGGAATAATCTATTGTTGAAATGGTTCAGACATTTCAAGCAGACTTGACTTTGAACTCTGAAGAAATCAGCATTTTGGGCCCAATAACGATAGATTATGTTGGTGTACAAATTAGAACCCAAATTAAGTTGGCATTAGATTTGAAGGACGGTAGATTGGCTTGAAGACATACATCTACCCAGCTTTGAAGGCCAGTTGTAACCTGGTAAACAAATTCACGAAATTTGGTCTTCGGTTTGAAGATTAGCTGTAGAGAACTTAGAATTTTACCACCTTTGAACATGTTAGAAATGAAATACATCATGATCTAGAGGTTCCAAAGGTACCCGCTCTCCAAGATTAGTCTCATGTGTTTGACTTCCCTGCTAAGAGTAGAATTAAGATATACCTGTTAGAACAAATGTTTTCATTGGAAACAAATGGAAGATTTGAGACTTTTAGGTGAGTGAAGAGAGACGCCCTCTACATTAGAAGGTTTGTCTTTGGTTAGAGAAATTTGTGGGATTGATACAATTAATCCCAAGTTTGAAAGTTATCCAGCTCTTACCTTTGGGTGTCATACCCAGATGAAAGATTGCCCTTTGATGGCAAACTTCCACTTTTGATCAAAACGACCCAGTACCTGAACCAAACTCTATTTTACCACCTTTGCGGTATGAATGATATGGCGTTTGTCTGACGCATTAACAACCTTTTCGAAAGAGAGGTTGGTCTGAAATGGCAAGAACTTATGAACTCATTTGAAGTCTACCTACCCACATGCTGATCACGCAAGTTAACTATTGACGCATACATTTCTTTTTCATACAGAGATAGAACACCTTATTGTTCTGTTTACTTGCAATCATTTGAAACCGGTGACTGGGCCGTTGCTAACTTTGTCGAAAGTAAAGTGTCAAGACGCTGCAATGCCAACTACAGCCTACCTCTGATTTGTTCAAGACTGGTTTACTCTCTGTTTACAT	1377	1
<i>Aspergillus fumigatus</i>	<i>easF</i>	Q4WZ60	ATGACCATCTGACACCGCGATTATCGATATTGCGCAGGCGCGCTGGAAAGCTCTATCCGAGACCAAGTGGTTGAAGGTTTGACCCAAAGAAAGTGAATAACCGCTGCCGCGCTGCTGTTTATTCACGAAAGGCAATCCAGCATTTGAAACCGCAATTCACGCGGCCGATTTCTTACCCGCGTCACGAAGAACTGTGCAATCTGAAAGCAGAAAGCTAGTAAATGGCAGCTTCCATTGCTCCAGGATTCACATGGGTTATCGACATGGGTTTCAGCATCGATGGATAAAGTCAATCTGCTGTGGAAGCGCTGGAAGAACAGAAAAATCTATCACTACTGTGCGCCTGGATCTGAGCTACTCTGAACTGGCAAGTAATTTTCAAGCTATTCCCGCGGTGCAATCTGCTGTGTTGGCCTGACGATTGGTAACTCTCTCGCGATAATGCGGCTAGTTTTCTGCGTAAACATCGCACAGAGCGCTCTGAGTACAGCCCCGACGCAAGTTCATTATCGTTAGCTGGATCTGTAAACTGCGCAGCAAAATTTCTGCTGGCATATACGCGCAGACGGTGTGCTGCCGTTTGCACTGGCCTCACTGTCTGACGCCAATAGCTGTTCCATCCGAAAGGTGATGCAAAATCTTCAACGAAGAGAGTGTGTTCTTCCATCCGAAATGGAAATCACGCGCTGGGCCGCTCATGAAGCCTGCTGATTACCCAGAGCAAGATATCCAACCTGGGTGGCGCTGGAAACGGTTATCTCCGCTGCGCGCAAAATTCGCTTTGGCTGCTATAAATACGATAAAGCAGAACGTGACACGCTGTTCCACAGCGCTGGTCTGGAAGATGGGCCGCTCTGACCGCACCGGATTGTGACGTGGCTTTTACCAACTGCGCCTGCGTCTGAAC	1017	2

FIG. 36 (cont'd)

[illegible]

FIG. 36 (cont'd)

FIG. 36 (cont'd)

FIG. 36 (cont'd)

Source Organism	Gene name	UniProt ID	Nucleotide sequence	NT length	SEQ ID NO:
<i>Epichloe chymi</i>		K0HDR9	A GAGAIACGTTGTACTTCGTTATGGGTTGTGTTCTTGGGGTTCTTGTCCTTGTGCAAGGTAGACCACTCTGTGATAGATGTAGACCTTGGGAGGGCTTGTGG CTTGATCTCACCAGTCTTCAACAGCTTCTTGTGAAGCTTTGATGTAGTGGTTTCATGTTCAACAGTGTGGTAGTGTGTGTCATGATGTCAGAAATACGATGCTGTCTT GTGGTACCGTTTGGATTGTGTCAGAAATCTCTGGTTGGAGAGCTTCCAAACCAGCTACTTACAAGATCGGTAGTGGTGTGAGTCGGATACGAACTGCTGTG TTGTGGTTTCTCTCTGAGAGATCCCAAGAAATCCCAATGTCATCAAGTATAGTTCCTTTGTACTACGTCTGCTGTTTCAACTCAACTGCTCTGTTTCAATCTGTGTGTA GATTTGCTAAAGACCAATTTGAGATTTGGTTTATAAGAAATCTGGTCATGAGCTACTGGTACTGCGCTGCCCGCGATTCTTCTTGCAAAATCTCACACTACTTTTGA AGGATTCACATCTACGAGTAACCTTCTTCTCAAGGTGACGCTACTGCTTGGTCTGAGCTGTGACTGTGAGTGTGGTGTGTCATGCACTCTGAAGTCTTACAAGATG GTATTGATCAAAATAGTGTGTGGTGGTGAATGTCCACCGCTGGTATTTGGTGTGATCTTCAAGAGTCTTCAAGAGTCTTGTGTTCTTCTGGTCCGGTTCTACTAG GTTTGGCACTCGATACGTTTTGGAGTACCAAGTGTGTACTGCAAACTGGTATTTGCTACGAAACACAAATATCAGGATCTTTCTGGGCTTTGAGAGGTGGAGGA GGTGTGACTTTTGGAGTTGATCTCAAGCTACTGTAGAGCTCTCCCAAGTACTCAACTGCTGTTCCTGTCACCTCCCAAGAGCTGACACTCTTGT GGGAAAGGCTATTTCCAGATTTGTTATCTTTTGGATTCTGTATACCAACAAAGAGCTCCAGGTCATTTGATATTACAGAACCATCTGAAGATATTTTGAACGCTG GTTGAAGTCTCTTCAACTACCAAGCTTTCTCATGCTCAACACTCTGTGCAACACATCTGCTTCTGAAAGAACAAATCTCAGCAAGCTTTATCTTG TAAGTTGCTGCTAATATCAACTCTGAATTGAGACTTGACTGATATCATCTCTGGTATTGGCAATCTTCTATGATGATCTCCGATGAACCTTTTGGT TCTCTAGAGGCTTTCCCACTGTGCTCAAGTTTGGTAAATGGCAATCGGTTCAAAAGCTTTTATTCACTCAAAATTTGGGTGGTGAAGTTGGCCTGAATAAG GCTTTAGACTCGCACTACCCAGCTCTGCTCATTTGGTATTACTACGTCTGCTGTGTAACCATCAATTGAAGCTAAAAAGTTGGCTCTGGATGA ATCACTAATAAGTATGATGCCAAATTTTGTACTATGCAACCTCTTTTAAAGTTTCTTACAGAAACTTAGTGACCAACCAAGAAAGAAATATCAAGAGGTTTTCTGG GGTGAAGGCGTTACAAGAGATTGGCTTCCAATAAGGCTAAATTAGATCCAGATGGTTTGTCACTCTAAGTTGGGTGTGGTCTTGAGCACTTGGGATGCTGAAG GGATGTGCTACCAACCAAGAAATAGAGTTTCTCAACCGTTGAGATCTCTTCAATCTTTTGAGTGTGTTTGCAAAGATACT	1809	10
<i>Epichloe inebrians</i>		ITDFY5	A GTACAACTTTGTGGGTCAGTCGCCGTGTGTGACTTTGGCTGGTTTGTGCTGTGGTTGTCACCTTGGTCTGAGTGTGTGATGACCTTGGGAACTTGTCTGGCACTCT GCTGCCATTGGGAAGGCTTCAACGAGCTATATCCAAAGGTAACTTGGTCAGAAATTAGACAGTGTGCTTCTGTTGTGTCACACTTGGAAATACGACCGCTTGTCTGCT AACTATCTCTTGGTTGTGATCTGTGGTGGAGAGCTTCTAACCTTCTACTTTGCAAGACTGGGTTTGGGAATCTGTGAACCGCTGAGGAAACTTGTCACTCT ATGACTTCTCAGGTGAAACAAAGAAAGTGTGTGTGCCAAGGTAGA TTGCCATTTGACTGCTGTGTCTCAATCCGCTCTTAACA TCCAATCTTCTGTGAGATTC GCTGTGCACCAAAATTTGAGATTGGTTTCAAGAATACTGTGCAGACTGTGGTGTAGTACTCTTCCCACTCTTTTCAAAATTCACAACTATGCTTGAAGAAT ATTAGTTTCCACAAAATTTGTTGCTGGTTCACAACTGGTTACGCTTCAGCTGTACTTGGGTCGGGCTGTATGCACTGGGGAAGTCTATGCTCTACGTTGCT CGAAAAGGTTACACCAATTTGGGTGGTGAAGTCCAACTGTGTGGTGCCTGGTGGTGTGTTCTTCCATTTCTTCCATTCCTTCTCCTCAGTAGAGTT GGCTGTGTAACGCTCTTGGAAATACCAAGTTGACTTTAAGGCTGACTAGTTACCAGTACGAAACCAAGAAATTTGATGCTGGGCTTTGAAAGGTTGGAG GTGGTGGTACATTTTGGTATTGTTACCAAGCCACTGTCTGTTTACCCTGACGACTCTGTACCCTTACTACTGTGATGATCAAGGCTGCTTCTCCTCACTCACTATT CTGAGCTGAAGGTGTGCAGAGAATTTGTGAGATTGCTTAGAGATTTTAAATTTGTGATATCTTGGTCAATAGTGTGTAGAGGTCCTGAGAAGCACTCTATCCAAG CTACCTTGAATTTGACTTTTGTCTAACATGATGAGTGAAGAGCTACGCTATGAAGTTGCTTTCTCTGCAAGTGGCTGACTATATCCATTCACCACTATCTCTGCACTTCC GCCAGAGTCAAAAGAGAGCTCTTCCGAAATTAAGAAATGAAGCCAGATATCTACCCACTCATACGGTATTTTGGAGGGTCCGCTCTGATTTCTTACCCTGCTCTC CAATCCGCTGAAGGTCCAACCTTATTTGGCCAGAAAATTTGCCAATTGAGATTTGCGATATTTGTCACCTTCACTTGGTGTGGTGAAGTGTGATGTTCTTAAAAAC ATTTGCTCATGATTCCTCAGCTTGGCTGGAAGCTGCTCAACTGTGATCCCTTGGTGGCGCGCTGAGGTAAGGTAAGTGTCTACCTTAGAG AACCTGACAGTGAAGTACCCAAATTTGTACTATTGACCCATCAGCTAAGATTTCTTACAGAAACTTAGGCGATCCACAAAGAACAAATTTCAAGCTAAGTAC TGGGTTGCTGATTAATACGCTAGATTGGCTATTAAGGCTAAGTTGGGCAAGTGTTTATCAACGATTCGGGATTTGGTCCGAAAAATTTGGGATGTG AGGATTTGTAGAAAGCTCAAGACTTTATGCTCAAGCATTCGCTTGTGTAAGAGTCGGTTGTCTTCTCTAC	1800	11

FIG. 36 (cont'd)

[illegible]

FIG. 36 (cont'd)

Source Organism	Gene name	UniProt ID	Nucleotide sequence	NT length	SEQ ID NO:
<i>Epichloe coenophiala</i>	<i>easE</i>	R9W261	ATGAGACACTTGTGACCTTGGTAGTAGGTTTCTCTTGACCTGGGGCTCTGTGCTCTTCAAGATCCACACTCTGTAGATGTAGACGGTGGGAACCAATGTTGGCC TGAATCTCACCAGTGGACCTCTATTTGATGGTAACTTTGGTTCAGTGCAGCAAGCTGGTCTGTGTCATGACCCACATACGATGCTGTGCTGTG GAGATGTTGGATTTGCTCGTAACTCAGGTTGGAGAGCTTCCACCAGCTATTCGACAGCTGGATCTGGGAGACTGGTCTGTGGTGAAGATGTTCTATGATTTG GGTGTTCTTCTTGAAGACCTCAAGAAATCCATGTCCACAGGAGTAGTGCCTATCTAGCTGTGAAGTCTACTCTGTGTTCAAGSTGGTCTTATGATTTG CTAAGGATCACAACTTGGATTAAGTAAAGAACTGGTATGATGCTACGGGTAGATCCGCTGCTCTGATTCATTACAAATTCATCACTACTTTTGGAAAGATAT TATACCAATGAATACCTTTGGTCCAGGTGAGCTCCGGTCTTGGTCCAGCGTTACTTTGGGTGCGGCTGTGCTTCACTCCGAAGTTTATAGCATGGTATTGATCA TAAGTACTCCGTTGTGGTGGTAAATGGCCCAACCGTTGGTATCGTTGGAGGTTTCTTGCAGGTGGTGGAGTTCTTCTGGTGGGTTTCCACCAGAGTTTGCTGT GATATGCTCTGMAATCAAGTTGTACGCCAACGCAAGTATGTTATGTCTACGACCAATCAAAATGTTTCTGGGCTTTTCGCGGGGTGGTGGTGGT ACTTTGGTGTGTACTCAAGCTACAGTAAGACGATCCCGATGATCCAACTGATGTTCTACTTTAGTTTGTCTACTAGAGCTGATACTCTCTGGGTGAAG GGCATCTCAGAGATTGTGAAGTATTTGGTCTGTGAACCAAAATGTTTCAAGGTCAAATGTATCATCAAGACCATCTGTGACATCTCAATGCTGGATGATGACTTA CATTTTCTCAAGATGACTAAGTCTGCATGCTGAACCTTTGTGCAACACACATGCTCTCGCTGTCGAGATCAAAATTCACACTACTCTGACTCTAAATCTGGTGTCCA ATATATTTCTGAAITGAGATTAGATGCTGATATTCACCAAGAGGAATGGTATGTTTCCAACTCTATGATGATTTCCAAAGAAATTTGTGCGTCTTCCGAGGTGCA TTGACTGTGCTCAAGTCTTGGTAAATACCAATTTGGTCCAAACGACTTATGTTTACTAGCACTGGGTGGTGTATGCTGCCAAATAGGGTTTATGATAGTCTGCCAT TCACCAGCTTGGAGATCAACAGCTACTGTTACCTACAGATCCGTTGAAGACTATCTATGAAGCTAAGAAATGGCTTTGAAGGAAATTAATAAGTACATG CAAATTTGATCTATGCAACACTCTTTTAAAGTTTTCATACAGAACTTGGAGACTCCAAATGAAGAAATCTCTCGGGGTGAAAAGTGTATACGAAGA GATTGGCTCTATTAAAGCTAAGTGGACCCAGATGGTTTGTTCATTCTTAAGTTGGGTGTTGGTAGTGAAGACTGGGATGTAAGGTATGTGTACCAACCTCAAA ACAGAGTTTCCCAACCATTCGCTTCTTGAAGTACTCTCTGCTGTTTGAAGACAT	1815	14
<i>Neotrophodinium bolii</i>	<i>easA_{iso} mense</i>	S5TC14	ATGTCTACTTCTACTTGTTCACCCCAATGCAATTCGGTAAATGTTGTTGCCAACACAAGTTGGTTTGTCTCCTCAATGACTAGATTGAGAGCTGATTAACGAAGGTTGTTCC ATTGCCATACGTTAAGACTACTACTGTCAAAGAGCTCTTTGCCAGGTTACTTTGTTGACTGAAGCCACCGCTATCTCTAGAAGAGCTAGAGGTTTCCCTCAACGTTCTC CAGATATCTGTGTCCTCCAAAGAACAAATCGCGGTTTGGAAAGAAAGTTGTGACGCTGTTTCACGCAAGGGTCTTACATCTGTTGCAATTTGTGGGCTACTGTGAGAGCTG CTGAAGTTGGTGTGTTGAAGACTAAGCGTTTCTGACTTGGTTCTCTCTCCGCGCTTCAGTTCTTCCAGGTGAAACCACTCCGATGGAAGTCTGTCTGATGACCAAATTAAC TCTACATGGTGTACTGTTTCAAGCCCTAAGAAGCGTGTGTTTGGAAAGCTGTTTCGATGGTGTGTAATGTCAGCGGTGCTAACGGTCTTCTTGATGATCAATCTTGCA ATCCCCATGTATACCAAGAGCTGATCAATGGGTTGTTGATTGAAACACAGATCTAGATTGCGTTTGGAAATTTAGAAAGTATTATGATGATTGAGAGTTGAGAGAAATCGGTAAT CGTTGGTATGAAGTTGTCTACTTTTCCAAGGTAAGGGTACTATGGATGATTGATATTCACCAATTCGAACTATTCATATGAGATTGAGAGAAATCGGTAAT GCTTACTTGCACTTGGTCTACTCTAGATGGGTGGAAGAAGAAGATCCCACTATTAGAACCTTCCAGCAAACTTCTCTGTAGAAATTTGGTGGGTGAGGTTAAAGTT AAGCCAGTCTGTTGGCTGGGTATAGCGTCCAGATCTGCTAAAGTTGGTTGATGAAACTTACTCTGATCACAGAAGATGGTGTGTTTTCGGTAGACACTACA TTTCTCAACCCAGATTGCAATTGAGATTGAAGTGGTTTGCCATTGCAAAAGTACACAGAGAAACTTTCTACATTTCTCTGATGAAGAGTTACTTGGATTACCCA TACTCTGAGAGATACATTACTTGAAACCAAGAGCAAGCTGTTTGTGGCT	1140	15

FIG. 36 (cont'd)

Source Organism	Gene name	UniProt ID	Nucleotide sequence	NT length	SEQ ID NO:
<i>Periglandula ipomoeae</i>	<i>eaxA₁₈₀</i> <i>mirase</i>	G9FM51	ATGTCACCTTCCAACTGTTCAAGAAATGCCATTGGGTACTCTGTTTGAAGCATAAAGATGTTTGTCTCCAAATGACATAGATTACAGAGCTGATAACCGGTGGTGTTC ATTGCCATAGCTTAAGACTTACTACGCTCAAGAGCTCTGTTACGGTACTTGTGTGATCTGAAGCTGTGCTATCTGTCCAGAGCCAAGGTTTCCCAACATCC CAGGTATCTGGCATGATTCTCAAAATCGCTGTTGGAAGGTGTGGTTGATGAAGTTCATCTAAGGGTTCGTATTGTGTGCAATTTGTGGCTACTGTGAGAGCTGT TGACCCAGATACTTTGACTTTAAACGCTTGGAAATGAAGTCTCTCTGAAGTTCAGTTGCTCCAGGTGAACCACTCCAAGACCATTTGTCCGAAGAAGAAATCCAA TCTTACATCTCGACTACGCTCAAGAGCTGCTAAGAACGCGCTCCACGAAGCGGTTTTGATGGTGTGAAATTCACGGTGCACACGCTTTTGTGATTGACCAATTTCTTACA ATCTTCTGTAAACAGAACCGATCAATGGGGTGGTCTCTTGAAGATGAGTCTAGATTGGTGTGAAATCACTAGAAAGAGTTATTGATGCTGTGGTFAACGATCA CGTTGGTGTAAAGTTGCTCTCTTGGTCTACCTTTCCAAGGTATGGGTACTATGGATGACTTGGTCCCAATTTTCATTTACTAGATTGAGAGAAATGGATATT GCTTACTTGCAATTTGGCTTAAGTGGGTGAAGAGGAGATCCATCCATGAAGCCCAAGATGTTCCACAAACCTCGTTAGAAATTTGGGGTGAAGAG CGTCCAAATTTTGGCTGGTGTAAACCCAGACTCCGCTAGAGCTTTGGTGTGATCAAACTTACTCTGAACAAACCAACGTTATGGTGTGTTTTCGGTAGACACTACAT TTCTAACCCAGATTTGCCATTTCAGATTGAAGATGGGTATTGCTTGCAGAAAGATACACAGAGATACTTCTACATCTCTGTTGGAAGGTACTTGGATTACCCAT TCTGTAAGGAATACTTGAAGCAAGGTGACCAAGAACTACTGTGCT	1140	16
			ATGTCACCTTCTAACTTGTCTACTCCATTGCAATTCGTTAAATGTTTGTGTCACACAAAGTTGGTTTTGTCTCCAAATGACTAGATTACAGAGCTGATAACGAAGGTGTTC ATTGCCATAGCTTAAGACTTACTACTGTCAAGAGCTCTTTGCCAGGTACTTTGTGTGACTGAAGCTACTCTATTTCTAGAGAGCTAGAGGTTTTCCCAACGTTTC CAGGTAATTTGGTCCCAAGAACAAATTGCTGTTGGAAGGAAAGTTGTGACGCTGTTCATGCTAAGGGTCTTACATTTGGTTGCAATTTGGGGCTACTGAGAGCTG CTGAAGTTGGTGTGTTTGAAGGCTAACGCTTTTCGACTTGGTTTTCTCTCCGCTGTTCCATGTTTCCAGAGTGAACCAACCAAGAGCTTTGTCTGATGATGAATTAAC TCTTACATCGGTGACTGTTCAAGCTGCTAAAAAGCCTGTCTTGAAGCTGGTTTCGACGGTGTGAAATGTCATGGTGTCTAACGGTTTTCTGATTGACCAATTTCTGCA ATCCCCATGTAACCAAGAACCGATCAATTGGGGTGGTGTGATGCAAAACACAGATCCAGATTCGTTTTGGAATTCACAGAGAGATTATCGATGCTGTGTTGGTAAAGACCA CGTTGGTATGAATTTGTCACCTTGGTCTACTTTTCCAGGTAAGGTAAGGTAAGTACTATGGATGACTTGTATTCACAAATTTGAACAATTCATATAGATTGAGAGAAATCGGTATC GCTTACTGCACTTGGCTAACTCTAGATGGGTGAAGAAGAACCCCAACTATCAGAACCCCAAGATATTCATAATGAACCTTTGTGAGAAATGTGGGGCAAGGAA AAGCCAGTCTTGTGGCTGGTTACGGTCCAGAACTGCTAAGTTGGTGTGATGAAACTTACTCTGATCACAAGACATCGGTGTCTGTTTTCGGTAGACATTACA TTTCTAACCCAGATTTCGCAATTCAGATTGAAGATGGGTTGCCATTGCAAAAGTACACAGAGAAACCTCTACATCTCTCTGATGAAGGTTACTTGGATTACCCA TACTCTGAAGAAATACATTACTGAAAAACAAGCAAGCTGTTTTGGCT	1140	17
<i>Epichloe coenophila</i>		R9W1H0			
<i>Claviceps purpurea</i>	<i>eaxA₁₈₀</i> <i>mirase</i>	M1W0Y0	ATGTCCACTTCACTTCAACACCGTTCCATTGCGTTAAACGTTTTGAACCAACAAGATCGTTTTTGTCCCAATGACTCTGTTTTCAGAGCCGATGATAACGGTGTTC ATTGTCTACATGAAGACTTTCACGCTCAAGAGCTAGTGTGCTGGTACTTTGTGGTACTTGAGCTGTGGCTATCTGTCCAGAACTAAGGTTTTCCCTAACGTCC CAGGTATCTGGAACAAGGATCAGATCGCTGCGTGGGAAGGAAAGTTGTGTGACGAAGTTCCATCTAAGGGTTCCTTCTATCTGGTTGCAACTTTTGGGCTACGGGTAGAGCC GCTGACCTTGAGGCTTGACATCTCAAGGTTGAAGTTGGAATCTCTCTGAAGTCCCAAGTTCAGAGTGAACCTACTCCACGCGCTTAGATGAAGATGAATCC AACAAATACATCTTGGACTACGTTCAAGGTGCTTAAGAACCGCTGCTGCTGCTGATGGTGTGAGATCCACGGTGTCAACGGTTTTCTTGTGATCAATTTCTT GCAATCTCTTGTAAACAGAACTGACCAATGGGGTGGTCTTATTGAAACCGTTCCCGTTTCGCTGTGAGATCACCAGAGGTTGTGATGCCGTGGGTACAGA CAGAGTGGGAAATGAAGTTGTCTTGTGTTACTTTCAAGGTATGGGTACTTGTGCTCCCTCAATTCGAACACTTCACTACTTGTGTGATGCCGTGGGTACAGA ATTGCTACTTTCGCTTGGCGAACTCCAGATGGGTGAAGAAGAACCCCACTATCAGAACTTCCACAGAACTTCCCAACTCAAACTTGTGTTCCAAATGTGGGGTAAAA AGCGCCCAATACTGTGGCTGGTTACGATCCAGATCCGCTAGAGCTTAGTTGATCAAACTTACTCCGATAGAAACCAACGTTTTGTTGTTTTCGGTAGACACTA CATCTTAACCCAGATTTCGCAATTCAGATTGCGCATGGGTATCGCTTTGCAAAAGTACACAGAGATACTTCTACATCCCACTGATGGTGAAGGTTACGTTGATTACC CATCTGTAAGGAATACTTGGATCAAGCTGATGAAGCTGCTGTGCTGGT	1140	18

FIG. 36 (cont'd)

Source Organism	Gene name	UniProt ID	Nucleotide sequence	N ^T length	SEQ ID NO:
<i>Batrachoseps chirensis</i>		M7UEF9	A T G C A T A G A G A T T A C A A T T C T C A G T A T T A G A A T T G C T C C A G A T A T G G T T C A T A G T T A A C G A T C C A G A T T C T T T T C A T A C T A T T T C A A T A A C A G A A C T A C A T A T T G A A A G A T C C A T C T T G T T A C A A G C A A A T T C A T A A C G A A T C A T C G T T T C A A T G T T A G A T G C C A T A A C A T A G A T G A G G A G A A A A G G T T A A T C T A T G T T C T C A A C A A A G G C T G T T G C A G C C A G A T G T T T A G C T A T C G C A C A A A G G C T G C A A C A T A T G A T A G A A G A G A G T T G A A G A A A A G A C C A G A T G A T G T A G A C A A A T G T C C A G T C C A T T T C T C A G A A G T T G T T T A A A T T T G T T G A T G A A A C C A A T G C A T T G T T A G A T T C T C A A G A A G A A C C A G A A T T G T T A G C T G T T T A A G A T A C A T T T T T G G G T A C A T T C G T G T G A T G A G A G C T T T C C A G T A T T G G T T A G C A A T T A A T T T G C C A C A A T C T T T A C T A G A A A A T T G A T T C C C A G G T T T T A A A T C A T T G A G A G A T G A T T G T A A A G A T G G G C T A G A A T T G C T G T C C A A G A C A A A A T T C A A G A A A A T T A A A A T G A T T C T T C A T C T T A C T A C A G T T T T G A T T G T T A T T G A T T G T A C T C C A A C A C C A G G T G A A C A G A T A G A A T T C A A T C C A G A T T G G T T G A T A G A A G A T T T T G C T G T T T G C A G G T A C T G A T A C T A C T A G T G T A C A C A T T C A C A A A C G C T T C T A C T A C A T T T A T C A T C T C A T C T G T T A T C A A A A T T T A G A T G A A T T G A C A G A C A T G A T C T C A T C A G A A C A T C G A T T G A C G T T G T C A A A G T T G C A A A G T T C A A A G A T T A C C A T A C T T G A C T G T G T T A A G A A T C A A T G A G A A T A C A A T G T T G G T G G T T T T G C C A A G A A T T G T C C A G A A T T G T T G T G A T G G T T A T T T A T T A T T G C C A G C T G G T A C A T A A T T C T C A A T C A A T C C T T T A C A T C A T A C G C A T C T G T T T T C C A T C A C A A A A G T G C A T C C A G A A G A T G G A T C A A G G A T G A A G A A A A G G A A T T G G A A A G T A C T T C G C A C C A T C T T C A A G G T T C A A G A G C T G T T G G G A T G A A T T T G G C A A C C A A G A A A T A T T G T T G T A T T G C T T A T T T T G T G C A A G A T T C G A A A T C G A A T T G T A C G A T A C T A C A A G A T C A A T G G A A T T G G G C T G A T C G T G T A A C A C A G T T A A C A G A T C A A G A T T T G T G G T T A A G A G A G A T A G A T G G G C A A A T A A T	1320	19
<i>Claviceps fusiformis</i>	<i>clo4</i>	A8C7R4	A T G T T G T A T T G G T T G T A T C A A G C A T T G C C A A C T C T T T G A C A A G A A T T T T A T G A C T G C T G G T T G T G T G T T C C A T G T G T T A T T C A T G G T A T T C T A A T T T G T A C T T C C A T C A T T G A G A A A C G T T C A G G T C C A A A T T G G G T G C A T G A C T G A T T G A C G T T T C T A C T G G A A C T G G A T A G A G G T G T G G T T A C T C T A C A G C A A T T C G A T A G A T G G C A T A A G C A T T A C A A T T C T A G T A T T A G A A T C G G T C C A A C G A G T T T C A T A C T A C A A A T T G A A T T A T A C G A T T A T C C A T A A A G C A G G T T T C A C T T G G T T G A A G A T A A A T C A T T T A C A A G C A T T C G G T G G T T A G A T G C T A T G A T C G A T C C A A G A A A T A C A G A A C T T A C A G A A C A C A T T T G G C A C C A T T A T A T C T C A A A G A G C T G T G A T G G T T A G T T T C A A A G A T G G A T G A T T T G G C A A T T T G T G G T C A A A A G A C T A C A A A A T G G C T G A A A T T G G T A A A A G A G T T A A C A T G G C T A G A G T T T G A C T A C A T T A C T A C A A T G A T C T G T A C A A T T G T T T C T A T G G A T A T T C T T G T G G A A T T G T A A T T A C C A T C C A T T T T T G G A A G C A T T T T G A A C A T A T A C T A T G G C T C A A A T T G G T A T T T G T C T T A C C A A G A T T G G C T A C T T G T T A T C T T G A T T C C A G G T A C A T T G G G C A A G A T A G A T C C A T C T T G G A C T A C T T T A T A G A A C T C T T G T G C T G A C T G T G T G A T G A A G A T G C A A A A C A A A G A G C T C T G A T G A T C A A T C A A T C A G A G A T T C C A T T C A A G A G A T A C T A C G A T T A G A C A C T A G A C T A G A T G C T A A C G A T A A G A A T A T A T T A T C A G A C A C A T T G A T G A A T T G T T T C T T A T T G C T G G T G G T A C A G A T A C T A C A G A T A C T A C A G G T T G G C T T T T T A T A T T A T C T A T T C T C T C C A T C T G T T G T A G A A A T T G G T A A G G A A T T G G A T G A A A A C G C T C T T T A T A G A A A C G G T T A G A T A C C A T A A A T T C A A A C T T T G C C A C T A C T A C A A C G C T G T A T T A A A A A C A A T A G A A T T T C T G T C C A G T T C C A A G A G T T G T T C C A A G A G T T G A T A C T G T T G G T T C A T T C A T T G C C A G C A G G T A C T G C T T T G T C T A T A A C A A C C A A A A T T C A T A A C C A A G A T A T T C C C A T C T C C A T T G T T T T C C A C A A A A G A G T A T T G G A T T G G T T G G T T G G T T G G T T G G T T G G T T A A G T A A A T G G A A T G T T G C T T T G G T A G A G G T T C A A G A C A A T G A T C G G T A C A T A G C A T A A T T G A A T T G A G A T G T G T G T G C T A T T C T T T T C A A G A T T C G A T A T G A C T T T T G A C A G C T A A A A A T G G T G A C G G T A G A T G G G T T G A T A G A T T G C T G T A A T T T G G A A T T T G G T T T T G T C T G A T A G A T G G T C A G G T G C T G A T A T	1533	20

FIG. 36 (cont'd)

Source Organism	Gene name	UniProt ID	Nucleotide sequence	NT length	SEQ ID NO:
<i>Claviceps paspali</i>		G8GV80	ATGCTACTACAGCATCTGGTGTAGGTGTTAGGTACTGCTGTGTTGCTGCGATTTTGCCATTTTGTCGTCAGTGTGTTACAAAGTGTGGTTCACCATTTGGAACCTACATCAGAGGTGAAGGTTACTCTAAGCAATTCGATTCATTACATAGAAGATACG ATTCTCCAGTTATAGAAATCGGTCCAAACCAATTTGCATCTACTACCTGGAACCTACAGAGTTCACGATTTATTTAAAGTGTGGTCTTAAATGGAGAAAGCATAACTCATTTCTACA GACATTTGGGTGGTTAGA TGCTATGGTTGAACCACTATTACAGAGCATATAGAACACATATGCTCCATTTGTCGACAGCAAGAGCTGTGTGATGGTGTGTTGCTTCCAAA ATTGAGAGGTGACTTGGATATGCTCGAGCTAGAATGTAGAAGCATATAGAGATGGTGAAGCTATTAAATAGGCAAGAGTTGCTCAAACTTTTGTACATCAATGAT CTTGCAATCTTA TTTTCAATCGATATTCATATACGATTTGATGGTCATCCATTTTGGAGAGCTTGAACAAATTTGTTGAAGGAACTTGGTGTGTTTAAAGTTA TCCCAATTTGTAGTGTGTTTCTTTAAATTCAGGTACAAAGTGTGAAGATTTAAAGCTGTTTGGAGCTTTTGAAGAGTGTGATGATCAAGAAATTT GAGAGTTCAATCTACTTCAACGACATTTCTACTAGAGATTCACATACAGAGATATAGCAATTAAGAAAGATGGTGAAGCTGTAAAGGCTATATTGTTCC AAAGCCATTGGATGATGTTTAAATTTGTTGCGAGGTGGTGTGCTACTACTACAGCTTACATACAGCATCAGCTATTTTCTATCTTCTTCCCAACTGTTTGTAAAGAC ATTGGTGCAGAAATGGATGCTCATTTCAATCATCAGAGATGAATGGATTACAACAGATACAATTTTGCCATATTGAACGCAATGTTTAAAGGAAACATTGAGA ATCGCTTCCAGTTCAGGTGTTTCCAGAGATTTGTTCCAGAGGTGGTATTTACTTTAGGTTCTTTTTCATTGCCAGAGGTACAGCTGTTTCTTATCATCAAGCT ATTTCTTTTATAGTATATTTCCCATCTCCCATCTTTTACAGCCAGAAAGATGGATTGGTCCAGAGAGCTGGTTAGATAAATGGAGCTTGTCTTTTCAAGAGG TCCAAGACAATGATTTGGTACTTCAATGGCATACTTGGAAATTAAGATGTACATTTGGCTATTTCTTTTCAAGATTCGAAATGACTTTTGCTGGTAAATTTGGGTAGAAGAT TGAGATCGTTGATAGTTGCTGAGCTAATTTGGATGATGTTGAAGTTAGAATTTTGAGACATAGATGGTCA	1503	21
<i>Claviceps purpurea</i>	<i>cla4</i>	M1WEN7	ATGCTTTGCAATGGTTACAACAACTAGACATGAATATCATGGACATGGATTTTGTGACTACATGTATCGCAATGATTTCTCATTGGTTTGAAGGTATCTATAA CGTTTACTTTTCATTAAGAAATATTCAGGTCCAAATGGCTGCA TTGCTGATTTCTACGCTTCTACTGGAACCTGGATTAGAGATGAAGGTTACTCTAAGCAAT TTTCAGATTGCAATGAACAACTACAACTCTCCAATCATCAGAAATCGGTCCAAACCAAGCTTACATACACAAGTTGAATTTTACGATGTTATTTTAAAGTCTGGTTCAAAG TGTTTGAAGGATAAATCATTTTACAAGTACTTCAATGGTTTGGATGCAATGATCGAATCATACAAATACAGAACTTACAGAACACATTTGGCTCCATATACGCTCAAA GAGCAATTGATGGTTTAGCACCAAAATGGATCAGATTTGACTAATTTGCTTCCAGGCAATGATGAGACAACTAAAAATGGTCAACAGTTAATCAATGGCAAAAGTTT TGAGAACTTTTATCTACATCAATGATCTGCTAATTTTGTGATATTTCTTGAACGATGGTGACGAATATCATCCATTTTGGAGCATTTGAACAAATGATGA CTCAATCTTGTTGTTGTTACATATCAATGGTTCCAATGGTTTGTCAATTAATTCAGGTACTCTTTTGCAGAGATTCATCTCTTACATACATTTTCAAAATTAATG ACAGCTTGGAAACGATGAGATATGAGAAAGCAAGAAATCTGAAGAAACAACTACAGAGATTTCTCATACAAGAGATATTTGCTTTAAAGGATGATGATGCTAG AAAGAAACTGCAATTCATACCATAGATGATGTTTAAATTTGCTGCTGGTGGTTCAAGATACAGCATATATACAGCTGTGCAATTTTACCATATTTTGTCTTC ACCAACAGTTAGAGAAAAATTTGGTTGTGAATTAAGATGAACATCTTCAATCATCAGAGATGAATTTGATTACAATGAAGATTCAAAATTTGCCATACTTGAACGCTGTTA TTAAGAAACTTTGAGAAATTCAGTTCAGTTCCTTCCAGAAATTTGTTCCAGAGGTGGTATTACAAATTTGCTCTTTTCAATTTACCAGAGGTACTGGTGT TCAATTAACACAACAAGCTATTTCTTTAATGAAAAGATTTTCCATTTGCCAATTTTACAGAAAGATGGATTTGGTCCAAAGTCTGTGGTTAGATAAATGGAA CATCGCTTTTCAAGAGGTCCAAGACAATGATTTGGTACTACATGGCTATTTTGGAAATTAAGATGTTATCGCATATTTCTTTTCAAGATTCGATATGGCTTTAACTG GTAATTTGTGGTGACCAATTGAGATGGGTGATAGATTTGTTCAGTTAATTTGGATGATGTTGAATTAACAAATTTTGGCTGATAGATGGACA	1521	22

48/60

Source Organism	Gene name	UniProt ID	Nucleotide sequence	N ^T length	SEQ ID NO:
<i>Claviceps purpurea</i> 20.1		M1VZB1	ATGGCAGTCTGTTGTAAGCTCTACTCAAAATGGCAGGTTAAACAGTTTGGTCTGGTTTATTTATCTTTCTGGCTGTGTCAGACACAACATCAAAATTTGCCA GGTCTTGGTACTCAATGGAGTGATTTGGTTTTAGATACCAATGGTCTACGGTAAACAAACTTCTACACATGATTTGGCATGAAGAAATACGGTCCCAATCGTTAG AGTTGCCCAATCAAGTGTGTTGCTGATTTGGAAACCTGTTAAGTCAGTTTGACATTTAAAGAACTACAGAAATCTTAAATTTATTTGAAATTTGTTGGTTTCAAGAC CAATTCACCAAGTTTCTCTACTGCTGATTTGAAATGCATAGAAAAATGGAAGAATTATGGCTCTCAAAATCTTCAATGGAAGTCTATGTTACCAAGTT ACCTCACATGTTGAAATGGCTATCAAGAGGAATCTAAGAGATGAGAGGTTGTTTGAATGTTTAAATGGTGTGTTTGTATTTGACTACAGATGATTTGGTG AATGTCTTTTGGTGAAATCAATCAAAATGTAGAAAAAGGGTAAAGAAGCTCAATACATCGAAGATTTGAAAAAGGTTCTCTGTTCTGCTGATGAAGTCACTTTCCCA TTTTTCAATTTGGCTGATTAAGTAGCATAAAAATTTTGGCATCTGTTTGGCATCTTAAATGCAATTAATGAAGATTTGGTTGAAATTTCAAGACAACTTTTGGGTGAAAT CCAAAAAGATTGAATCTGATGCTACATCAAGATACATTTGTTGAAAAATTTGTTCCAAGCTGAAGAAATAAAGAATCACAATCGAAGATCTTTTGACAAAT GCTCAAACTTTTATATGCAAGGTTCTGATCTACAGCTACTACATTTGACTTATTTGATTTGGTCAATTTGTAAGACCCAGAAATGAGAGATGCAATGTTTGAAGGAAT GAGAAGATCTACCTGGTGAATTTACTGAACCCAGATTGAGAGAATTCGCAATGTTAAATCAACAGTTTGAAGAACTTTAGAGAGTTTACTCTTCAGCTCCAGCATCTTAC CAAGACAGTTTCCAAAGGTGGTGTCTACTGTGGTGTTATTACTGTGACAGAGTACTACAGTTGCTGCACAGGATAACAATGCAATAGAGATCCAGCTATCTCG AAAACCCAGATGTTTGTATGCCACAAAGATGGGCTAATCCAACCTAGAGCTATGAAGAGCCCTTTATGCCATTTGGTAGAGGTTCAAGATCAATGTATATAATCTGGTAA TGTT	1320	23
<i>Claviceps purpurea</i> 20.1	<i>cla-4</i>		ATGAAATGGCATGTGTTTCAATCATATCCACAAATGGCAGGTGTGCTGTTTGGTTGTTCTATCTTCGGTTCTTTAGAAGCATAGCTTCAAGGTGCTTGGCCAAATGGT TTTTAAAAATGGAATAGAAGATAGTTTCCAAAAACATGTAGAGCTAAAGTTTCAAAGGATGAAGATGTTTGGTTGTTGATCGATGTGCTCATATTGGTCCCAATTTGTTAGA GTTGCCACAGATAAAGTTATTTGTGCAGATTTGGATGCTGTTAAGTCTATCTATGATTAAGAAACATACAGAAAACTGATTTTATAAATGATGATTACCAAGACC AATTCACCAAACTTTCTCTACTGTGACGTGATTTGTCATAGAAATGGAAGAATGTTAGCTTCTCAATGTCAGAACTTCTTATGAAACATGATGCCACAAATTA AATCTCATGTTGATTTGGCTATCCAAAGAAATGAAGGAAGATCAAGGCCAAGAGGTGTTATGATGTTTAAATGGTCTTTGTTATGACTACAGATTTTGATCGGTGA ATTATCTTTGGTGAATCAATTCAAATGTGTTGAAAAAGGGTAAAGAATCAATACATGGAAGATTTTGAAGATATTCTTCTATCGGTGCATACAGAGTTACATCCCAT TTTTCTTTTGGTGGCTGATAGATACTCAAAATATTTTGGCATTTGTTAAAGTAAAAATTTCTACTAGAGAATTAAGGAATATTCAGACAACTCAATTTGGTAGATAC CAAAAGAAAGTTGAAGAAATCCAGCAAGCTAAGCAACATTCGTTGCAAGATGTTCCAAGCTGAAAAAGGATGAAGATCGCATCGGTGCACATTTTGGACAA CGCAAACTGTTGATGCTGGTTCGTGATACTACAGATCAACTTGACATATTTGATTTGGTCTGTGTTGAAGAGCCAGATTTGAGAGATGCTGTTTGAAGGAAT TGAGAACATTACCGCCGATTTACTGAAGCAGATTTGAGAGATTTGCCATGTTTAAATAGAACATCGAAGAACTTTAAGAGTTTACTCTTCAGTCCAGCATTTGT ACCAAGACGTGTGTTCCCAAGGTGGTGTCTCATATTGGTGTTTACTGTGTCGAAGGTACTACAGTGTGCACAGCATATACAAATGCAATAGAGATCCAGCAATCTTC GAAACCCAGTGTTTTTTGATCCACAAGATGGGTTAATCCAACATGAAGCAATGCAAGGATCTATGCCATTTGGTAGAGTTTGAAGGTTCAAGAGTTTGTATCGGTATTCAAT TGCGTACATCAATGATAGAGATTTGGCTGCTGTAGATTTTGTAGAAATTTCCAAACGCAAGAGTTTCTGCTAAGAAAGGCATGTGCAGATAGAGATATGGATTTCTACTGT TTACTTTTGTGTTGCTCCAAAGGGTAAAGATGTTTGTGATCGAAGG	1467	24

FIG. 36 (cont'd)

[illegible]

FIG. 36 (cont'd)

Source Organism	Gene name	UniProt ID	Nucleotide sequence	NT length	SEQ ID NO:
<i>Epichloe coenophiala</i>	<i>clad</i>	R9W253	ATGATTTTACCTTGGTTGTCACAAATGAGATCAGTTCTTTGGGTACTATTTTCTTGACATATATTTTGGTATTTTGACITCCAITAGTITTTACACITGTTTACAGATTGTA CTTCCATCCATTGAGAAAAATCCAGGTCGAAGAACAGGTGCTTTAACTACATCTACGGTTCTCTGGAACCTGGATTAGAGATGAAGGTTACTCAAAAATGTTTAAATC CATTGCAATAAACAAATACAAATTTGTATCATCAGATCGGTCCAAACATCTATATCAACCAACAGAAATCTTGATGAAATTTTAAAGTTGGTTCTACTACATGGAGA AAGGATCTTCATTTTACAAGTACTCAATGGTTTGGATGCAATGATCGAACCACTCAACAGAACTTACAGAACACATTTGGTCCCTATATACGCCACAAAGATCAAT CGATCTTCAACTCCAAAATGCGATGTTGGTTTACAGCTGAAAGAAATGGCAAAATCTTTGAAACTGGTGAACCGAGTTAACTGCTTAAAAATTTTGGAACTT TATCAACATCTATGATGTGTTGTTGTTACTACAAGATATTGTTGCTGTAATATGATGTTTACCCTCAATTTTGAAGAGCATTTGATTTGTTGATGACACATCAT GGTTGAGTTTAACTACCAATGAGGTATGATCTTTGGGTTTGAATCCAGGTACATCTTTTGCAAGTTTAACTGCTGCAITCGGTACATTTTGAAGTACTGTAAAGGA ATGGAACGATGAGAAGAAATGGAACAGCTGATCAATGAAGATTAAGAGATTCACATGAAGAGATTTTGGCAATCGATCCAAACGATCAAAATTAATAA AGAAAGTTTCCACATCCATTAGAAGATATTTTAAATTCATTTGCTGGTGGTTCAGATACCTACATCTTAACACTGCTGCTTTTATGTTTGTCTCTCAGAG AGTTCAATCTAAATGGTTGCTGATTAGATCATGCTGTTATTAAGATACAGTTCGATTACAAATTAAGATTTGGCCATCTTAACGCTGTTATTAAAGA AACTTAAGAAATTCATGTCAGTTCCAGGTGTTATCCAGAGATTTGTTCCAGAGAGTGGTATGAAATTTGGGTTCTGTAAATTTGCCAGCTGGTACAGTTGTTCAATTT CTCAATTGGCAATCCATTCACGAAACTATCTCCCATCCCTGATAAGTTTATTCAGAAAGATGTTGGGTGACGATAAGGAAATCAATCGATAAGGTGGAACATCGC TTTTCAAGAGGTCCAGACAAATGTTATGGTACTACATGGCTTACATGGAATGAGATGTTTTAGCATATTTCTTTTCAAGATTCAGTTTAAATTTGACTGGTCTTGG TGGTGACAAATTGAGATGGGTTGATAGATTCGTTTCTGTTAAATTTGGATGATGTTTGAAGTTACTACTGTTAAGGATAGATGGACA	1518	27
		R9VXN6	ATGATTTTACCTTGGTTGTCACAAATCAGTTCTTTAGGTACTATTTCTTGACATATTTTGGTATTTTGACTCCAITAGTITTTACATCAGTTTACAGATTGTA CTTTCATCCAATGAGAAAAATCCAGGTCGAAGAACCTGGTCTTTGACATCTTTTACGGTTTCTACTGGAACCTGGATTAGAGATGAAGGTTACTCAAAAATGTTTAAATC CATTGCAATAAACAAATACAAATTTGTATCATCAGATCGGTCCAAACATCTATATCAACCAACAGAACTTTGATGAAATTTTAAAGTTGGTTCTACTACATGGAGA AAGGATCTTCATTTTACAAGTACTCAATGGTTTGGATGCAATGATCGAACCACTCAACAGAACTTACAGAACACATTTGGTCCCTATATACGCCACAAAGATCAAT TGAATGTTGACTCCAAAATTTGCAATGATGATTTGGTTGTTACAGCTGAAAGAAATGGCAAAATCTATCGAAACCGGTGAACCAAGTTAACTGTTAAAAATTTTGAAGC TTTATCAACATCTATGATGTTGTTACCTTTGACTCACAAGATATTCATTTGCTCAATACGATGGTTACCATCCAATTTTGGAAAGCATTTGATGATGACACAATC ATG6TTGATGATCACTACCAATGATGGGTATGATCTTGGGTTTGGATCCAGGTACTCTTTTGGCAAGTTTAACTGCTGCAITCGGTACATTTTGAAGTACTGTAAAGG AATGGAACGATGAAGATGAAGAAATACAAAATTAAGAACTGCTGTAATCTTGAAGATTTCTCAATGAAGAGATTTTGGCAATCGATCCAAACGATCAAAATTAATAA AAGAAAGTTGTTCCACATCCATTGGAAGATATTTTAAATTCATGCTGGTGGTTCAGATACCTACATCTTATACAGCTGCAITGCTCTTCTTCTGATGTTTGGTCTCTCA GAAGTTCTTAAATTTGGTTGCTGAAATTTGGATCAAGCATCATCTGTTATAGAGATCTTTGCAATTAAGATCCAAAATTTGGCATACTTAAACGCTGTTATTAA AGAACATTAAAGAAATTCATGTCAGTTCCAGGTGTTTGGCAAGAGTTTGGTCCAGAGGTGGTATGAAATTTGGGTTCTGTAAATTTGCCAGCTGGTACTGTGTTTCA ATTTCAATTAAGCAATCCATTCACGAAACAAATTTTCTCTCTCTGATAAGTTTATTCAGAAAGATGTTGGGTGACGATAGAAAGTCAATCGAAAGTGGGAACA TCGCTTTTCAAGAGGTCCAGACAAATGATTCGGTACTACATTAGCTTACATGGAATTAAGATGATCTTGGCATATTTCTTTTCAAGATTCGAGTTTAAATTTGACTGGT TCTTGGTGGTACAAAATTTGAGATGGGTTGATAGATTCGTTTCTGTTAAATTTGGATGATGTTTGAAGTTTAACTGTTAAGGATAGATGGGCA	1518	28

FIG. 36 (cont'd)

Source Organism	Gene name	UniProt ID	Nucleotide sequence	NT length	SEQ ID NO:
<i>Neophodium holi</i>		S5SW12	ATGATTTTACCTTGGTTGCTCAATGGCAATCAGTTCCTTACGTTACCTATTTCTTGACATATATTTTGGTTATTTTGACTCCATAGTTTTCATACAGTATACAGATTAIA CTTTTCATCCAATGAGAAAAATCCAGGTCGAAGAACTGGTCTTGACATCTTTTACGTTTCTACTGGAACCTGGATTAGAGATGAAGGTTACTCAAAATTTGTTAAATC CATTGATTAACAAATACAAATTTCTATATCATCAGATCGGTCCCAACACATGTTTCATATACACACACACACATGATGAAATTTTAAAGTTGGTACTACATGGAGA AAGGATTTCTCATTTTACAAGTACTTCAATGGTTTAGATGCAATGCAACCACTCAATACAGAACTTACAGAACACATTTGGCTCATATACGCAACAAAGATCAAT TGATGGTTTGACTCCAAAATTTGCATGATGATTTGGTTGTTACAGCTGAAAGAAATGGCAAAAGTCTATCGAAAACGGTGAACCAAGTTAAACATTTTGAAGAAC TTTGTCAAACATCTATGATGTTGTACACCTTTGTACTCACAAGATATTCATTTGTCTCAATACGATGGTTACATCCATTTTGGAGAGCATTTGAAATTTGTGATGACACAATC ATGGTTTGATGATCACTACCAATGATGGGTATGATCTTGGTTTGTATTCAGCTGAAAGAAATGGCAAAAGTCTATCGAAAACGGTGAACCAAGTTAAACATTTTGAAGAAC AATGGAACGATGAAGATGAAGAAATACAAAATTAGMAACTGCTGAACTCATTTAGAGATCTTTCGATACAAATAGATCCAAAATTTGGCAATCGATCCAAACAAACGAAATTA AAGAAAGTTTGTCACATCCATTGGAAGATATTTTAAATTCATCGCTGGTGGTTCAGATCTACATCTTATACAGCTGCAATGCTCTTCTTCTTCTTCTTCTCTCTG AAGTTTCATCTAAATTTGGTTGCTGAAATTTGGAATCAAGCATCATCTGTTATAGAGATCTTTCGATACAAATAGATCCAAAATTTGGCAATCGATCCAAACAAACGAAATTA GAAACATTAAGAAATTTCAATGTCAGGTTTCCAGGTTTGTTCAGAGAGTGGTATGAATTTGGGTTCTGTTAAATTTGCCAGCTGGTACTGTTGTTTCAAT TTCTCAATTTGGCAATCCATTTCAACGAAACAAATTTCTCTTCCAGACAAAGTTTATTCAGAAAGATGGTTGGGTGACGATAGAAAGTCAATCGAAAAGTTGGAAACATC GCTTTTCAAGAGGTCGAAGACAAATGATCGGTACTACATTTGGCTTACATGGAATTAAGATGTTGTTTGGCATATTTCTTTTCAAGATTGCGAGTTTAAATTTGACTGGTTC TTGGTGGACAAAATGAGATGGGTTGATAGATTTGTTCTGTAAATTTGGATGATGTTGAAGTTACAATCGTTAAGGATAGATGGGCA	1518	29
			ATGGAACAACTTCACTACAGCTTCTACTGTTTCTATTTTCAGAACTCGGTTTAAATTTGGCAAGATGTCACAAATTAACAAGCACTCTGGGCTTGGCATTTTACT ACATGTTGTTGCTGTTTGTACAGCAGTATTAAGTGGTGTGTTACAGATGTTACTTCCATCCATGAGAAATGTTCCAGGTCCAAAAATTTGGCTGCATTGACAAACTCTA CGCATTTCTACTGGAATTTGGATTAGAGATGAAGGTTATTCAGAGATTTTCTGCTTTTGCATAAGTACTCAACTCACCATCATCAGAAATCGGTCCCAAATTTCTGTTCAITA CAAAACCAACGAGATGATTTTCGATGTTATTTTAAAGGTTGGTTCAAAAGTGGAAAGAAAGATAACTCTTTTACAAGTACTTCAACGGTTTGGATGCTATGATTTGATCCAGC ACAAATATAGAACTTACAGATCACAATTTGGCACCATTATACGCTCAAGAGAGCAAGTTAATGATTTGGCTCCAAAATTTGCAATATTTTGTATCTCAGCTGCAAAAGATG GAAAAATCAATGAACAACTCTGAAGCTGTTAACATGTTAAGGTTTGAAGACTTTTATCAACATCTATGATTTTGCATAATTTTGTCTACATGATATTTCTTTTAAATCGA ATACGATGGTTACCATTTTGGAAAGCAATTTGAACATTTGATGACTCAATCATGTTGGTTGTTTATTCAGGTACATCTTTTGTCAAGTTTAAATCTTCTTACACTAC TTTTATGAAGTACTGTAAGGGTTGGAAACGATGAAGATAGAGATAGAGATACAAAGATTTGATGAAAAACCAAGAAATGAGAGATTCACACATGAAGAGATAGCTTAGCTATGA ACTCAACGATTGGCAAGGATACGTTGTTCCAAACCATTTGAACGATATTTTAAATTTGTTGCGAGGTGGTTTCAGATCTACATCTTACACATAGCTTGTGCTTTC TTTTATATCTTATCTTCCAGAAATATATGCAAAATTTGGTTAAAGAAATAGATGAATGTTGCTTTTATAGAGATCTTTTCGATTAACATTAAGAATCAAAATTTTGCCA TATTTGAATGCTGTTTAAAGAAACATTAAGAAATTTCTGTCAGGTTGTTGCAAGAAATTTGTTCCAGAACTAGCTACTACATTTGGGTTCTGTTTATTTGGCA GCTGGTACTGCTGTTTCTTATTTCTCAACAATCAATTTCTTTCATGAACAACTCTTCCCACTCAGCAAGAAAGTTTATTCAGAAAGATGGTTGGGTAAATGAAGCTCAAG ATTGGATAAGTGGAACTGTCATTTTCAAGAGGTCGAAGCAATGATGTTGGTACTTCTTAGCTTACTTGGCAATTAAGATGTTGTTTGGCATACTTTTGTCAAGATTCG AAATGGCTTTGACTGGTAAATTTGGTGGTACAGATTTGAGATGGGTTGATAGATTTTGTCTGTAAATTTGGATGATGTTGAAGTTAAATTTGTGAGAGATAGATGGAAT	1536	30
<i>Metarhizium acridum</i>	<i>clad</i>	E9EAT5			

GGTAAAGATGTTTGATCGAAAGCATCT

GGTAAAGATGTTTGATCGAAAGCATCT

[illegible]

54/60

PCT/SG2022/050840

FIG. 37

Source Organism	Gene name	UniProt ID	Amino acid Sequence	AA length	SEQ ID NO:
<i>Aspergillus fumigatus</i>	<i>dnalW</i>	Q50EL0	MKAANASSAEAYRILSRAFRDNEQDLWWHSTAPMFAMKILETANYTTPCQYQLITYKEVPSGCGYPTNSAPRWLSILTRYGTPELSINCSINRYTIFEPINQHTGT DKDPFNTHAIWESLQHLPIEKSIDLEWFRHFHDKDLTINSEESAFIANDRLVGGTIRTCNKIALDLKGRFAKTYIYPALKAVVTGKTHIELVFGSVRLAVREPRILPPLN MLEEYRSGSKSTASPRVSCDLTSPAKSRKIKYLLEQWVSEAMEDIWLTGGRRDASTLEGSLVRELWDLQLSPGKSYPPYLPGLVPIPERLPIMANFTLHQNDPVP EPQVYFTTGMNDMAVDALTTFFERRGWSEMARYETTLKSYYPHADHDKLNYLHAYISFYRDRTPYLSVYLQSFETGDWAVANLSESKVKCQDAACQPTALPPDLSK TGYYVSGLH	459	37
	<i>easF</i>	Q4WZ60	MTISAPPIIDIRQAQLESSIPDQVVEGLTKVEKTLTALLFYSTKGIGHWNHRSHADFYPRHEELCLKAEASKMAASIAQDSLVIDMGSAEMDKVILLLEALEEQKSKSYCAL DLSYSELASNFQAIPVDYRFRHYVFAALHGTFDGGLHWLQNPADIRNRPRIILFGITIGNFSRDNAASFIRNAGSALSTSPGTQSIIVSISDCKLPTKILRAYTADGVVPFALAS LSYANSILFHPKGDRIKIFNEEDWYFHESEWNHALGRHEASLITQSKDQLGAPLETIVIVRRDEKIRFGCSKYDKAERDQLFHSAGIEDAAVWTAPDCDVAFYQLRLIN	339	38
<i>Claviceps purpurea</i>	<i>easC</i>	M1WA44	MASEVSVASSGSEHSGAQKCPFDQGLSSMDSDSRLRDLISRENRKIPERAVHARGAGAVGEFEVTHDVSIDICIDIMILGVGKTKPCVVRFTTTLERGSAESVRDVKG MAIKHFTQDGNWDDWVCLNIPMFFRDPSPKPDMMVHAQRDPDTTNVANPSRWWEFVCNNHETLHMVMFQFSDFGTFMFDYRSMGSAHYAKVMWMPDGSWKYVH WFIASDQGNFETGHOAKIGADDAESATRDLYOSLERGEYPSVTKVQVDPDAPKPLNLDVTKHNLGNVPPDIDVPGRTLIGKTLKKGPDQDYEEIEQLAFSPS RLVHGVASEDPMLOARLFAYPDAQKHLRIGPNLIDLPAWRTKILADGSRPEKAEAMAPQKVPSEHADWVSQVKSSSWSEPNETDYKFPREFWKAPLRLKEAFQNSLV VNMAKSVSCVPADMRRQKVYSTLAIADLADRVRTMTTEEVE	473	39
	<i>easD</i>	Q4WZ66	MASVESRIAITGGASGIGAAATCRLLAERGAALVCVCDISPKNFDLKISIKKINPSTKVHCATVDVTSSVEVRQWIEGIDFGLHGAVNAAAGIAQAGAGMRNTPTIAEEVDE EWTRIMNTNLNGVYCTREEVRAMKGLPATDRSINVNGSIASVSHMPDYVAYGTSKACAYFTTCVAADAEPGLIRINNVSFVNTNTPMLPQFAPMAKTFEEIESYKKE GLSIEAEDVARTIVWLLSEDSRPVFGANINVGACMP	261	40
<i>Claviceps purpurea</i>	<i>easG</i>	M1WEN5	MTVLLTGGTGRATAKIHAGIFRQTNVPELVASRSSAGTAENIRKFDWLDEETFPNALSDVDQGMKPSVWMLCPPLVDLATPVKIFDFAVSQNVKKFVLSASVQKGGPA MGKIHGHLDISKDVTYTLRPTWFMENFTKGEIQCEAIRDSTVYSATENGKIPSPVVDIARVAACALTAETLKNSDHILQGPDLITYDEVAQALTVGLGRKITHTKMTEG ELAEKIMEEGVTPEEATYMHAAIDMSMIKSGSEFVVSDVEKWEVTGVKPRGFNFALSEKAAWRANK	290	41
	<i>easE</i>	- / GenBank: P3133859, 1 (for <i>A. indologenus</i>)	MGQSRGILGGVRQLILVILVGAYLSRLSAVDDDRHDCRCRPGPCWPTVSHWSTINESIGGALAHVKPIAHVCHQSGQDSSACEQVLCESIDSKWRASHITGALQDWWV EGGAESNQTCYLRSGPAGSCHQGRIPLYSAAVKSASDVQKVDFTRQHNLRIRNTGHDGSGRSGDPSVEIHTHHLSVQYHPNFRPAGSSRQSPAGQPAVTVGA GILLGLDYARGASEGWVGGECPTVGAAGGLQGGGVSSWLSYHGLAVDNVLEVEVYAKGEWIANAHQNPDLFWALRGGGGGTGVVTCATLQVHPDLPVSVD AVVTGSRADATFWSHGAALLRALQFLNNHGTAGQFLRNTDDDTVQASLTMYFSNLTPYAVADERMDPLRRALEHNGHPYQLTSRFLPQISSTFRHTADRYPDYTGILM GSVLVSLDLFNSATGPAAALQHFARLPMTPDDLLFTSNLGGRVSLNRDPASTAMHPGWRDAAQLNFVRGVGAPSLAAKATALHELTVQMARLYELEPAFQISYRNIG DPSERRSREVVWGSNNYARLVEVKRRWDPEGLIFSKLIGDGDWDADAEGMCRQTRQGAWNVAVKWQSLGSLASVW	621	42
<i>Aspergillus japonicus</i> / <i>Aspergillus indologenus</i>					
<i>Neophodium loli</i>	<i>easE</i>	S5TDB9	MRHFVTVVGGFLSWGFLSLQDPPSCRPWPCPDSDHQWTSINASIDGNLVHVQVGVSCDHPHYDAVACGDVIDLSRNSGWRASNPATLQDWIMETSGDNE SCLLVSSSERPQEIPCHQGRILPYSAAVKSTAHVQGVIRFAKHNLRLVKNITGHDATGRSAAPDSLQIHTYFKDIHYDNFLVHGDATGSGPAAVTILGAGVHVSEVYKHGI DHKYSVGGECPTVGVGGFLQGGGVSSWGSFTRGLAVDNVLEVVYANAEIVANEIHNQNDLFWALRGGGGGTGGVVTQATVRAFPDDPTVSTLVLSSTRADTSF WKAISRLSLRSCNQVQWVHQDLITRPSVDILNAGLTHFNSNMVTHAETTLHQPHIASLESDQSLTSLTSKFVANINSLDADLHPRGIGTLQTSMMISNELFGSGEGLT VAQVFEKLPIDPNLDTSLNIGGCCAANKGLDTAHPAWRSSAHILTVYRSVFEPSIEAKKALKETNKYMPILYSMQPSFKYSYRNLDGDPNEKNYQEVFWGEEKYKRLASIK AKLIDPDGLFISKLVGSGEDWDTEGMCYCPQNRVSQPIRSIKLYFLSLVKOT*	606	43

FIG. 37 (Cont'd)

Source Organism	Gene name	UniProt ID	Amino acid Sequence	AA length	SEQ ID NO:
<i>Epichloe finkii</i>		R9W1Q5	MRYVTVFMGLLFSWGFISLLQGRPSRCRPWEACWPDSHOWTISNASIDGNLVHVQPVGSVCHDPEYDAVACGDVLDLSRNSGWRASNPATLQDWIWIETGSGDN ESCLLVSSERSQEPCHQGRPLYSAAVKSTAHVQSVVRFAKDHNLRVKNKTGHDATGRSAAPDSLIQHTYFLKDIHYHDNFQAQGDATGSGPAVTLAGVMHSEVYKH GIDHKYSVVGEGCPTVGAVGGFLQGGGVSSHSFTKGLAVDNVLEQVVTANLVANHEHQNDQFLWALRGGGGGTGGVVTQATVRAFPDDPTVSTLVVTSRADTTLL WEKAISRLSILRFCNQNVHIGQLITRPSDILNAGLTILHFSNMVTVSHAEITLQPHIASILREIQSAALSCKFVANINSELRDADIHPRGIGTLQTSMMISDELFSGSEGPS TVAQVFGKLPIGNDILFTSNLGGRIANAKALDTAIHPAWRRAAQLVTVRAVGPSPGIEGKLSALENLTSQDIPILYSVDPNAKSYRNLGDPQCEQFQARYWGLDNYARLAAIKA KAKLDPDGLFISKLVGSEHWDAGMICYQPCQNRVSQPLRSLOQLSVLQDTLE	605	44
		G9FN46	MHRLGPVACITLAGVFWAQSGHCRPWEPCWPSTAQWEAFNESIQGNLVRIRPIASVCHGLEIDAACANLSNLIVDSGWRASNPSTLQDWVWESGVAEEACH MTSPGEQRGSACHQGRPLYSVVVQSTSDIQSSVRFASDHNLRVKNKTGHDACAGSSSPNSFQJHTNLLKSIFHENFVARGSTTCSGPAVTLAGVMHSEVYAHGVE NGYTIVGGECPTVGAVGGFLQGGGVSSHSFTKGLAVDNVLEQVVTANLVANHEHQNDQFLWALRGGGGGTGGVVTQATVRAFPDDPTVSTLVVTSRADTTLL TEGVRELLRLQYFNQHLHPQQLVWTGPEKDSIQATLELHFANMTDEAHAMKLSELRLPILSIHHISTISYRVQKRASSELRMKPDYPPQVQILQGSVLSTAVFQSAEGPTL IARFSELTYSRNDILFTSNLGGRIANAKALDTAIHPAWRRAAQLVTVRAVGPSPGIEGKLSALENLTSQDIPILYSVDPNAKSYRNLGDPQCEQFQARYWGLDNYARLAAIKA KWDPNGLFTRSGVGSSEDWDVEGICRKSRLAQALELLKGPYILE	602	45
<i>Epichloe elymi</i>	<i>ease</i>	K0HDR9	MRYVTVFMGLLFSWGFISLLQGRPSRCRPWEACWPDSHOWTISNASIDGNLVHVQPVGSVCHDPEYDAVACGDVLDLSRNSGWRASNPATLQDWIWIETGSGDNE SCLLVSSERSQEPCHQGRPLYSAAVKSTAHVQSVVRFAKDHNLRVKNKTGHDATGRSAAPDSLIQHTYFLKDIHYHDNFQAQGDATGSGPAVTLAGVMHSEVYKHG IDHKYSVVGEGCPTVGAVGGFLQGGGVSSHSFTKGLAVDNVLEQVVTANLVANHEHQNDQFLWALRGGGGGTGGVVTQATVRAFPDDPTVSTLVVTSRADTTLL EKAISRLSILRFCNQNVHIGQLITRPSDILNAGLTILHFSNMVTVSHAEITLQPHIASILREEQSAALSCKFVANINSELRDADIHPRGIGTLQTSMMISDELFSGSEGPSTVA QVFGKLPIGNDILFTSNLGGRIANAKALDTAIHPAWRRAAQLVTVRAVGPSPGIEGKLSALENLTSQDIPILYSVDPNAKSYRNLGDPQCEQFQARYWGLDNYARLAAIKA LDPDGLFISKLVGSEHWDAGMICYQPCQNRVSQPLRSLOQLSVLQDT	603	46
		I7DFY5	MYNLLGPVACITLAGVLVWLSHGHCRCRPWEPCWPSAAHWKAFNESIQGNLVRIRPIASVCHGLEIDAACANLSLVDSGWRASNPSTLQDWVWESGNTAEETCH SMTSPGEQRGSACHQGRPLYSAAVKSTAHVQSVVRFAKDHNLRVKNKTGHDACAGSSSPNSFQJHTNLLKNISFHENFVARGSTTGYGPAVTLAGVMHSEVYAHGA EKGTYILGECPTVGAVGGFLQGGGVSSHSFTKGLAVDNVLEQVVTANLVANHEHQNDQFLWALRGGGGGTGGVVTQATVRAFPDDPTVSTLVVTSRADTTLLFWT EGVRELLRLRDFNLLHPGQLVVRGPEKHSIQATLELHFANMTDEAYAMKLSELRLPILSIHHISTISYRVQKRASSELRMKPDYPPHYGILQGSVLSTAVFQSAEGPTLLA RKSELTMRFSDILFTSNLGGRIANAKALDTAIHPAWRRAAQLVTVRAVGPSTKGLSTLENLTSRDTPLYSIDPSAKISYRNLGDPQCEQFQARYWGLDNYARLAAIKAKW DPNELFTRSGVGSSENWDVEGICRKSQDHAQAFALLKVGLSH	600	47
<i>Claviceps fusiformis</i>		A8C7R9	MYRLGLPIACIALAWFFTWAPSGRCRCRPWETCWPVSADWSALNESMQGNLIRIPVASVCHGSEYEAACAANVMVDSGWRASNPRTLQDWIWIETGNTAQES CFDFTTWPGYHHRSTDCHQGRPLYSAAVESTSDIQSCVKFANHHNLRVKNKGHDATGRSSAPHSFQJHTNLLSHENFVRPGSTTGHGPAVTLAGVMHSEVYAHG VKNAYTILGECPTVGAVGGFLQGGGVSSHSFTKGLAVDNVLEQVVTANLVANHEHQNDQFLWALRGGGGGTGGVVTQATVRAFPDDPTVSTLVVTSRADTTLLTMF WTEGVRELLRVQHFNMDHIPQQLVMTPTDTSMDQATLELHFANMTDEAHVTLNLSQGLSTLENLTSRDTPLYSIDPSAKISYRNLGDPQCEQFQARYWGLDNYARLAAIKAKW GQSHVASKLSQLPLGSDIMFTSNLGGRIANAKALDTAIHPAWRRAAQLVTVRAVGPSTKGLSTLENLTSRDTPLYSIDPSAKISYRNLGDPQCEQFQARYWGLDNYARLAAIKAKWDPHFMKSLG VGSENNWDVEGICRKSILGPFVERISAILKIERWKN	581	48

FIG. 37 (Cont'd)

Source Organism	Gene name	UniProt ID	Amino acid Sequence	AA length	SEQ ID NO:
<i>Aspergillus lentulus</i>	<i>casE</i>	A0A0S7DKV5	MTLIFSHLGAFLGCIWLFSGTLTCRCPGEPWPAASEWIALINTILRGDLLEVRVPAHYCHDPYYPACQNLADLARQSGWRASQPGALQGWIWETGRTDEITCHAHSPRGARCHQGRIPLYSAAVESVDQVAAVRFAQRRHVRVLRVNTGHDTAGSSAPDSQIHTHRMKQIEYHNDNFRVSSDIDQGPVAVSGAGVLLGEMVARGARDGWWWVGGECTPGATGGFLOGGGVSHFNGLAVDNVLEFVATKAEVNVANSSQDLFWALRGGGGGTGGVVTATMRVHNDPVCISEAVVSGHNNLSLWTRGVAGLFSVLRSFNQGGIPQGFILQPLSEHQVNASLTLYSMNATTRAAENMLSVKVELSTLPLFASRCLSKVSDVLRKESDILPANYGILTGSVLVSEDFNSEQGPILHLANQLVQFPMGPGDILLFTSNLGGNVTANTEKHTDTSMHQAWRQAHLINYRVSVTPTAQEKARSLEELHVSQMRKLYNIEPGRFVSYRNLGDHLEGDAPQVYWGANYRRILLEKRWDPEDLFSVQLGVSGEGWADDQMSTMTMSTPTPIDIRQSKFESSIP	601	49
			MRHFVTFVVVGHLLSWGFLSSIQDPPSCRCRPWPCWPSDSHQWTSINASIDGNLVHVQPVGSVCHDPHYDAVACGDVIDLSRNSGWRASNPATILQDWIWFETGSGDNE		
<i>Epichloe coenophiala</i>		R9W261	SCLLVSSSERPQEIPECHQGRILPLYSAAVKSTAHVQGVIRFAKDHNLRVKNKTGHDAATGSAAPDSLIQHTYFLKDIHYHNDNHLVHGDATGSGPAVTLGAGVVHVYKHGIDHKYSVVGGEPTGVIGVGGFLQGGVSSVSGFTRGLAVDNVLEQVVTANAEVLVIANEHQNDQLFWALRGGGGGTGGVVTQATVRAFPPDPTWVSTLVLSSTRADTSF		50
			WVKAISRLSILRSCNQNVHQLITRPSVDILNAGLTLHFSNMNTNVLHAETLLQPHIASLSEDDQSTLTLSKFVANINSELRLDADIHPRGIGTLQTSMMISNELFGSSEGPLTVAQVFGKLPIGPNDLFTSNLGGCAANKGLDTAHPAWRSSAHLVTYVRSVPSIEAKKLAKETITNKYMPILYSMQPSEKVSRYRNLGDPNEKNYQEVFWGGEKYKRLASIKAKLDPPDGLFISKLVGSGEDWDTEGMCYQPNRVSOPLRSIKLYFLSVLKDT	605	
<i>Neotyphodium lolii</i>		S5TC14	MSTSNLFTPLQFGKCLLQHKLVLSPMTRFRADNCGVPLPVYKTYTCORASLPGTLLTTEATASRRARGFPNVPGWISQEQIAGWKEVVDAVHAAGSYIWLQLWATGRAAEVGVKANGFDLVSSSAVPVSPGPTPRALSDEINSYIGDFVQAANKNAVLEAGDFGVELHGANGFLIDQLQSPCNQRTDQWGGGCIENRSRFGLETRRVIDAVGKDHVGMKLSLWSTFQGMGTMDLLIPQFEHFIMRLREIGIAYLHLANSRWVEEDPTIRTHPDIIHNETFVRMWGKEKPVLLAGGYGPESAKLVWDEYSDHKNIGVVFGRRHYISNPDLPFRLLKMGGLPLQKYNRETFTYIPFSDGEGYLDYPYSEETENKKQAVLA	380	51
			MSTSNLNELPFGTSVLKHKVLSLPMTRFRADNCGVPLPVYKTYAQRASVHGTLLITEAIVCAICPRAKGFNPNGIWHDSQJAAWKGVVVDEVHSGSVIWLQLWATGRAVDPDLTSLNGLELKSSEVPVAPGEPTRPLSEEEIGSYIFDYAQGAKNNAVLEAGDFGVELHGANGFLIDQLQSCNRRITDQWGGGCIENRSRFGLETRRVIDAVGNDHVGVKLSPWSTFQGMGTMDLLIPQFEHFITRLREMDIAYLHLANSRWVEEDPSIKTHPDVHNETFVRMWGKEKPVLLAGGYNPDSARLLVDQTYSEQNNVMVWVFGRRHYISNPDLPFRLLKMGGLQRYNRDFTYIPFSGEGYLDYPCKEYLKQGDQETTVAA	380	52
<i>Epichloe coenophiala</i>	<i>casE^{Δ-180}mutant</i>	R9W1H0	MSTSNLFTPLQFGKCLLQHKLVLSPMTRFRADNCGVPLPVYKTYTCORASLPGTLLTTEATASRRARGFPNVPGWISQEQIAGWKEVVDAVHAAGSYIWLQLWATGRAAEVGVKANGFDLVSSSAVPVSPGPTPRALSDEINSYIGDFVQAANKNAVLEAGDFGVELHGANGFLIDQLQSPCNQRTDQWGGGCIENRSRFGLETRRVIDAVGKDHVGMKLSLWSTFQGMGTMDLLIPQFEHFIMRLREIGIAYLHLANSRWVEEDPTIRTHPDIIHNETFVRMWGKEKPVLLAGGYGPESAKLVWDEYSDHKNIGVVFGRRHYISNPDLPFRLLKMGGLPLQKYNRETFTYIPFSDGEGYLDYPYSEETENKKQAVLA	380	53
			MSTSNLNTVYVPGKVLNHHKVLSPMTFRADDNCGVPLPVYKTYAQRASVVRGTLLVTDAVACPRTKGFNPVPGVWKNKQJAAWKEVVDEVHSGKSFVWLQLWATGR		
<i>Claviceps purpurea</i>		M1W0Y0	AADLEALTSCGLKLESSEVPVAPGEPTRPRALDEIQIYLDVYVQGAKNNAVHGDGVEIHGANGFLVDQFIQSSCNRRITDQWGGGCIENRSRFGLETRRVIDAVGHD		54
			RVGMKLSPWSTFQGMGTMDLLIPQFEHFITCLREMDIAYLHLANSRWVEEDPSIRTHPDHFNQTFVQMMWGKKRPILAGGYDPDSARLLVDQTYSDRNNVLVFGGRHYISNPDLPFRLLRMGIALQKYNRDTFYIPCSGEGYVYVPCKEYLDQADEAAVAG	380	

FIG. 37 (Cont'd)

Source Organism	Gene name	UniProt ID	Amino acid Sequence	AA length	SEQ ID NO:
<i>Botrytis cinerea</i>	<i>clo4</i>	M7UEF9	MHRDYNSSVIRIADPMVHNDPFFSTFNRTTYLKDPSLYKQISLINESIVSMILDPHEHLRQRQVNSMFSTKAVDSMAPDVAIAQKAANMMKRGEEKRPVDMYRLSRSISSEVLFKILFDEPMHLLDSQEQPELLAGLDLFTGLTFWLMRAFPVIGWALNLPQSLTRKLPGEKSLRDCDCERWARMVARQNSREITKNDDSSNTVFDLLLTPTTPEPRSEFSPDILVDEAFLEAFVAGDTTGNITTNNAFYLLSSPSYSKILDELTAHGTHSETFDCCNVVQRLPLTA/VKESMRITHTVGGVLPRIVPDGVDGVMFMPAGTISQSIHS LHHNASVPSPPEKFDPERWIKDEEKELEKYAFPSKSRACLGMINLANQETVWVIAFCARFEIELYDTSRSMEWADRGNTVNRSPVKLLVKRDRWANN	440	55
<i>Claviceps fusiformis</i>		A8C7R4	MILLWLYQALPTSLTRILLTAGLCVPCALVIHGIYNLYFHPRLNV7PGPKLGALTDLYAFYWNWIRGVYSKQFDRWHKHYNSSVIRIGPNNDVHTTQVELYDVVHKAGSTWLKDKSPYKHFGGLDAMIDPREYRTRTHLAPLYSQRAVDGLVSKMDDDLAIGCQKTTKMAENGKAVNMARVLTLSMSILYNLFMSDILWECNDYHPFLEAFEHMAQIWFLSPYPLATCLSLIPGTSIARLAPSWTTFMNSCAAACWDEDAKQASDDQSDIRDSKRYALKHTDANDKSIIPAPLDFLFSFIAGGDTDTTATGCAFFYLSSPSVCRKLVKELDENASFRINGLDYHKKIQTLPYLNAVIKETLRSVPVPGCLPRVVPPEGGITVGSFHLPGATALSTTQQAISLNQDIFPSPCFSPERWIGPAAAGLDKWNVA/AFGRGRQCIGTTLAYLEIRCVAVYFSSRFDMTLTAKNGDGRHWVDREAVNLDTVLEVLSDRWSGARY	511	56
<i>Claviceps paspali</i>		G8GY80	MSTTASWSWVLTACVAALIPFVAAYVNWVHHPLRTVPGRLAAVTDYAFYWNVIRGEYSKQFDSLHRRVDSVPIRIGPNHLHTIQPKFYDIIFKVGSKWRKHNSFYRIHFGGLDAMVEPHYRAYRTHIAPLYAQRVADGLVPKLRGDLDM5AARMLEAYRDGEANMARVAQTLLSTMILHILFSDIPLYDCDGHHPLEAVEQLKETWFLGYPQLLAVLSLIPGTRFARLNAWVWTTFTKYCTSWYQEDLRVQSTSNESHSTRDHTKRYLAIKERDGDGKKSIVPKPLDDVFNFVAGGADTTATTYTTASAIIFYLSSPTVCCKTLVAELDAHSSIIIRDELNYNRIOQLPYLNAVVKETLRIAPVPVPGCLPRVVPPEGGITLGSFSIPAGTAVSLSHQAI5FNDDIFSPHSFRPERWIGWPEAAAGLDKWNVA/AFSRGPRQCIGTSMAYLEIRCTLAYFFSRFEMTTLTGNGRRRLRVVDRFVAANLDDVEVRLHHRWS	501	57
<i>Claviceps purpurea</i>		M11WEN7	MSLQW/LQQTRHLSWVWILLTICALISPLVLKGIWVYVHPLRNP6PKLAALTDFYAFYWNWIRDEGYSKQFSRLHEQYNSPIRIGPNNVHTTQVEFYDVVFKSGSKWLKDKSPYKYNGLDAMIPEYQYRTRTHIAPLYAQRADIDGLAPKLRSDLTNSASGMIMRQTKNGQTVNMMAKVLRTLSMILHILFSDISLNDGDYHPFLEAFQQLMTQSWLFVTPYPMVPMVLSLIPGTSFARFNSSYTTFSNVCTAWNDEDMRKQRESEEQSTRDHTKRYLSLKDDARKKTAIPYPLDDVFNFVAGGADTTATTYTTACAFYHILLSPTVRELNLVWELDEHSSIRDEFDYNKQNLNPLYNAVIKETLRSVPVPGSLPRIVPQGGITGTSFSLPAGTGV5ITQQAISFNEKIFPLPHSFLPERWIGPKSVGLDKWNIAFSRGRPRQCIGTTIAYLEIRCVAVYFSSRFDMALTGNGGDQLRWVDRFVAVNLDVVELQILADRWIT	507	58
<i>Claviceps purpurea</i> 20.1		M11VZB1	MAVHWKSVSQLAGTLVLALFYFELVLSRPTSLPGPWYSKWTDLVFRYQWFGYKQJTYTHDLHKYGPVIRVAPNQVAVADLTQVSVYTIKETYRKTIFYELLVSRPIQTVFSTADVELHRLKRLIMASQMSSESLKSMPLQVTSHVELAQRMKESKDRGVIDVFKWGLFMTTDDVIGELSGESQMLEKGGKTKQYIEDLENVSSVSADRTFPLFFHLADKYDKILPLFRSKAINRRLVEYSRQSLGRYQKQVESDATSAKYTFVEKLFQAEKDNKMTFEDILTNAQTFIAAGSDTTATTLTYLW5ICKRPLRDALLKELRTPGDFTEPDLRELPLFNQTVTEETLRVYSSAPASLPRAPVPGGAHVGGYLSEGTVAQAQAYTMHRDPAIFENPDVDFPQQRWANPTRAMKEAFMPFGRGSRSMYKSGNV	440	59
<i>Claviceps purpurea</i> 20.1		M11W6N5	MKLVHVQSVPCLAGVAVLVVHFGSL5EAYVQGAWPMVFKMDPRRYPKTCRAKYSKDE5DWLLIDVAHIGPIRVAPDKVIVADLDVKSITYTIKETYRKTDFYKLITSRPIQTIFSTGDVDLHRKIRRLIASCMSSESLKTMMPQIKSHVDLAIQRMKEESKRGVIDVFKWGLFMTTDDIGELSGESQMLEKGGKKNKQYIEDLE5SIAAYRVTFPF6WLA DRY5NLIPLFKGKISITRRLKEY5RQSLGRYQKQVESDATSAAKQTFVAKMFOAEKDDKIAFGDILTNAQTLVAGSDTTATTLTYLW5VCKRPLRDALLKELRTPGDFTEADLRDPLFNRTIETTLRVYSSVPALLPRAPVPGGAHIGGYLSEGTVAQAQAYTMHRDPAIFENPDVDFPQQRWANPTKAMKEASMPFGRGSRVCIGIHLAYIELRLAAARFLEFPNARVSAKEGMSDRDMDSTVTVFLMSPKGRKCUIE	489	60

FIG. 37 (Cont'd)

Source Organism	Gene name	UniProt ID	Amino acid Sequence	AA length	SEQ ID NO:
<i>Colletotrichum gloeosporioides</i>		T0KET3	MALTSVSSSSQLLLSYISIGLLYRLFFHPLRNIPGPWCAAAATSWYEFYQDVLDGHYKDYPELHAKYGVPRVSRVHVHYNPEYKEVYNGTKYTKDPDYSVMIDPEEHKQRRNTVKSICSTRQMDQLAPSLDVVRAMNRAQBSYDRGAPLNIAQLWSSVTVDTIMSVLFDRCMNFDSEDEMPPLDAMTKFADNFLTKEHFLIMNRLAVGLPMSIAGMIIPGFAAFKQCEWGEIEDKQAKGLTTASDGRPTYFDLLRSNAKMPNGREALVDEAFVLCFAGDTTIGIGLSLGYLLKNPEKLNKMLDELMTVKTSAEGLFEYRELCLNPLYLRLSSPVGITPRVPAGGVYAGHFLPEGSTVSCAIRTHIDNPDIFFPERFERPWLGEQGWALERYFVFSKGPMSMYICLANLFTFRNMSLYTKDDTTTQWADGPAARIESVKVNIASVKM	497	61
		T0KX90	MALKLGGQSLSADAPRIFVGLVYAVGLVAYRLLFHLRNPGRPWAATWYEFYQDVLDGHYKDYPELHAKYGVPRVSRVHVHYNPEYKEVYNGTKYTKDPDFFQSGGKIYSIIMLIDPEAHKQRRNTVKSIFSPKQMDQLAPVLDVVKRAMARAQBSFEKGEAISMQPFWQAVTVDTIMPLFNRMNMLVDQDEFFPFLDIMEKFAQNFLTKHFPFLIHLAMAPMSIAQKLLPGVAQFRHQCEWQIEQEDKQAGIDTASDGRSTYFDTLTKNTKMYHKLSRALVDALALCFAGDTTISFGLTFGTYYLRLHPDKLEKVLEELKTGTGNSGLVEYRDISSLPYLSATIKELRLSSPVGPIIPRRVPKGGATVDGYLPEGTTVSQTLRTHDNPDLFAEKEFIPERWLGEQGWALERYFVFSKGPMSCLGMNVAVVEMVLSIANFFSRFMSLYKDTETAIWIDSAARIWKPIRVKIDSIKEHP	511	62
<i>Epichloe coenophiala</i>	clad	R9W253	MILPWLSQLRSVSLGTFLTLVLVLTFTSVRLYFHLRKPGRPTGALTTFYGFYWNWIRDEGYSKLENPLHKQYNSCIIRGNPHVHINQPETDEFKVGSTWRKDSFYKYFNGLDAMIEPTQYRTYRTHLAPYAQRSIDSTPKLHVLDLVYTAERMAKSIETGEPNVNKKILRTLSTSMMLYLSQDILLSEYDGYHPFLKAFELLMTQSWLMWNYPMMGMILGLIPGTSFAKFNAAFGTFLKYCKEWNDEDERIQKLETAESLRDHSMMKRYLAIDPNQIKKKVPHPLEIDFNFIAGGSDTTSYTAACAFYVLSSEVHLSKLVAEILDHASSVKIDTFDYNKIQNLPLYLNAVIKETLRISCPVPGCIPRVVPEGGMNLGSLNLPAGTVVSSISQLAIHFNETIFSPDKFIPERWLGGDDKESIDKWNIAFSRGPQCIGTTLAYMELRCVLAYFFSRFEKLTGSCGDKLRWVDRFVSVNLDVDEVTVKDRWT	506	63
<i>Epichloe coenophiala</i>		R9VXN6	MILPWLSQLRSVSLGTFLTLVLVLTFTSVRLYFHLRKPGRPTGALTTFYGFYWNWIRDEGYSKLENPLHKQYNSHIIRGNPHVHINQPOAFDEFKVGTTWRKDSFYKYFNGLDAMIEPTQYRTYRTHLAPYAQRSIDGLTPKLHDDLVTYTAERMAKSIENGEPVNMVKILRTLSTSMMLYLYSQDIPLSQYDGYHPFLFAELLMTQSWLMINYPMGMILGLIPGTSFAKFNAAFGTFLKYCKEWNDEDERIQKLETAESLRDHSMMKRYLAIDPNNEIKKKVPHPLEIDFNFIAGGSDTTSYTAACAFHVLSSSEVHLSKLVAEILDHDOASSVIRDTFDYNKIQNLPLYLNAVIKETLRISCPVPGCLPRVVPVEGGMNLGSLNLPAGTVVSSISQLAIHFNETIFSSPDKFIPERWLGGDRKSIEKWNIAFSRGPQCIGTTLAYMELRCVLAYFFSRFEKLTGSCGDKLRWVDRFVSVNLDVDEVTVKDRWA	506	64
<i>Neonophodium holti</i>		S5SW12	MILPWLSQLRSVSLGTFLTLVLVLTFTSVRLYFHLRKPGRPTGALTTFYGFYWNWIRDEGYSKLENPLHKQYNSHIIRGNPHVHINQPOAFDEFKVGTTWRKDSFYKYFNGLDAMIEPTQYRTYRTHLAPYAQRSIDGLTPKLHDDLVTYTAERMAKSIENGEPVNMVKILRTLSTSMMLYLYSQDIPLSQYDGYHPFLFAELLMTQSWLMINYPMGMILGLIPGTSFAKFNAAFGTFLKYCKEWNDEDERIQKLETAESLRDHSMMKRYLAIDPNNEIKKKVPHPLEIDFNFIAGGSDTTSYTAACAFHVLSSSEVHLSKLVAEILDHDOASSVIRDTFDYNKIQNLPLYLNAVIKETLRISCPVPGCLPRVVPVEGGMNLGSLNLPAGTVVSSISQLAIHFNETIFSSPDKFIPERWLGGDRKSIEKWNIAFSRGPQCIGTTLAYMELRCVLAYFFSRFEKLTGSCGDKLRWVDRFVSVNLDVDEVTVKDRWA	506	65
<i>Metarhizium acridum</i>		E9EAT5	MENNFTTASTVSISEGLWQRSLQQAASWALIIFTCAVLLPAVITGVRLYFHLRNPVGPGLAALTNYAFYWNWIRDEGYSRRESFALHKYNSPIRIGPNVSHVTNQPDDEDFVKVGSKKWKKDNFYYKFNGLDAMIDPAQYTYRSHLAPYAQRVNDLAPKLHKDLSAAAKMEKSMKTEAVNMVVKVLRITLSTSMMLNLYSHDHSISLEYDGYHPELEAFELMTQSWLWIFIPGTGTSFAKFNSVYTFMKYCKGWNDEDMRIQRLTENQELRDSHMKRYLAMNSNDWAKDNVNPPLNIDFNFIAGGSDTTSYTLACAFYILSPEIYAKLVKELDENWAFHRTFDYNIQNLPLYLNAVIKETLRISVPVPGCLPRVPSGTTLGSLVYPAGTAVSISQSIHFETIFSPPEKFIPERWLGNVGAQRDLKWNVAFSRGPRCIGTSLAYLELRCVLAYLSRFEMALTGNGCDRLRWVDRFVAVNLDDEVTVKDRWN	512	66

FIG. 37 (Cont'd)

Source Organism	Gene name	UniProt ID	Amino acid Sequence	AA length	SEQ ID NO:
<i>Metarhizium acridum</i>		E9DSJ7	MAVHVKSQLAGLTVALFYFVLRSRPTKLPGPWYKSWTDLVRYQWYFKQIYTHLHKKYGPVIRVAPQVAVADLETVKSYYTIKE TYRKTKFYELLVSRIPI QTVFSTADVELHRKLRRLMASQMSSESLKSMPLQVTSHELVAIQRMKEESKORGVID/FKWC/LFMTTIDVIGELSGESGQMLE KGKKTQVIEDLENVSSVSADRTTFFPF HIADKYDKILPLFRSKIAINRLRLVYSROSIGRYQKQVESDTSYAKYTFVEKLFQAEKDNKTTFEDILTNAQT/HIAGSDTTATTLTYIWSICKRPELRDALLKELRPLPGDFTE PDLREL/FNQTVETLRVYSSAPASLPRAPVPGGAHVGGYYLSEGTVAQAQYTMHIRDPAIFENPDVDPQRWANPTRAMKEAFMPFGRGSRSMYKSGNV	440	67
		E9FX7	MANIESTADVYHHRKLRLMSAQLSESLKSLPAITSRVELAIQRMKEDMTQTRGFVDVFKWCLFMATDVIGELA/GESFRMLEKGEKNQYIRDLEGCVLSAVRIAFPR VIA/LARKYLP/PIFQKVVQQA/RILGYAEQSLQRYQSLIDQNPEVPKQ/IVTKMFKAREDKKLSFSEVINAQGLV/AGSDTTSNSLTLYLLWSVRCRPELRDALVKELRTLPDD FTEHDLRELPLISQCCEETLRILYSAA/PALLSREVPQGGVGLGYWLPGGTTVATQAYTMHRRHPDIPFPNDEFNPRWAAPT/KAMKEAFMAFGRP/ICIGI/HLAYIELRL AAARFFQEPTAYMSEFREGMSDGMNETHYI/MSPKGKRCLEKAS	379	68
<i>Metarhizium robertsii</i>	<i>clo4</i>	E9F392	MESNDTTSFTLSISERGQIW/QWLPQPOQAS/WTII/AFTALAAVL/PAVTTGVVRL/YFHPIR/VVPGPK/LAALT/NFYAFYVW/WIRDEGYSKRFGAL/HKYNSPIR/IGPNSVH TNQPEYFDVIFKVGSKWKSDFYKYNGLDAMIDPAQYRTYRSHLAP/YAQR/VNDLAP/KLHKD/LSSAAKMEGH/KGEAINMTSMILHNL/YSHD/ISLIEYDGYHPFLE AFEQLMITOSW/LFVSYPI/PAMLLGLIP/GTSFAKFNASF/TTFMKYCKD/WNDEDMRIQ/LAEDQELRDS/HMKRYLAMDSNDS/ADK/VVP/NPLED/INFVAGSDTTSYTL ACAFFYILSP/EIYAKLVKELDENAP/IRDTFDYIKIQNL/NLNAV/KETLRISVP/PGCLPR/VPEGGTTLGSVYLP/TGTAV/SISQSQSIFHEKIPSP/EPK/PERW/IGNEAORLDK W/WAFSRGPRQCI/GTSLAY/LELRCV/LAYF/LSRFEM/ALTGNCGR/LRWVDRF/VAV/NLDDVEIK/LLRDRWN	515	69
		G9FN49	MSLKWLYQAQYAFWTWVLTFTFCISITLPLVMIGIYNLYFHP/LRNVPGPK/LAALT/NLYAFYVW/WIRDEGYSRQFSALHKYNSIIRVGP/NHVHTTQVELYD/VIFKAGSKW RKEKSYKYFNGIDAMIENPQYRTYRTHLAP/YAQR/IDDLAP/KYGD/LSAARM/KIMTETGKTINM/VKVLRT/LSMILHNFYS/IDSLINEYDGYHPFTEAEFEQLMITOS W/LFVTPMV/PMLLGLIP/GTRFAKFNSSYTTFMNYCNAW/NDEDRKQASDDQSVRDS/HMKRYLAIKNDDEQKSIIPNPLDD/VFNFAGGSDTTSYTTACAFYILSP/ VCTKL/VREIDEHSSIRDTFDYTIQI/LPYLNAV/KETLRISVP/PGCLPR/VPEGGVTLGSFSLPAGTAV/SISQQAISFENNEJESSHSFIPERWIG/PEAVGLDKWNI/AFSRGP RQCI/GTTLAY/LELRSV/LAYFFSRFEMTLTGNCGR/LRWVDRF/VAV/NLDDVE/LVLLRDRWG	506	70
<i>Saccharomyces cerevisiae</i>	FAD1	P38913	MQLSKAAEMCYETNSYLHIDQKSIQASTQEAIRLTRKYLSEIFVRWSP/LNGEISFSYNGGKDCQVLLLLYLSC/LWEYFFIKAQNSQDPDEFQSPMQRLPTVFIDQEEITFP TLENFVILETSERYCLSLYESQSGASVNMADAFRDFIKIYPT/EAIVIGIRHTIDP/GEALKPIQRITSSNWPDMRLQPL/HWDLTNIW/SFLLYSNEPICGLYGKGF/ISIGGI NNSLPNPHLRKDSNNPALHFEWEIHAFGKDAEGERSAINTSPISVVDKERFSKYHDNYYPGWYLVDDTLERAGRIKN*	307	71
<i>Saccharomyces cerevisiae</i>	PD11	P17967	MKFSAGAVLSWSSLLIASSVFAQQEAVAPEDSAVVKLATDSFNEYQSHDLV/LAEFFAP/WCGHCKNMAPEVYKAAETLVEKNITL/IAQIDCTENODDLCMEHNIPGFP/SLKI FKNSDVNNISDYEGPRTAE/AVQFM/KQSQP/AVAVADL/PAYLAV/ETFTV/VQSGKIDAFNATFYSMANKHFN/DYDFVSAENADDDFKLSIYLP/SA/MD/EPVYVYNGK KADIADAD/VFEKW/LQVEALPYFGEIDGSVFAQYV/ESGLPLGY/LFYND/EELEEYKPLFTELAKKNRGLM/NFVSIDARKEGRHAGLN/NMKEQPLFAI/HDMTEDLKYGLPQ LSEEA/DELSDKIVLESKAI/ESLVDK/LGQDASPIV/KSQE/IFENQDSSV/FQLVGKNH/DEIVNDPKDVLVLYAP/WCGHCKRLAPTYQ/ELADTYANATSDVLI/IAKIDHTEND VRGWIEGYPTIVLYPGGKKS/ESVVVQGSRS/IDSLFDHIKENGHFDVDGKALY/EAQEKAAE/EADADA/EI/AD/ED/IAHDEL*	523	72