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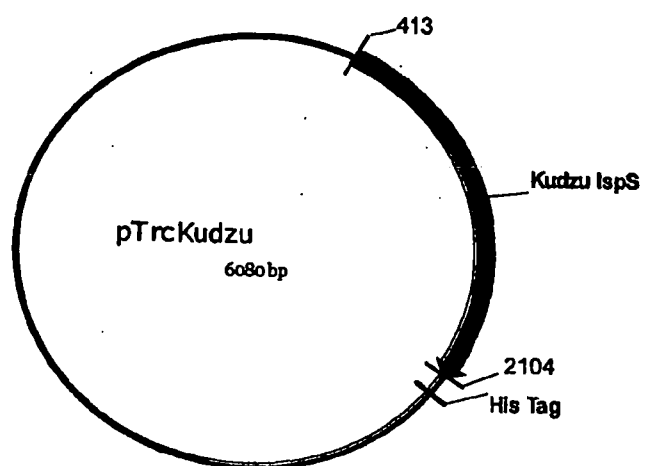
Figure 2

Figure 3A

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Figure 3B

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Figure 3C

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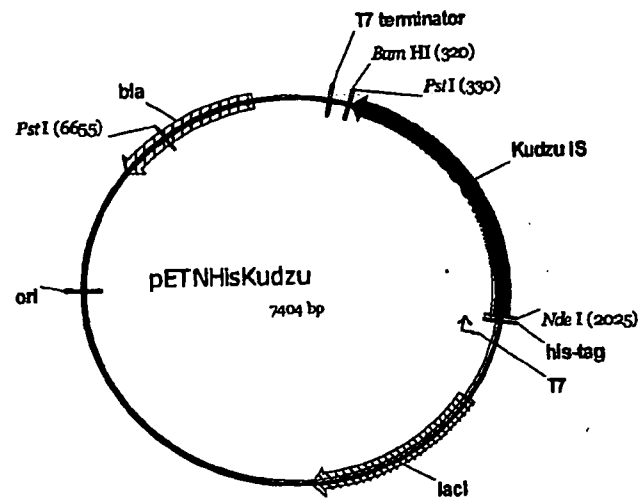


Figure 5A

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Figure 5B

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Figure 5C

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Figure 6

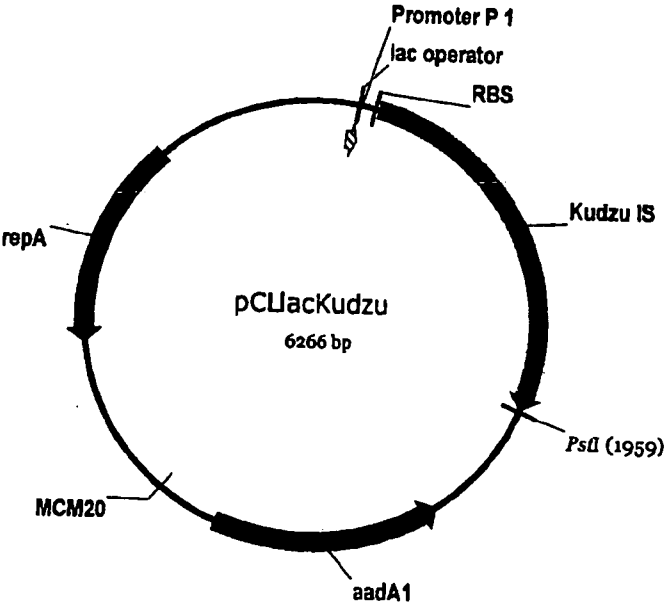


Figure 7A

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Figure 7B

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Figure 7C

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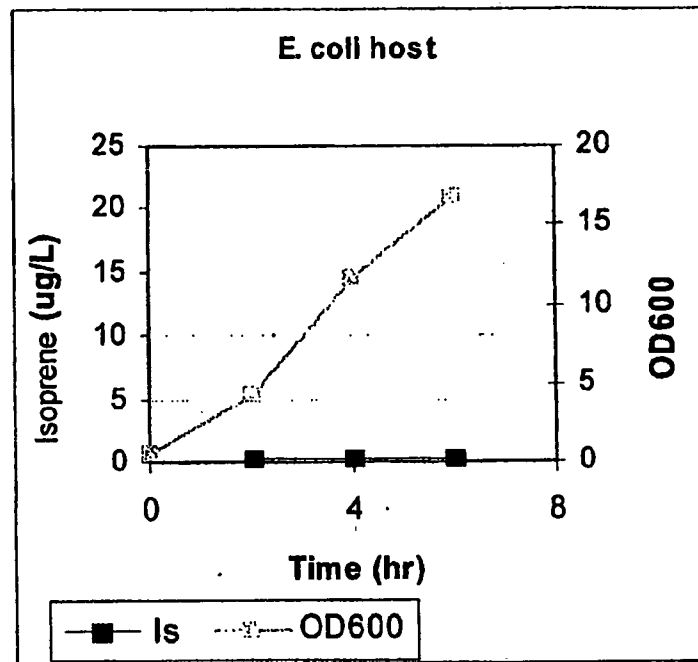
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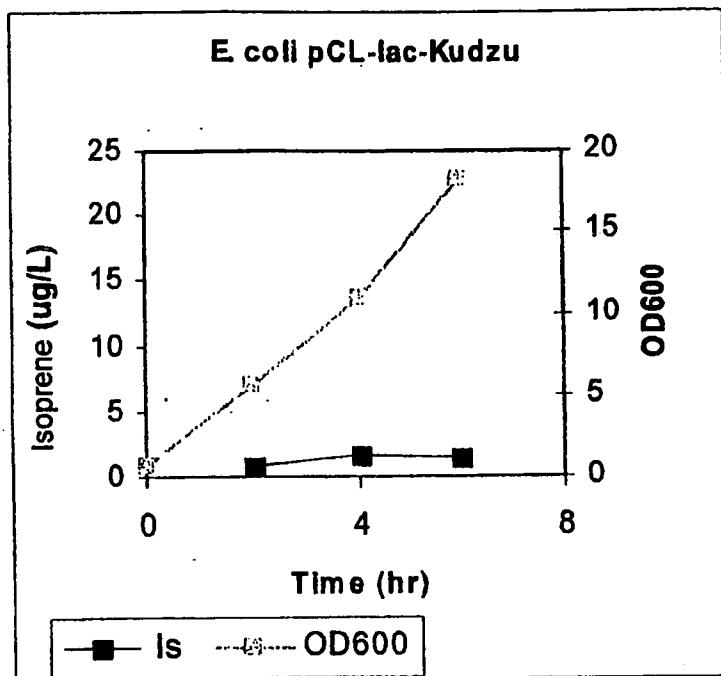
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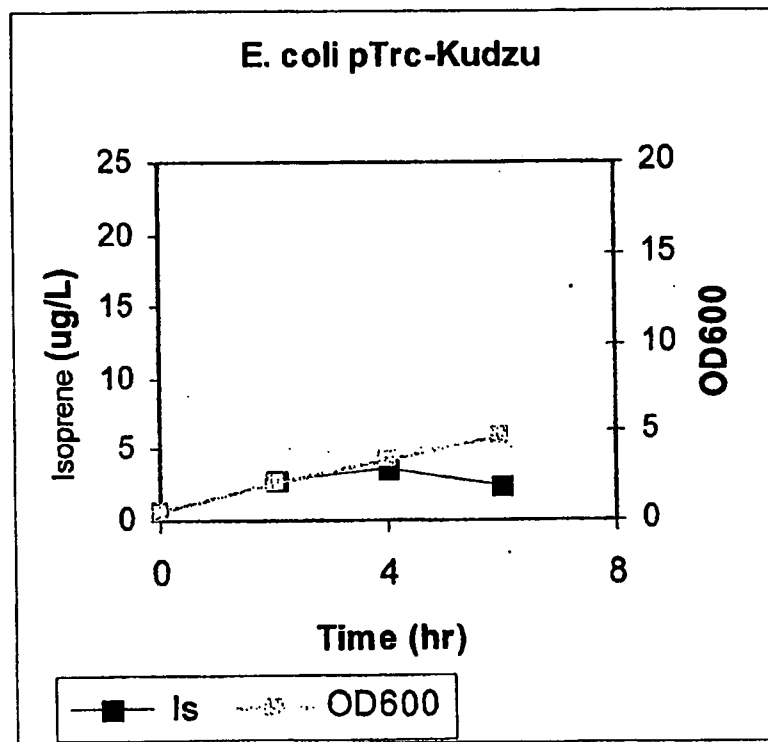
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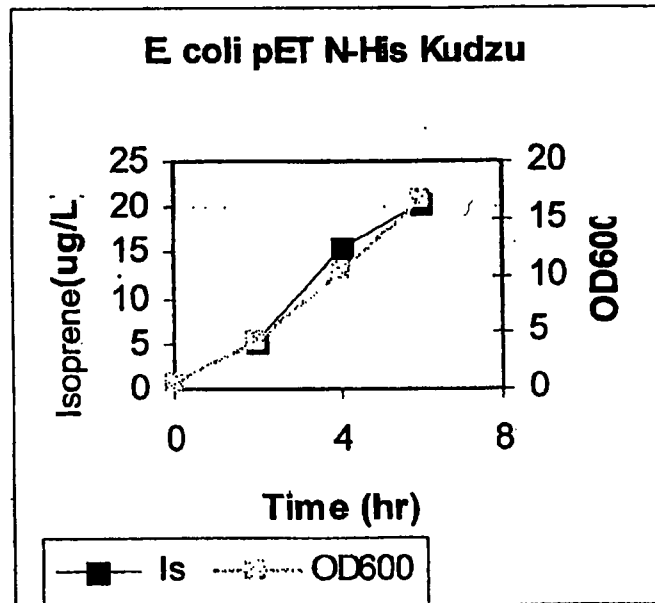
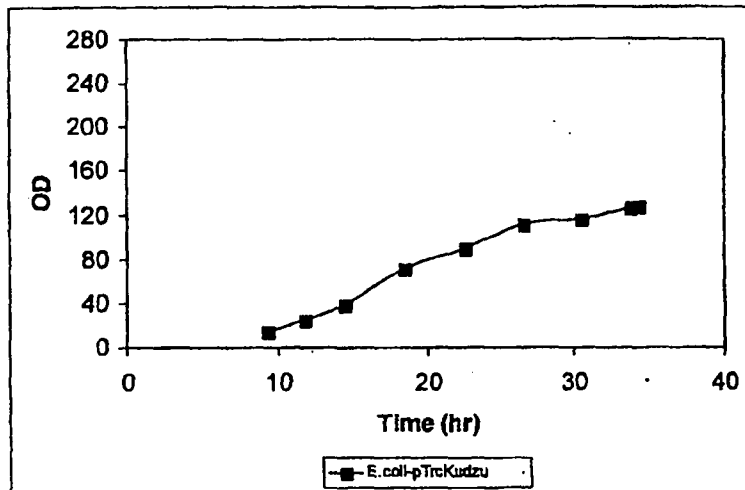
Figure 8D

Figure 9

A.



B.

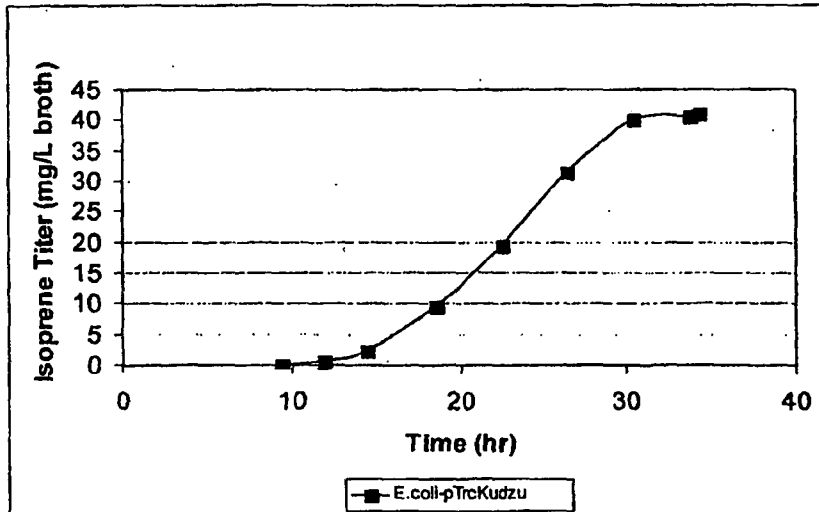


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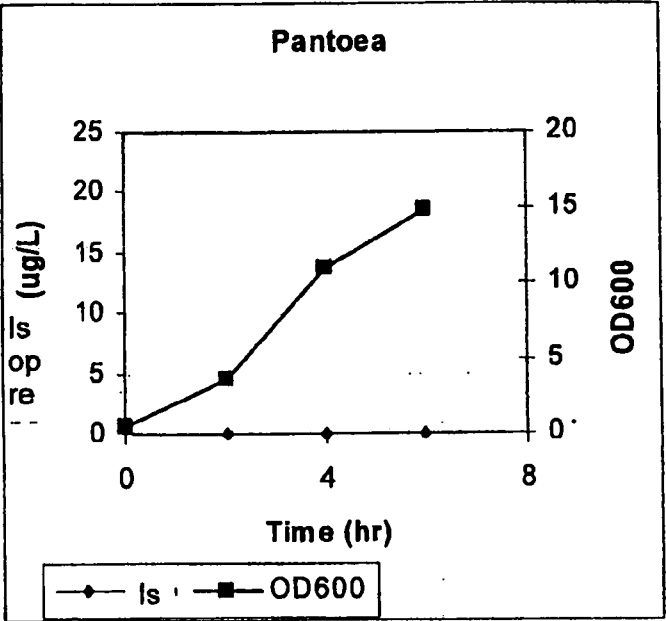


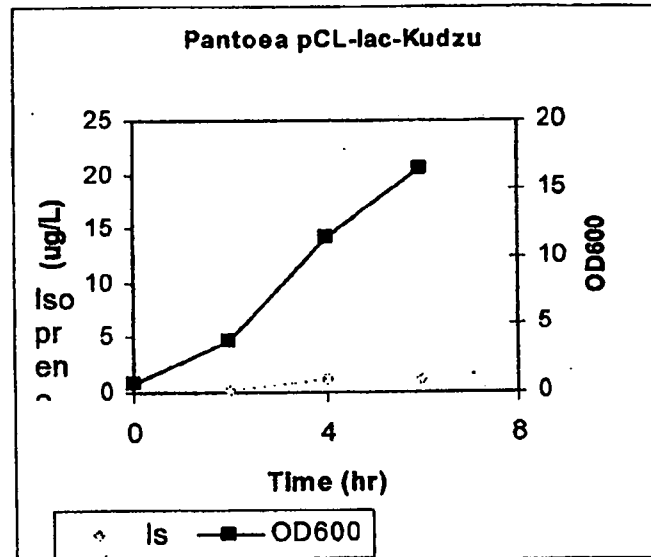
Figure 10B

Figure 10C

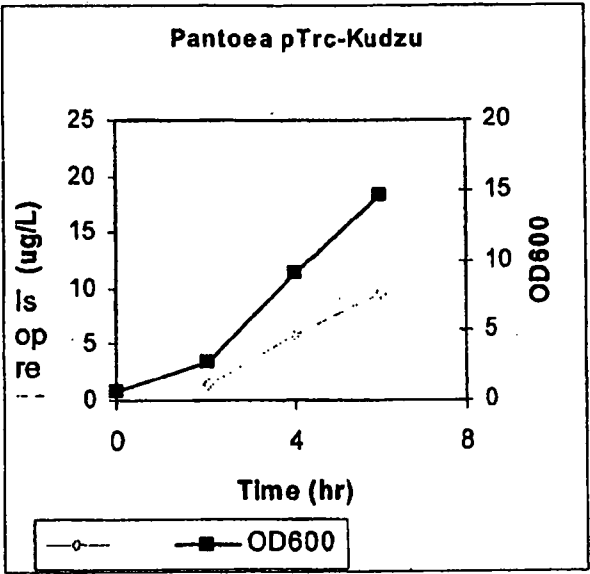


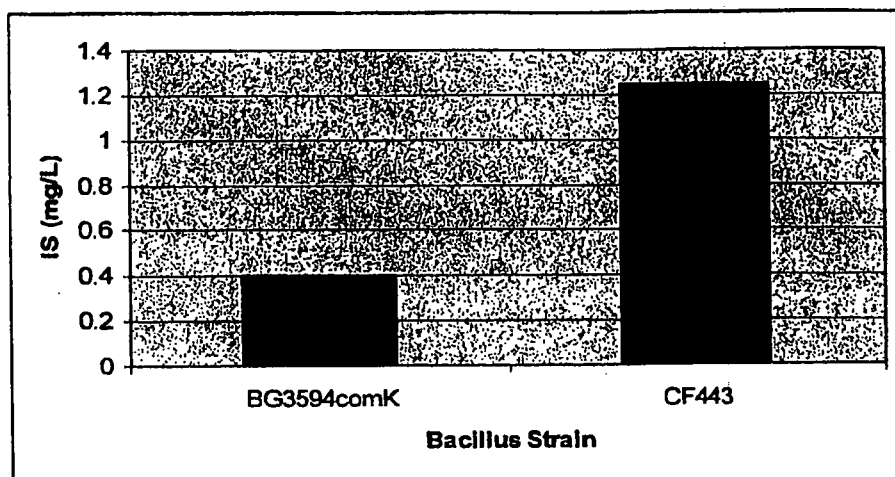
Figure 11

Figure 12A

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Figure 12B

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Figure 12C

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attttataaactcattccctgatctcgacttcgttcttttttacctctcgggttatgagttagt
tcaaattcgttcttttttaggttctaaatcggtttttcttggaattgtgctgttttatccttta
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(SEQ ID NO:57)

Figure 13

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GCTCGAGGAGAAGGCGACCAAACCTCGAGGAGGAGGTGCGATGTATGATCAACAGAGTTGACACC
CAACCCCTGTCTTTGCTGGAGCTGATCGACGATGTGCAGCGGTTGGGTTTGACTTATAAATTCG
AGAAGGACATTATCAAGGCACTGGAGAACATTGTGCTCCTCGACGAGAACAAGAACAAGTC
TGATCTTCACGCTACCGCTCTCTCTTTCCGACTTCTTCGACAACACGGCTTCGAGGTGTCGCAG
GACGTCTTCGAGAGATTTAAGGACAAGGAGGGAGGATTTAGCGGCGAGCTGAAGGGAGACGTTG
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AGCTCGTACATTTTCCATCACTCACCTTAAGAATAACCTTAAGGAGGGAATTAACACCAAGGTG
GCCGAGCAGGTTTCTCAGCCCTGGAGCTCCCCTACCACCAACGGCTCCATAGACTGGAGGCTC
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GCTGGACTTCAATATGGTTTCAGACGCTGCACCAAAGGAGTTGCAGGACCTGTCTCGATGGTGG
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CGGTCTTGTGACTATCATCGACGACGTCTACGATGTCTACGGCACACTCGACGAGTTGCAGCTG
TTCCTGACGCCGTCGAGCGATGGGATGTGAACGCCATTAATACTCTCCCTGACTATATGAAGC
TGTGCTTCCTGGCTCTGTACAACACTGTCAACGATACCTCGTACTCTATCCTCAAGGAGAAGGG
ACACAACAATCTCTCCTACTTGACCAAATCCTGGCGAGAAGTGTGCAAGGCTTTTCTGCAGGAG
GCTAAATGGTCCAAATAACAAGATCATTCTGCTTTTTCTAAATACCTGGAAAATGCCTCGGTGT
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(SEQ ID NO:8)

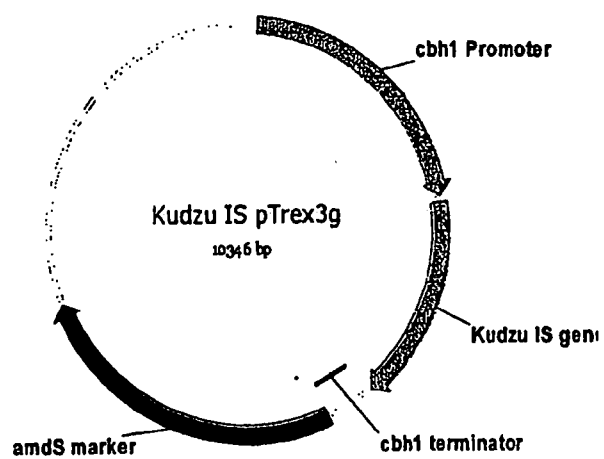
Figure 14

Figure 15A

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1  TCGACCGGTG AGAAGAACAG CATCGGGACA AGGGAAGGAA GAACAAAGAC AAAGAAAACA
61 AAAGAAAGCA ATTGAAAACA AAACAAAACA ATTTTCATTC CTTCTCTTAT CATTCCTTTT
121 CTTTTCTTTT CTCTCATFCA ACGCACTCCA TCGTATCCGT ATTCCTCTTA TTTTTCTCTT
181 TTCTCTATAT CCATTTCTTT CTCTCTAGGT GTGTCCTCTC TCTCTCTTCA ATTTCTCTAC
241 TCCGCATTCC AACGCATCCT TCCCCAACCC TCCCATTTC TCCTTACGGC CCGATAGCGA
301 TCGTCTTTCC CTCGTATCA CTCGTACCG GCCCTCCTC TGCACGTAA CTCCTACGT
361 ATTTACCATA TCATAAAGTT TTTCCGACG CTTATCGCTG ACCCCTGTC GCCCTCCTAT
421 TGGCTTCGGG ATTATCTTCT TGTCATAAG GTGATCCATG CTTCTGAAG ATTCGGAAA
481 TGTGTCCACT TTGGCGGGGA ATCATTCCAT CCACCTCTT CTCTCTCGCT TTCCTCATTC
541 GCGCTCCCC TTCCGCTCT CATTTGGTCT CCGCTCCGT TTTGCTTTCG CGATGTTACT
601 TGGGGAGAGG TGGGATAATC CTTTCGCAA AACTCGGTTT GACGCTCCC ATGGTATAAA
661 TAGTGGGTGG TGGACAGGTG CCTTCGCTTT TCTTTAAGCA AGAGAATCCC ATGTCTTGA
721 CTATCACGAA TTCACATACA TTATGAAGAT CACCGCTGTC ATTGCCCTT TATTCTCACT
781 TGCTGCTGCC TCACCTATTC CAGTTGCCGA TCCTGGTGTG GTTTCAGTTA GCAAGTCATA
841 TGCTGATTTT CTTCTGTTT ACCAAAGTTG GAACACTTTT GCTAATCTG ATAGACCCAA
901 CCTTAAGAAG AGAAATGATA CACCTGCAAG TGGATATCAA GTTGAAGAAG TCGTAATTTT
961 GTCACGTAC GGTGTAGGG CCCCTACAAA AATGACTCAA ACCATGCGTG ATGTCACTCC
1021 TAATACATGG CCAGAATGGC CCGTTAAATT AGGATATATT ACACCAAGAG GTGAACACTT
1081 GATCACTCTT ATGGCGGTT TTTACCGTCA AAAATTCCAG CAACAAGGAA TCCTTTCTCA
1141 GGGCTCCTGT CTTACTCCTA ACTCCATATA TGTCTGGCT GACGTGATC AGCGTACTTT
1201 AAAAATGGT GAAGCATTCC TTGCTGGTTT GGCACCACAA TGTGGCTTGA CAATTCATCA
1261 CCAACAAAAT CTTGAGAAAG CTGATCCTCT TTTTCATCCC GTTAAAGCTG GAACCTGCTC
1321 TATGGATAAA ACTCAAGTTC AACAAAGTGT TGAGAAGGAG GCACAACTC CTATAGATAA
1381 TTTGAATCAA CATTACATCC CCTTTTAGC TTTAATGAAT ACAACATTAA ATTTTAGTAC
1441 TTCTGCCTGG TGCCAAAAC ACTCTGCTGA TAAATCCTGT GACCTAGGTT TATCCATGCC
1501 TTCTAAATTG TCCATAAAG ATAATGGTAA CAAGGTCGCA TTGGATGGAG CTATTGGTCT
1561 ATCCTCTACT TTGGCCGAGA TTTTCTTCT TGAATATGCT CAAGGCATGC CTCAGCTGC
1621 TTGGGGTAAC ATCCACTCAG AGCAAGAGTG GGCTTCCTG CTAAAGTGC ATAATGTTCA
1681 ATTCGATTTG ATGGCCCGAA CACCTTATAT TGCTCGACAT AACGGTACTC CTTTATTGCA
1741 AGCTATATCA AATGCCCTTA ATCCCAACGC CACTGAATCA AAACCTCCAG ATATTTACC
1801 TGATAACAAA ATATTGTTCA TTGCAGGTCA TGACACAAAT ATTGCTAATA TAGCCGGCAT
1861 GTTAAATAG CGTTGGACAT TACCAGGTCA ACCAGATAAT ACTCCTCCAG GTGGTCCCT
1921 AGTATTTGAA CGTCTGCTG ATAAAAGTGG AAAACAATAT GTTCTGTAT CTATGGTTTA
1981 TCAACACTA GAACAACTTC GATCAGAC TCCCTTTCT CTAAATCAGC CTGCCGGATC
2041 TGTTCAACTT AAAATCCAG GTTGCAATGA TCAAACAGCC GAGGGTACT GTCTCTTTC
2101 CTTAAATACA AGAGTTGTTT CCCAATCTGT TGAACCTGGA TGCCAACTTC AATAATGAGG
2161 ATCCAAGTAA GGGAAATGAGA ATGTGATCCA CTTTAAATTC CTAATGAATA CATGCCATTA
2221 GTTCTTTTCT TTTGTTCTTT ATGTCGTTT TCGATGGTAC GGCCGTTGTC AATCTCAGTT
2281 TGTGTGCTTG GTTGACGCTT GGTTCAAAT CTGTTCACT CATGAATCTT TTACCATTTT
2341 ACCACACGTT TATACCATTC TCTCATAGAA TCTTCATCAA ACCATCTCGG GGTAGAGTG
2401 GAAAGAAAGT CTTGTCTTT TATTTCTTT TTTCCATCTT CAAGGCTTTT CTTTCTTCC
2461 TCCTCTCTCGT TCATCTTGAG GTTTGACGTG TCTGTTTGA ATTTGAGCT GTTGACGAT
2521 CTTATTTTTT GTTTTGCGAA AACGAAGCGC TTTACTCTCT TCATCAGTTG GACGATTGTA
2581 CCTTTGAAAA CCAACTACTT TTGCATGTTT TGTATAGAAA TCAATGATAT TAGAATCCCA
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2701 GCATTTGCCA AGGATGTTTT CATTAATCAA GAACGAAAGT TAGGGGATCG AAGACGATCA
2761 GATACCGTCG TAGTCTTAAC CATAAACTAT GCCGACTAGG GATCGGGCAA TGTTTCATTT
2821 ATCGACTTGC TCGGCACCTT ACGAGAAATC AAAGTCTTTG GGTTCGGGG GGAGTATGGT
2881 CGCAAGGCTG AAACCTAAAG GAATTGACGG AAGGGCACCA CAATGGAGTG GAGCCTGCGG
2941 CTTAATTTGA CTCACACCGG GGAAACTCAC CAGGTCCAGA CATAGTAAGG ATTGACAGAT
3001 TGAGAGCTCT TTCTTGATTC TATGGGTGGT GGTGCATGGC CGTCTTAGT TGGTGGAGTG
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3181 AGGCAATAAC AGGTCTGTGA TGCCCTTAGA TGTTCTGGGC CGCACGCGCG CTACACTGAC
3241 GGAGCCAACG AGTTGAAAAA AATCTTTTGA TTTTATATCC TTGGCGGAA GGTCTGGGTA
3301 ATCTTGTTAA ACTCCGCTGT GCTGGGGATA GAGCATTGCA ATTATTGCGG CCGCTCTCA
3361 ATTCGATGTT GCAGATTTTA CAAGTTTTTA AATGTATTT CATTATTACT TTTATATGC
3421 CTAATAAAAA AGCCATAGTT TAATCTATAG ATAACTTTT TTCCAGTGCA CTAACGGACG

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Figure 15B

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3601 TTTACAGCAA TTTTAAACAA ACATCGTTCA CCTCGTTTAA GGATATCTTG TGTATGGGGT
3661 GTTGACTTGC TTTATCGAAT AATTACCGTA CCTGTAATTG GCTTGCTGGA TATAGCGGTA
3721 GTCTAATATC TAGCAAAAAT CTTTGGGGTG AAAAGGCTTG CAATTTACG ACACCGAACT
3781 ATTTGTCATT TTTTAATAAG GAAGTTTCC ATAAATTCCT GTAATTCTCG GTTGATCTAA
3841 TTGAAAAGAG TAGTTTTGCA TCACGATGAG GAGGGCTTTT GTAGAAAGAA ATACGAACGA
3901 AACGAAAATC AGCGTTGCCA TCGCTTTGGA CAAAGCTCCC TTACCTGAAG AGTCGAATTT
3961 TATTGATGAA CTTATAACTT CCAAGCATGC AAACCAAAG GGAGAACAAG TAATCCAAGT
4021 AGACACGGGA ATTGGATTCT TGGATCACAT GTATCATGCA CTGGCTAAAC ATGCAGGCTG
4081 GAGCTTACGA CTTTACTCAA GAGGTGATTT AATCATCGAT GATCATCACA CTGCAGAAGA
4141 TACTGCTATT GCACTTGGTA TTGCATTCAA GCAGGCTATG GGTAACCTTG CCGGCGTTAA
4201 AAGATTTGGA CATGCTTATT GTCCACTTGA CGAAGCTCTT TCTAGAAGCG TAGTTGACTT
4261 GTCGGGACGG CCTATGCTG TTATCGATT GGGATTAAAG CGTGAAAAGG TTGGGGAATT
4321 GTCCCTGTGA ATGATCCCTC ACTTACTATA TTCCTTTTCG GTAGCAGCTG GAATTACTTT
4381 GCATGTTACC TGCTTATATG GTAGTAATGA CCATCATCGT GCTGAAAGCG CTTTTAAATC
4441 TCTGGCTGTT GCCATGCGCG CGGCTACTAG TCTTACTGGA AGTTCTGAAG TCCCAAGCAC
4501 GAAGGGAGTG TTGTAAGAT GAATTTGGATT ATGTCAGGAA AAGAAGCACA ATTTTGCAATC
4561 CAAATTGTCT AAATTTTAGA GTTGCTTGA AACAATAGAA CCTACTTGC TTTATAATTA
4621 CGTTAATTAG AAGCGTTATC TCGTGAAGGA ATATAGTACG TAGCCGTATA AATTGAATTG
4681 AATGTTACAG TTATAGAATA GAGACACTTT GCTGTTCAAT GCGTCGTCAC TTACCATACT
4741 CACTTTATTA TACGACTTTA AGTATAAACT CCGCGGTTAT GGTAAAATTA ATGATGCACA
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4861 CCATAGCTTC AAAATGTTTC TACTCCTTTT TTACTCTTCC AGATTTTCTC GGACTCCGCG
4921 CATCGCCGTA CCACTTCAAA ACACCCAAGC ACAGCATACT AAATTTTCCC TCTTCTTCC
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5101 TTTTTTTTTT TAGTTTTTTT CTCTTTCAGT GACCTCCATT GATATTTAAG TTAATAACG
5161 GTCTTCAATT TCTCAAGTTT CAGTTTCAAT TTTCTTGTTT TATTACAAC TTTTCTACTT
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5281 TCGGCATAGT ATATCGGCAT AGTATAATAC GACAAGGTGA GGAACATAAC CATGGCCAAG
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5461 GACGACGTGA CCCTGTTTAT CAGCGCGGTC CAGGACGAGG TGGTGCCGGA CAACACCCTG
5521 GCCTGGGTGT GGGTGCGCGG CCTGGACGAG CTGTACGCCG AGTGGTCGGA GGTGCTGTCC
5581 ACGAACTTTC GGGACGCGCT CGGGCCGGCC ATGACCGAGA TCGGCGAGCA GCGTGGGGG
5641 CGGGAGTTCG CCCTGCGCGA CCCGGCCGGC AACTGCGTGC ACTTCGTGGC CGAGGAGCAG
5701 GACTGACACG TCCGACGCGG GCCACGCGGT CCCAGGCCTC GGAGATCCGT CCCCCTTTTC
5761 CTTTGTGCGAT ATCATGTAAT TAGTTATGTC ACGCTTACAT TCACGCCCTC CCCCACATC
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6061 CTCACACCAT AGGCAGATAA CGTTCCCCAC CGGCTCGCCT CGTAAGCGCA CAAGGACTGC
6121 TCCCAAAGAT CCTAGGCGGG ATTTTGCCGA TTTCCGCCCT AAGGAACCGG AACACGTAGA
6181 AAGCCAGTCC GCAGAAACGG TGCTGACCCC GGATGAATGT CAGCTACTGG GCTATCTGGA
6241 CAAGGGAAAA CGCAAGCGCA AAGAGAAAGC AGGTAGCTTG CAGTGGGCTT ACATGGCGAT
6301 AGCTAGACTG GCGGTTTTTA TGGACAGCAA GCGAACCGGA ATTGCCAGCT GGGGCGCCT
6361 CTGGTAAGGT TGGGAAGCCC TGCAAAGTAA ACTGGATGGC TTTCTTGCCG CCAAGGATCT
6421 GATGGCGCAG GGGATCAAGA TCTGATCAAG AGACAGGATG AGGATCGTTT CGCATGATTG
6481 AACAAGATGG ATTGCACGCA GGTCTCCGG CCGCTTGGGT GGAGAGGCTA TTCGCTATG
6541 ACTGGGCACA ACAGACAATC GGCTGCTCTG ATGCCGCCGT GTTCCGGCTG TCAGCGCAGG
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6661 AGGCAGCGCG GCTATCTGCG CTGGCCACGA CGGGCGTTCC TTGCGCAGCT GTGCTCGACG
6721 TTGTCACTGA AGCGGGAAGG GACTGGCTGC TATTGGCGGA AGTGCCGGGG CAGGATCTCC
6781 TGTCTCTCTG CCTTGCTCCT GCCGAGAAAG TATCCATCAT GGCTGATGCA ATGCGGCGGC
6841 TGCATACGCT TGATCCGGCT ACCTGCCCAT TCGACCACCA AGCGAAACAT CGCATCGAGC
6901 GAGCACGTAC TCGGATGGAA GCCGGTCTTG TCGATCAGGA TGATCTGGAC GAAGAGCATC
6961 AGGGGCTCGC GCCAGCCGAA CTGTTCCGCA GGCTCAAGGC GCGCATGCCC GACGCGGAGG

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Figure 15C

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7021 ATCTCGTCGT GATCCATGGC GATGCCTGCT TGCCGAATAT CATGGTGGA AATGGCCGCT
7081 TTTCTGGATT CAACGACTGT GGCCGGCTGG GTGTGGCGGA CCGCTATCAG GACATAGCGT
7141 TGGATACCCG TGATATTGCT GAAGAGCTTG GCGGCGAATG GGCTGACCGC TTCTTCGTGC
7201 TTTACGGTAT CGCCGCTCCC GATTCGCAGC GCATCGCCTT CTATCGCCTT CTTGACGAGT
7261 TCTTCTGAAT TGA AAAAGGT ACCAAGTTTA CTCATATATA CTTTAGATTG ATTTAAAACT
7321 TCATTTTAA TTTAAAGGA TCTAGGTGAA GATCCTTTTT GATAATCTCA TGACCAAAT
7381 CCCTTAACGT GAGTTTTCGT TCCACTGAGC GTCAGACCCC GTAGAAAAGA TCAAAGGATC
7441 TTCTTGAGAT CCTTTTTTTC TGCGCGTAAT CTGCTGCTTG CAAACAAAAA AACCACCGCT
7501 ACCAGCGGTG GTTTGTTTGC CGGATCAAGA GCTACCAACT CTTTTCCTGA AGGTAAGTGG
7561 CTTACAGAGA GCGCAGATAC CAAATACTGT CTTCTAGTG TAGCCGTAGT TAGGCCACCA
7621 CTTCAAGAAC TCTGTAGCAC CGCCTACATA CCTCGCTCTG CTAATCCTGT TACCAAGTGGC
7681 TGCTGCCAGT GGCGATAAGT CGTGTCTTAC CGGGTTGGAC TCAAGACGAT AGTTACCGGA
7741 TAAGGCGCAG CGGTCGGGCT GAACGGGGGG TTCGTGCACA CAGCCCAGCT TGGAGCGAAC
7801 GACCTACACC GAACTGAGAT ACCTACAGCG TGAGCATTGA GAAAGCGCCA CGCTTCCCAG
7861 AGGGAGAAAG GCGGACAGGT ATCCGGTAAG CCGCAGGGTC GGAACAGGAG AGCGCACGAG
7921 GGAGCTTCCA GGGGGAAACG CCTGGTATCT TTATAGTCCT GTCGGGTTTC GCCACCTCTG
7981 ACTTGAGCGT CGATTTTGT GATGCTCGTC AGGGGGGCGG AGCCTATGGA AAAACGCCAG
8041 CAACGCGGCC TTTTACGGT TCCTGGCCTT TTGCTGGCCT TTTGCTCACA TGTTCTTTCC
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8161 TCGCCGAGC CGAACGACCG AGCGCAGCGA G
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(SEQ ID NO:11)

Figure 16

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1 GAATTCAAAA CAAATGTGT GCAACCTCCT CCCAGTTTAC TCAGATTACC GAGCATAATT
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121 AAAATGACCT GAAGGTGGAA AAGCTCGAGG AGAAGGCGAC CAAACTCGAG GAGGAGGTGC
181 GATGTATGAT CAACAGAGTT GACACCCAAC CCCTGTCTTT GCTGGAGCTG ATCGACGATG
241 TGCAGCGGTT GGGTTTGACT TATAAATTCG AGAAGGACAT TATCAAGGCA CTGGAGAACA
301 TTGTGCTCCT CGACGAGAAC AAGAAGAACA AGTCTGATCT TCACGCTACC GCTCTCTCTT
361 TCCGACTTCT TCGACAACAC GGCTTCGAGG TGTCGCAGGA CGTCTTCGAG AGATTTAAGG
421 ACAAGGAGGG AGGATTTAGC GCGGAGCTGA AGGGAGACGT TCAGGGTCTT CTCTCCTTGT
481 ACGAGGCGTC CTACCTGGGA TTCGAGGGAG AGAACCTCCT GGAGGAAGCT CGTACATTTT
541 CCATCACTCA CCTTAAGAAT AACCTTAAGG AGGGAATTAA CACCAAGGTG GCCGAGCAGG
601 TTCTCACGC CCTGGAGCTC CCCTACCACC AACGGCTCCA TAGACTGGAG GCTCGTTGGT
661 TCCTGGACAA ATATGAGCCA AAGGAGCCTC ATCATCAGTT GCTGTTGGAG TTGGCCAAGC
721 TGGACTTCAA TATGGTTCAG ACGCTGCACC AAAAGGAGTT GCAGGACCTG TCTCGATGGT
781 GGACCGAGAT GGGATTGGCC TCGAAGCTGG ATTTTGTCCG TGACCGACTT ATGGAGGTCT
841 ATTTTGGGC CCTTGGAAAT GCGCCTGACC CCCAGTTCGG AGAGTGCCGG AAGGCGGTGA
901 CGAAGATGTT CGGTCTTGTG ACTATCATCG ACGACGTCTA CGATGTCTAC GGCACACTCG
961 ACGAGTTGCA GCTGTTCACT GACGCCGTCG AGCGATGGGA TGTGAACGCC ATTAATACTC
1021 TCCTGACTA TATGAAGCTG TGCTTCCTGG CTCTGTACAA CACTGTCAAC GATACCTCGT
1081 ACTCTATCCT CAAGGAGAAG GGACACAACA ATCTCTCCTA CTTGACCAA TCCTGGCGAG
1141 AACTGTGCAA GGCTTTTCTG CAGGAGGCTA AATGGTCCAA TAACAAGATC ATTCCTGCTT
1201 TTTCTAAATA CCTGGAAAAT GCCTCGGTGT CGAGCTCTGG CGTCGCCCTT CTGGCCCTT
1261 CTTACTTCTC CGTCTGCCAG CAGCAGGAGG ATATTTCGTA TCATGCTCTT AGATCGCTGA
1321 CCGATTTTCA CGGCCTCGTG CGATCTTCCT GCGTGATTTT TCGGTGTGT AATGACCTTG
1381 CGACCTCTGC TGCTGAGCTG GAACGAGGCG AACTACAAA TTCCATTATT TCTTACATGC
1441 ACGAAAACGA TGGAACATCT GAAGAACAGG CTAGAGAGGA ACTGCCAAAG TTGATCGACG
1501 CCGAGTGGAA GAAGATGAAC AGAGAGCGGG TGTCCGACTC TACCCTGCTT CCCAAGGCCT
1561 TCATGGAGAT CGCCGTGAAC ATGGCTCGAG TTTCCCATTG TACTTACCAG TACGGTGACG
1621 GCCTGSGTCG TCCGGAATAC GCTACAGAGA ACCGAATCAA GCTGCTGCTC ATCGACCCCT
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(SEQ ID NO:12)

Figure 17

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1 GAATTCAACA AAAATGTGCT CTGTTTCCAC TGAGAACGTG TCCTTTACTG AGACTGAGAC
61 TGAAGCACGT AGAAGCGCCA ACTACGAACC CAACTCCTGG GATTATGACT TTCTGCTGTC
121 TTCTGACACC GACGAGTCGA TCGAGGTTTA TAAGGATAAG GCCAAGAAAC TTGAGGCCGA
181 GGTCAAGACGA GAGATTAAACA ACGAGAAGGC CGAGTTCCTG ACCCTTCTTG AGCTGATCGA
241 CAACGTTCAA CGACTTGGTC TTGGTTACCG TTTTCAATCC GATATCCGAC GTGCATTGGA
301 TCGATTGTGC TCGTCCGGAG GTTTCGATGG TGTGACTAAG ACGTCGCTGC ACGCCACAGC
361 TCTTTCCTTC AGACTGTTGC GGCAGCATGG ATTTGAGGTT TCCCAGGAAG CCTTTTCTGG
421 TTTCAAGGAT CAGAACGGAA ACTTTTGGGA GAATCTCAAG GAGGACACCA AGGCCATCCT
481 GTCGTTGTAT GAGGCCTCGT TCCTGGCTCT TGAGGGCGAG AATATTCTGG ATGAGGCTCG
541 GGTTTTTCGCT ATTTTCGCACC TGAAGGAGTT GTCGGAGGAA AAGATCGGAA AGGAACTGGC
601 CGAGCAGGTC AACCATGCAC TTGAACTTCC CCTGCATCGA CGTACCCAGC GACTGGAGGC
661 CGTGTGGAGC ATCGAGGCGT ACAGAAAAAA GGAGGATGCT AATCAGGTTT TGCTCGAACT
721 CGCTATCCTC GACTATAACA TGATTAGAG CGTGTACCAG CGTGACTTGC GAGAGACAAG
781 CCGGTGGTGG CGACGGGTGG GACTGGCCAC GAAGCTCCAC TTTGCTAAAG ATCGATTGAT
841 TGAGTCGTTT TACTGGGCAG TGGGTGTGGC CTTTGAGCCT CAGTACTCCG ACTGCCGAAA
901 CTCCGTTGCA AAGATGTTTT CTTTGTGCAC TATCATCGAC GACATCTACG ATGTTTACGG
961 CACTCTCGAT GAACTCGAAC TCTTCACGGA CGCTGTGCGA CGATGGGATG TGAATGCCAT
1021 TAATGATCTG CCAGATTATA TGAAGTTGTG TTTCTTGGCG CTCTACAACA CAATTAATGA
1081 AATTGCCTAC GACAACCTCA AGGACAAGGG AGAGAACATT CTGCCCTACC TTACTAAAGC
1141 CTGGGCCGAC CTGTGTAACG CCTTTTGTGCA GGAAGCCAAG TGGCTCTATA ACAAATCTAC
1201 TCCTACATTT GATGACTACT TCGGCAACGC TTGGAAGTCT TCCAGCGGCC CTCTCCAGTT
1261 GATCTTCGCT TACTTTGCAG TGGTCCAGAA CATCAAGAAA GAGGAGATTG AGAACCTCCA
1321 GAAGTATCAC GACATCATCT CCCGACCTTC GCACATCTTT CGACTGTGCA ATGACCTTGC
1381 CTCCGCATCC GCTGAGATTG CCCGAGGAGA AACAGCCAAT TCTGTGTCGT GTTACATGCG
1441 TACAAAGGGC ATCTCCGAGG AGCTGGCTAC CGAGTCTGTG ATGAACCTGA TCGATGAAAC
1501 CTGTAAGAAG ATGAACAAAG AGAAACTGGG CGGTTCTCTG TTCGCCAAAC CATTTGTTGA
1561 AACC CGCATC AATCTGGCTC GTCAGTCTCA TTGTACTTAC CATAACGGTG ACGCGCACAC
1621 TTCGCCGGAC GAATTGACCC GTAAGCGTGT GCTTTCGGTG ATTACCGAGC CGATCCTGCC
1681 GTTCGAAAGA TAATAGGATC C
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(SEQ ID NO:13)

Figure 18A

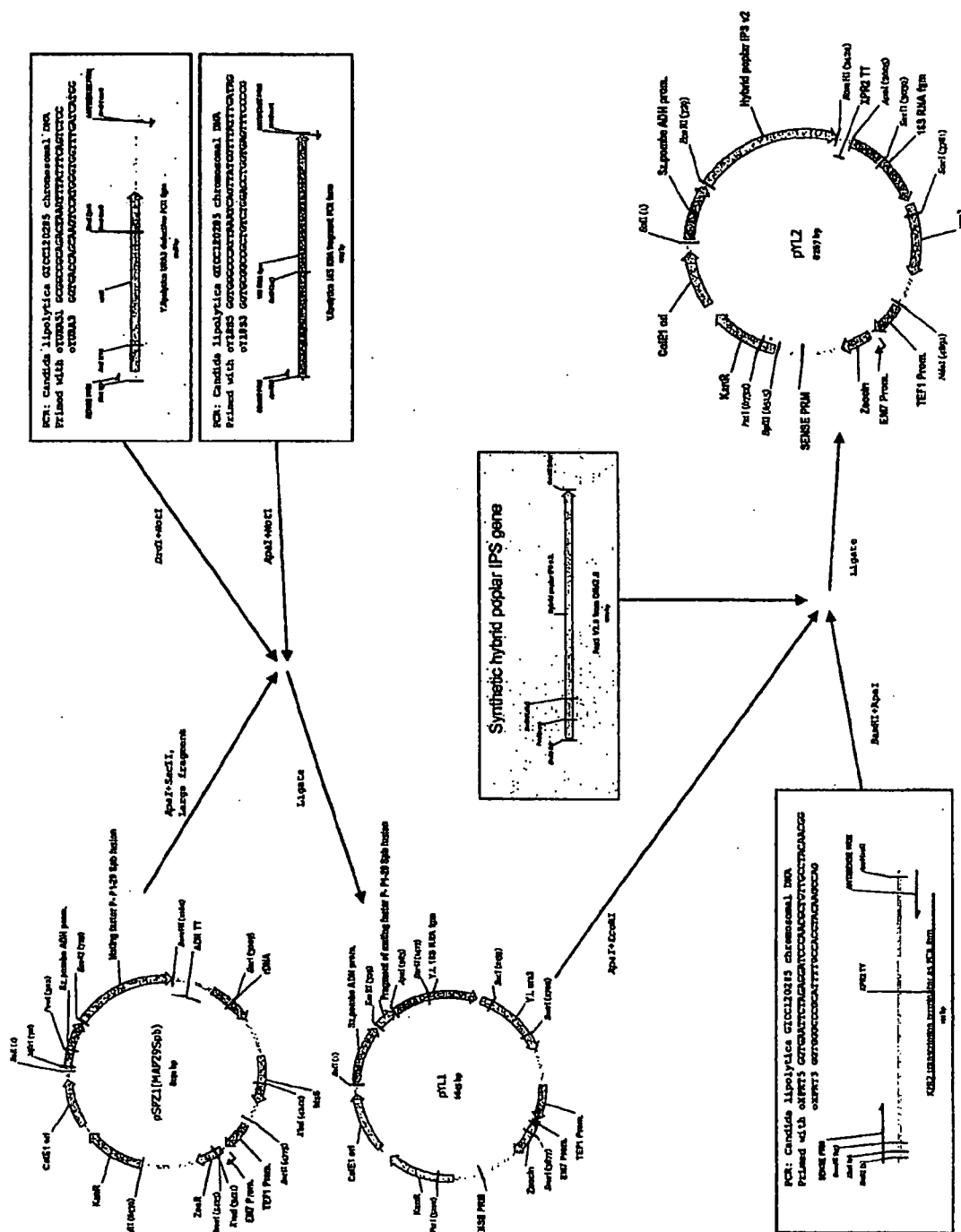


Figure 18B

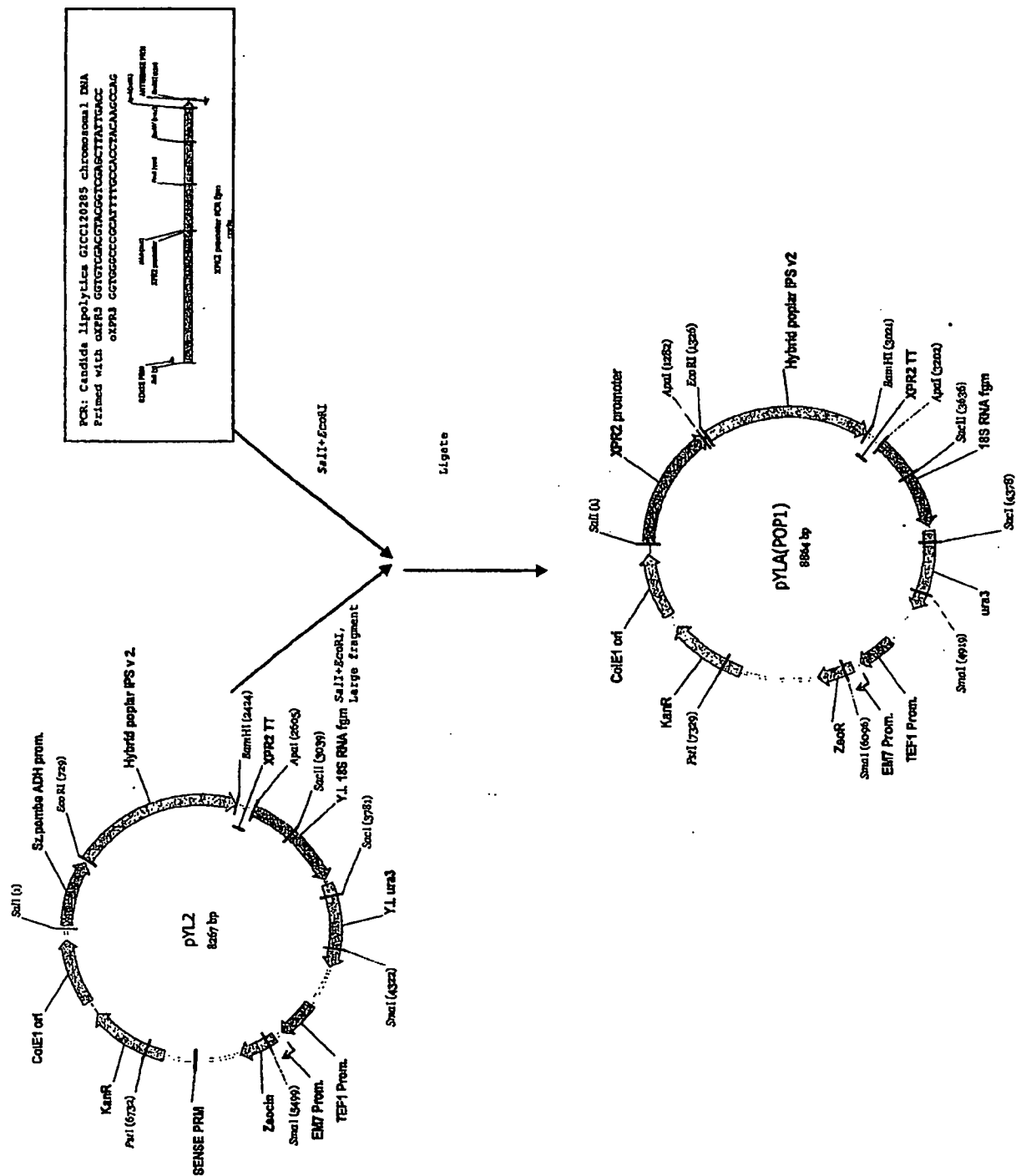


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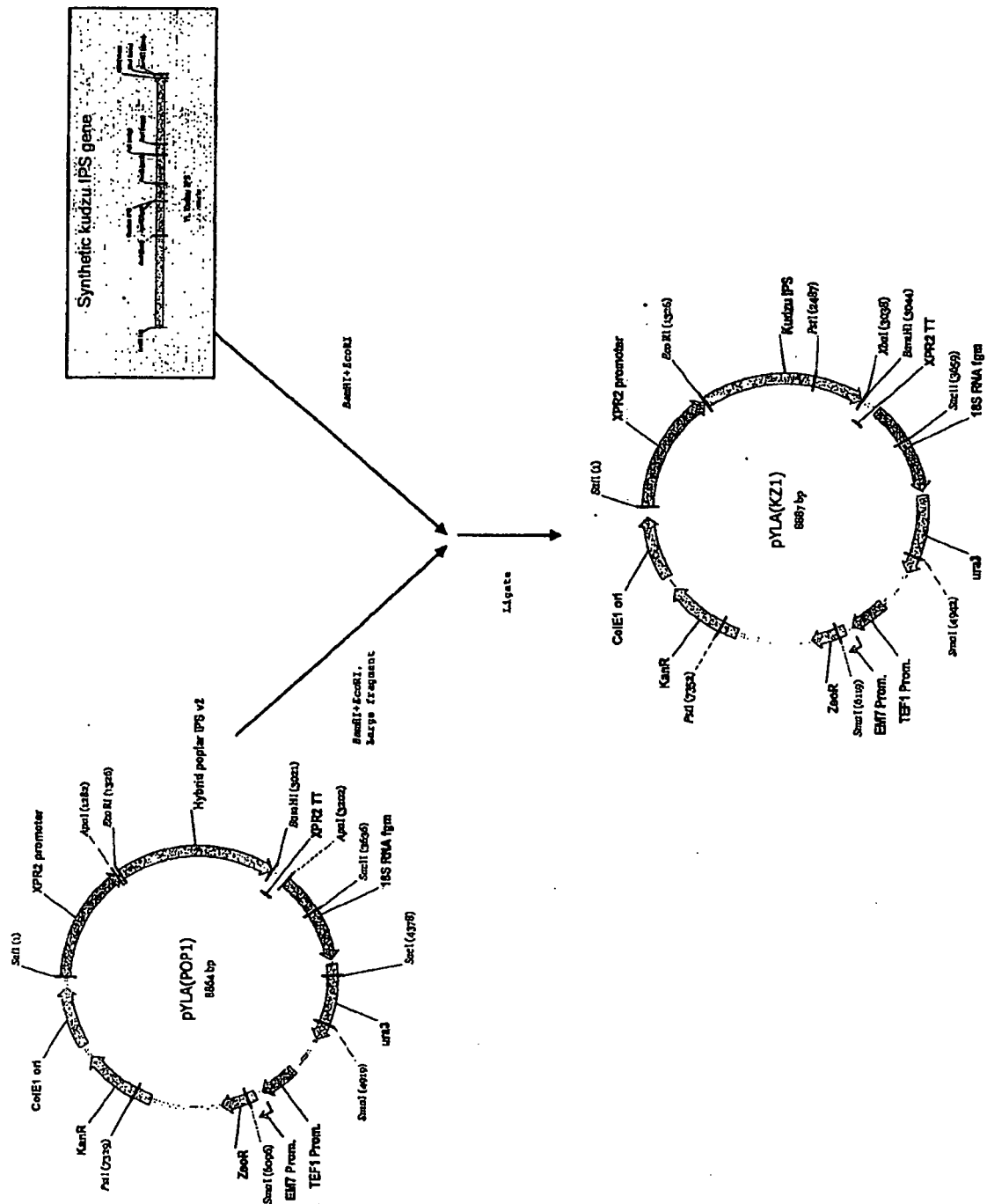


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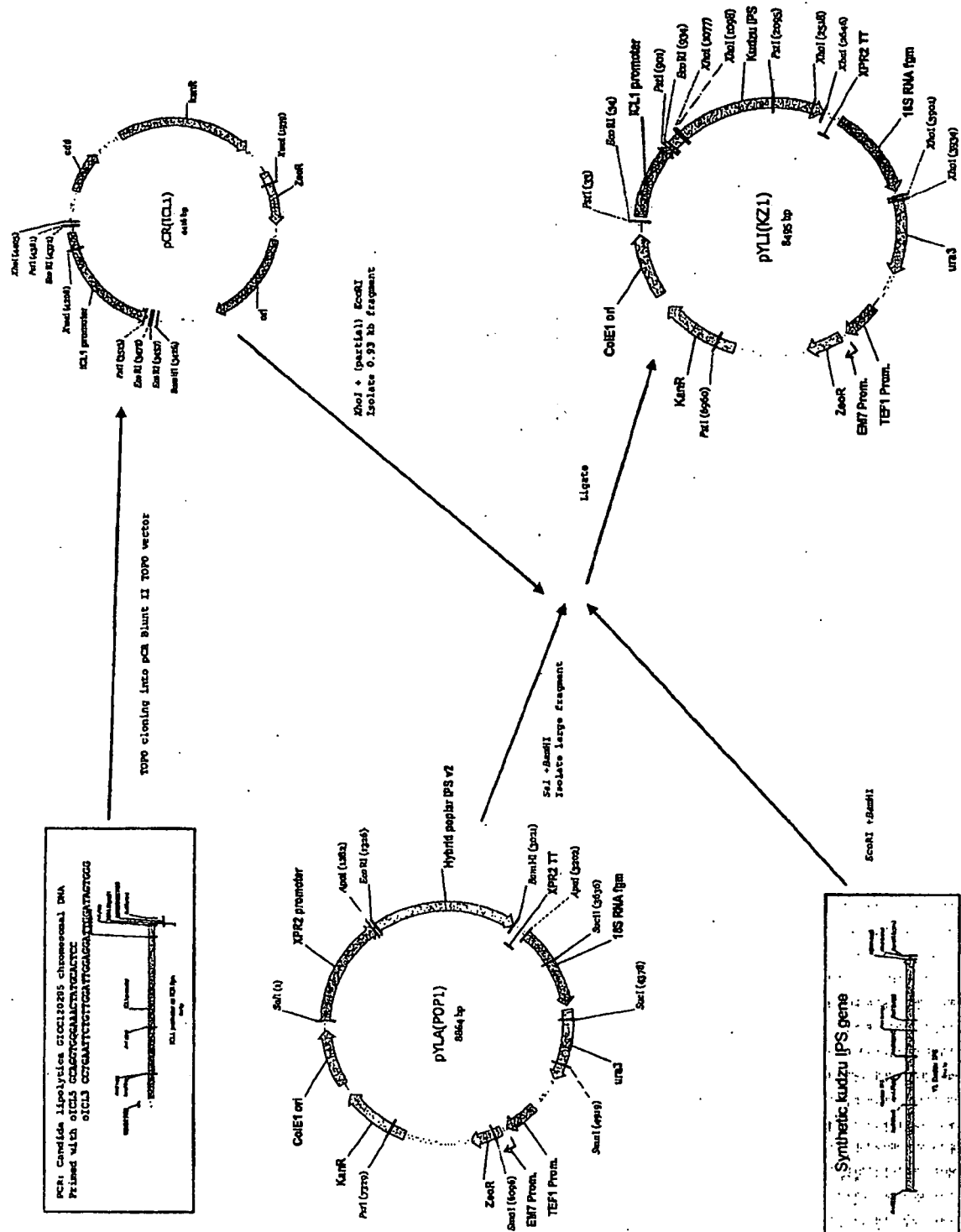


Figure 18E

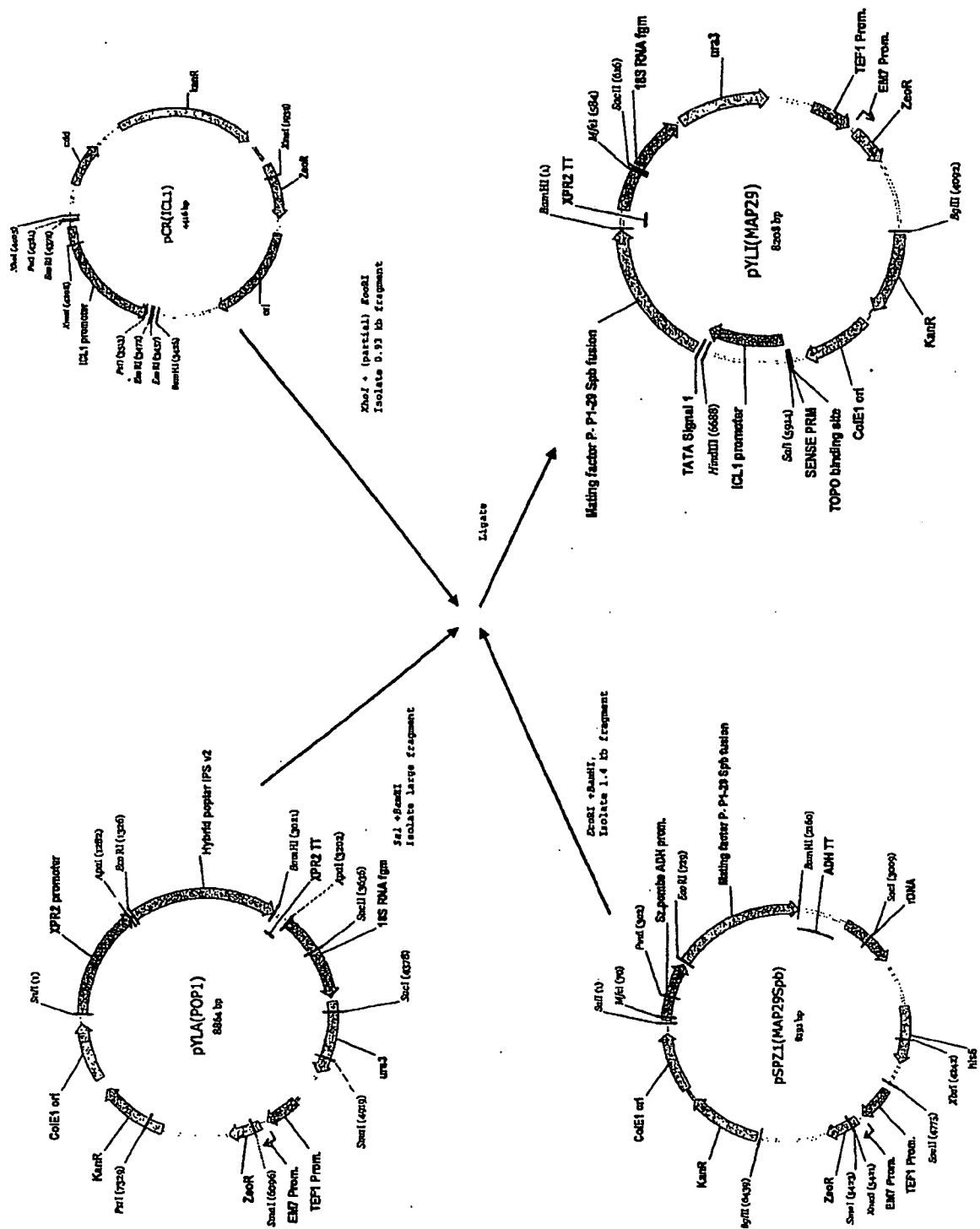


Figure 18F

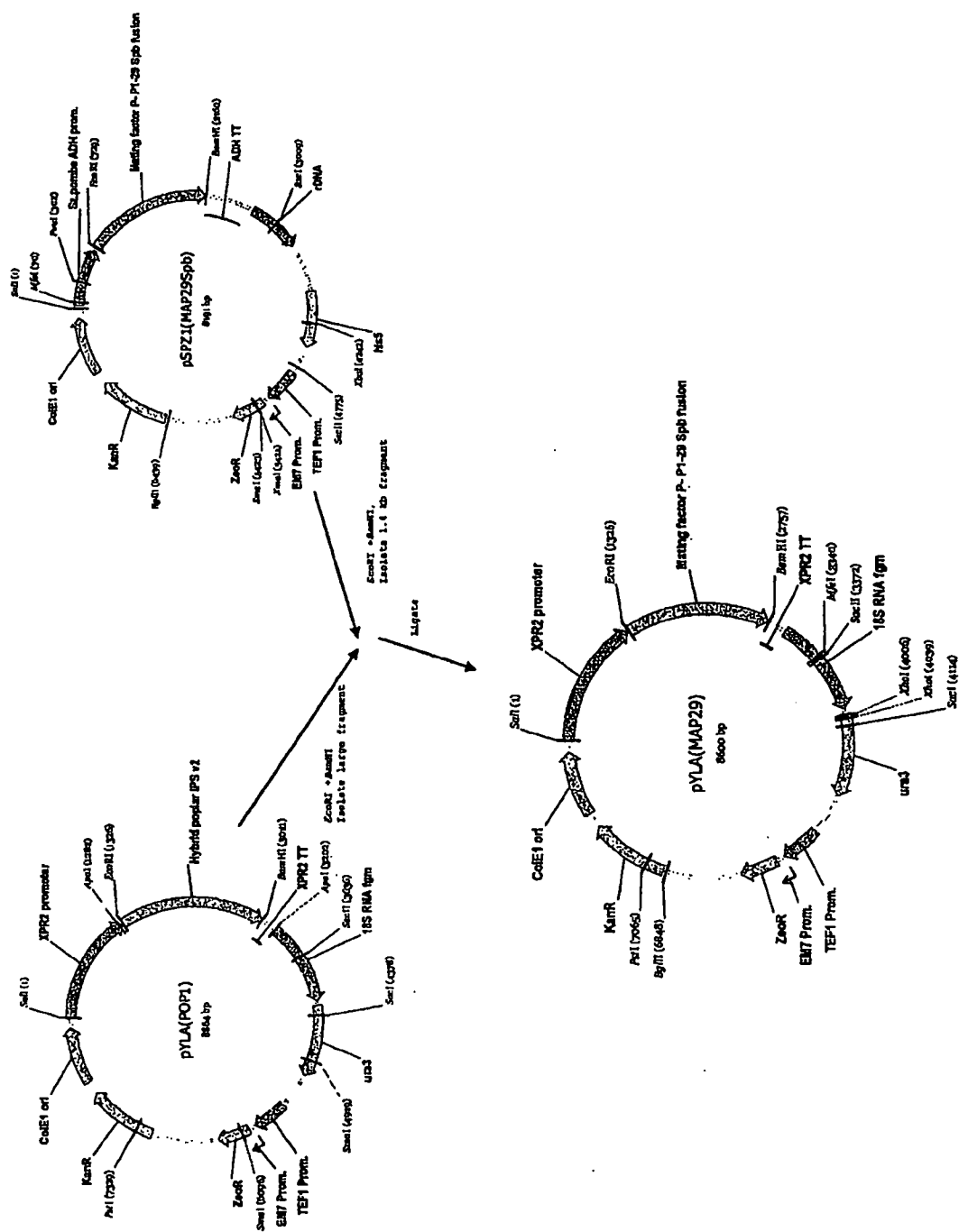


Figure 19A

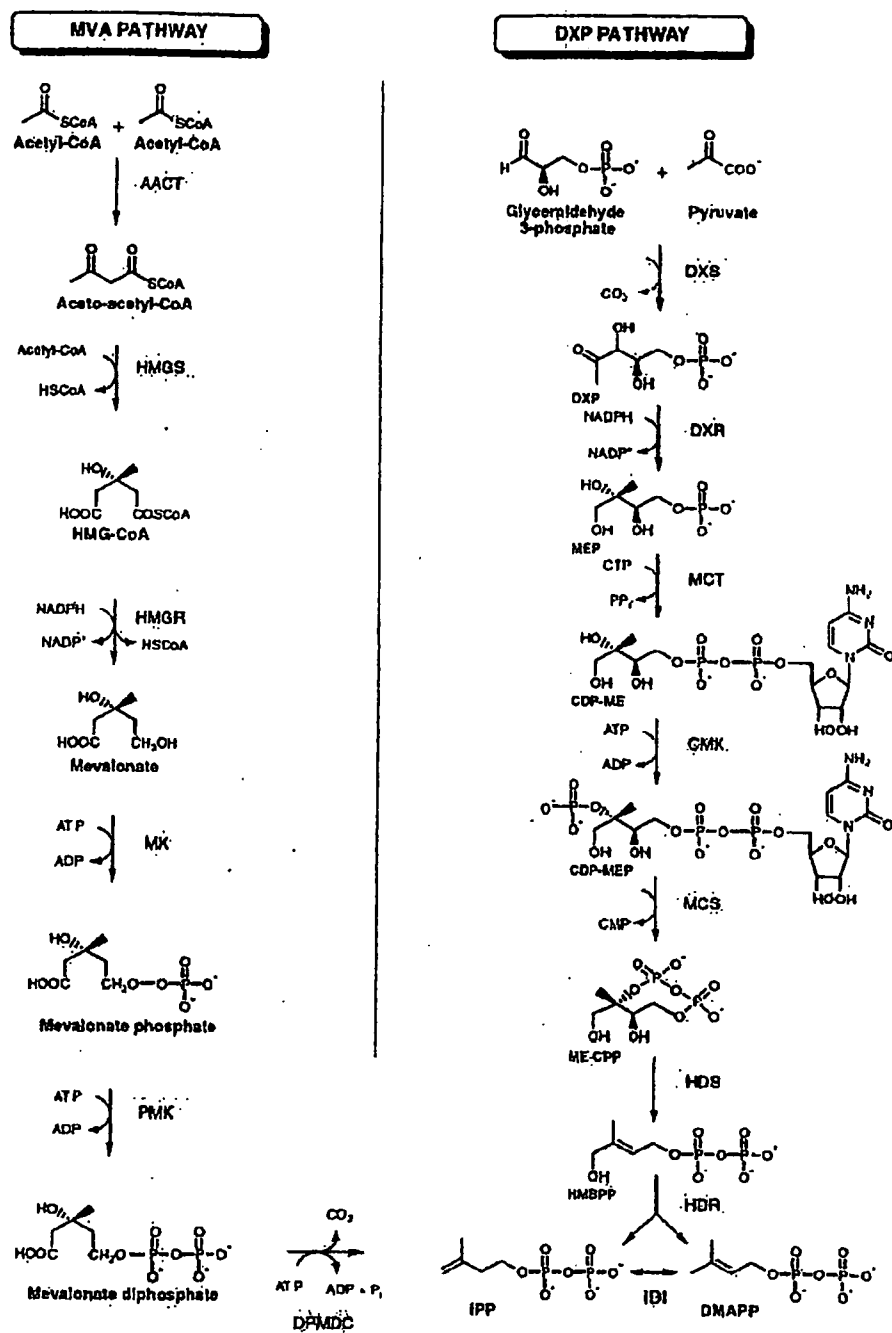


Figure 19B

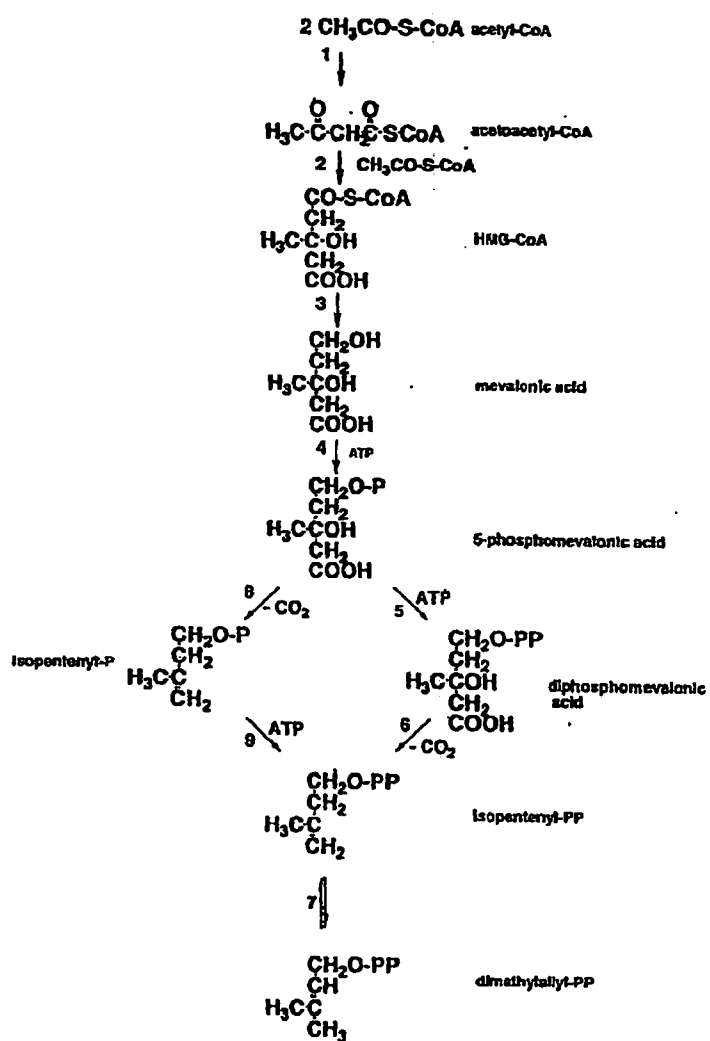


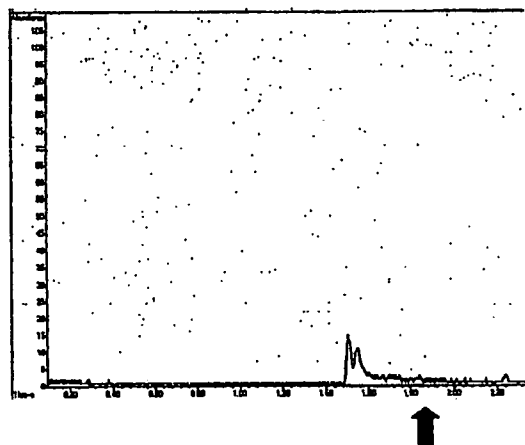
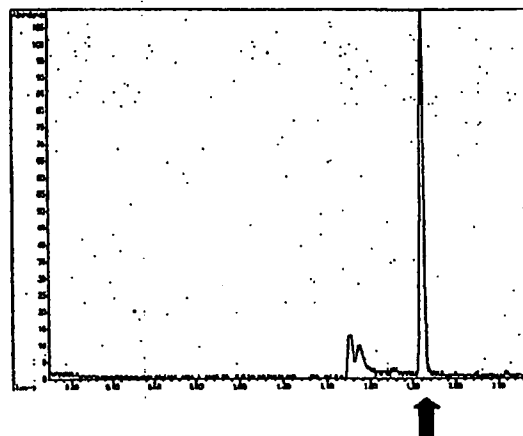
Figure 20***Y. lipolytica* CLIB122:: pYLA(MAP29)*****Y. lipolytica* CLIB122:: pYLA(KZ1)**

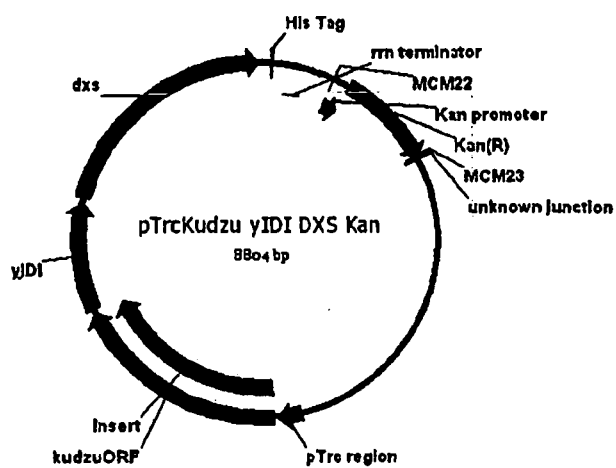
Figure 21

Figure 22A

1-

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Figure 22B

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Figure 22C

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Figure 22D

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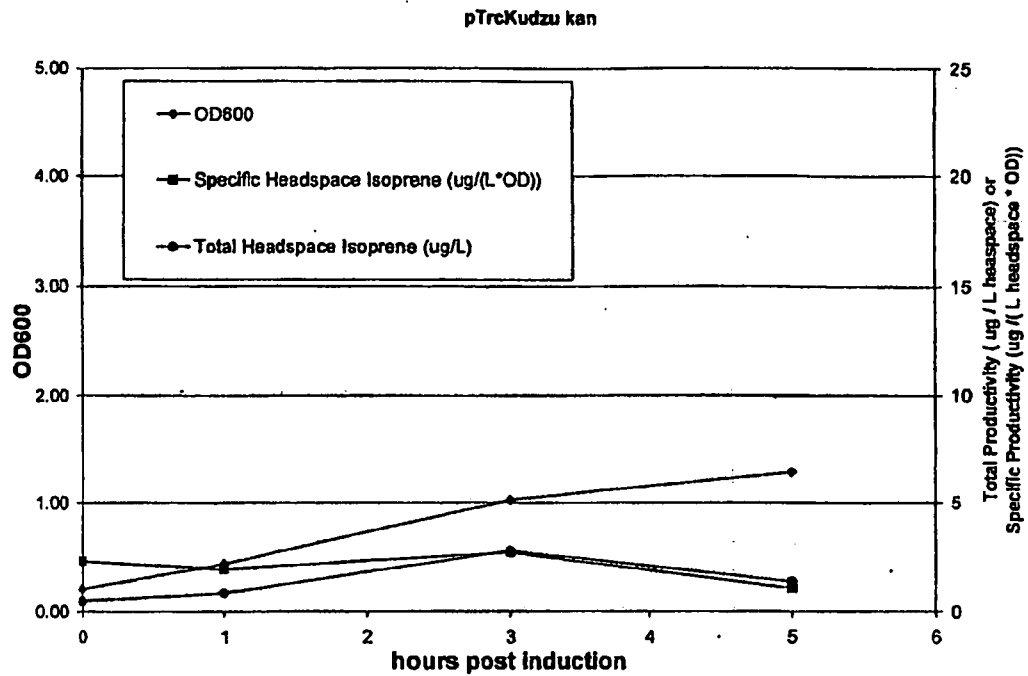
Figure 23A

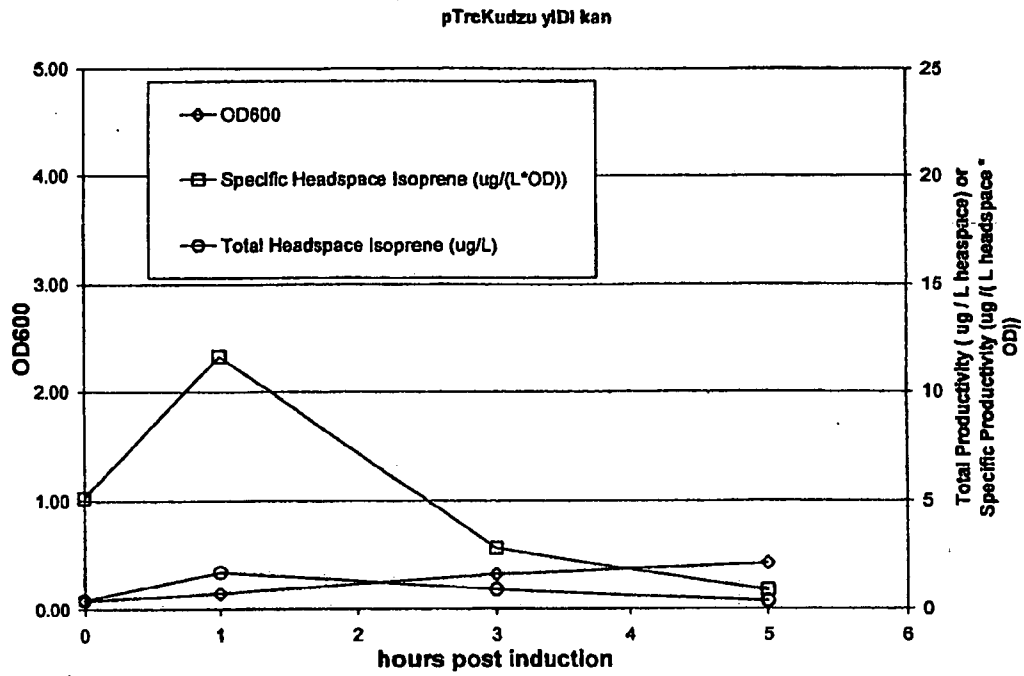
Figure 23B

Figure 23C

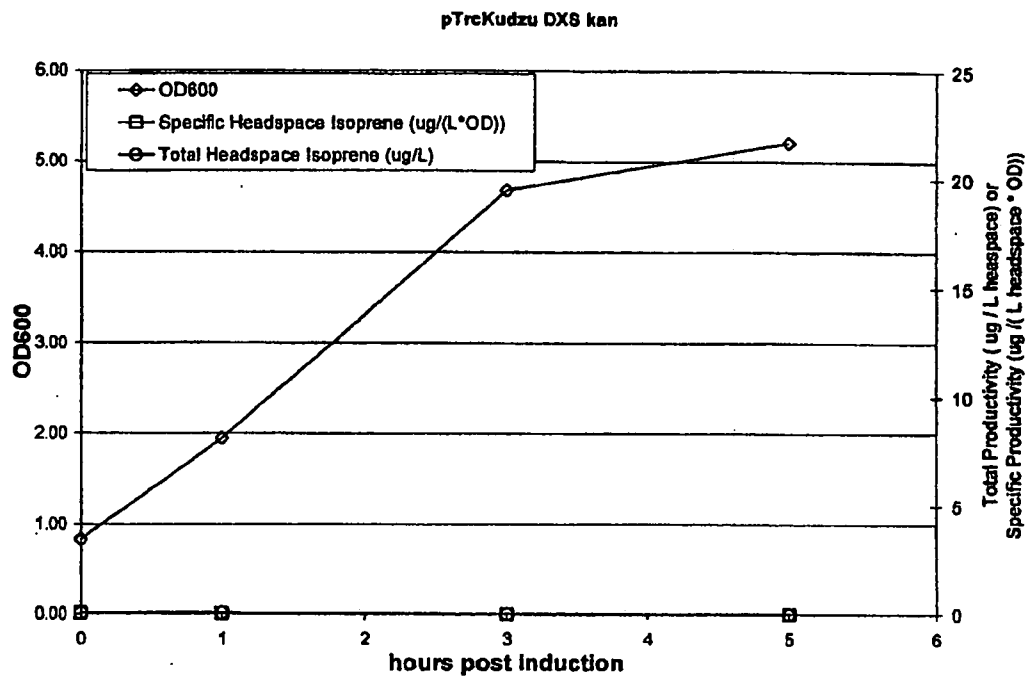


Figure 23D

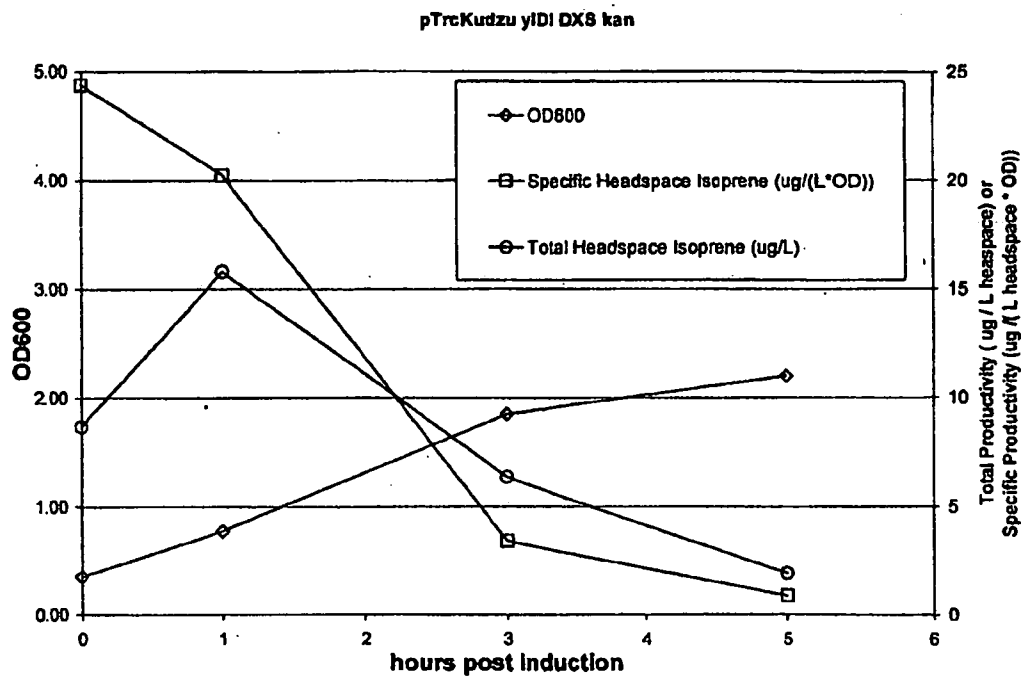


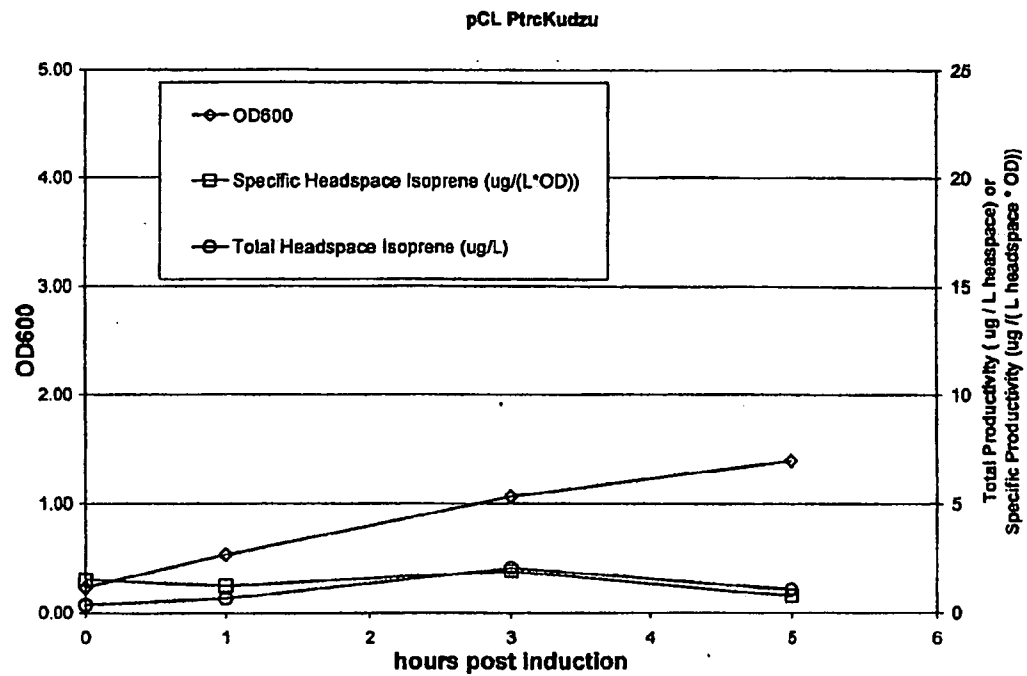
Figure 23E

Figure 23F

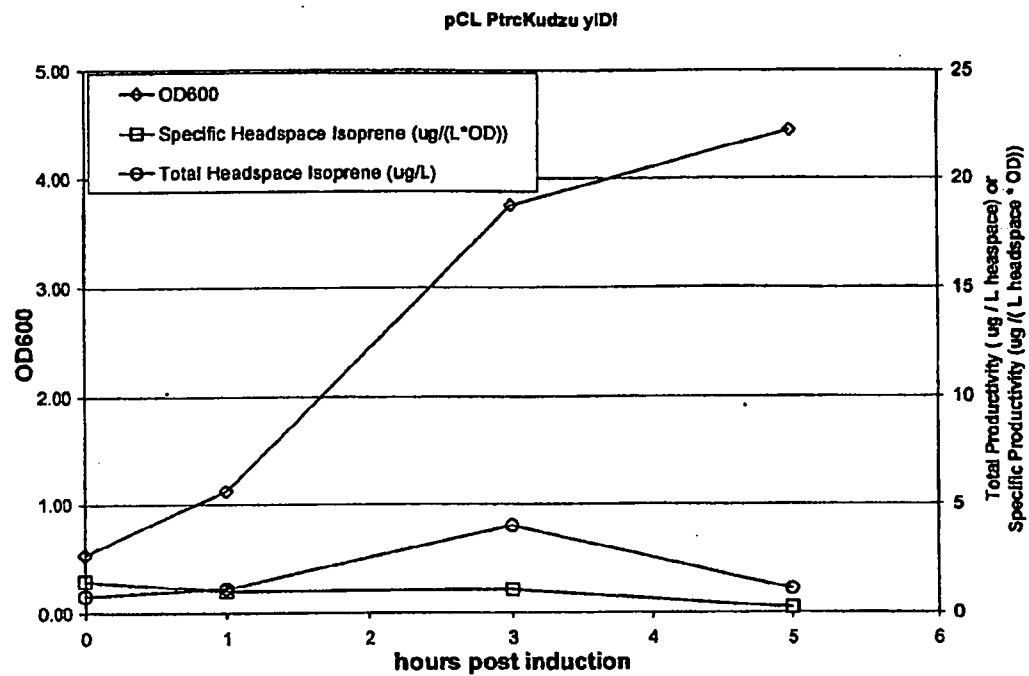


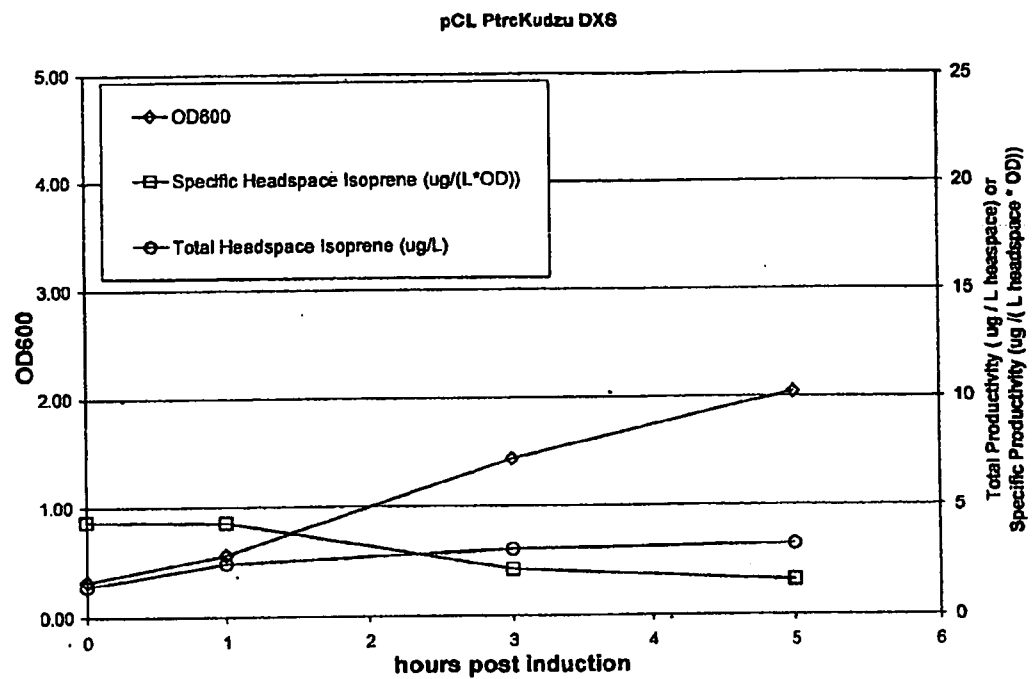
Figure 23G

Figure 23H

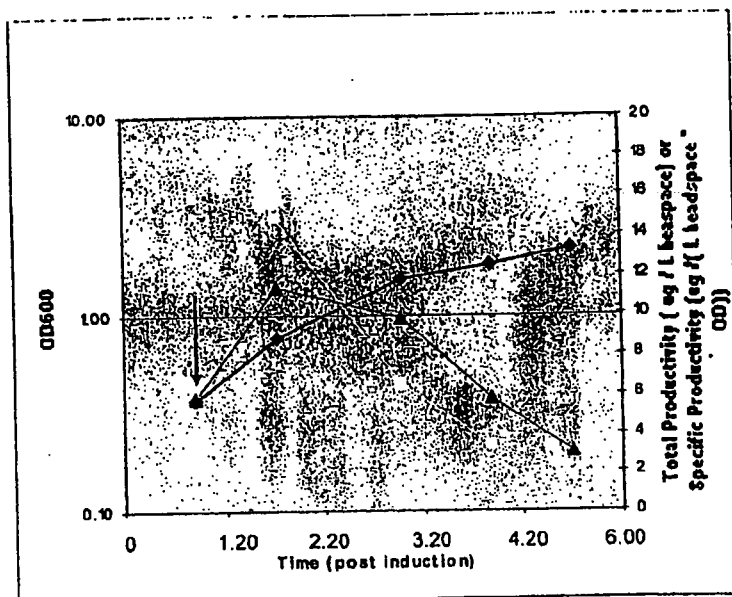


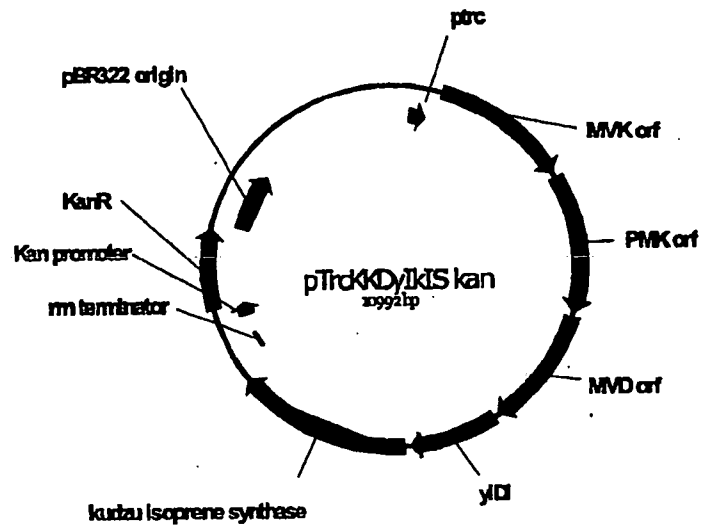
Figure 24

Figure 25A

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Figure 25B

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Figure 25C

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Figure 25D

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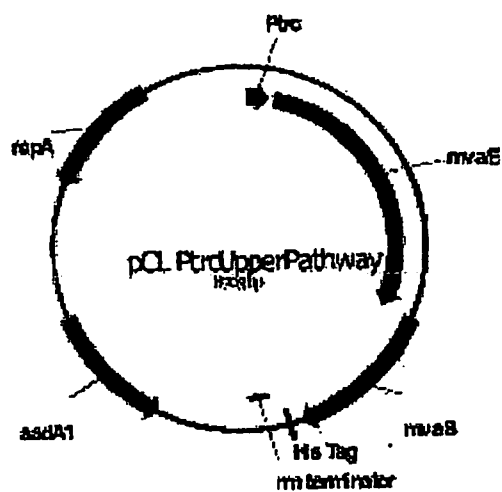
Figure 26

Figure 27A

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Figure 27B

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Figure 27C

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Figure 27D

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Figure 28

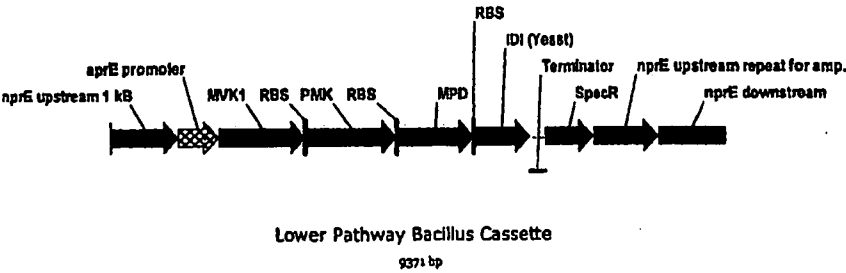


Figure 29A

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Figure 29B

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Figure 29C

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Figure 29D

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Figure 30

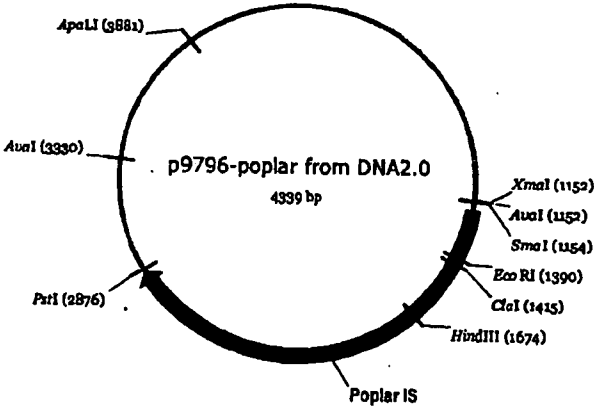


Figure 31A

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Figure 31B

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Figure 32

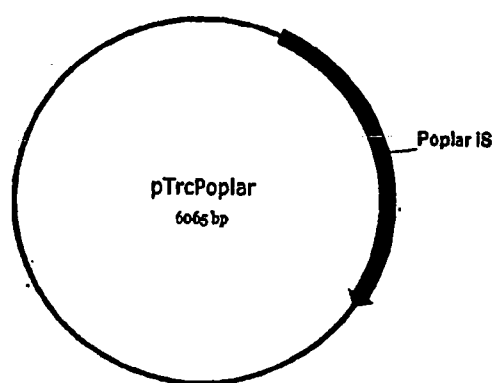


Figure 33A

5' -

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Figure 33B

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Figure 33C

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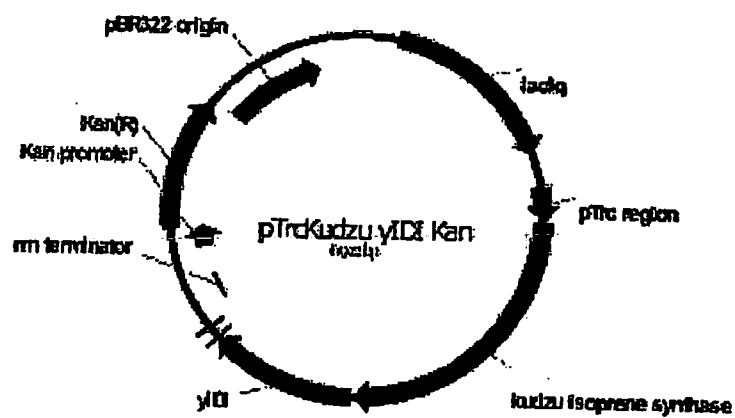
Figure 34

Figure 35A

5' -

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Figure 35B

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Figure 35C

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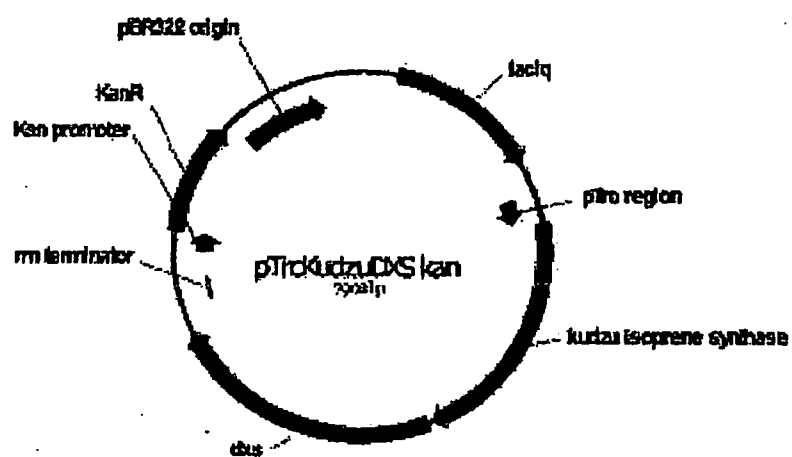
Figure 36

Figure 37A

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Figure 37B

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Figure 37C

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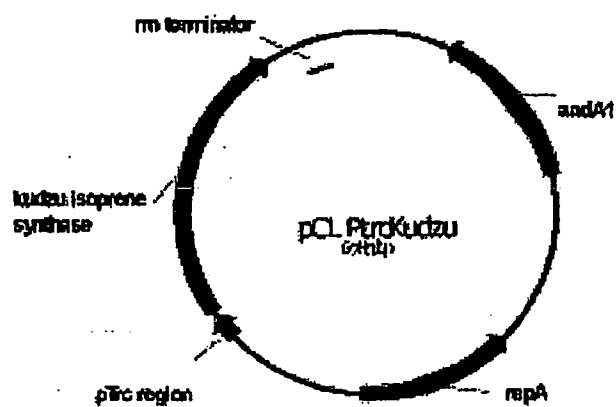
Figure 38

Figure 39A

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Figure 39B

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Figure 39C

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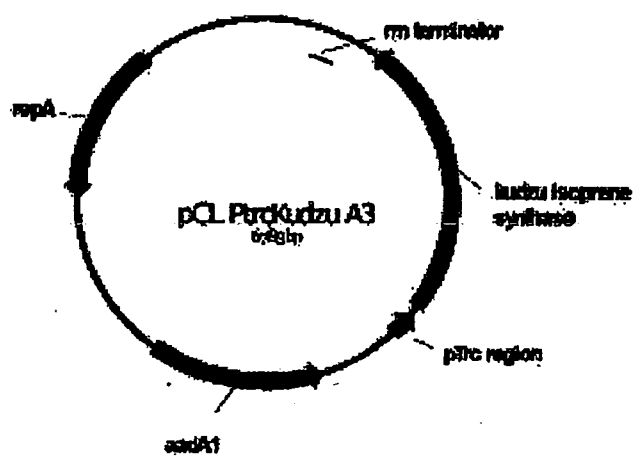
Figure 40

Figure 41A

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Figure 41B

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Figure 41C

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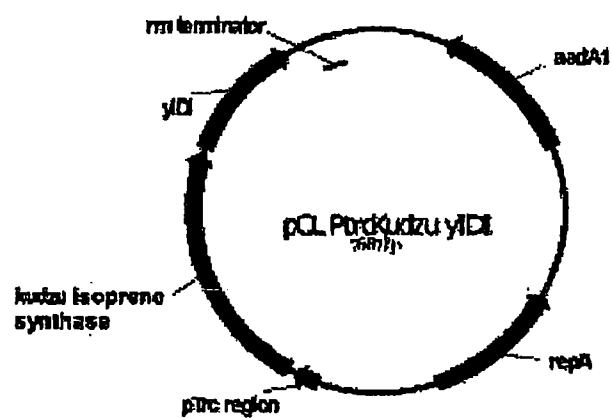
Figure 42

Figure 43A

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Figure 43B

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Figure 43C

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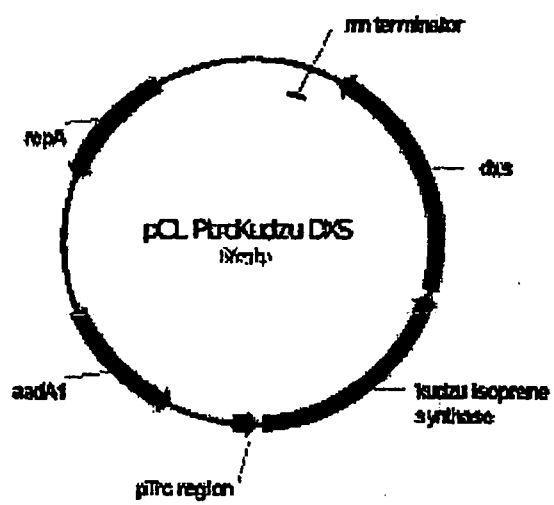
Figure 44

Figure 45A

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Figure 45B

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Figure 45C

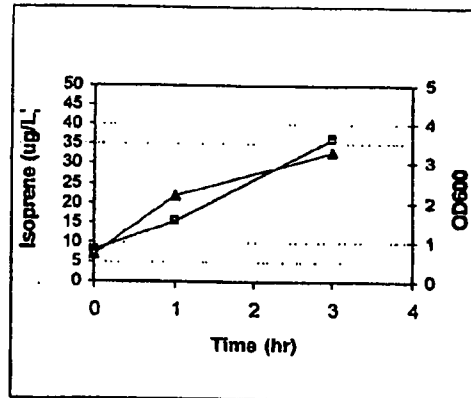
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Figure 45D

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(SEQ ID NO:55)

Figure 46A

A.

**Figure 46B**

B.

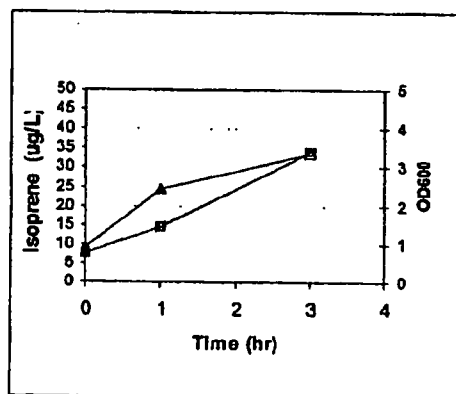
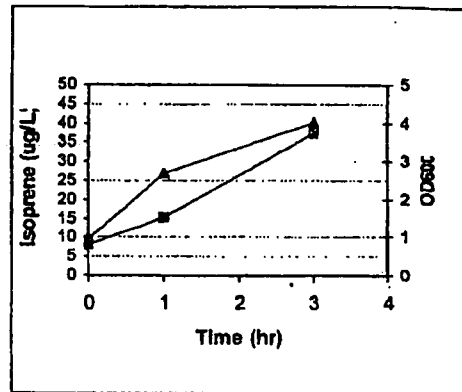


Figure 46C

C.

**Figure 46D**

D.

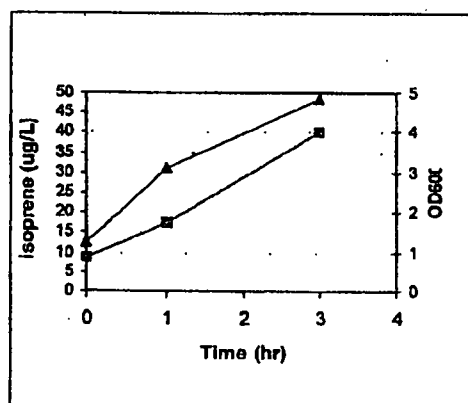


Figure 46E

E.

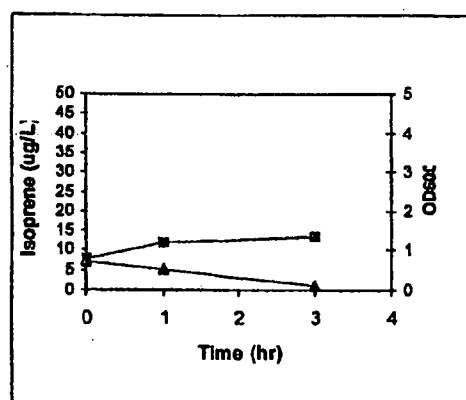


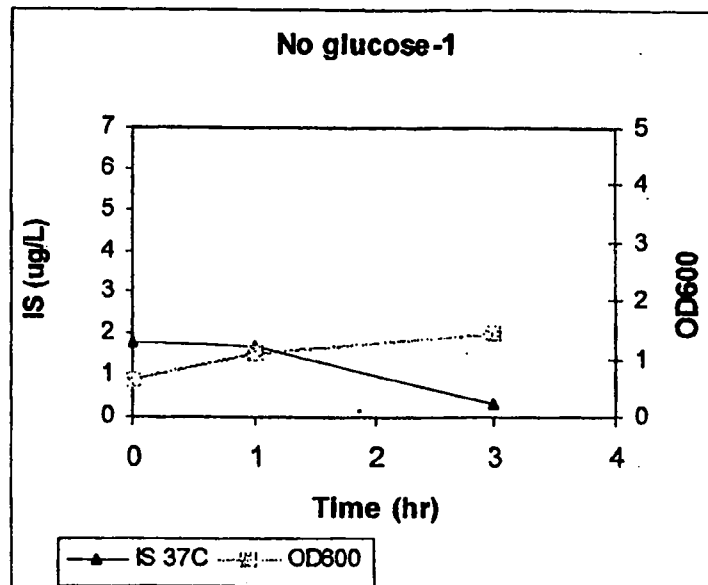
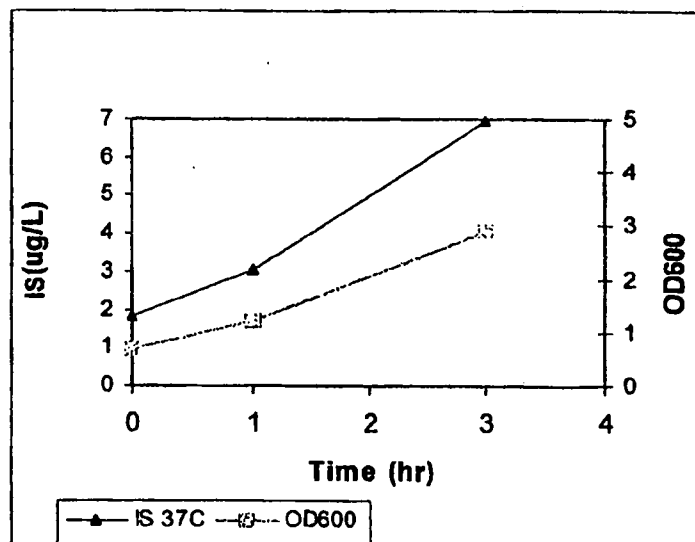
Figure 47A**Figure 47B**

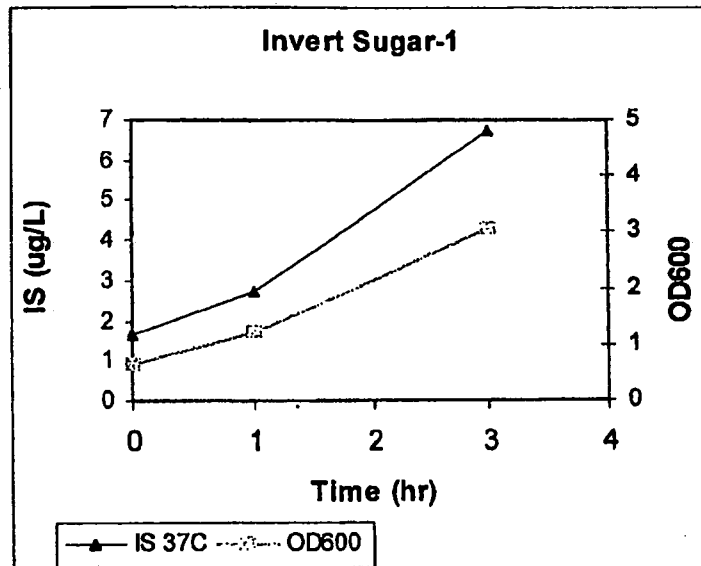
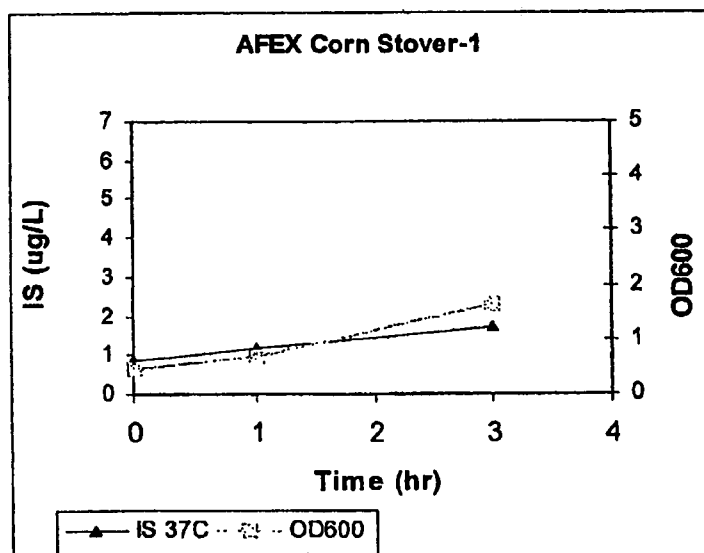
Figure 47C**Figure 47D**

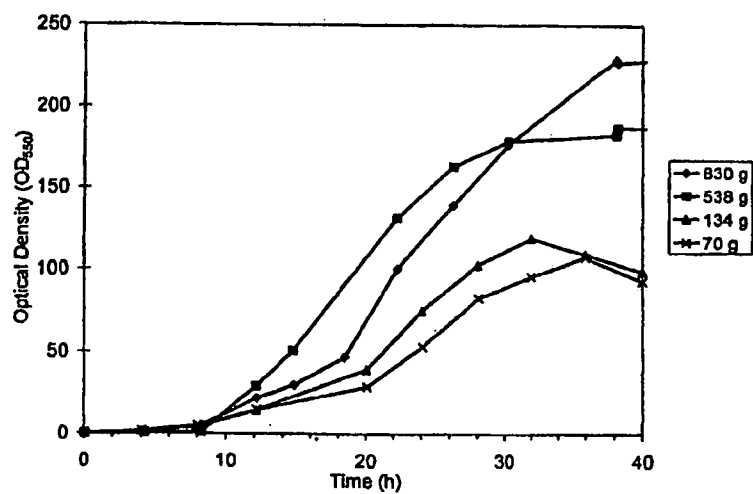
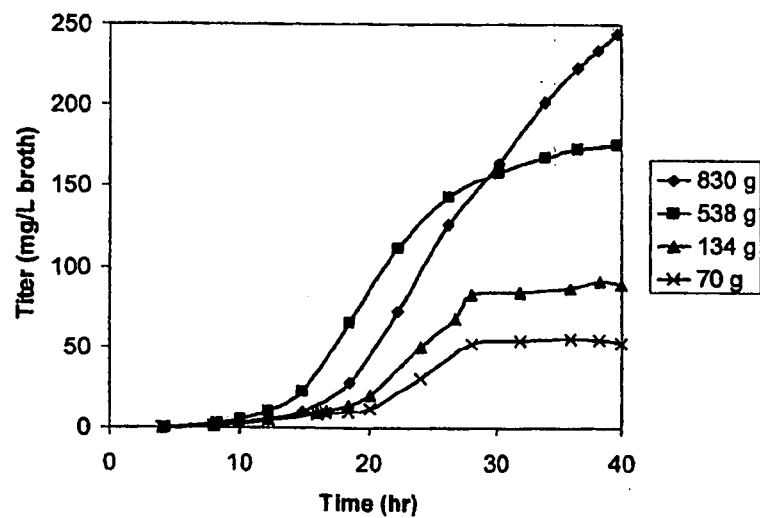
Figure 48A**Figure 48B**

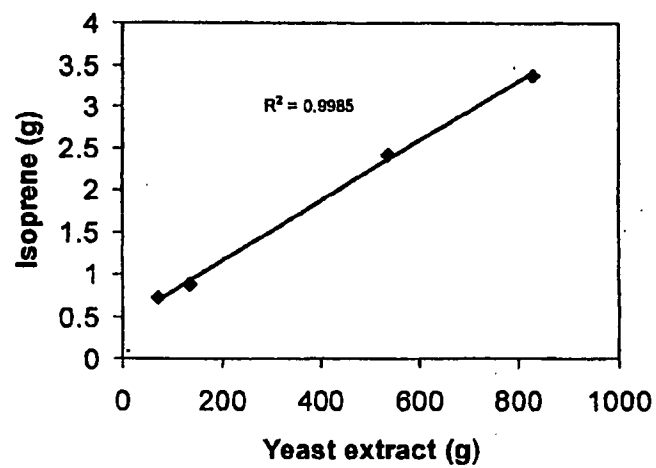
Figure 48C

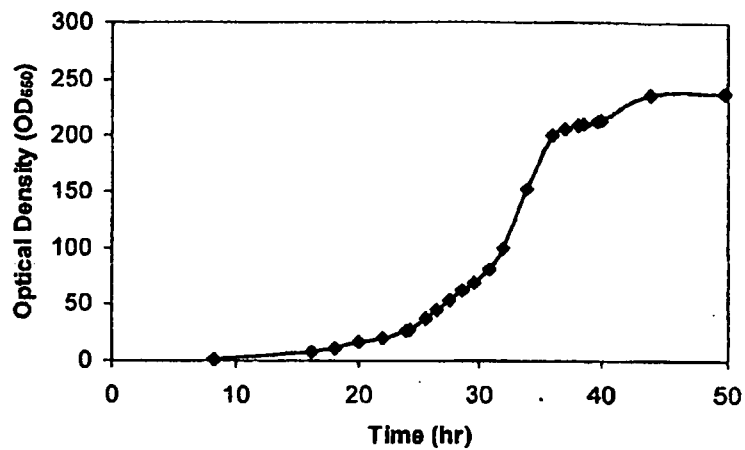
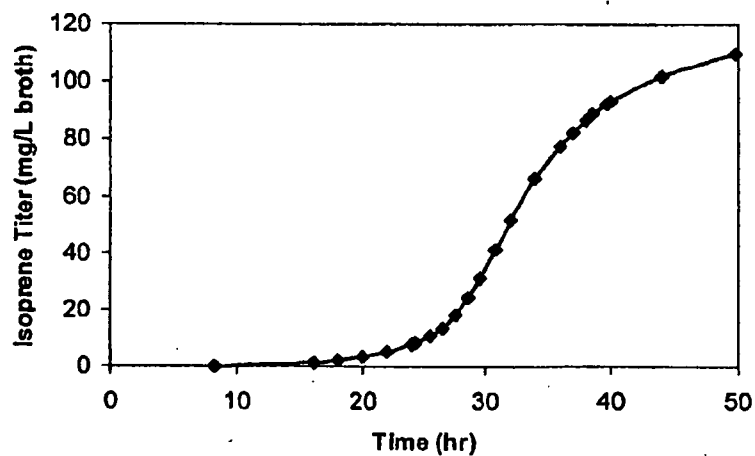
Figure 49A**Figure 49B**

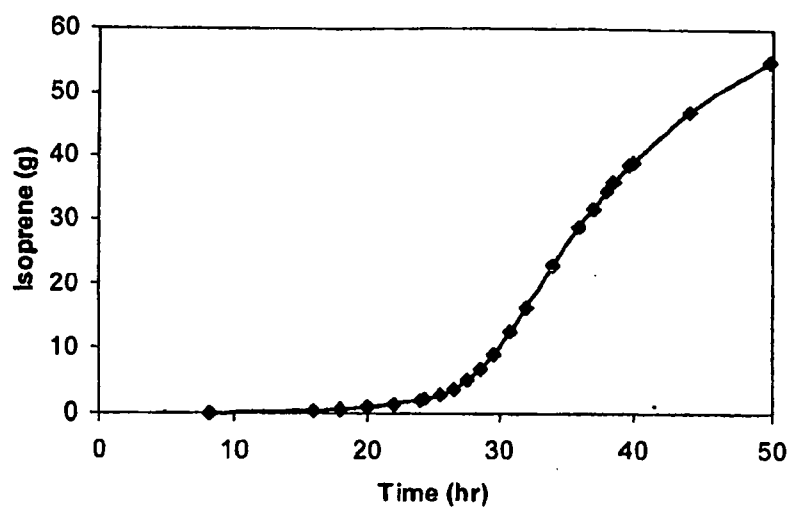
Figure 49C

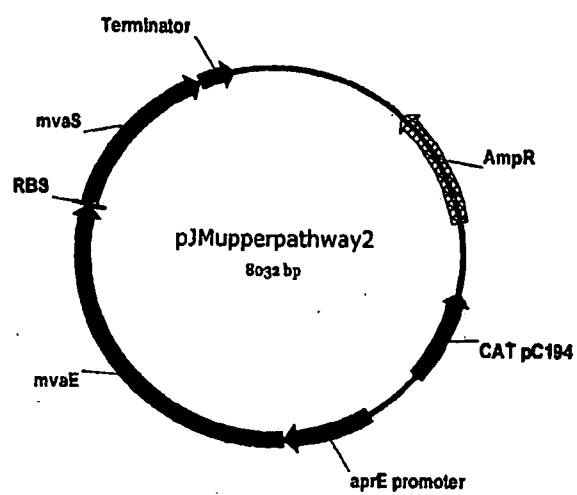
Figure 50

Figure 51A

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t a t c c a c a g a a t c a g g g g a t a a c g c a g g a a g a a c a t g t g a g c a a a a g g c c a g c a a a a g g c c a g
g a a c c g t a a a a a g g c c g c g t t g c t g g c g t t t t t c c a t a g g c t c c g c c c c c t g a c g a g c a t c a c
a a a a t c g a c g c t c a a g t c a g a g g t g g c g a a a c c c g a c a g g a c t a t a a a g a t a c c a g g c g t t t c
c c c t g g a a g c t c c c t c g t g c g c t c t c c t g t t c c g a c c c t g c c g t t a c c g g a t a c c t g t c c g c
c t t t c t c c c t t c g g a a g c g t g g c g c t t t t c t a t a g c t c a c g c t g t a g g t a t c t c a g t t c g g t g
t a g g t c g t t c g c t c c a a g c t g g g c t g t g t g c a c g a a c c c c c g t t c a g c c c g a c c g c t g c g c c t
t a t c c g g t a a c t a t c g t c t t g a g t c c a a c c c g g t a a g a c a c g a c t t a t c g c c a c t g g c a g c a g c
c a c t g g t a a c a g g a t t a g c a g a g c g a g g t a t g t a g g c g g t g c t a c a g a g t t c t t g a a g t g g t g g
c c t a a c t a c g g c t a c a c t a g a a g a a c a g t a t t t g g t a t c t g c g c t c t g c t g a a g c c a g t t a c c t
t c g g a a a a a g a g t t g g t a g c t c t t g a t c c g g c a a c a a a c c a c c g c t g g t a g c g g t g g t t t t t
t g t t t g c a a g c a g c a g a t t a c g c g c a g a a a a a a g g a t c t c a a g a a g a t c c t t t g a t c t t t t c t
a c g g g g t c t g a c g c t c a g t g g a a c g a a a a c t c a c g t t a a g g g a t t t t g g t c a t g a g a t t a t c a a
a a a g g a t c t t c a c c t a g a t c c t t t t a a a t t a a a a t g a a g t t t t a a t c a a t c t a a a g t a t a t a
t g a g t a a a c t t g g t c t g a c a g t t a c c a a t g c t t a a t c a g t g a g g c a c c a t c t c a g c g a t c t g t
c t a t t t c g t t c a t c c a t a g t t g c c t g a c t c c c c g t c g t g t a g a t a a c t a c g a t a c g g g a g g g c t
t a c c a t c t g g c c c c a g t g c t g c a a t g a t a c c g c g a g a c c c a c g c t c a c c g g c t c c a g a t t t a t c
a g c a a t a a a c c a g c c a g c c g g a a g g g c c g a g c g c a g a a g t g g t c c t g c a a c t t t a t c c g c c t c c
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c g g g a t a a t a c c g c g c c a c a t a g c a g a a c t t t a a a a g t g c t c a t c a t t g g a a a c g t t c t t c g g
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c a a c t g a t c t t c a g c a t c t t t t a c t t t c a c c a g c g t t t c t g g g t g a g c a a a a c a g g a a g g c a a
a a t g c c g c a a a a a g g g a a t a a g g g c g a c a c g g a a a t g t t g a a t a c t c a t a c t c t t c c t t t t c
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g a a a a t a a c a a a t a g g g g t t c c g c g c a c a t t t c c c c g a a a a g t g c c a c c t g a c g t c t a a g a a
a c c a t t a t t a t c a t g a c a t t a a c c t a t a a a a a t a g g c g t a t c a c g a g g c c c t t t c g t c t c g c g c
g t t t c g g t g a t g a c g g t g a a a a c c t c t g a c a c a t g c a g c t c c c g g a g a c g g t c a c a g c t t g t c t
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g g c t g g c t t a a c t a t g c g g c a t c a g a g c a g a t t g t a c t g a g a g t g c a c c a t a g a t c t g g a g c t g
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g g t a a t a t a t t g a a t t a c c t t t a t t a a t g a a t t t t c c t g c t g t a a t a a t g g g t a g a a g g t a a t
t a c t a t t a t t a t t g a t a t t t a a g t t a a a c c a g t a a a t g a a g t c c a t g g a a t a a t a g a a g a g a
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t c a g a a a g g t a t a a a t c a t a a a a c t c t t t g a a g t c a t t c t t t a c a g g a g t c c a a a t a c c a g a g a
a t g t t t t a g a t a c a c c a t c a a a a a t t g t a t a a a g t g g c t c t a a c t t a t c c c a a t a a c c t a a c t c
t c c g t c g c t a t t g t a a c c a g t t c t a a a a g c t g t a t t t g a g t t t a t c a c c c t t g t c a c t a a g a a a
a t a a a t g c a g g g t a a a a t t t a t a t c c t t c t t g t t t t a t g t t t c

Figure 51B

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Figure 51C

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Figure 52

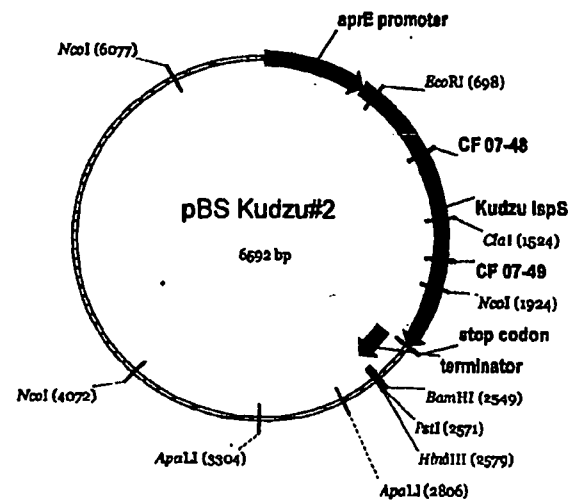


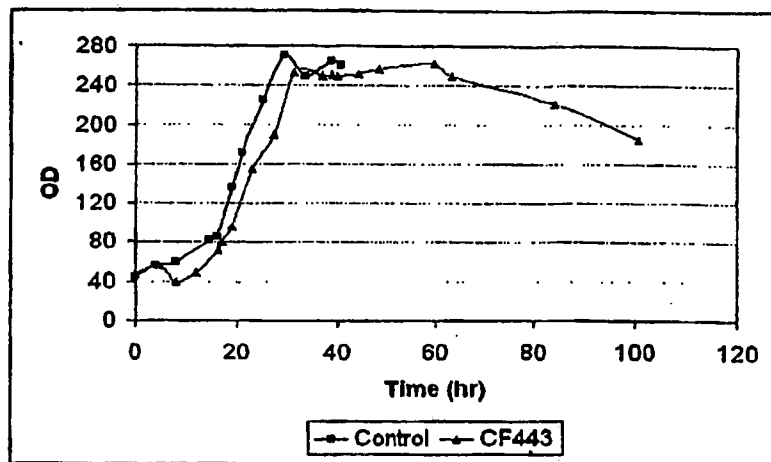
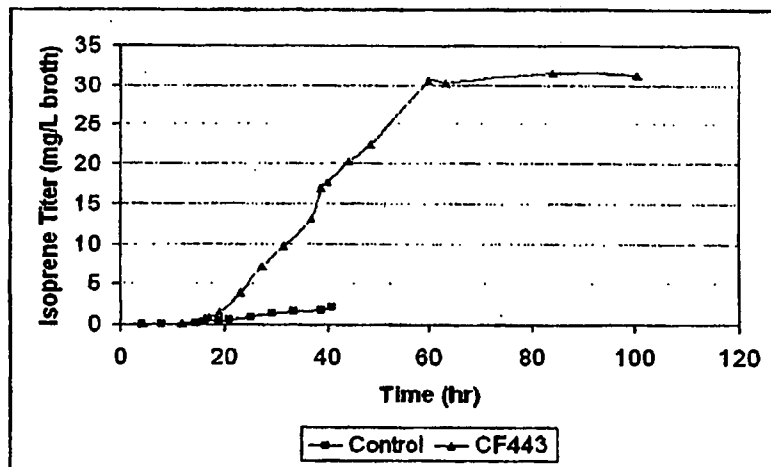
Figure 53A**Figure 53B**

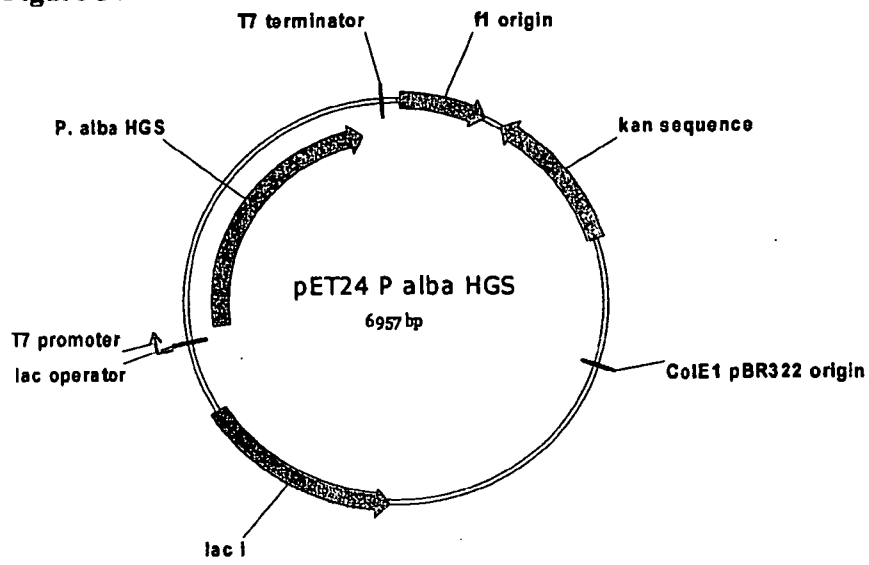
Figure 54

Figure 55A

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Figure 55B

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Figure 56

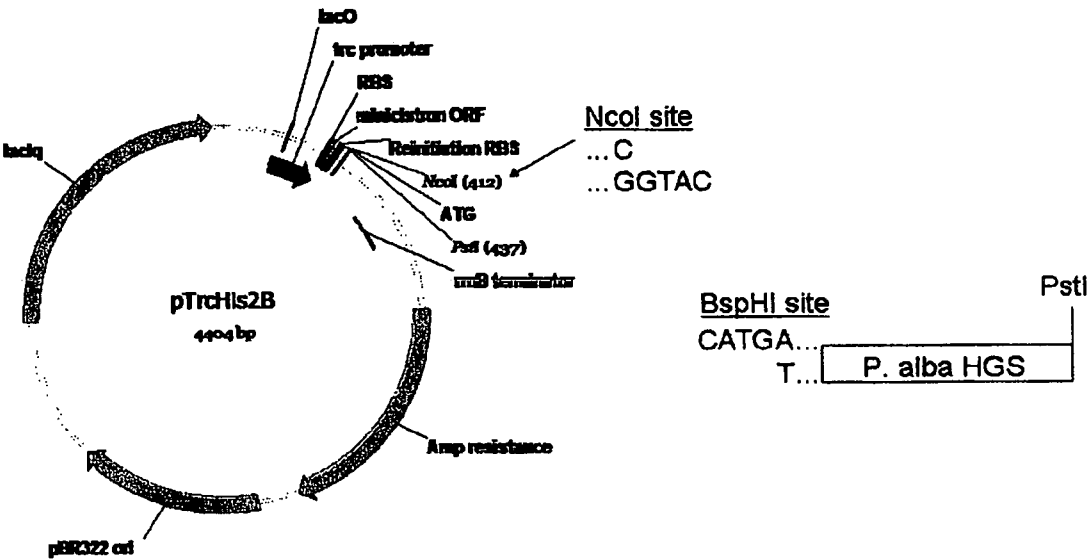


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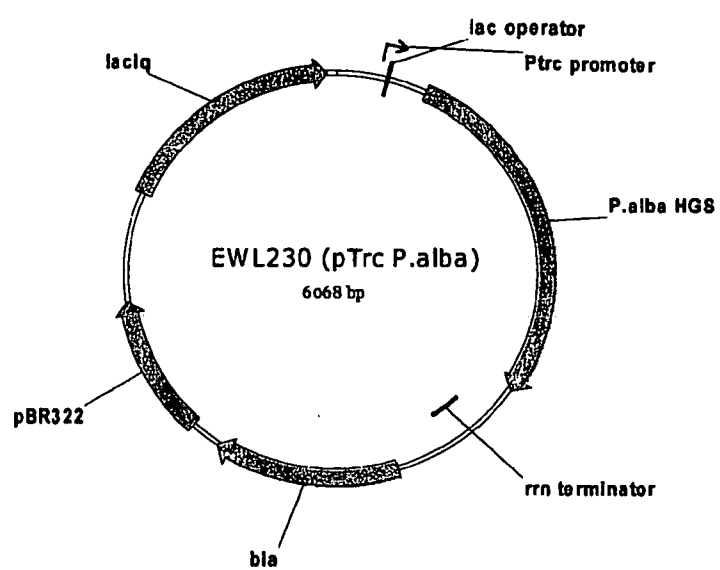


Figure 58A

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Figure 58B

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Figure 59

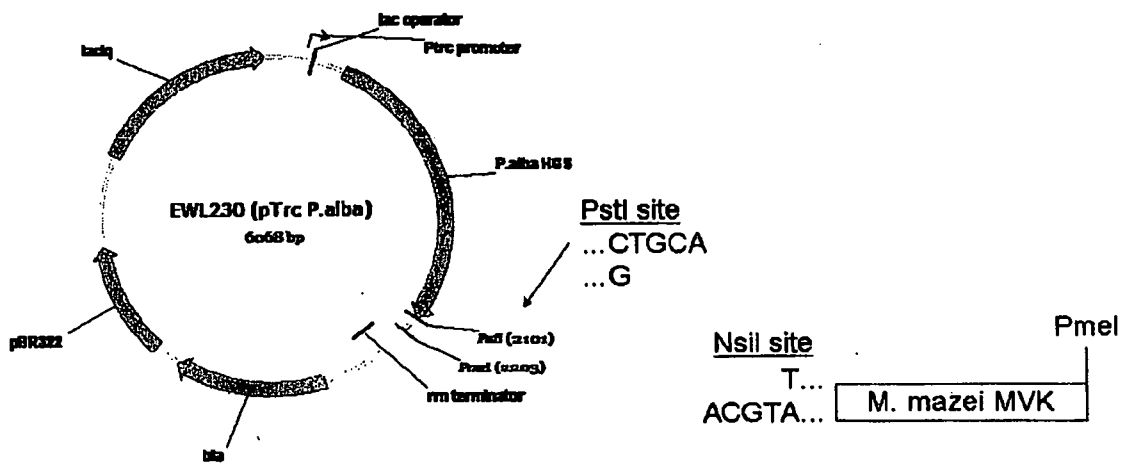


Figure 60

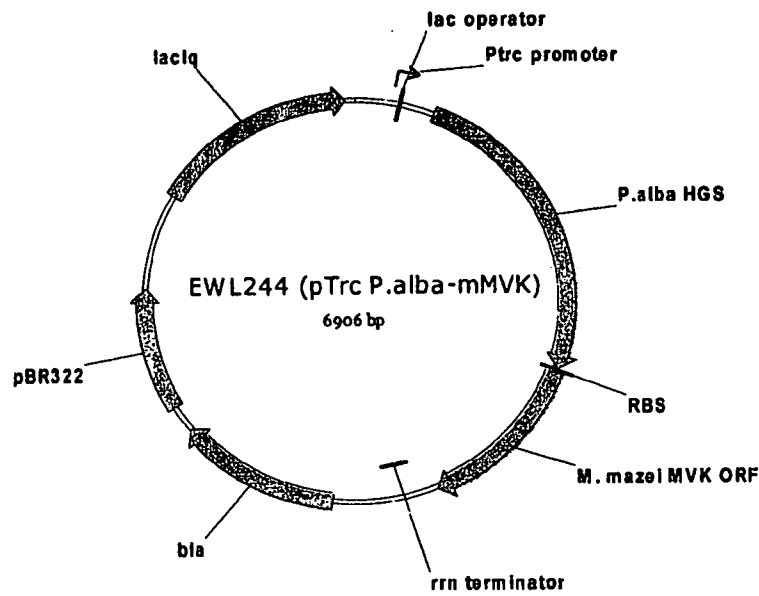


Figure 61A

1-

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Figure 61B

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Figure 62

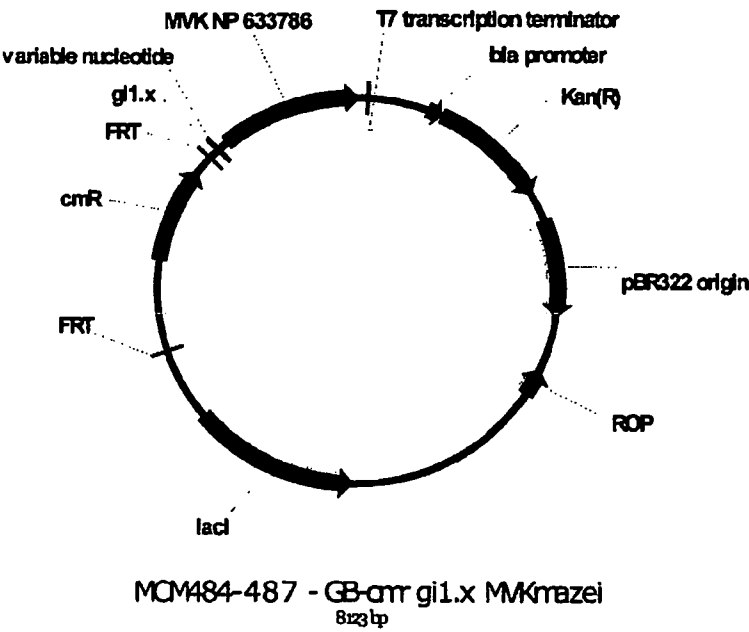


Figure 63C

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Figure 64A

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Figure 64C

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Figure 65A

1-

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Figure 65B

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Figure 65C

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Figure 66A

1-

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Figure 66B

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Figure 66C

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Figure 67A

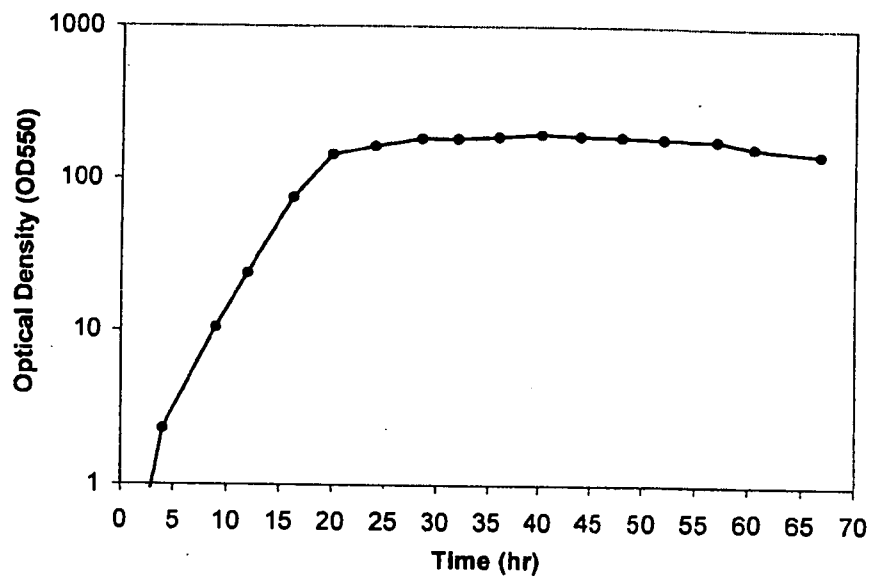


Figure 67B

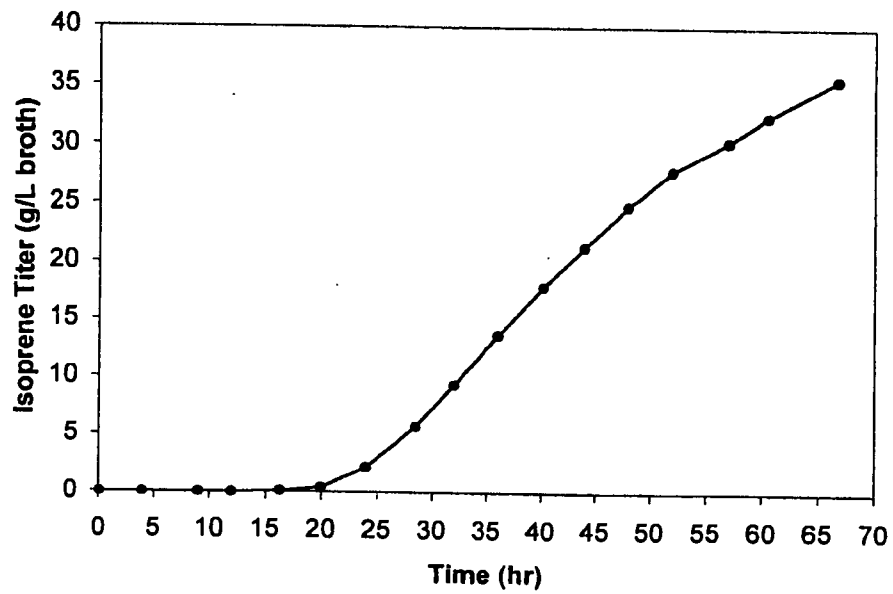


Figure 67C

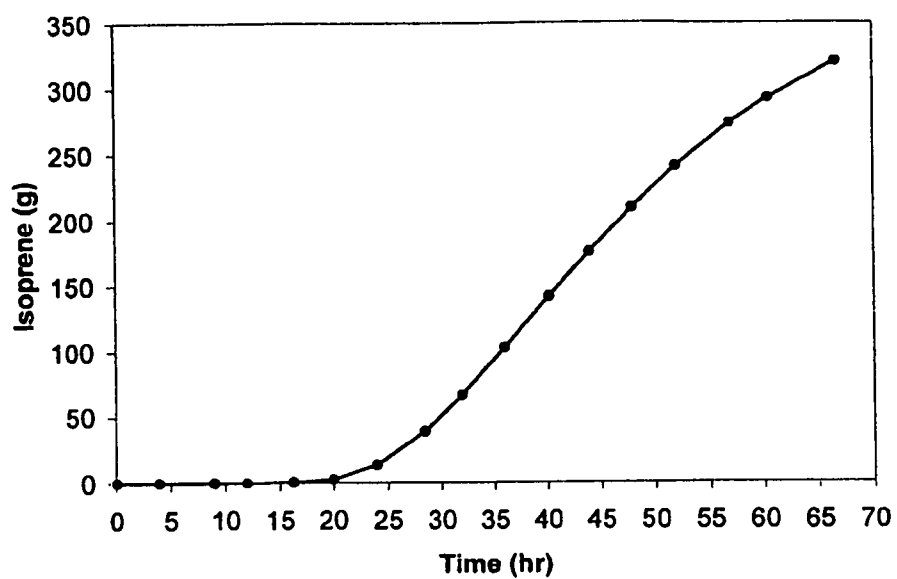


Figure 67D

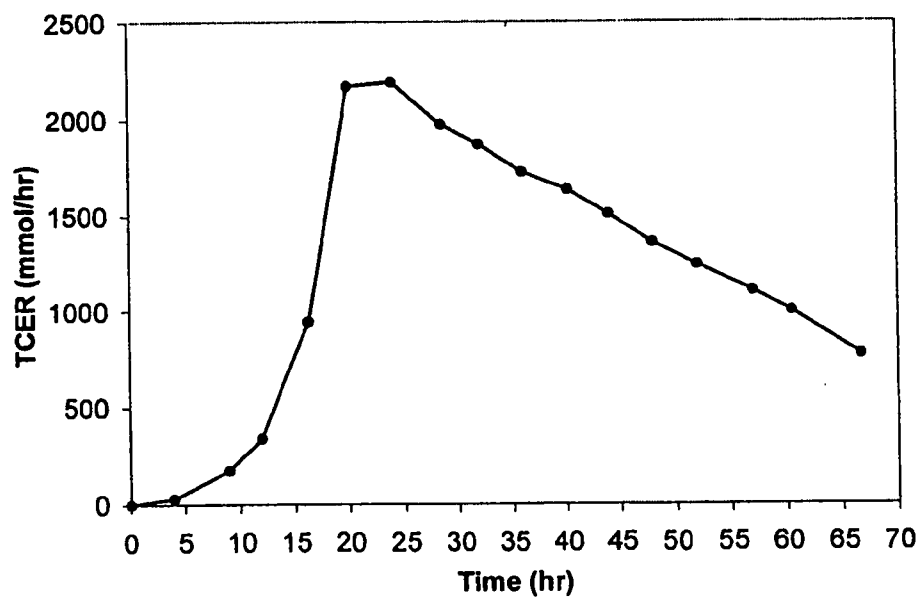


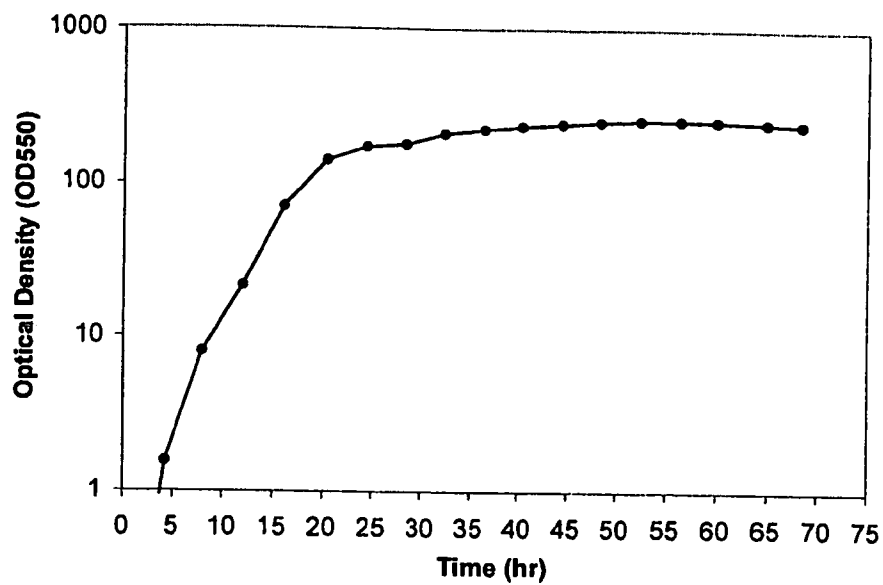
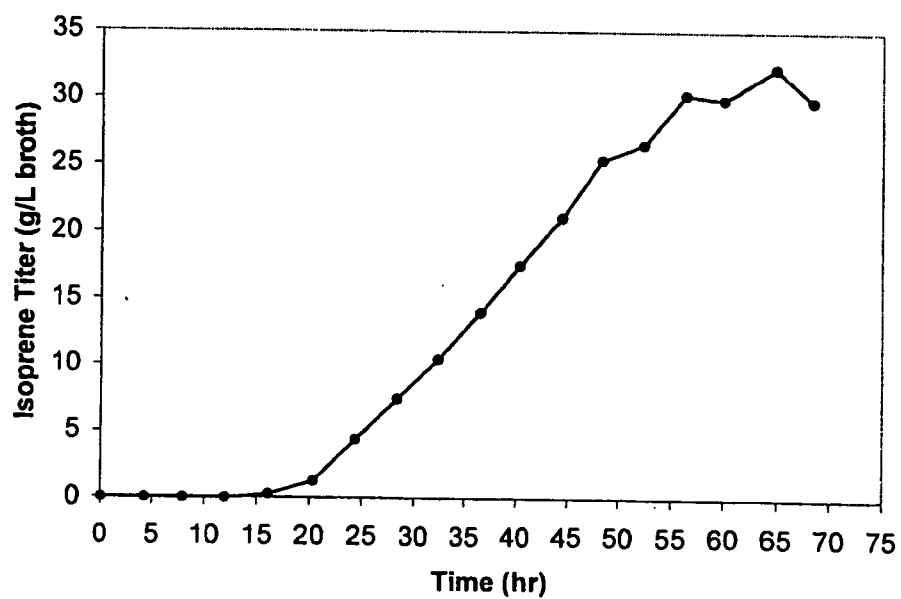
Figure 68A**Figure 68B**

Figure 68C

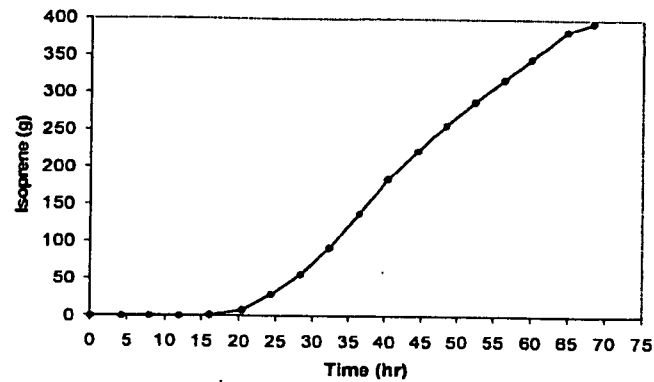


Figure 68D

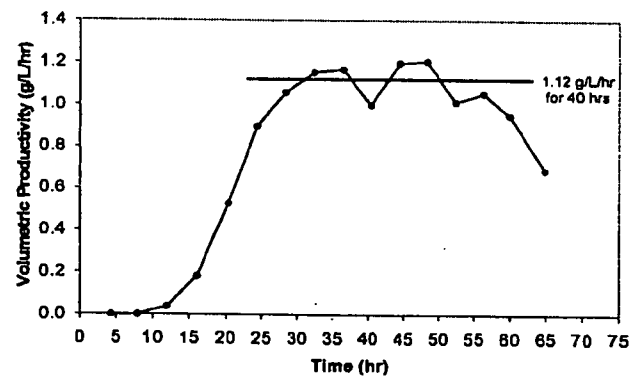


Figure 68E

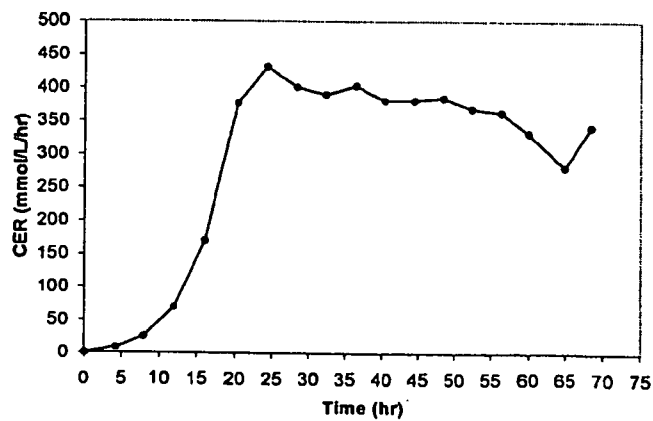


Figure 69A

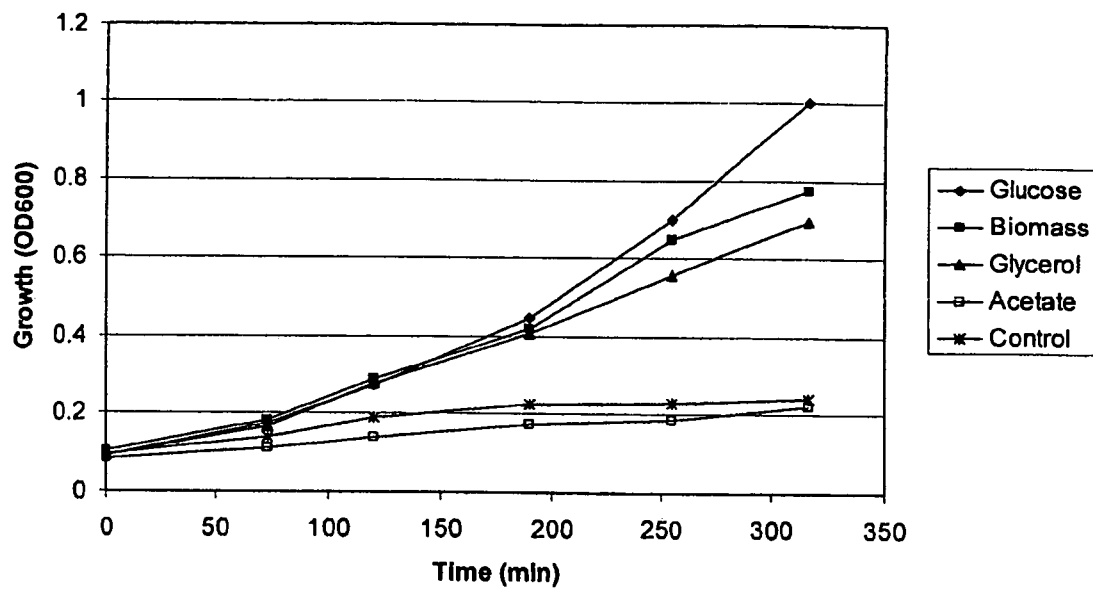


Figure 69B

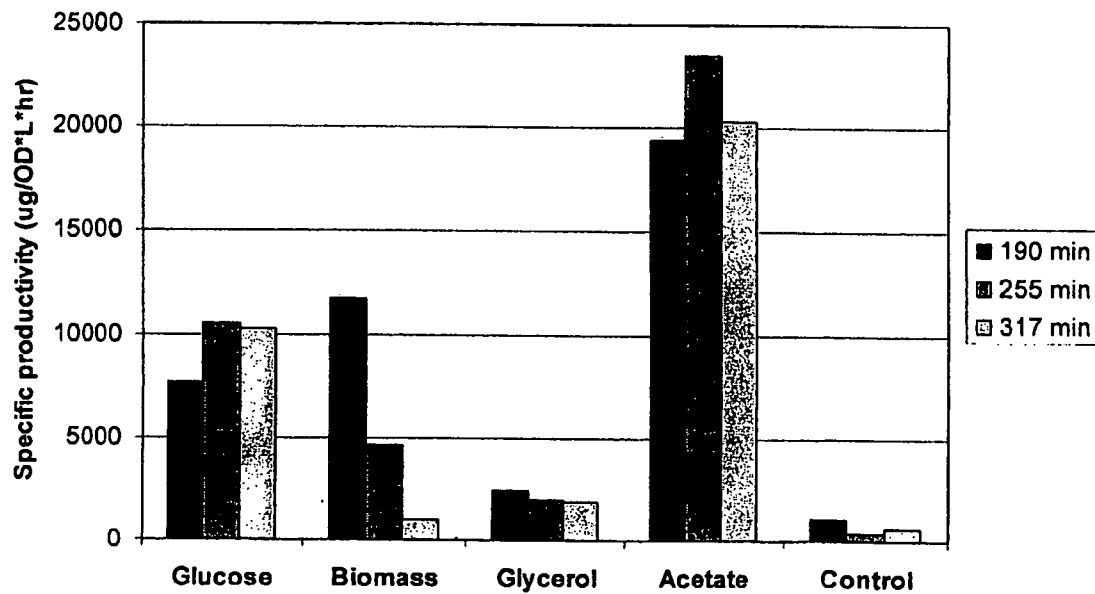


Figure 69C

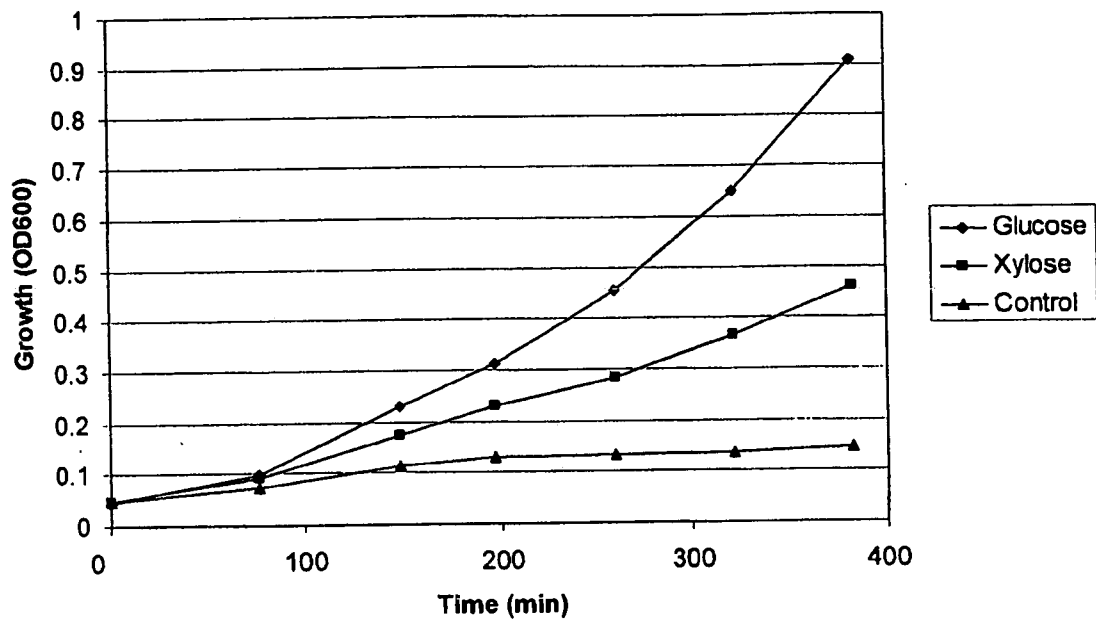


Figure 69D

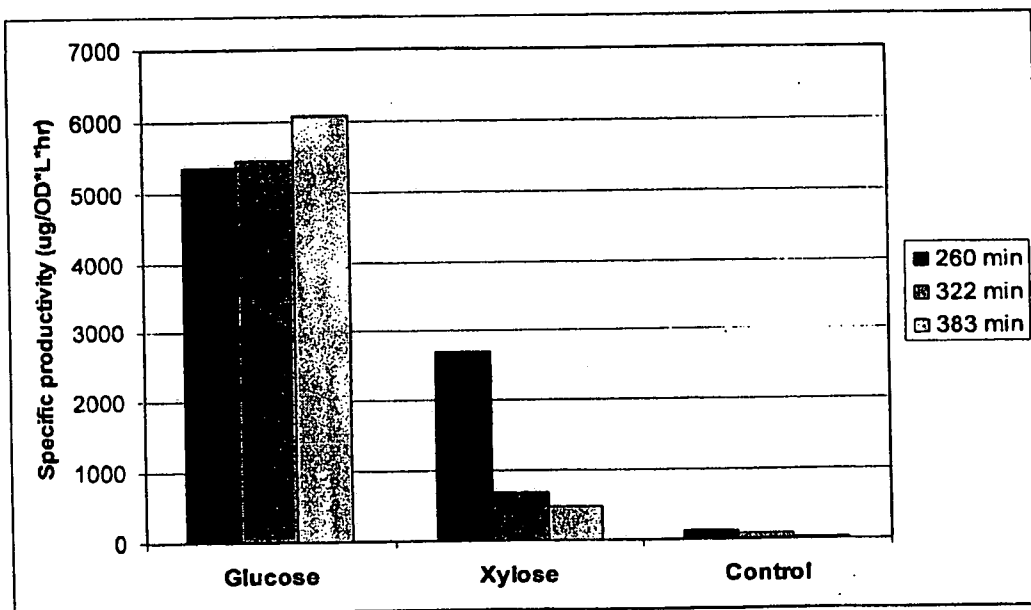


Figure 70A

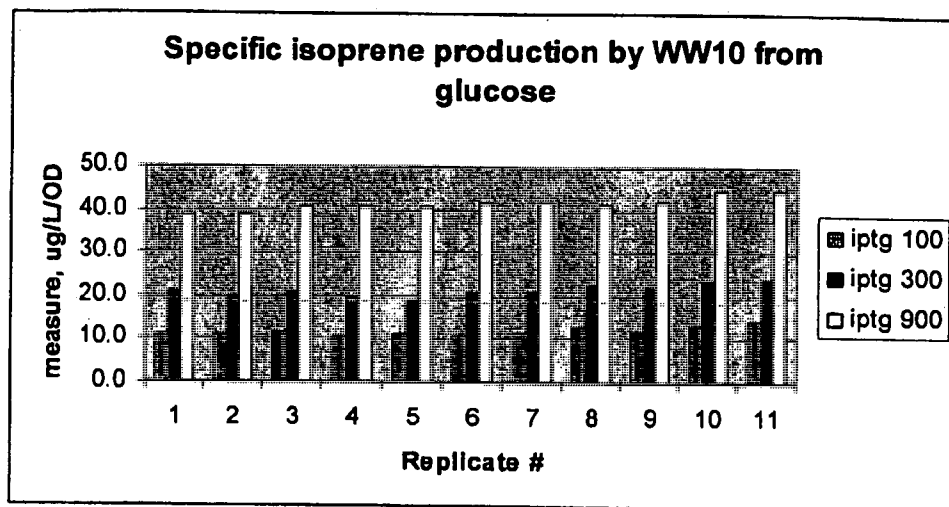


Figure 70B

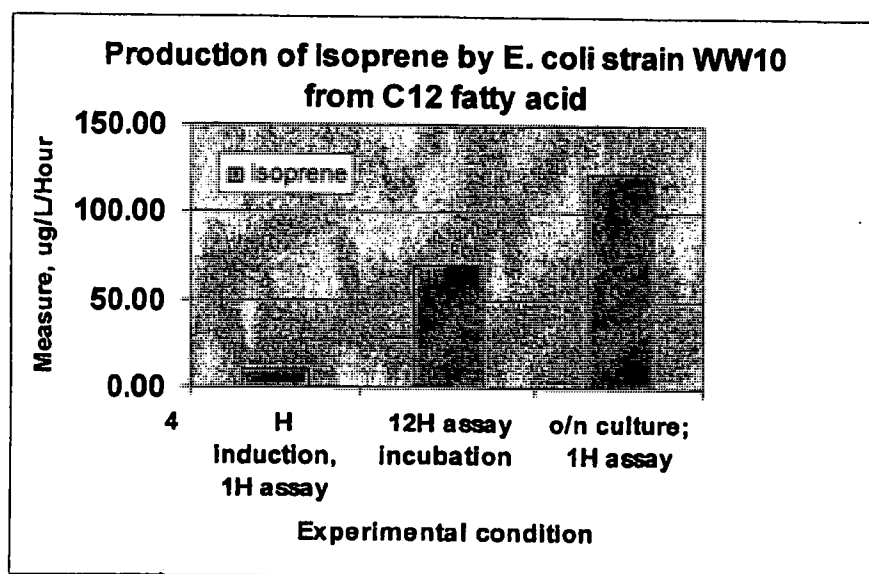


Figure 71

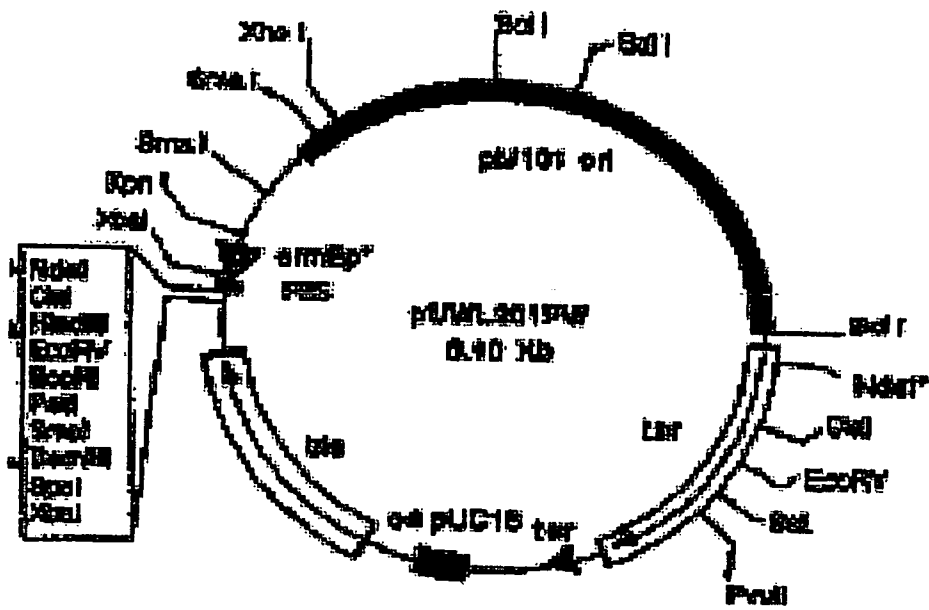


Figure 72

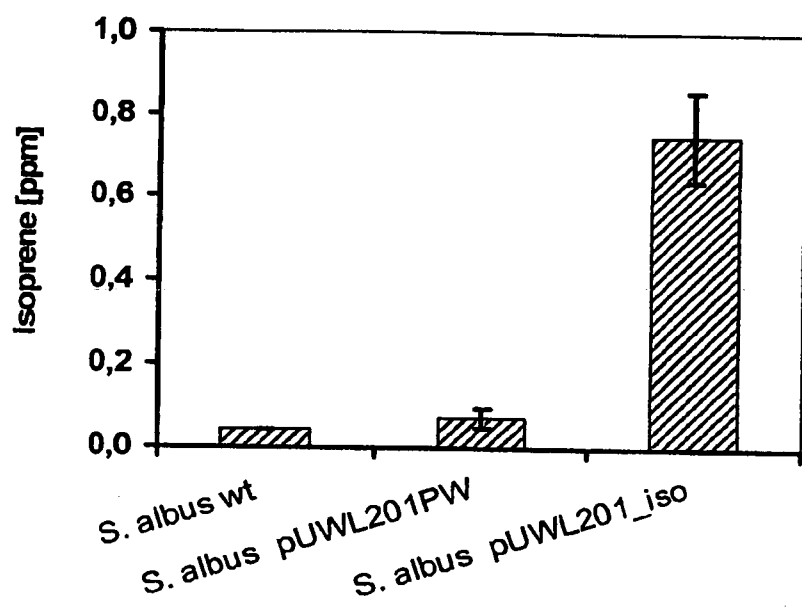


Figure 73A

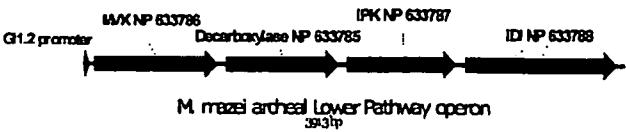


Figure 73C

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(SEQ ID NO:113)

Figure 74A

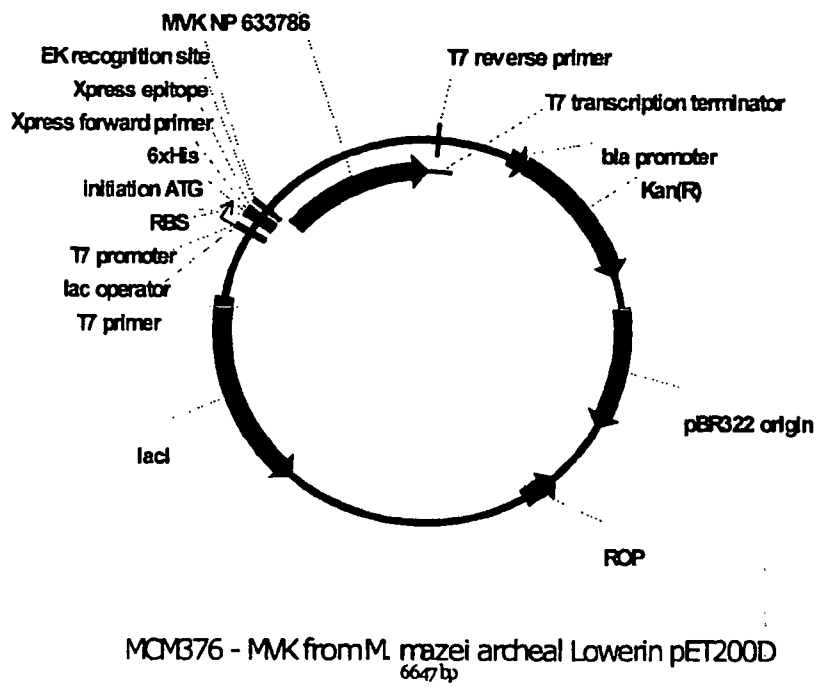


Figure 74B

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Figure 74C

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Figure 75A

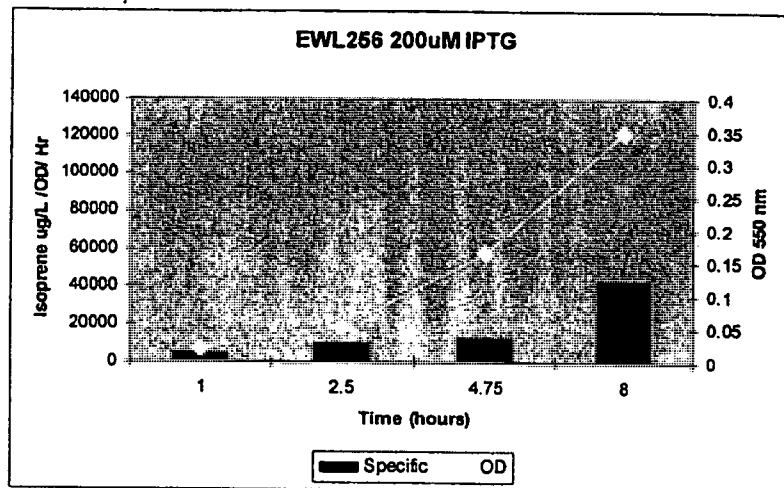


Figure 75B

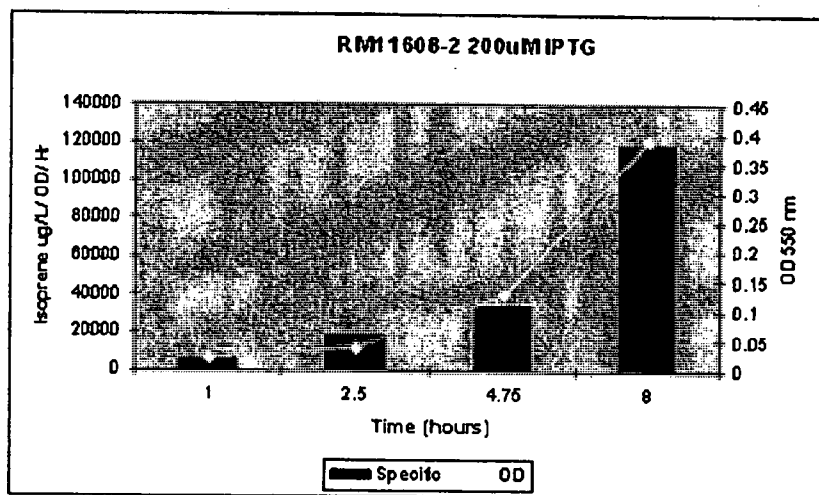


Figure 75C

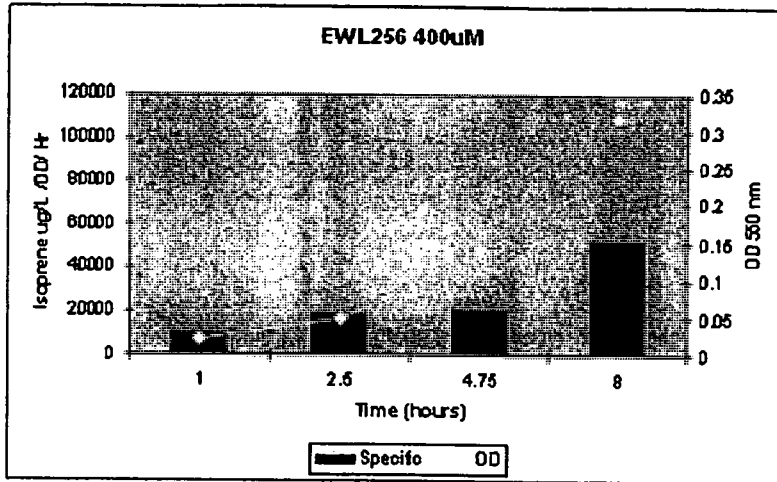


Figure 75D

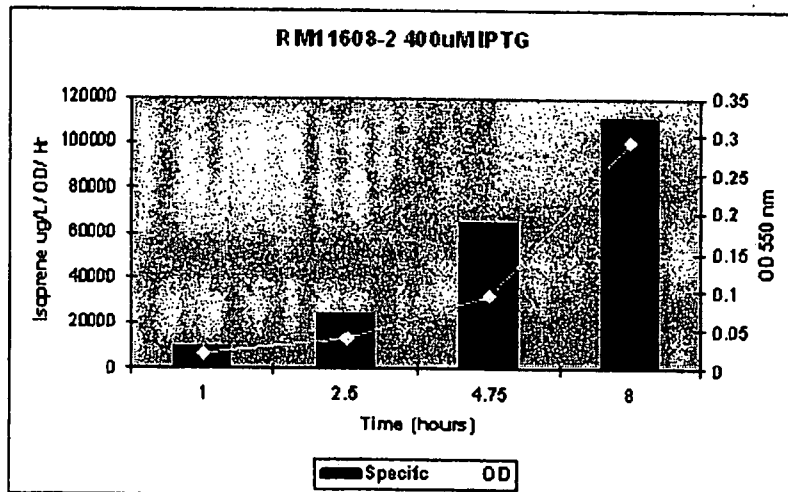
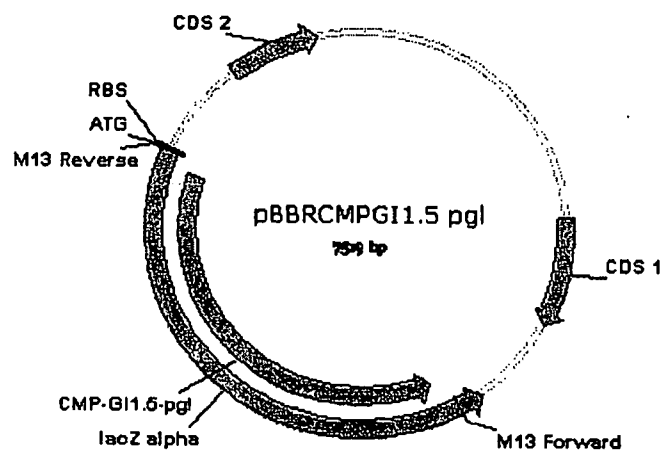


Figure 76

CDS 2: Gentamycin resistance gene; CDS1: E. coli replication protein.

Figure 77A

1-

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Figure 77B

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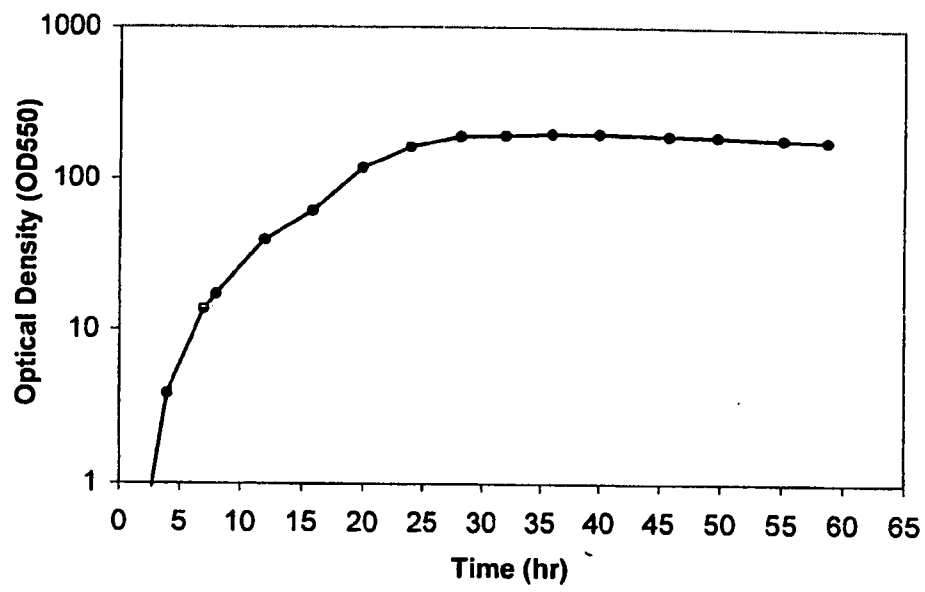
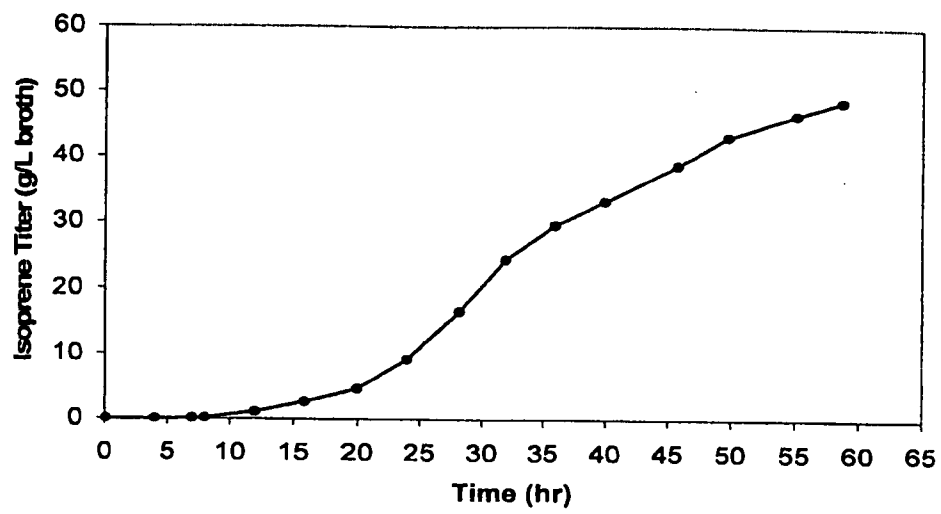
Figure 78A

Figure 78B



Titer 78C

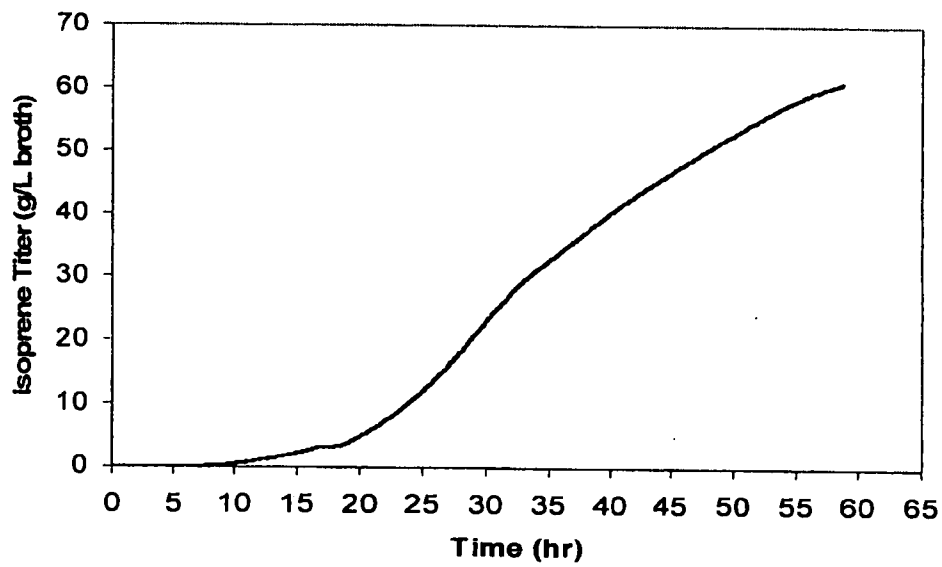


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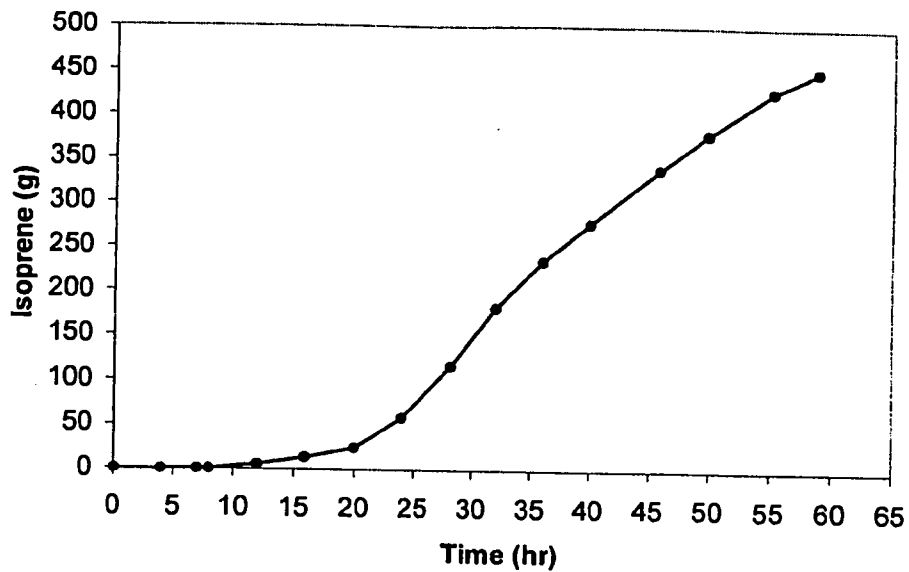


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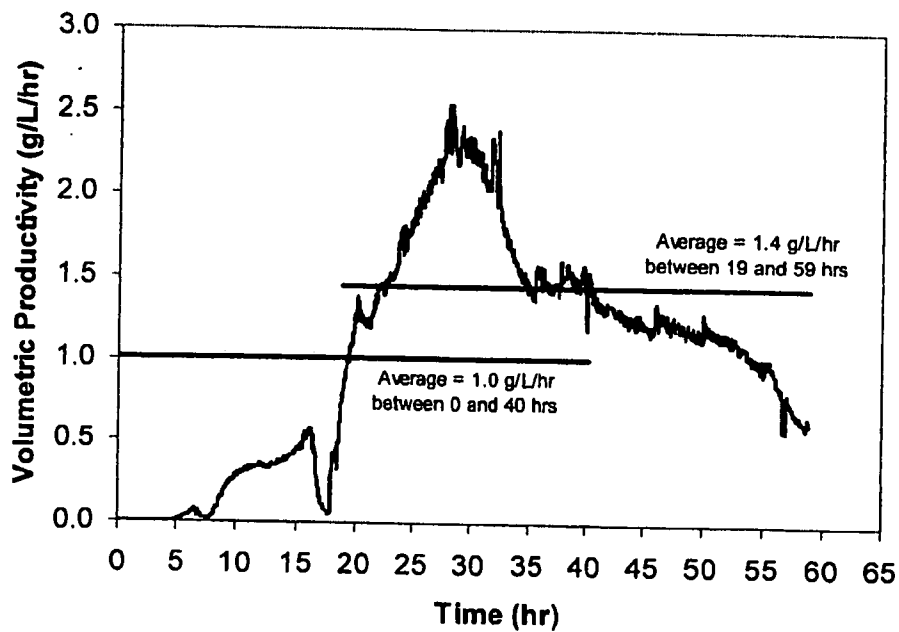


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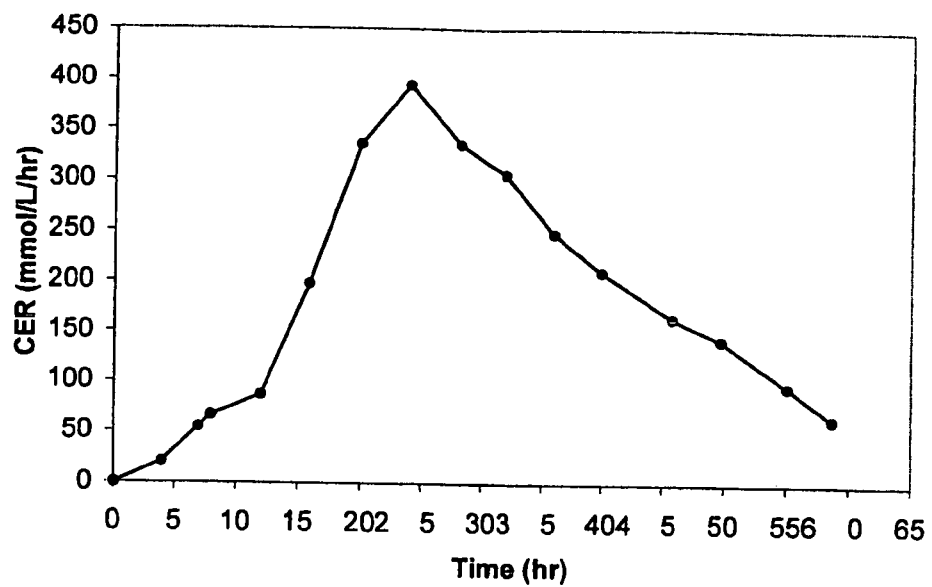


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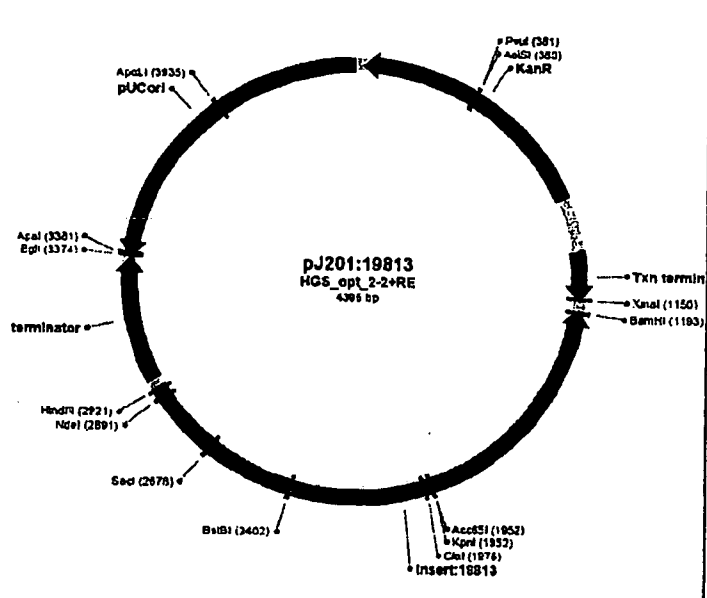


Figure 79B

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Figure 79C

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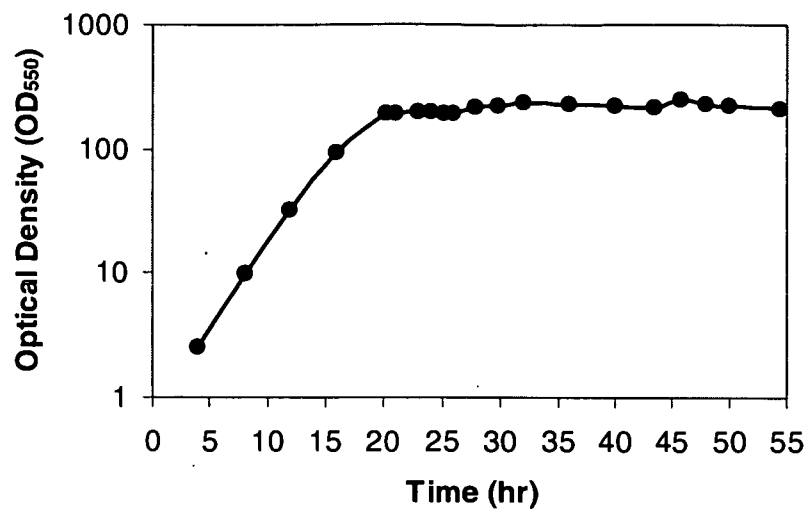
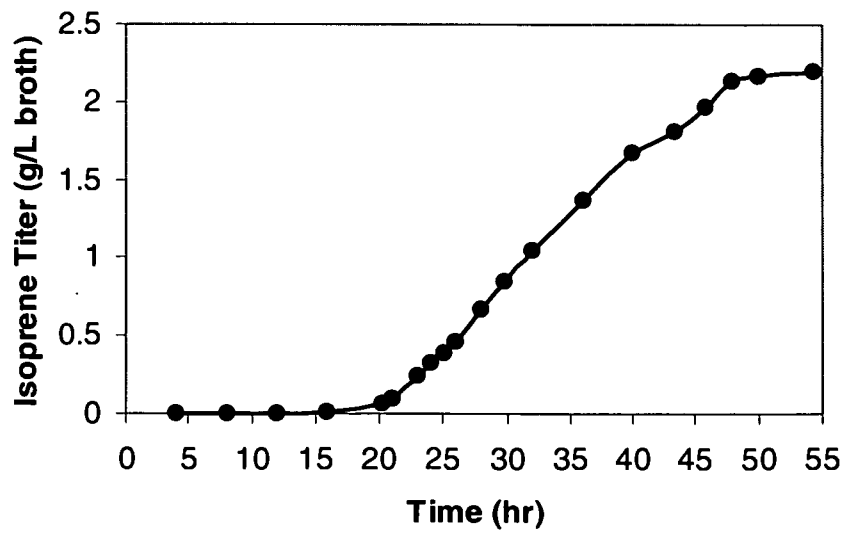
Figure 80**Figure 81**

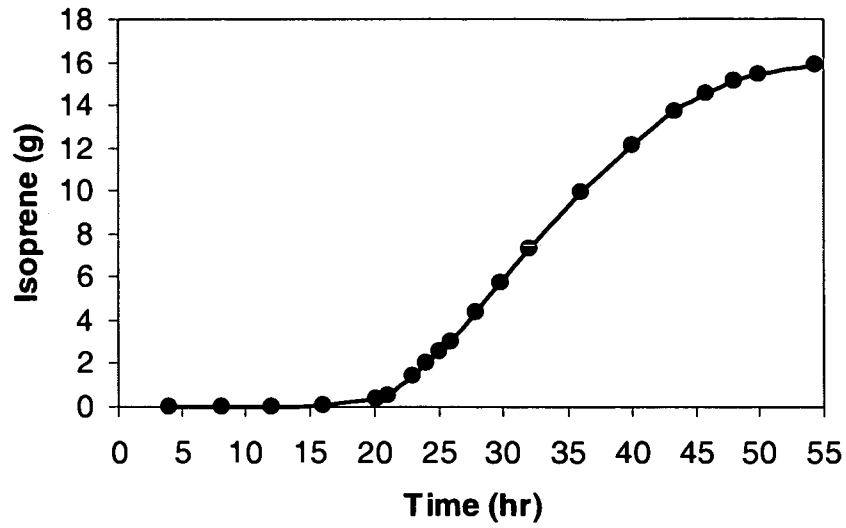
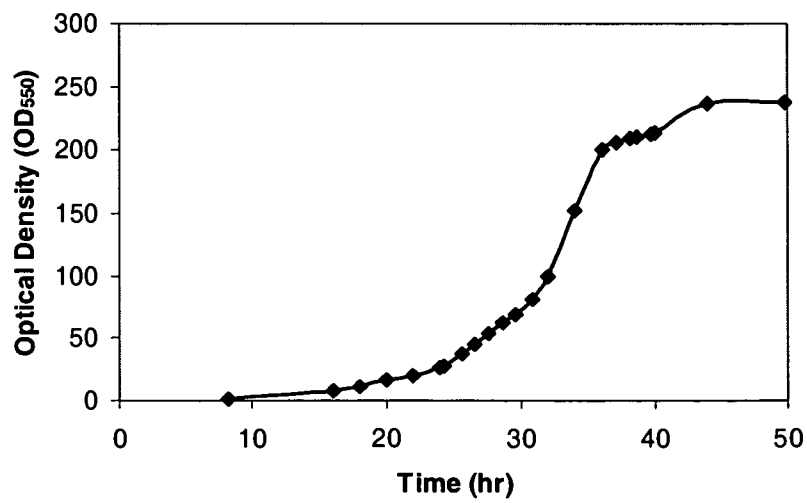
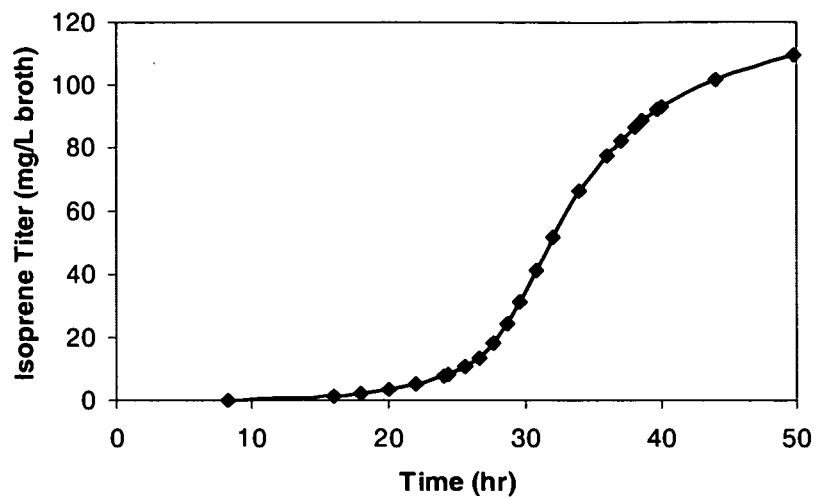
Figure 82**Figure 83**

Figure 84**Figure 85**