Fig. 1

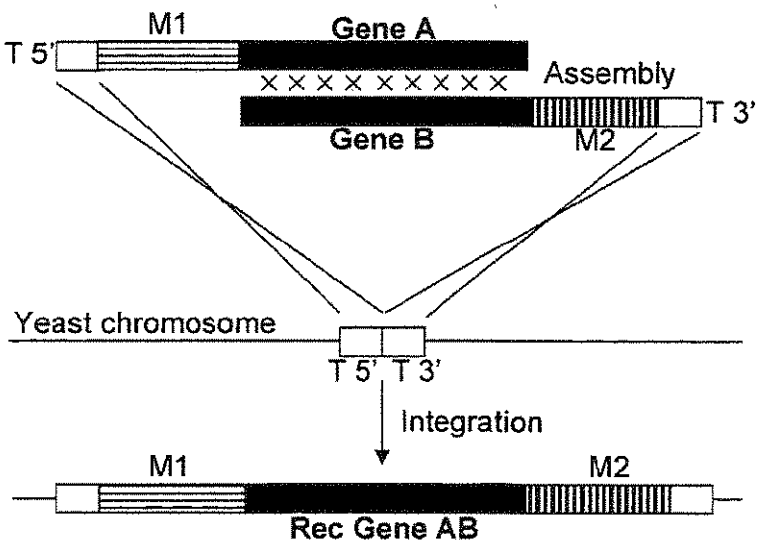
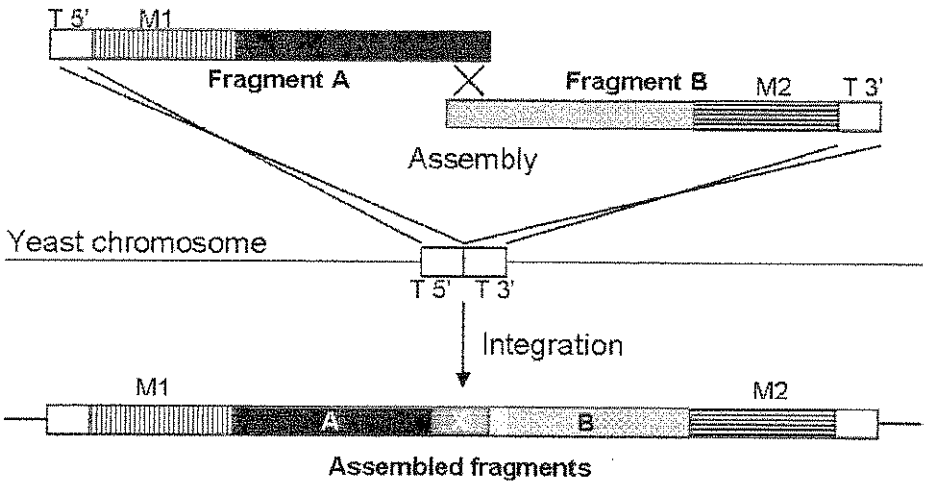

M1
Gene A
T 5'
Assembly
T 3'
Gene B
M2
Yeast chromosome
T 5'
T 3'
Integration
M1
M2
Rec Gene AB

Fig. 2


T 5'
M1
Fragment A
Fragment B
M2
T 3'
Assembly
Yeast chromosome
T 5'
T 3'
Integration
M1
A
B
M2
Assembled fragments

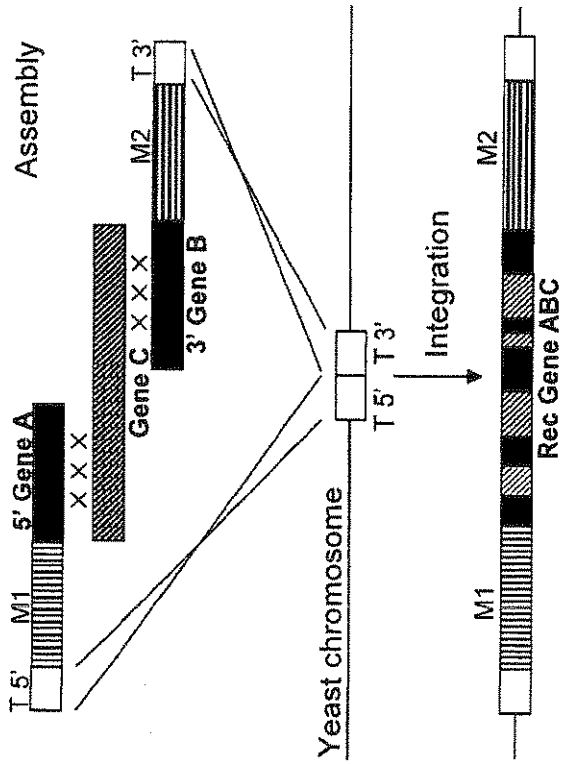

Assembly
T 3'
M2
3' Gene B
Gene C
X X X
X X X
5' Gene A
M1
T 5'
Yeast chromosome
T 5'
T 3'
Integration
M2
Rec Gene ABC
M1

Fig. 3

Fig. 4

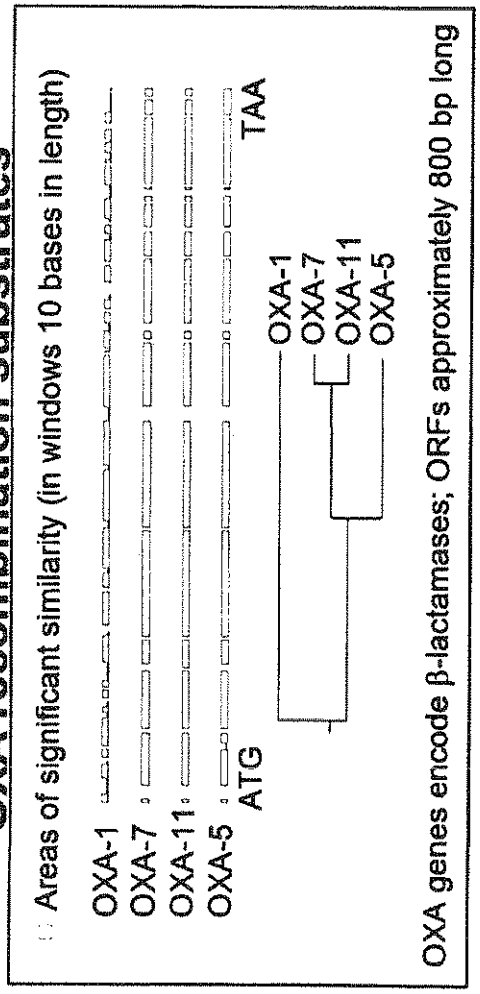

OXA recombination substrates
Areas of significant similarity (in windows 10 bases in length)
OXA-1
OXA-7
OXA-11
OXA-5
ATG
TAA
OXA-1
OXA-7
OXA-11
OXA-5
OXA genes encode β-lactamases; ORFs approximately 800 bp long

Fig. 5:

>Fe02 11-7

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SEQ ID NO1

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ASEGIIGG

SEQ ID NO 2

>Fe03 11-7

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SEQ ID NO 3

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ASEGIIGG

SEQ ID NO 4

>Fe04 11-7

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SEQ ID NO 5

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LYLNKLSASKENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWVEKETEVYFFAFNMDIDNESKLPLRKSIPTKIR
ESEGIIGG

SEQ ID NO 6

Fig. 5 continued

>Fe05 11-7

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GAGGGGCAATACAAGTTTCAGCTGTTCCCGTATTTCAACAAATCGCCAGAGAAGTTGGCGAAGTAAGAATGCAGAAATACC
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CTGGTGTCGCATGGTGGGTTGGTTGGGTTGAGAAGGGAGCAGAGGTTTACTTTTTCGCATTTAACATGGATATAGACAAC
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SEQ ID NO 7

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MASEGIIGG

SEQ ID NO 8

>Fe06 11-7

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CGCATGGTGGGTTGGGTGGGTTGAGAAGGAGACAGAGGTTTACTTTTTCGCCTTTAACATGGATATGGACAACGAAAGTAA
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SEQ ID NO 9

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MESEGIIGG

SEQ ID NO 10

>Fe10 11-7

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TCATAAAGAATGAGCATCAG**ATTTTCAAATGGGACGGAAA**GCCAAGAGCCATGAA**ACAATGGGAAAGAGACTTGAGCTTA**
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ATCTTAAAAAATTTTCATATGGTAACCAGAATATCAGTGGTGGCATTGACAAAT**TCTGGT**TGGA**GGGTCAGCTTAGAATTT**
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AAGAGGCTTTGGTAACGGAGGCTGCGCCTGAATATCTTGTGCATTCAAAAACTGGTTTTTCTGGTGTGGGAACTGAGTCA
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SEQ ID NO 11

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MASEGIIGG

SEQ ID NO 12

Fig. 5 continued

>Fe11 11-7

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TCGCATGGTGGGTTGGGTGGGTTGAGAAGGAGACAGAGGTTTACTTTTTCGCATTTAACATGGATATAGACAACGAAAAT
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SEQ ID NO 13

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MASEGIIGG

SEQ ID NO 14

Fig. 6:

>Fe09 11-5
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TTAGCTCGTGCATCAAAGGAATATCTTCCAGCATCAACATTTAAGATCCCCAACGCAATTATCGGCCTAGAGACTGGTGTCA
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CGCATGGTGGGTTGGGTGGGTTGAGAAGGAGACAGAGGTTTACTTTTTCGCCTTTAACATGGATATAGACAACGAAAGTAA
GTTGCCGCTAAGAAAATCCATTCCCACCAAAATCATGGAAAGTGAGGGCATCATCATTGGTGGCTAA

SEQ ID NO 15

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ESEGIIIGG

SEQ ID NO 16

>Fe13 11-5
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CGCATGGTGGGTTGGGTGGGTTGAGAAGGAGACAGAGGTTTACTTTTTCGCCTTTAACATGGATATAGACAACGAAAGTA
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SEQ ID NO 17

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MESEGIIGG

SEQ ID NO 18

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SEQ ID NO 19

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SEQ ID NO 20

Fig. 6 continued

>Fe16 11-5
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SEQ ID NO 21

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SEQ ID NO 22

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SEQ ID NO 23

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MESEGIIIGG

SEQ ID NO 24

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SEQ ID NO 25

MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNDLARASKEYLPASTFKIPNAIIGLETGVIKNEHQ
VFKWDGKPRAMKQWERDLSLRGAIQVSAVPVFQQIAREVGEVRMQRYLKKFSYGSQNISGGIDKFWLEDQLRISAVNQVEFLES
LYLNKLSASKENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWVGKETEVYFFAFNMDIDNESKLPLRKSIPTKI
MESEGIIGG

SEQ ID NO 26

Fig. 6 continued

>Fe19 11-5
ATGAAAACATTTGCCGCATATGTAATTACTGCGTGTCTTTCAAGTACGGCATTAGCTAGTTCAATTACAGAAAATACGTTTTG
GAACAAAGAGTTCTCTGCCGAAGCCGTCAATGGTGTTTTTCGTGCTTTGTAAAAGTAGCAGTAAATCCTGCGCTACCAATA
ACTTAGCTCGTGCATCAAAGGAATATCTTCCAGCATCAACATTTAAGATCCCCAACGCAATTATCGGCCTAGAAACTGGTGT
CATAAAGAATGAGCATCAGGTTTTCAAATGGGACGGAAAGCCAAGAGCCATGAAACAATGGGAAAGAGACTTGAGCTTAAG
AGGGGCAATACAAGTTTCAGCGGTTCCCGTATTTCAACAAATCGCCAGAGAAGTTGGCGAAGTAAGAATGCAGAAATATCTT
AAAAAATTTTCATATGGTAACCAGAATATCAGTGGTGGCATTGACAAATTCTGGTTGGAGGGTCAGCTTAGAATTTCCGCAG
TTAATCAAGTGGAGTTTCTAGAGTCTCTATTTTTAAATAAATTGTCAGCATCAAAAGAAAATCAGCTAATAGTAAAAGAGGCT
TTGGTAACGGAGGCTGCGCCTGAATATCTTGTGCATTCAAAAACTGGTTTTTCTGGTGTGGGAACTGAGTCAAATCCTGGTG
TCGCATGGTGGGTTGGTTGGGTTGAGAAGGGAGCAGAGGTTTACTTTTTCGCATTTAACATGGATATAGACAACGAAAATA
AGTTGCCGCTAAGAAAATCCATTCCCACCAAATCATGGCAAGTGAGGGCATCATTGGTGGCTAA

SEQ ID NO 27

MKTFAAYVITACLSSTALASSITENTFWNKEFSAEAVNGVFVLCKSSSKSCATNNLARASKEYLPASTFKIPNAIIGLETGVIKNEHQ
VFKWDGKPRAMKQWERDLSLRGAIQVSAVPVFQQIAREVGEVRMQKYLKKFSYGNQNISGGIDKFWLEGQLRISAVNQVEFLES
LFLNKLSASKENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWVEKGAEVYFFAFNMDIDNENKLPLRKSIPTKI
MASEGIIGG

SEQ ID NO 28

>Fe20 11-5
ATGAAAACATTTGCCGCATACGTAATTACTGCGTGTCTTTCAAGTACGGCATTAGCTAGTTCAATTACAGAAAATACGTTTTG
GAACAAAGAGTTCTCTGCCGAAGCCGTCAATGGTGTTTTCGTGCTTTGTAAAAGTAGCAGTAAATCCTGCGCTACCAATGAC
TTAGCTCGTGCATCAAAGGAATATCTTCCAGCATCAACATTTAAGATCCCCAACGCAATTATCGGCCTAGAAACTGGTGTCA
TAAAGAATGAGCATCAGATTTTCAAATGGGACGGAAAGCCAAGAGCCATGAAGCAATGGGAAAGAGACTTGACCTTAAGAG
GGGCAATACAAGTTTCAGCTGTTCCCGTATTTCAACAAATCGCCAGAGAAGTTGGCGAAGTAAGAATGCAGAAATACCTTAA
AAAATTTTCATATGGTAACCAGAATATCAGTGGTGGCATTGACAAATTCTGGTTGGAGGGTCAGCTTAGAATTCCCGCAGTT
AATCAAGTGGAGTTTCTAGAGTCTCTATTTTTAAATAAATTGTCAGCATCAAAAGAAAATCAGCTAATAGTAAAAGAGGCTTT
GGTAACGGAGGCGGCACCTGAATATCTTGTGCATTCAAAAACTGGTTTTTCTGGTGTGGGAACTGAGTCAAATCCTGGTGT
CGCATGGTGGGTTGGTTGGGTTGAGAAGGGAGCAGAGGTTTACTTTTTCGCATTTAACATGGATATAGACAACGAAAATAA
GTTGCCGCTAAGAAAATCCATTCCCACCAAAATCATGGCAAGTGAGGGCATCATTGGTGGCTAA

SEQ ID NO 29

MKTFAAYVITACLSSTALASSITENTFWNKEFSAEAVNGVFVLCKSSSKSCATNDLARASKEYLPASTFKIPNAIIGLETGVIKNEHQ
IFKWDGKPRAMKQWERDLTLRGAIQVSAVPVFQQIAREVGEVRMQKYLKKFSYGNQNISGGIDKFWLEGQLRIPAVNQVEFLES
LFLNKLSASKENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWVEKGAEVYFFAFNMDIDNENKLPLRKSIPTKI
MASEGIIGG

SEQ ID NO 30

>Fe21 11-5
ATGAAAACATTTGCCGCATATGTAATTATCGCGTGTCTTTCGAGTACGGCATTAGCTGGTTCAATTACAGAAAATACGTCTTG
GAACAAAGAGTTCTCTGCCGAAGCCGTCAATGGTGTCTTCGTGCTTTGTAAAAGTAGCAGTAAATCCTGCGCTACCAATGAC
TTAGCTCGTGCATCAAAGGAATATCTTCCAGCATCAACATTTAAGATCCCCAACGCAATTATCGGCCTAGAAACTGGTGTCA
TAAAGAATGAGCATCAGGTTTTCAAATGGGACGGAAAGCCAAGAGCCATGAAGCAATGGGAAAGAGACTTGACCTTAAGAG
GGGCAATACAAGTTTCAGCTGTTCCCGTATTTCAACAAATCGCCAGAGAAGTTGGCGAAGTAAGAATGCAGAAATACCTTAA
AAAATTTTCCTATGGCAGCCAGAATATCAGTGGTGGCATTGACAAATTCTGGTTGGAAGACCAGCTTAGAATTTCCGCAGTT
AATCAAGTGGAGTTTCTAGAGTCTCTATATTTAAATAAATTGTCAGCATCTAAAGAAAACCAGCTAATAGTAAAAGAGGCTTT
GGTAACGGAGGCGGCACCTGAATATCTAGTGCATTCAAAAACTGGTTTTTCTGGTGTGGGAACTGAGTCAAATCCTGGTGT
CGCATGGTGGGTTGGGTGGGTTGAGAAGGAGACAGAGGTTTACTTTTTCGCCTTTAACATGGATATAGACAACGAAAGTAA
GTTGCCGCTAAGAAAATCCATTCCCACCAAAATCATGGAAAGTGAGGGCATCATTGGTGGCTAA

SEQ ID NO 31

MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNDLARASKEYLPASTFKIPNAIIGLETGVIKNEHQ
VFKWDGKPRAMKQWERDLTLRGAIQVSAVPVFQQIAREVGEVRMQKYLKKFSYGSQNISGGIDKFWLEDQLRISAVNQVEFLES
LYLNKLSASKENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWVEKETEVYFFAFNMDIDNESKLPLRKSIPTKI
MESEGIIGG

SEQ ID NO 32

Fig. 6 continued

>Fe22 11-5
ATGAAAACATTTGCCGCATATGTAATTATCGCGTGTCTTTCGAGTACGGCATTAGCTGGTTCAATTACAGAAAATACGTCTTG
GAACAAAGAGTTCTCTGCCGAAGCCGTCAATGGTGTCTTCGTGCTTTGTAAAAGTAGCAGTAAATCCTGCGCTACCAATGAC
TTAGCTCGTGCATCAAAGGAATATCTTCCAGCATCAACATTTAAGATCCCCAACGCAATTATCGGCCTAGAAACTGGTGTCA
TAAAGAATGAGCATCAGGTTTTCAAATGGGACGGAAAGCCAAGAGCCATGAAGCAATGGGAAAGAGACTTGACCTTAAGAG
GGGCAATACAAGTTTCAGCTGTTCCCGTATTTCAACAAATCGCCAGAGAAGTTGGCGAAGTAAGAATGCAGAAATACCTTAA
AAAATTTTCCTATGGCAGCCAGAATATCAGTGGTGGCATTGACAAATTCTGGTTGGAAGACCAGCTTAGAATTTCCGCAGTT
AATCAAGTGGAGTTTCTAGAGTCTCTATATTTAAATAAATTGTCAGCATCTAAAGAAAACCAGCTAATAGTAAAAGAGGCTTT
GGTAACGGAGGCGGCACCTGAA**CAT**CTAGTGCATTCAAAAACTGGTTTTTCTGGTGTGGGAACTGAGTCAAATCCTGGTGT
CGCATGGTGGGTTGGGTGGGTTGAGAAGGAGACAGAGGTTTACTTTTTCGCCTTTAACATGGACATAGACAACGAAAGTAA
GTTGCCGCTAAGAAAATCCATTCCCACCAAAATCATGGAAAGTGAGGGCATCATTGGTGGCTAA

SEQ ID NO 33

MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNDLARASKEYLPASTFKIPNAIIGLETGVIKNEHQ
VFKWDGKPRAMKQWERDLTLRGAIQVSAVPVFQQIAREVGEVRMQKYLKKFSYGSQNISGGIDKFWLEDQLRISAVNQVEFLES
LYLNKLSASKENQLIVKEALVTEAAPEHLVHSKTGFSGVGTESNPGVAWWVGWVEKETEVYFFAFNMDIDNESKLPLRKSIPTKI
MESEGIIGG

SEQ ID NO 34

>Fe23 11-5
ATGAAAACATTTGCCGCATAT**TTA**ATTATCGCGTGTCTTTCGAGTACGGCATTAGCTGGTTCAATTACAGAAAATACGTCTTG
GAACAAAGAGTTCTCTGCCGAAGCCGTCAATGGTGTCTTCGTGCTTTGTAAAAGTAGCAGTAAATCCTGCGCTACCAATGAC
TTAGCTCGTGCATCAAAGGAATATCTTCCAGCATCAACATTTAAGATCCCCAACGCAATTATCGGCCTAGAAACTGGTGTCA
TAAAGAATGAGCATCAGGTTTTCAAATGGGACGGAAAGCCAAGAGCCATGAAGCAATGGGAAAGAGACTTGACCTTAAGAG
GGGCAATACAAGTTTCAGCTGTTCCCGTATTTCAACAAATCGCCAGAGAAGTTGGCGAAGTAAGAATGCAGAAATACCTTAA
AAAATTTTCCTATGGCAGCCAGAATATCAGTGGTGGCATTGACAAATTCTGGTTGGAAGACCAGCTTAGAATTTCCGCAGTT
AATCAAGTGGAGTTTCTAGAGTCTCTATATTTAAATAAATTGTCAGCATCTAAAGAAAACCAGCTAATAGTAAAAGAGGCTTT
GGTAACGGAGGCGGCACCTGAATATCTAGTGCATTCAAAAACTGGTTTTTCTGGTGTGGGAACTGAGTCAAATCCTGGTGT
CGCATGGTGGGTTGGGTGGGTTGAGAAGGAGACAGAGGTTTACTTTTTCGCCTTTAACATGGATATAGACAACGAAAGTAA
GTTGCCGCTAAGAAAATCCATTCCCACCAAAATCATGGAAAGTGAGGGCATCATCAT**TGGTGGCTTA**

SEQ ID NO 35

MKTFAAYLIIACLSSTALAGSITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNDLARASKEYLPASTFKIPNAIIGLETGVIKNEHQ
VFKWDGKPRAMKQWERDLTLRGAIQVSAVPVFQQIAREVGEVRMQKYLKKFSYGSQNISGGIDKFWLEDQLRISAVNQVEFLES
LYLNKLSASKENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWVEKETEVYFFAFNMDIDNESKLPLRKSIPTKI
MESEGIIIGG

SEQ ID NO 36

>Fe24 11-5
ATGAAAACATTTGCCGCATATGTAATTATCGCGTGTCTTTCGAGTACGGCATTAGCTGGTTCAATTACAGAAAATACGTCTTG
GAACAAAGAGTTCTCTGCCGAAGCCGTCAATGGTGTCTTCGTGCTTTGTAAAAGTAGCAGTAAATCCTGCGCTACCAATGAC
TTAGCTCGTGCATCAAAGGAATATCTTCCAGCATCAACATTTAAGATCCCCAACGCAATTATCGGCCTAGAAACTGGTGTCA
TAAAGAATGAGCATCAGGTTTTCAAATGGGACGGAAAGCCAAGAGCCATGAAGCAATGGGAAAGAGACTTGACCTTAAGAG
GGGCAATACAAGTTTCTGCTGTTCCCGTATTTCAACAAATCGCCAGAGAAGTTGGCGAAGTAAGAATGCAGAAATACCTTAA
AAAATTTTCCTATGGCAGCCAGAATATCAGTGGTGGCATTGACAAATTCTGGTTGGAAGACCAGCTTAGAATTTCCGCAGTT
AATCAAGTGGAGTTTCTAGAGTCTCTATATTTAAATAAATTGTCAGCATCTAAAGAAAACCAGCTAATAGTAAAAGAGGCTTT
GGTAACGGAGGCGGCACCTGAATATCTAGTGCATTCAAAAACTGGTTTTTCTGGTGTGGGAACTGAGTCAAATCCTGGTGT
CGCATGGTGGGTTGGGTGGGTTGAGAAGGAGACTGAGGTTTACTTTTTTGCTT**CTAACATGGA**CATAGACAATGAGAGTAA
ATTGCCGTCAAGAAAATCCATTTCAACGAAAATCATGGCAAGTGAAGGCATCATCAT**TGGTGGCTAA**

SEQ ID NO 37

MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNDLARASKEYLPASTFKIPNAIIGLETGVIKNEHQ
VFKWDGKPRAMKQWERDLTLRGAIQVSAVPVFQQIAREVGEVRMQKYLKKFSYGSQNISGGIDKFWLEDQLRISAVNQVEFLES
LYLNKLSASKENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWVEKETEVYFFASNMDIDNESKLPSRKSISTKI
MASEGIIIGG

SEQ ID NO 38

Fig. 7

OXA11 (parental)

ATGAAAACATTTGCCGCATATGTAATTATCGCGTGTCTTTCGAGTACGGCATTAGCTGGT
TCAATTACAGAAAATACGTCTTGGAACAAAGAGTTCTCTGCCGAAGCCGTCAATGGTGTC
TTCGTGCTTTGTAAAAGTAGCAGTAAATCCTGCGCTACCAATGACTTAGCTCGTGCATCA
AAGGAATATCTTCCAGCATCAACATTTAAGATCCCCAACGCAATTATCGGCCTAGAAACT
GGTGTCATAAAGAATGAGCATCAGGTTTTCAAATGGGACGGAAAGCCAAGAGCCATGAAG
CAATGGGAAAGAGACTTGACCTTAAGAGGGGCAATACAAGTTTCAGCTGTTCCCGTATTT
CAACAAATCGCCAGAGAAGTTGGCGAAGTAAGAATGCAGAAATACCTTAAAAAATTTTCC
TATGGCAGCCAGAATATCAGTGGTGGCATTGACAAATCCTGGTTGGAAGACCAGCTTAGA
ATTTCCGCAGTTAATCAAGTGGAGTTTCTAGAGTCTCTATATTTAAATAAATTGTCAGCA
TCTAAAGAAAACCAGCTAATAGTAAAAGAGGCTTTGGTAACGGAGGCGGCACCTGAATAT
CTAGTGCATTCAAAAACTGGTTTTTTCTGGTGTGGGAACTGAGTCAAATCCTGGTGTCGCA
TGGTGGGTTGGGTGGGTTGAGAAGGAGACAGAGGTTTACTTTTTCGCCTTTAACATGGAT
ATAGACAACGAAAGTAAGTTGCCGCTAAGAAAATCCATTCCCACCAAAATCATGGAAAGT
GAGGGCATCATTGGTGGCTAA

SEQ ID NO 39

OXA07 (parental)
ATGAAAACATTTGCCGCATATGTAATTACTGCGTGTCTTTCAAGTACGGCATTAGCTAGT
TCAATTACAGAAAATACGTTTTGGAACAAAGAGTTCTCTGCCGAAGCCGTCAATGGTGTT
TTCGTGCTTTGTAAAAGTAGCAGTAAATCCTGCGCTACCAATAACTTAGCTCGTGCACCA
AAGGAATATCTTCCAGCATCAACATTTAAGATCCCCAACGCAATTATCGGCCTAGAAACT
GGTGTCATAAAGAATGAGCATCAGATTTTCAAATGGGACGGAAAACCAAGAGCCATGAAA
CAATGGGAAAGAGACTTGAGCTTAAGAGGGGCAATACAAGTTTCAGCGGTTCCCGTATTT
CAACAAATCGCCAGAGAAGTTGGCGAAGTAAGAATGCAGAAATATCTTAAAAAATTTTCA
TATGGTAACCAGAATATCAGTGGCGGCATTGACAAATTCTGGTCGGAGGGTCAGCTTAGA
ATTTCCGCAGTTAATCAAGTGGAGTTTCTAGAGTCTCTATTTTTAAATAAATTGTCAGCA
TCAAAAGAAAATCAGCTAATAGTAAAAGAGGCTTTGGTAACGGAGGCTGCGCCTGAATAT
CTTGTGCATTCAAAAACTGGTTTTTCTGGTGTGGGAACTGAGTCAAATCCTGGTGTCGCA
TGGTGGGTTGGTTGGGTTGAGAAGGGAGCAGAGGTTTACTTTTTCGCATTTAACATGGAT
ATAGACAACGAAAATAAGTTGCCGCTAAGAAAATCCATTCCCACCAAAATCATGGCAAGT
GAGGGCATCATTGGTGGCTAA

SEQ ID NO 40

OXA05 (parental)
ATGAAAACCATAGCCGCATACTTAGTTACTTCCTGTTTTTCAAGCACCGCGCTCTCAAAG
TCTATTTCTGAAAATTTGGTGTGGAATAAAGAATTTTCTAGTGAATCCGTACATGGCGTT
TTTGTACTTTGTAAAAGTAGTAGCAATTCCTGTACTACAAATAATGCGGCACGTGCATCT
ACAGCCTATATTCCAGCATCAACATTCAAAATTCCTAATGCTCTAATAGGTCTTGAAACC
GGCGCCATAAAAGATGAACGGCAGATTTTCAAATGGGACGGCAAGCCCAGAGCCATGAAA
CAATGGGAAAAAGACTTAAGGCTAAGGGGCGCTATACAGGTTTCTGCGGTTCCGGTATTT
CAACAAATTGCCAGAGAAGTTGGCGAAATGAGAATGCAAAGATATCTTAACCTGTTTTCA
TACGGTAACGCCAATATAGGGGGAGGCATTGACAAATTCTGGCTAGAGGGTCAGCTTAGA
ATCCCAGCATTCAATCAAGATAAATCTTTAGAGTCGCTCTTCCTGAATAATTTGCCAGCA
TCAAAAGCAAATCAACTAATAGTAAAAGAGGCAATAGTTACAGAAGCTACGCCAGAATAT
ATTGTTCATTCAAAAACTGGGTATTCCGGTGTTGGCACAGAATCAAGTCCTGGTGTCGCT
TGGTGGGTTGGTTGGGTAGGGAAAGGAGCTGAGGTTTACTTTTTTGCATTTAACATGGAC
ATAGACAATGAGAATAAATTGCCGTCAAGAAAATCCATTTCAACGAAAATCATGGCAAGT
GAAGGCATCATCATTGGTGGCTAA

SEQ ID NO 41

Fig. 8

a) >OUL3-05-II

ATGAAAACATTTGCCGCATATGTAATTATCGCGTGTCTTTCGAGTACGGCATTAGCTGGTTC
AATTACAGAAAATACGTCTTGGAACAAAGAGTTCTCTGCCGAAGCCGTCAATGGTGTCTTCG
TGCTTTGTAAAAGTAGCAGTAAATCCTGCGCTACCAATGACTTAGCTCGTGCATCAAAGGAA
TATCTTCCAGCATCAACATTCAAAATTCCTAATGCTCTAATAGGTCTTGAAACCGGCGCCAT
AAAAGATGAACGGCAGGTTTTCAAATGGGACGGCAAGCCCAGAGCCATGAAGCAATGGGAAA
AAGACTTAAAGCTAAGGGGCGCTATACAGGTTTCTGCTGTTCCGGTATTTCAACAAATTGCC
AGAGAAGTTGGCGAAATAAGAATGCAAAAATACCTTAACCTGTTTTCATACGGCAACGCCAA
TATAGGGGGAGGCATTGACAAATTCTGGCTAGAAGGTCAGCTTAGAATCTCAGCATTCAATC
AAGTTAAATTTTTAGAGTCGCTCTACCTGAATAATTTGCCAGCATCAAAAGCAAACCAACTA
ATAGTAAAAGAGGCAATAGTTACAGAAGCAACTCCAGAATATATAGTTCATTCAAAAACTGG
GTATTCCGGTGTTGGCACAGAATCAAGTCCTGGTGTCGCTTGGTGGGTTGGTTGGGTAGAGA
AAGGAACTGAGGTTTACTTTTTTGCTTTTAACATGGACATAGACAATGAGAGTAAATTGCCG
TCAAGAAAATCCATTCC**CACCAAAATCATGGCAAGTGAGGGCATCATTGGTGGCTAAGCTGT**
GAAGATCCCAGCAAAGGCTTA

SEQ ID NO 42

MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNDLARASKE
YLPASTFKIPNALIGLETGAIKDERQVFKWDGKPRAMKQWEKDLKLRGAIQVSAVPVFQQIA
REVGEIRMQKYLNLFSYGNANIGGGIDKFWLEGQLRISAFNQVKFLESLYLNNLPASKANQL
IVKEAIVTEATPEYIVHSKTGYSGVGTESSPGVAWWVGWVEKGTEVYFFAFNMDIDNESKLP
SRKSIPTKIMASEGIIGG.

SEQ ID NO 43

Fig. 8 (continued).

b) >OUL3-05-III

ATGAAAACATTTGCCGCATATTTAGTTCTCGCGTGTCTTTCGAGTACGGCATTAGCTGGTTC
AATTACAGAAAATACGTCTTGGAACAAAGAGTTCTCTGCCGAAGCCGTCAATGGTGTCTTCG
TGCTTTGTAAAAGTAGCAGTAAATCCTGCGCTACCAATGACTTAGCTCGTGCATCAAAGGAA
TATCTTCCAGCATCAACATTTAAGATCCCCAACGCAATTATCGGTCTAGAAACTGGTGTCAT
AAAGAATGAGCATCAGGTTTTCAAATGGGACGGAAAGCCAAGAGCCATGAAGCAATGGGAAA
GAGACTTGACCTTAAGAGGGGCAATACAAGTTTCAGCTGTTCCCGTATTTCAACAAATCGCC
AGAGAAGTTGGCGAAATAAGAATGCA**GAAATATCTTAAAAAATTTTCATATGGTAACCAGAA**
TATCAGTGGTGGCATTGACAAATTCTGGCTAGAAGGTCAGCTTAGAATCTCAGCATTCAATC
AAGTTAAATTTTTAGAGTCGCTCTACCTGAATAATTTGCCAGCATCAAAAGA**AAATCAGCTA**
ATAGTAAAAGAGGCTTTGGTAACGGAGGCTGCGCCTGAATATCTTGTGCATTCAAAAACTGG
TTTTTCTGGTGTGGGAACTGAGTCAAATCCTGGTGTCGCATGGTGGGTTGGTTGGGTTGAGA
AGGGAGCAGAGGTTTACTTTTTCGCATTTAACATGGATATAGACAACGAAAATAAGTTGCCG
CTAAGAAAATCCATTCCCACCAAAATCATGGCAAGTGAGGGCATCATTGGTGGCTAA

SEQ ID NO 44

MKTFAAYLVLACLSSTALAGSITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNDLARASKE
YLPASTFKIPNAIIGLETGVIKNEHQVFKWDGKPRAMKQWERDLTLRGAIQVSAVPVFQQIA
REVGEIRMQKYLKKFSYGNQNISGGIDKFWLEGQLRISAFNQVKFLESLYLNNLPASKENQL
IVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWVEKGAEVYFFAFNMDIDNENKLP
LRKSIPTKIMASEGIIGG.

SEQ ID NO 45

Fig. 8 (continued).

c) >OUL3-05-IV

ATGAAAACATTTGCCGCATATGTAATTATCGCGTGTCTTTCGAGTACGGCATTAGCTAGTTC
AATTACAGAAAATACGTCTTGGAACAAAGAGTTCTCTGCCGAAGCCGTCAATGGTGTCTTCG
TGCTTTGTAAAAGTAGCAGTAAATCCTGCGCTACCAATGACTTAGCTCGTGCATCAAAGGAA
TATCTTCCAGCATCAACATTTAAGATCCCCAACGCAATTATCGGCCTAGAAACTGGTGTCAT
AAAGAATGAGCATCAGGTTTTCAAATGGGACGGAAAGCCAAGAGCCATGAAGCAATGGGAAA
GAGACTTGACCTTAAGAGGGGCAATACAAGTTTCAGCTGTTCCCGTATTTCAACAAATCGCC
AGAGAAGTTGGCGAAATAAGAATGCA**GAAATATCTTAAAAAATTTTCATATGGTAACCAGAA**
TATCAGTGGTGGCATTGACAAATTCTGGTTGGAGGGTCAGCTTAGAATTTCCGCAGTTAATC
AAGTGGAGTTTCTAGAGTCTCTATTTTTAAATAAATTGTCAGCATCAAAAGAAAATCAGCTA
ATAGTAAAAGAGGCTTTGGTAACGGAGGCTGCGCCTGAATATCTTGTGCATTCAAAAACTGG
TTTTTCTGGTGTGGGAACTGAGTCAAATCCTGGTGTCGCATGGTGGGTTGGTTGGGTTGAGA
AGGGAGCAGAGGTTTACTTTTTCGCATTTAACATGGATATAGACAACGAAAATAAGTTGCCG
CTAAGAAAATCCATTCCCACCAAAATCATGGCAAGTGAGGGCATCATTGGTGGCTAA

SEQ ID NO 46

MKTFAAYVIIACLSSTALASSITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNDLARASKE
YLPASTFKIPNAIIGLETGVIKNEHQVFKWDGKPRAMKQWERDLTLRGAIQVSAVPVFQQIA
REVGEIRMQKYLKKFSYGNQNISGGIDKFWLEGQLRISAVNQVEFLESLFLNKLSASKENQL
IVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWVEKGAEVYFFAFNMDIDNENKLP
LRKSIPTKIMASEGIIGG.

SEQ ID NO 47

Fig. 8 (continued).

d) >OUL3-05-IX

ATGAAAACATTAGCCGCATATTTAGTTCTAGTTTTTTATGCAAGCACCGCGCTCTCAGAGTC
AATTACAGAAAATTTGGCGTGGAATAAAGAATTTTCTAGTGAATCCGTACATGGCGTTTTTG
TACTTTGTAAAAGTAGTAGCAATTCCTGTACTACAAATAATGCGGCACGTGCATCTACAGCC
TATATTCCAGCATCAACATTCAAAATTCCTAATGCTCTAATAGGTCTTGAAACCGGCGCCAT
AAAAGATGAACGGCAGGTTTTCAAATGGGACGGAAAGCCAAGAGCCATGAAGCAATGGGAAA
GAGACTTAAAGCTAAGGGGCGCTATACAGGTTTCTGCTGTTCCGGTATTTCAACAAATTGCC
AGAGAAGTTGGCGAAATAAGAATGCAAAAATACCTTAACCTGTTTTCATACGGCAACGCCAA
TATAGGGGGAGGCATTGACAAATTCTGGCTAGAAGGTCAGCTTAGAATCTCAGCATTCAATC
AAGTTAAATTTTTAGAGTCGCTCTACCTGAATAA**ATTGTCAGCATCAAAAGAAAA**CCAACTA
ATAGTAAAAGAGGCAATAGTTACAGAAGCAACTCCAGAATATATAGTTCATTCAAAAACTGG
TTTTTCTGGTGTTGGCACAGAATCAAGTCCTGGTGTCGCTTGGTGGGTTGGTTGGGTAGAGA
AAGGAACTGAGGTTTACTTTTTTGCTTTTAACATGGACATAGACAATGAGAGTAAATTGCCG
TCAAGAAAATCCATT**CCCACCAAAATCATGGCAAGTGAGGGCATCATTGGTGGCTAA**

SEQ ID NO 48

MKTLAAYLVLVFYASTALSESITENLAWNKEFSSESVHGVFVLCKSSSNSCTTNNAARASTA
YIPASTFKIPNALIGLETGAIKDERQVFKWDGKPRAMKQWERDLKLRGAIQVSAVPVFQQIA
REVGEIRMQKYLNLFSYGNANIGGGIDKFWLEGQLRISAFNQVKFLESLYLNKLSASKENQL
IVKEAIVTEATPEYIVHSKTGFSGVGTESSPGVAWWVGWVEKGTEVYFFAFNMDIDNESKLP
SRKSIPTKIMASEGIIGG.

SEQ ID NO 49

Fig. 8 (continued).

e) >OUL3-05-X

ATGAAAACATTTGCCGCATATGTAATTATCGCGTGTCTTTCGAGTACGGCATTAGCTGGTTC
AATTACAGAAAATACGTCTTGGAACAAAGAGTTCTCTGCCGAAGCCGTCAATGGTGTCTTCG
TGCTTTGTAAAAGTAGCAGTAAATCCTGCGCTACCAATGACTTAGCTCGTGCATCAAAGGAA
TATCTTCCAGCATCAACATTTAAGATCCCCAACGCAATTATCGGCCTAGAAACTGGTGTCAT
AAAGAATGAGCATCAGGTTTTCAAATGGGACGGAAAGCCAAGAGCCATGAAGCAATGGGAAA
GAGACTTGACCTTAAGAGGGGCAATACAAGTTTCAGCTGTTCCCGTATTTCAACAAATCGCC
AGAGAAGTTGGCGAAGTAAGAATGCAGAAATATCTTAA**AAAATTTTCATATGGTAACCAGAA**
TATCAGTGGTGGCATTGACAAATTCTGGTTGGAAGGTCAGCTTAGAATT**TCCGCAGTTAATC**
AAGTGGAGTTTCTAGAGTCTCTATTTTTAAATAAATTGTCAGCATCAAAAGAAAATCAGCTA
ATAGTAAAAGAGGCTTTGGTAACGGAGGCTGCGCCTGAATATCTTGTGCATTCAAAAACTGG
TTTTTCTGGTGTGGGAACTGAGTCAAATCCTGGTGTCGCATGGTGGGTTGGTTGGGTTGAGA
AGGGAGCAGAGGTTTACTTTTTCGCATTTAACATGGATATAGACAACGAAAATAAGTTGCCG
CTAAGAAAATCCATTCCCACCAAAATCATGGCAAGTGAGGGCATCATTGGTGGCTAA

SEQ ID NO 50

MKTFAAYVIIACLSSTALAGSITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNDLARASKE
YLPASTFKIPNAIIGLETGVIKNEHQVFKWDGKPRAMKQWERDLTLRGAIQVSAVPVFQQIA
REVGEVRMQKYLKKFSYGNQNISGGIDKFWLEGQLRISAVNQVEFLESLFLNKLSASKENQL
IVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWVEKGAEVYFFAFNMDIDNENKLP
LRKSIPTKIMASEGIIGG.

SEQ ID NO 51

Fig. 9 :

a) >ADH Kluyveromyces

ATGTCTGCTCACGAAATCCCAAAGACCCAGAAAGGTGTTATCTTCTACGAGACCG
GTGGTAAGCTGGAATACAAGGACATCGATGTCCCAACCCCAAAGGCCAACGAGC
TTTTGGTCAACGTCAAGTACTCCGGTGTGTGCCACACTGACTTGCACGCCTACCAC
GGTGACTGGCCATTGCCAGTTAAGTTGCCTCTAGTCGGTGGCCACGAGGGTGCCG
GTGTCGTTGTCGCCATGGGTGAGAACGTCAAGGGCTGGAAGGTCGGTGACTTGGC
CGGTATCAAGTGGTTGAACGGCTCCTGTATGTCCTGTGAGTCCTGTGAGTTGGGT
AACGAGTCCAACTGTCCAGAGGCTGACTTGTCCGGTTACACCCACGACGGTTCTT
TCCAGCAGTACGCTACTGCCGATGCCGTCCAGGCCGCTAAGATCCCAGCTGGCGC
TGACCTTGCTGAGATCGCCCCAATCCTGTGTGCCGGTATCACTGTCTACAAGGCTT
TGAAGTCTGCTAACTTGCAGGCCGGTGACTGGGTTGCCATCTCCGGTGCCGCCGG
TGGTTTGGGTTCCCTAGCCGTCCAGTACGCCAAGGCCATGGGTTACCGTGTCTTG
GGTATCGACGGTGGTGAGGAGAAGGAGCAGCTCTTCAGACAGTTGGGTGGTGAG
GTCTTCATCGACTTCAGAACCTGCAAGGACATCGAGGGTGAGATCATCAAGGCCA
CCAACGGTGGTGCTCACGGTGTCATCAACGTCTCTGTCTCCGAGGCCGCCATCGA
GTCCTCTACCAACTACGTCAGAGCCAACGGTACCGTCGTCTTGGTCGGTTTGCCA
GCTGGCGCCAAGTGCAAGTCTGACGTTTTCAACCAGGTCGTCAAGTCCATCTCTA
TCGTCGGTTCTTACGTCGGTAACAGAGCTGACACCAGAGAGGCTCTAGACTTCTT
CGTCCGTGGTTTGGTCAGATCTCCAATCAAGGTTGTCGGTCTATCTACTCTACCAG
AGATTTTCGAGAAGATGGAGAAGGGCCAAATTGTTGGCAGATACGTTGTCGACA
CCTCCAACTAA
SEQ ID NO 52

b) >ADH Saccharomyces

ATGTCTATCCCAGAAACTCAAAAAGGTGTTATCTTCTACGAATCCCACGGTAAGT
TGGAATACAAAGATATTCCAGTTCCAAAGCCAAAGGCCAACGAATTGTTGATCAA
CGTTAAATACTCTGGTGTCTGTCACACTGACTTGCACGCTTGGCACGGTGACTGG
CCATTGCCAGTTAAGCTACCATTAGTCGGTGGTCACGAAGGTGCCGGTGTCGTTG
TCGGCATGGGTGAAAACGTTAAGGGCTGGAAGATCGGTGACTACGCCGGTATCA
AATGGTTGAACGGTTCTTGTATGGCCTGTGAATACTGTGAATTGGGTAACGAATC
CAACTGTCCTCACGCTGACTTGTCTGGTTACACCCACGACGGTTCTTTCCAACAAT
ACGCTACCGCTGACGCTGTTCAAGCCGCTCACATTCCTCAAGGTACCGACTTGGC
CCAAGTCGCCCCCATCTTGTGTGCTGGTATCACCGTCTACAAGGCTTTGAAGTCTG
CTAACTTGATGGCCGGTCACTGGGTTGCTATCTCCGGTGCTGCTGGTGGTCTAGGT
TCTTTGGCTGTTCAATACGCCAAGGCTATGGGTTACAGAGTCTTGGGTATTGACG
GTGGTGAAGGTAAGGAAGAATTATTCAGATCCATCGGTGGTGAAGTCTTCATTGA
CTTCACTAAGGAAAAGGACATTGTCGGTGTGTTCTAAAGGCCACTGACGGTGGTG
CTCACGGTGTCATCAACGTTTCCGTTCCGAAGCCGCTATTGAAGCTTCTACCAGAT
ACGTTAGAGCTAACGGTACCACCGTTTTGGTCGGTATGCCAGCTGGTGCCAAGTG
TTGTTCTGATGTCTTCAACCAAGTCGTCAAGTCCATCTCTATTGTTGGTTCTTACGT
CGGTAACAGAGCTGACACCAGAGAAGCTTTGGACTTCTTCGCCAGAGGTTTGGTC
AAGTCTCCAATCAAGGTTGTCGGCTTGTCTACCTTGCCAGAAATTTACGAAAAGA
TGGAAAAGGGTCAAATCGTTGGTAGATACGTTGTTGACACTTCTAAATAA
SEQ ID NO 53

Fig. 9 (continued)

c) >Clon A02

ATGTCTATCCCAGAAACTCAAAAAGGTGTTATCTTCTACGAATCCCACGGTAAGT
TGGAATACAAAGATATTCCAGTTCCAAAGCCAAAGGCCAACGAATTGTTGATCAA
CGTTAAATACTCTGGTGTCTGTCACACTGACTTGCACGCTTGGCACGGTGACTGG
CCATTGCCAGTTAAGCTACCATTAGTCGGTGGTCACGAAGGTGCCGGTGTCGTTG
TCGGCATGGGTGAAAACGTTAAGGGCTGGAAGATCGGTGACTACGCCGGTATCA
AATGGTTGAACGGTTCTTGTATGGCCTGTGAATACTGTGAATTGGGTAACGAATC
CAACTGTCCAGAGGCTGACTTGTCCGGTTACACCCACGACGGTTCTTTCCAGCAG
TACGCTACTGCCGATGCCGTCCAGGCCGCTAAGATCCCAGCTGGCGCTGACCTTG
CTGAGATCGCCCCAATCCTGTGTGCCGGTATCACTGTCTACAAGGCTTTGAAGTCT
GCTAACTTGCAGGCCGGTGACTGGGTTGCCATCTCCGGTGCCGCCGGTGGTTTGG
GTTCCCTAGCCGTCCAGTACGCCAAGGCCATGGGTTACCGTGTCTTGGGTATCGA
CGGTGGTGAGGAGAAGGAGCAGCTCTTCAGACAGTTGGGTGGTGAGGTCTTCATC
GACTTCAGAACCTGCAAGGACATCGAGGGTGAGATCATCAAGGCCACCAACGGT
GGCGCTCACGGTGTCATCAACGTCTCTGTCTCCGAGGCCGCCATCGAGTCCTCTA
CCAACTACGTCAGAGCCAACGGTACCGTCGTCTTGGTCGGTTTGCCAGCTGGCGC
CAAGTGCAAGTCTGACGTTTTCAACCAGGTCGTCAAGTCCATCTCTATCGTCGGTT
CTTACGTCGGTAACAGAGCTGACACCAGAGAGGCTCTAGACTTCTTCGTCCGTGG
TTTGGTCAGATCTCCAATCAAGGTTGTCGGTCTATCTACTCTACCAGAGATTTTCG
AGAAGATGGAGAAGGGCCAAATTGTTGGCAGATACGTTGTCGACACCTCCAACT
AA

SEQ ID NO 54

d) >Clon A03

GCCATGGGTGAGAATGTCTATCCCAGAAACTCAAAAAGGTGTTATCTTCTACGAA
TCCCACGGTAAGTTGGAATACAAAGATATTCCAGTTCCAAAGCCAAAGGCCAAC
GAATTGTTGATCAACGTTAAATACTCTGGTGTCTGTCACACTGACTTGCACGCTTG
GCACGGTGACTGGCCATTGCCAGTTAAGCTACCATTAGTCGGTGGTCACGAAGGT
GCCGGTGTCGTTGTCGCCATGGGTGAGAACGTCAAGGGCTGGAAGGTCGGTGACT
TGGCCGGTATCAAGTGGTTGAACGGCTCCTGTATGTCCTGTGAGTCCTGTGAGTT
GGGTAACGAGTCCAACTGTCCAGAGGCTGACTTGTCCGGTTACACCCACGACGGT
TCTTTCCAGCAGTACGCTACTGCCGATGCCGTCCAGGCCGCTAAGATCCCAGCTG
GCGCTGACCTTGCTGAGATCGCCCCAATCCTGTGTGCCGGTATCACTGTCTACAA
GGCTTTGAAGTCTGCTAACTTGCAGGCCGGTGACTGGGTTGCCATCTCCGGTGCC
GCCGGTGGTTTGGGTTCCCTAGCCGTCCAGTACGCCAAGGCCATGGGTTACCGTG
TCTTGGGTATCGACGGTGGTGAGGAGAAGGAGCAGCTCTTCAGACAGTTGGGTG
GTGAGGTCTTCATCGACTTCAGAACCTGCAAGGACATCGAGGGTGAGATCATCAA
GGCCACCAACGGTGGTGCTCACGGTGTCATCAACGTCTCTGTCTCCGAGGCCGCC
ATCGAGTCCTCTACCAACTACGTCAGAGCCAACGGTACCGTCGTCTTGGTCGGTT
TGCCAGCTGGCGCCAAGTGCAAGTCTGACGTTTTCAACCAGGTCGTCAAGTCCAT
CTCTATCGTCGGTTCTTACGTCGGTAACAGAGCTGACACCAGAGAGGCTCTAGAC
TTCTTCGTCCGTGGTTTGGTCAGATCTCCAATCAAGGTTGTCGGTCTATCTACTCT
ACCAGAGATTTTCGAGAAGATGGAGAAGGGCCAAATTGTTGGCAGATACGTTGT
CGACACCTCCAACTAA

SEQ ID NO 55

Fig. 9 (continued)

e) >Clon A05

ATGTCTATCCCAAAGACCCAGAAAGGTGTTATCTTCTACGAGACCGGTGGTAAGC
TGGAATACAAGGACATCGATGTCCCAACCCCAAAGGCCAACGAGCTTTTGGTCAA
CGTCAAGTACTCCGGTGTGTGCCACACTGACTTGCACGCCTACCACGGTGACTGG
CCATTGCCAGTTAAGTTGCCTCTAGTCGGTGGCCACGAGGGTGCCGGTGTCGTTG
TCGCCATGGGTGAGAACGTCAAGGGCTGGAAGGTCGGTGACTTGGCCGGTATCA
AGTGGTTGAACGGCTCCTGTATGTCCTGTGAGTCCTGTGAGTTGGGTAACGAGTC
CAACTGTCCAGAGGCTGACTTGTCCGGTTACACCCACGACGGTTCTTTCCAGCAG
TACGCTACTGCCGATGCCGTCCAGGCCGCTAAGATCCCAGCTGGCGCTGACCTTG
CTGAGATCGCCCCAATCCTGTGTGCCGGTATCACTGTCTACAAGGCTTTGAAGTCT
GCTAACTTGCAGGCCGGTGACTGGGTTGCCATCTCCGGTGCCGCCGGTGGTTTGG
GTTCCCTAGCCGTCCAGTACGCCAAGGCCATGGGTTACCGTGTCTTGGGTATCGA
CGGTGGTGAGGAGAAGGAGCAGCTCTTCAGACAGTTGGGTGGTGAGGTCTTCATC
GACTTCAGAACCTGCAAGGACATCGAGGGTGAGATCATCAAGGCCACCAACGGT
GGTGCTCACGGTGTCATCAACGTCTCTGTCTCCGAGGCCGCCATCGAGTCCTCTAC
CAACTACGTCAGAGCCAACGGTACCGTCGTCTTGGTCGGTTTGCCAGCTGGCGCC
AAGTGCAAGTCTGACGTTTTCAACCAGGTCGTCAAGTCCATCTCTATCGTCGGTTC
TTACGTCGGTAACAGAGCTGACACCAGAGAGGCTCTAGACTTCTTCGTCCGTGGT
TTGGTCAGATCTCCAATCAAGGTTGTCGGTCTATCTACTCTACCAGAGATTTTCGA
GAAGATGGAGAAGGGCCAAATTGTTGGCAGATACGTTGTCGACACCTCCAACTA
A

SEQ ID NO 56

f) >Clon A06

ATGTCTATCCCAGAAACTCAAAAAGGTGTTATCTTCTACGAATCCCACGGTAAGT
TGGAATACAAAGATATTCCAGTTCCAAAGCCAAAGGCCAACGAATTGTTGATCAA
CGTTAAATACTCTGGTGTCTGTCACACTGACTTGCACGCTTGGCACGGTGACTGG
CCATTGCCAGTTAAGCTACCATTAGTCGGTGGTCACGAAGGTGCCGGTGTCGTTG
TCGGCATGGGTGAAAACGTTAAGGGCTGGAAGATCGGTGACTACGCCGGTATCA
AATGGTTGAACGGTTCTTGTATGGCCTGTGAATACTGTGAATTGGGTAACGAGTC
CAACTGTCCAGAGGCTGACTTGTCTGGTTACACCCACGACGGTTCTTTCCAACAA
TACGCTACTGCCGATGCCGTCCAGGCCGCTAAGATCCCAGCTGGCGCTGACCTTG
CTGAGATCGCCCCAATCCTGTGTGCCGGTATCACTGTCTACAAGGCTTTGAAGTCT
GCTAACTTGCAGGCCGGTGACTGGGTTGCCATCTCCGGTGCCGCCGGTGGTTTGG
GTTCCCTAGCCGTCCAGTACGCCAAGGCCATGGGTTACCGTGTCTTGGGTATCGA
CGGTGGTGAGGAGAAGGAGCAGCTCTTCAGACAGTTGGGTGGTGAGGTCTTCATC
GACTTCAGAACCTGCAAGGACATCGAGGGTGAGATCATCAAGGCCACCAACGGT
GGTGCTCACGGTGTCATCAACGTCTCTGTCTCCGAGGCCGCCATCGAGTCCTCTAC
CAACTACGTCAGAGCCAACGGTACCGTCGTCTTGGTCGGTTTGCCAGCCGGCGCC
AAGTGCAAGTCTGACGTTTTCAACCAGGTCGTCAAGTCCATCTCTATCGTCGGTTC
TTACGTCGGTAACAGAGCTGACACCAGAGAGGCTCTAGACTTCTTCGTCCGTGGT
TTGGTCAGATCTCCAATCAAGGTTGTCGGTCTATCTACTCTACCAGAGATTTTCGA
GAAGATGGAGAAGGGCCAAATTGTTGGCAGATACGTTGTCGACACCTCCAACTA
A

SEQ ID NO 57

Fig. 9 (continued)

g) >Clon A10

ATGTCTATCCCAGAAACTCAAAAAGGTGTTATCTTCTACGAGACCGGTGGTAAGC
TGGAATACAAGGACATCGATGTCCCAACCCCAAAGGCCAACGAGCTTTTGGTCAA
CGTCAAGTACTCCGGTGTGTGCCACACTGACTTGCACGCCTACCACGGTGACTGG
CCATTGCCAGTTAAGTTGCCTCTAGTCGGTGGCCACGAGGGTGCCGGTGTCGTTG
TCGCCATGGGTGAGAACGTCAAGGGCTGGAAGGTCGGTGACTTGGCCGGTATCA
AGTGGTTGAACGGCTCCTGTATGTCCTGTGAGTCCTGTGAGTTGGGTAACGAGTC
CAACTGTCCAGAGGCTGACTTGTCCGGTTACACCCACGACGGTTCTTTCCAGCAG
TACGCTACTGCCGATGCCGTCCAGGCCGCTAAGATCCCAGCTGGCGCTGACCTTG
CTGAGATCGCCCCAATCCTGTGTGCCGGTATCACTGTCTACAAGGCTTTGAAGTCT
GCTAACTTGCAGGCCGGTGACTGGGTTGCCATCTCCGGTGCCGCCGGTGGTTTGG
GTTCCCTAGCCGTCCAGTACGCCAAGGCCATGGGTTTACCGTGTCTTGGGTATCG
ACGGTGGTGAGGAGAAGGAGCAGCTCTTCAGACAGTTGGGTGGTGGAGGTCTTC
ATCGACTTCAGAACCTGCAAGGACATCGAGGGTGAGATCATCAAGCCCACCAAC
GGTGGTGCTCACGGTGTCATCAACGTCTCTGTCTCCGAGGCCGCCATCGAGTCCT
CTACCAACTACGTCAGAGCCAACGGTACCGTCGTCTTGGTCGGTTTGCCAGCTGG
CGCCAAGTGCAAGTCTGACGTTTTCAACCAGGTCGTCAAGTCCATCTCTATCGTC
GGTTCTTACGTCGGTAACAGAGCTGACACCAGAGAGGCTCTAGACTTCTTCGTCC
GTGGTTTGGTCAGATCTCCAATCAAGGTTGTCGGTCTATCTACTCTACCAGAGATT
TTCGAGAAGATGGAGAAGGGCCAAATTGTTGGCAGATACGTTGTCGACACCTCCA
ACTAA

SEQ ID NO 58

h) >Clon A11

ATGTCTATCCCAGAAACTCAAAAAGGTGTTATCTTCTACGAATCCCACGGTAAGT
TGGAATACAAAGATATTCCAGTTCCAAAGCCAAAGGCCAACGAATTGTTGATCAA
CGTTAAATACTCTGGTGTCTGTCACACTGACTTGCACGCTTGGCACGGTGACTGG
CCATTGCCAGTTAAGCTACCATTAGTCGGTGGTCACGAAGGTGCCGGTGTCGTTG
TCGGCATGGGTGAAAACGTTAAGGGCTGGAAGATCGGTGACTACGCCGGTATCA
AATGGTTGAACGGTTCTTGTATGGCCTGTGAATACTGTGAATTGGGTAACGAATC
CAACTGTCCTCACGCTGACTTGTCTGGTTACACCCACGACGGTTCTTTCCAGCAGT
ACGCTACTGCCGATGCCGTCCAGGCCGCTAAGATCCCAGCTGGCGCTGACCTTGC
TGAGATCGCCCCAATCCTGTGTGCCGGTATCACTGTCTACAAGGCTTTGAAGTCT
GCTAACTTGCAGGCCGGTGACTGGGTTGCCATCTCCGGTGCCGCCGGTGGTTTGG
GTTCCCTAGCCGTCCAGTACGCCAAGGCCATGGGTTACCGTGTCTTGGGTATCGA
CGGTGGTGAGGAGAAGGAGCAGCTCTTCAGACAGTTGGGTGGTGAGGTCTTCATC
GACTTCAGAACCTGCAAGGACATCGAGGGTGAGATCATCAAGGCCACCAACGGT
GGTGCTCACGGTGTCATCAACGTCTCTGTCTCCGAGGCCGCCATCGAGTCCTCTAC
CAACTACGTCAGAGCCAACGGTACCGTCGTCTTGGTCGGTTTGCCAGCTGGCGCC
AAGTGCAAGTCTGACGTTTTCAACCAGGTCGTCATGTCCATCTCTATCGTCGGTTC
TTACGTCGGTAACAGAGCTGACACCAGAGAGGCTCTAGACTTCTTCGTCCGTGGT
TTGGTCAGATCTCCAATCAAGGTTGTCGGTCTATCTACTCTACCAGAGATTTTCGA
GAAGATGGAGAAGGGCCAAATTGTTGGCAGATACGTTGTCGACACCTCCAACTA
A

SEQ ID NO 59