SEQUENCE LISTING

<110> Intrexon Corporation

<120> Site-Specific Serine Recombinases and Methods of Their Use

<130> SP8830A

<140> Not yet assigned
<141> 2005-02-08

<160> 21

<170> PatentIn version 3.3

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<211> 1638
<212> DNA
<213> Artificial

<220>
<223> synthetic gene

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aaggaactca tgaacaagat cctcaccgcc atcgagatcc cctacgagct gaagatggag 180

atcggcagcg gcgagagcat cgacggcaga cccgtgttca aggagtgcct gaaggatctg 240

gaggagggca agtaccaggc catcgccgtg aaggagatca ccaggctgag cagaggcagc 300

tacagcgacg ccggccagat cgtgaacctg ctgcagagca agcggctcat catcatcacc 360

ccctacaagg tgtacgaccc cagaaacccc gtcgacatgc ggcagatccg gttcgagctg 420

ttcatggcca gggaggagtt cgagatgacc cgggagagaa tgaccggcgc caagtacacc 480

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aaaaccagca agctggaccc cgtggaggac gaggccaagg tggtgcagct catcttcaac 600

atcttcctga acgggctgaa cggcaaggac tacagctaca cagccatcgc cagccacctc 660

accaatctgc agatccctac ccccagcggc aagaagcggt ggaaccagta caccatcaag 720

gccatcctgc agaacgaggt gtacatcggc accgtgaagt acaaggtgcg ggagaaaacc 780

aaggacggca agcggaccat caggcctgag aaggagcaga tcgtggtgca ggacgcccac 840

gcccctatca tcgacaagga gcagttccag cagagccagg tgaagatcgc caacaaggtg 900

cccctgctgc ccaacaagga cgagttcgag ctgagcgagc tggccggagt gtgcacctgc 960

agcaagtgcg gcgagcctct gagcaagtac gagagcaagc gcatccggaa gaacaaggat 1020

ggcaccgaga gcgtgtacca cgtgaagtcc ctcacctgca agaagaacaa gtgcacctac 1080

gtgcggtaca acgacgtgga gaacgccatc ctggattacc tgagcagcct gaacgacctg 1140

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agcaacatga aaaccaagaa gcagatgagc gagcacctga gccagaagga gaaggagctt 1260

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ctgcggatgg tgctgaagga cgtgatcgtg aacatgaccc agaagcgcaa gggccccatc 1560

cccgcccagt tcgagatcac acccatcctg cggttcaact ttatcttcga tctcaccgcc 1620

accaacagct tccactag 1638

<210> 2
<211> 545
<212> PRT
<213> Bacillus subtilis phage SPBc2

<400> 2

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Gly Tyr Leu Arg Arg Ser Arg Gln Asp Met Glu Arg Glu Lys Arg Thr
20 25 30

Gly Glu Asp Thr Leu Thr Glu Gln Lys Glu Leu Met Asn Lys Ile Leu
35 40 45

Thr Ala Ile Glu Ile Pro Tyr Glu Leu Lys Met Glu Ile Gly Ser Gly
50 55 60

Glu Ser Ile Asp Gly Arg Pro Val Phe Lys Glu Cys Leu Lys Asp Leu
65 70 75 80

Glu Glu Gly Lys Tyr Gln Ala Ile Ala Val Lys Glu Ile Thr Arg Leu
85 90 95

Ser Arg Gly Ser Tyr Ser Asp Ala Gly Gln Ile Val Asn Leu Leu Gln
100 105 110

Ser Lys Arg Leu Ile Ile Ile Thr Pro Tyr Lys Val Tyr Asp Pro Arg
115 120 125

Asn Pro Val Asp Met Arg Gln Ile Arg Phe Glu Leu Phe Met Ala Arg
130 135 140

Glu Glu Phe Glu Met Thr Arg Glu Arg Met Thr Gly Ala Lys Tyr Thr
145 150 155 160

Tyr Ala Ala Gln Gly Lys Trp Ile Ser Gly Leu Ala Pro Tyr Gly Tyr
165 170 175

Gln Leu Asn Lys Lys Thr Ser Lys Leu Asp Pro Val Glu Asp Glu Ala
180 185 190

Lys Val Val Gln Leu Ile Phe Asn Ile Phe Leu Asn Gly Leu Asn Gly

195 200 205

Lys Asp Tyr Ser Tyr Thr Ala Ile Ala Ser His Leu Thr Asn Leu Gln
210 215 220

Ile Pro Thr Pro Ser Gly Lys Lys Arg Trp Asn Gln Tyr Thr Ile Lys
225 230 235 240

Ala Ile Leu Gln Asn Glu Val Tyr Ile Gly Thr Val Lys Tyr Lys Val
245 250 255

Arg Glu Lys Thr Lys Asp Gly Lys Arg Thr Ile Arg Pro Glu Lys Glu
260 265 270

Gln Ile Val Val Gln Asp Ala His Ala Pro Ile Ile Asp Lys Glu Gln
275 280 285

Phe Gln Gln Ser Gln Val Lys Ile Ala Asn Lys Val Pro Leu Leu Pro
290 295 300

Asn Lys Asp Glu Phe Glu Leu Ser Glu Leu Ala Gly Val Cys Thr Cys
305 310 315 320

Ser Lys Cys Gly Glu Pro Leu Ser Lys Tyr Glu Ser Lys Arg Ile Arg
325 330 335

Lys Asn Lys Asp Gly Thr Glu Ser Val Tyr His Val Lys Ser Leu Thr
340 345 350

Cys Lys Lys Asn Lys Cys Thr Tyr Val Arg Tyr Asn Asp Val Glu Asn
355 360 365

Ala Ile Leu Asp Tyr Leu Ser Ser Leu Asn Asp Leu Asn Asp Ser Thr
370 375 380

Leu Thr Lys His Ile Asn Ser Met Leu Ser Lys Tyr Glu Asp Asp Asn
385 390 395 400

Ser Asn Met Lys Thr Lys Lys Gln Met Ser Glu His Leu Ser Gln Lys
405 410 415

Glu Lys Glu Leu Lys Asn Lys Glu Asn Phe Ile Phe Asp Lys Tyr Glu
420 425 430

Ser Gly Ile Tyr Ser Asp Glu Leu Phe Leu Lys Arg Lys Ala Ala Leu
435 440 445

Asp Glu Glu Phe Lys Glu Leu Gln Asn Ala Lys Asn Glu Leu Asn Gly
450 455 460

Leu Gln Asp Thr Gln Ser Glu Ile Asp Ser Asn Thr Val Arg Asn Asn
465 470 475 480

Ile Asn Lys Ile Ile Asp Gln Tyr His Ile Glu Ser Ser Ser Glu Lys
485 490 495

Lys Asn Glu Leu Leu Arg Met Val Leu Lys Asp Val Ile Val Asn Met
500 505 510

Thr Gln Lys Arg Lys Gly Pro Ile Pro Ala Gln Phe Glu Ile Thr Pro
515 520 525

Ile Leu Arg Phe Asn Phe Ile Phe Asp Leu Thr Ala Thr Asn Ser Phe
530 535 540

His
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<213> Artificial

<220>
<223> Synthetic gene

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tacaagaact acagcgacgc cggcttcagc ggcggcaagc tggagagacc cgccatcacc 180

gagttgatcg aggacggcaa gaacaacaag ttcgacacca tcctggtgta caagctggac 240

cggctgagca gaaacgtgaa ggacaccctg tacctggtga aggacgtgtt caccgccaac 300

aacatccact tcgtgagcct gaaggagaac atcgacacca gcagcgccat gggcaatctg 360

ttcctcacac tgctgagcgc aattgccgag ttcgagcggg agcagatcaa ggaacggatg 420

cagttcggcg tgatgaacag agccaagagc ggcaagacca ccgcctggaa aacccctcca 480

tacggctacc ggtacaacaa ggacgagaaa accctgagcg tgaacgagct ggaggccgcc 540

aatgtgaggc agatgttcga catgatcatc agcggctgca gcatcatgag catcaccaac 600

tacgcccggg acaacttcgt gggcaacacc tggacccacg tgaaggtgaa gcggatcctg 660

gagaacgaga cctacaaagg cctggtgaag taccgggagc agacctttag cggcgatcac 720

caggccatca tcgacgaaaa gacctacaac aaggcccaga tcgccctggc ccacagaacc 780

gacaccaaga ccaacaccag acccttccag ggcaagtaca tgctgagcca catcgccaag 840

tgcggctact gtggcgcccc tctgaaggtg tgcaccggca gggccaagaa tgacggcacc 900

cggagacaga cctacgtgtg cgtgaacaag accgagagcc tggccagaag gagcgtgaac 960

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tacgtgatcg acgtgctgta taagctgcag cacgacaagg agtacctgaa gaagatcaag 1080

aaggacgaca acatcatcga tatcaccccc ctgaagaagg agatcgagat catcgacaag 1140

aagattaacc ggctgaacga cctgtacatc aacgacctca tcgacctgcc caagctgaag 1200

aaagacatcg aggagctgaa ccacctgaag gacgactaca ataaggccat caagctgaac 1260

tacctggaca agaagaacga ggacagcctg ggcatgctca tggacaacct ggacatccgc 1320

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accatggaca atatcgacat catcttcaag ttctag 1416

<210> 4
<211> 471
<212> PRT
<213> Putative recombinase of bacteriophage SF370.1

<400> 4

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Glu Glu Gly Tyr Ser Ile Gln Gly Gln Ile Glu Ala Leu Thr Lys Tyr
20 25 30

Cys Glu Ala Met Glu Trp Lys Ile Tyr Lys Asn Tyr Ser Asp Ala Gly
35 40 45

Phe Ser Gly Gly Lys Leu Glu Arg Pro Ala Ile Thr Glu Leu Ile Glu
50 55 60

Asp Gly Lys Asn Asn Lys Phe Asp Thr Ile Leu Val Tyr Lys Leu Asp
65 70 75 80

Arg Leu Ser Arg Asn Val Lys Asp Thr Leu Tyr Leu Val Lys Asp Val
85 90 95

Phe Thr Ala Asn Asn Ile His Phe Val Ser Leu Lys Glu Asn Ile Asp
100 105 110

Thr Ser Ser Ala Met Gly Asn Leu Phe Leu Thr Leu Leu Ser Ala Ile
115 120 125

Ala Glu Phe Glu Arg Glu Gln Ile Lys Glu Arg Met Gln Phe Gly Val
130 135 140

Met Asn Arg Ala Lys Ser Gly Lys Thr Thr Ala Trp Lys Thr Pro Pro
145 150 155 160

Tyr Gly Tyr Arg Tyr Asn Lys Asp Glu Lys Thr Leu Ser Val Asn Glu
165 170 175

Leu Glu Ala Ala Asn Val Arg Gln Met Phe Asp Met Ile Ile Ser Gly
180 185 190

Cys Ser Ile Met Ser Ile Thr Asn Tyr Ala Arg Asp Asn Phe Val Gly
195 200 205

Asn Thr Trp Thr His Val Lys Val Lys Arg Ile Leu Glu Asn Glu Thr
210 215 220

Tyr Lys Gly Leu Val Lys Tyr Arg Glu Gln Thr Phe Ser Gly Asp His
225 230 235 240

Gln Ala Ile Ile Asp Glu Lys Thr Tyr Asn Lys Ala Gln Ile Ala Leu
245 250 255

Ala His Arg Thr Asp Thr Lys Thr Asn Thr Arg Pro Phe Gln Gly Lys
260 265 270

Tyr Met Leu Ser His Ile Ala Lys Cys Gly Tyr Cys Gly Ala Pro Leu
275 280 285

Lys Val Cys Thr Gly Arg Ala Lys Asn Asp Gly Thr Arg Arg Gln Thr
290 295 300

Tyr Val Cys Val Asn Lys Thr Glu Ser Leu Ala Arg Arg Ser Val Asn
305 310 315 320

Asn Tyr Asn Asn Gln Lys Ile Cys Asn Thr Gly Arg Tyr Glu Lys Lys
325 330 335

His Ile Glu Lys Tyr Val Ile Asp Val Leu Tyr Lys Leu Gln His Asp
340 345 350

Lys Glu Tyr Leu Lys Lys Ile Lys Lys Asp Asp Asn Ile Ile Asp Ile
355 360 365

Thr Pro Leu Lys Lys Glu Ile Glu Ile Ile Asp Lys Lys Ile Asn Arg
370 375 380

Leu Asn Asp Leu Tyr Ile Asn Asp Leu Ile Asp Leu Pro Lys Leu Lys
385 390 395 400

Lys Asp Ile Glu Glu Leu Asn His Leu Lys Asp Asp Tyr Asn Lys Ala
405 410 415

Ile Lys Leu Asn Tyr Leu Asp Lys Lys Asn Glu Asp Ser Leu Gly Met
420 425 430

Leu Met Asp Asn Leu Asp Ile Arg Lys Ser Ser Tyr Asp Val Gln Ser
435 440 445

Arg Ile Val Lys Gln Leu Ile Asp Arg Val Glu Val Thr Met Asp Asn
450 455 460

Ile Asp Ile Ile Phe Lys Phe
465 470

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<211> 1503
<212> DNA
<213> Synthetic gene

<400> 5
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gccgaggatc tggatgtgag cggagccgtg gacccccttcg acagaaagcg gagacccaac 180

ctggccagat ggctggcctt tgaggagcag cccttcgatg tgatcgtggc ctacagagtg 240

gacaggctga cccggagcat tagacacctc cagcagctgg tgcactgggc cgaggaccac 300

aagaaactgg tggtgagcgc cacagaggcc cacttcgata ccaccacccc ctttgctgca 360

gtggtgatcg ccctgatggg cacagtggcc cagatggagc tggaggccat caaggagagg 420

aatcggtctg ccgcccactt caatatcagg gccggcaagt acagaggaag cctgcctcct 480

tggggctacc tgcccacaag agtggatggc gagtggagac tggtgcctga ccctgtgcag 540

agggagagaa tcctggaagt gtatcaccgc gtggtggaca atcacgagcc tctgcacctg 600

gtggcccacg acctgaatag gagaggcgtg ctgtccccca aggattactt cgcccagctc 660

cagggcagag agcctcaggg cagagagtgg tctgccaccg ccctgaaaag atctatgatc 720

agcgaggcca tgctgggcta cgccaccctg aatggcaaga ccgtgaggga tgatgatgga 780

gcccctctgg tgagagccga gcccatcctg acaagggaac agctggaggc tctgagagcc 840

gaactggtga aaaccagcag agccaagcct gccgtgagca cacctagcct gctgctgaga 900

gtgctgttct gtgccgtgtg tggcgagcct gcctacaagt ttgccggcgg aggcagaaag 960

caccccggt acagatgtag gagcatgggc ttccctaagc actgcggcaa tggcaccgtg 1020

gccatggccg aatgggacgc cttttgcgag gagcaagtgc tggatctgct gggagatgcc 1080

gagaggctgg agaaagtgtg ggtggccgga tccgattctg ccgtggaact ggccgaagtg 1140

aatgctgaac tggtggacct gaccagcctg atcggcagcc ctgcctatag agccggaagc 1200

cctcagagag aagccctgga cgccagaatt gccgccctgg ccgccagaca ggaggaactg 1260

gagggactgg aggccagacc ttctggctgg gagtggagag agaccggcca gagattcggc 1320

gattggtgga gggagcagga taccgccgcc aagaacacct ggctgcggag catgaacgtg 1380

aggctgacct tcgacgtgag aggcggcctg accagaacca tcgacttcgg cgacctccag 1440

gagtatgagc agcacctgag actgggaagc gtggtggaga gactgcacac aggcatgtcc 1500

tag 1503

<210> 6
<211> 500
<212> PRT
<213> Putative recombinase of mycobacteriophage Bxb1

<400> 6

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Thr Ser Pro Glu Arg Gln Leu Glu Ser Cys Gln Gln Leu Cys Ala Gln
20 25 30

Arg Gly Trp Asp Val Val Gly Val Ala Glu Asp Leu Asp Val Ser Gly
35 40 45

Ala Val Asp Pro Phe Asp Arg Lys Arg Arg Pro Asn Leu Ala Arg Trp
50 55 60

Leu Ala Phe Glu Glu Gln Pro Phe Asp Val Ile Val Ala Tyr Arg Val
65 70 75 80

Asp Arg Leu Thr Arg Ser Ile Arg His Leu Gln Gln Leu Val His Trp
85 90 95

Ala Glu Asp His Lys Lys Leu Val Val Ser Ala Thr Glu Ala His Phe
100 105 110

Asp Thr Thr Thr Pro Phe Ala Ala Val Val Ile Ala Leu Met Gly Thr
115 120 125

Val Ala Gln Met Glu Leu Glu Ala Ile Lys Glu Arg Asn Arg Ser Ala
130 135 140

Ala His Phe Asn Ile Arg Ala Gly Lys Tyr Arg Gly Ser Leu Pro Pro
145 150 155 160

Trp Gly Tyr Leu Pro Thr Arg Val Asp Gly Glu Trp Arg Leu Val Pro
165 170 175

Asp Pro Val Gln Arg Glu Arg Ile Leu Glu Val Tyr His Arg Val Val
180 185 190

Asp Asn His Glu Pro Leu His Leu Val Ala His Asp Leu Asn Arg Arg
195 200 205

Gly Val Leu Ser Pro Lys Asp Tyr Phe Ala Gln Leu Gln Gly Arg Glu
210 215 220

Pro Gln Gly Arg Glu Trp Ser Ala Thr Ala Leu Lys Arg Ser Met Ile
225 230 235 240

Ser Glu Ala Met Leu Gly Tyr Ala Thr Leu Asn Gly Lys Thr Val Arg
245 250 255

Asp Asp Asp Gly Ala Pro Leu Val Arg Ala Glu Pro Ile Leu Thr Arg
260 265 270

Glu Gln Leu Glu Ala Leu Arg Ala Glu Leu Val Lys Thr Ser Arg Ala
275 280 285

Lys Pro Ala Val Ser Thr Pro Ser Leu Leu Leu Arg Val Leu Phe Cys
290 295 300

Ala Val Cys Gly Glu Pro Ala Tyr Lys Phe Ala Gly Gly Gly Arg Lys
305 310 315 320

His Pro Arg Tyr Arg Cys Arg Ser Met Gly Phe Pro Lys His Cys Gly
325 330 335

Asn Gly Thr Val Ala Met Ala Glu Trp Asp Ala Phe Cys Glu Glu Gln
340 345 350

Val Leu Asp Leu Leu Gly Asp Ala Glu Arg Leu Glu Lys Val Trp Val
355 360 365

Ala Gly Ser Asp Ser Ala Val Glu Leu Ala Glu Val Asn Ala Glu Leu
370 375 380

Val Asp Leu Thr Ser Leu Ile Gly Ser Pro Ala Tyr Arg Ala Gly Ser
385 390 395 400

Pro Gln Arg Glu Ala Leu Asp Ala Arg Ile Ala Ala Leu Ala Ala Arg
405 410 415

Gln Glu Glu Leu Glu Gly Leu Glu Ala Arg Pro Ser Gly Trp Glu Trp
420 425 430

Arg Glu Thr Gly Gln Arg Phe Gly Asp Trp Trp Arg Glu Gln Asp Thr
435 440 445

Ala Ala Lys Asn Thr Trp Leu Arg Ser Met Asn Val Arg Leu Thr Phe
450 455 460

Asp Val Arg Gly Gly Leu Thr Arg Thr Ile Asp Phe Gly Asp Leu Gln
465 470 475 480

Glu Tyr Glu Gln His Leu Arg Leu Gly Ser Val Val Glu Arg Leu His
485 490 495

Thr Gly Met Ser
500

<210> 7
<211> 1359
<212> DNA
<213> Synthetic gene

<400> 7
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atcttcatcg acggcggcta cagcggcagc aacatgaaca gacccgccct gaacgagatg 180

ctgagcaagc tgcacgagat cgatgccgtg gtggtgtaca ggctggacag gctgagcaga 240

agccagaggg acaccatcac cctcatcgag gagtacttcc tgaagaacaa cgtggagttc 300

gtgagcctga gcgagaccct ggacaccagc agcccttcg gcagagccat gatcggcatc 360

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gacgtgatcg acaccaagct gtacatcaac gaggaggagg ccaagcagct gcagctcatc 540

tacgatatct tcgaggagga gcagagcatc accttcctgc agaagcggct gaagaagctg 600

ggcttcaagg tgcggaccta caaccggtac aacaactggc tcaccaacga cctgtactgc 660

ggctacgtga gctacaagga caaggtgcac gtgaagggga tccacgagcc catcatcagc 720

gaggagcagt tctaccgggt gcaggagatc ttcacccgca tgggcaagaa ccccaacatg 780

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gccgacaagc tggaggagtt gatcatcaac cgggtgaaca actacagctt cgccagccgg 1020

aacgtggata aggaggacga gctggacagc ctgaatgaga agcttaagat cgagcacgcc 1080

aagaagaagc gcctgttcga cctgtacatt aacggcagct acgaggtgag cgagctggac 1140

tccatgatga acgacatcga cgcccagatc aactactacg agagccagat cgaggccaac 1200

gaggagctga agaagaacaa gaagatccag gagaacctgg ccgacctggc caccgtggat 1260

ttcgacagcc tggagttcag ggagaagcag ctgtacctga agtccctcat caataagatc 1320

tacatcgacg gggagcaggt gaccatcgag tggctgtag 1359

<210> 8
<211> 452
<212> PRT
<213> Putative recombinase of bacteriophage A118

<400> 8

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Asn Tyr Ser Ile Gln Ala Gln Thr Glu Lys Leu Thr Ala Leu Cys Arg
20 25 30

Ser Lys Asp Trp Asp Val Tyr Asp Ile Phe Ile Asp Gly Gly Tyr Ser
35 40 45

Gly Ser Asn Met Asn Arg Pro Ala Leu Asn Glu Met Leu Ser Lys Leu
50 55 60

His Glu Ile Asp Ala Val Val Val Tyr Arg Leu Asp Arg Leu Ser Arg
65 70 75 80

Ser Gln Arg Asp Thr Ile Thr Leu Ile Glu Glu Tyr Phe Leu Lys Asn
85 90 95

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

Phe Gly Arg Ala Met Ile Gly Ile Leu Ser Val Phe Ala Gln Leu Glu
115 120 125

Arg Glu Thr Ile Arg Asp Arg Met Val Met Gly Lys Ile Lys Arg Ile
130 135 140

Glu Ala Gly Leu Pro Leu Thr Thr Ala Lys Gly Arg Thr Phe Gly Tyr
145 150 155 160

Asp Val Ile Asp Thr Lys Leu Tyr Ile Asn Glu Glu Glu Ala Lys Gln
165 170 175

Leu Gln Leu Ile Tyr Asp Ile Phe Glu Glu Glu Gln Ser Ile Thr Phe
180 185 190

Leu Gln Lys Arg Leu Lys Lys Leu Gly Phe Lys Val Arg Thr Tyr Asn
195 200 205

Arg Tyr Asn Asn Trp Leu Thr Asn Asp Leu Tyr Cys Gly Tyr Val Ser
210 215 220

Tyr Lys Asp Lys Val His Val Lys Gly Ile His Glu Pro Ile Ile Ser
225 230 235 240

Glu Glu Gln Phe Tyr Arg Val Gln Glu Ile Phe Thr Arg Met Gly Lys
245 250 255

Asn Pro Asn Met Asn Arg Asp Ser Ala Ser Leu Leu Asn Asn Leu Val
260 265 270

Val Cys Ser Lys Cys Gly Leu Gly Phe Val His Arg Arg Lys Asp Thr
275 280 285

Met Ser Arg Gly Lys Lys Tyr His Tyr Arg Tyr Tyr Ser Cys Lys Thr
290 295 300

Tyr Lys His Thr His Glu Leu Glu Lys Cys Gly Asn Lys Ile Trp Arg
305 310 315 320

Ala Asp Lys Leu Glu Glu Leu Ile Ile Asn Arg Val Asn Asn Tyr Ser
325 330 335

Phe Ala Ser Arg Asn Val Asp Lys Glu Asp Glu Leu Asp Ser Leu Asn
340 345 350

Glu Lys Leu Lys Ile Glu His Ala Lys Lys Lys Arg Leu Phe Asp Leu
355 360 365

Tyr Ile Asn Gly Ser Tyr Glu Val Ser Glu Leu Asp Ser Met Met Asn
370 375 380

Asp Ile Asp Ala Gln Ile Asn Tyr Tyr Glu Ser Gln Ile Glu Ala Asn
385 390 395 400

Glu Glu Leu Lys Lys Asn Lys Lys Ile Gln Glu Asn Leu Ala Asp Leu
405 410 415

Ala Thr Val Asp Phe Asp Ser Leu Glu Phe Arg Glu Lys Gln Leu Tyr
420 425 430

Leu Lys Ser Leu Ile Asn Lys Ile Tyr Ile Asp Gly Glu Gln Val Thr
435 440 445

Ile Glu Trp Leu
450

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<211> 1410
<212> DNA
<213> Synthetic gene

<400> 9
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aagtgggtgc ccgtggagta cctggacaac gatgtgagcg ccagcaccgg caagaggaga 180

cccgcctacg agcagatgct ggccgacatc accgccggca agatcgccgc cgtggtggcc 240

tgggacctgg ataggctgca caggagaccc atcgagctgg aggccttcat gagcctggcc 300

gatgagaaaa gactggccct ggccaccgtg gccggcgacg tggacctggc caccccccag 360

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agactcgagc tggaaaccct gtacggcgag ctggacagac tggccgtgga gagagccgag 1140

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aagctgcagg ccaggcagca ggaccaggag aggctgagag tgttcgacgg catccccctg 1260

ggcacccctc aggtggccgg catgattgcc gagctgagcc ccgatagatt cagggctgtg 1320

ctggatgtgc tggccgaggt ggtggtgcag cccgtgggca agagcggcag aatcttcaac 1380

cccgagcggg tgcaggtgaa ctggagatag 1410

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<211> 469
<212> PRT
<213> Putative recombinase of bacteriophage PhiRv1

<400> 10

Met Arg Tyr Thr Thr Pro Val Arg Ala Ala Val Tyr Leu Arg Ile Ser
1 5 10 15

Glu Asp Arg Ser Gly Glu Gln Leu Gly Val Ala Arg Gln Arg Glu Asp
20 25 30

Cys Leu Lys Leu Cys Gly Gln Arg Lys Trp Val Pro Val Glu Tyr Leu
35 40 45

Asp Asn Asp Val Ser Ala Ser Thr Gly Lys Arg Arg Pro Ala Tyr Glu
50 55 60

Gln Met Leu Ala Asp Ile Thr Ala Gly Lys Ile Ala Ala Val Val Ala
65 70 75 80

Trp Asp Leu Asp Arg Leu His Arg Arg Pro Ile Glu Leu Glu Ala Phe
85 90 95

Met Ser Leu Ala Asp Glu Lys Arg Leu Ala Leu Ala Thr Val Ala Gly
100 105 110

Asp Val Asp Leu Ala Thr Pro Gln Gly Arg Leu Val Ala Arg Leu Lys
115 120 125

Gly Ser Val Ala Ala His Glu Thr Glu His Lys Lys Ala Arg Gln Arg
130 135 140

Arg Ala Ala Arg Gln Lys Ala Glu Arg Gly His Pro Asn Trp Ser Lys
145 150 155 160

Ala Phe Gly Tyr Leu Pro Gly Pro Asn Gly Pro Glu Pro Asp Pro Arg
165 170 175

Thr Ala Pro Leu Val Lys Gln Ala Tyr Ala Asp Ile Leu Ala Gly Ala
180 185 190

Ser Leu Gly Asp Val Cys Arg Gln Trp Asn Asp Ala Gly Ala Phe Thr
195 200 205

Ile Thr Gly Arg Pro Trp Thr Thr Thr Leu Ser Lys Phe Leu Arg
210 215 220

Lys Pro Arg Asn Ala Gly Leu Arg Ala Tyr Lys Gly Ala Arg Tyr Gly
225 230 235 240

Pro Val Asp Arg Asp Ala Ile Val Gly Lys Ala Gln Trp Ser Pro Leu
245 250 255

Val Asp Glu Ala Thr Phe Trp Ala Ala Gln Ala Val Leu Asp Ala Pro
260 265 270

Gly Arg Ala Pro Gly Arg Lys Ser Val Arg Arg His Leu Leu Thr Gly
275 280 285

Leu Ala Gly Cys Gly Lys Cys Gly Asn His Leu Ala Gly Ser Tyr Arg
290 295 300

Thr Asp Gly Gln Val Val Tyr Val Cys Lys Ala Cys His Gly Val Ala
305 310 315 320

Ile Leu Ala Asp Asn Ile Glu Pro Ile Leu Tyr His Ile Val Ala Glu
325 330 335

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

Asp Ala Ala Glu Ala Glu Thr Ile Arg Leu Glu Leu Glu Thr Leu Tyr
355 360 365

Gly Glu Leu Asp Arg Leu Ala Val Glu Arg Ala Glu Gly Leu Leu Thr
370 375 380

Ala Arg Gln Val Lys Ile Ser Thr Asp Ile Val Asn Ala Lys Ile Thr
385 390 395 400

Lys Leu Gln Ala Arg Gln Gln Asp Gln Glu Arg Leu Arg Val Phe Asp
405 410 415

Gly Ile Pro Leu Gly Thr Pro Gln Val Ala Gly Met Ile Ala Glu Leu
420 425 430

Ser Pro Asp Arg Phe Arg Ala Val Leu Asp Val Leu Ala Glu Val Val
435 440 445

Val Gln Pro Val Gly Lys Ser Gly Arg Ile Phe Asn Pro Glu Arg Val
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Gln Val Asn Trp Arg
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<210> 11
<211> 99
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<220>
<223> SPBc2 attP site

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tatctgtttt ttaagatact tactactttt cttagtgga 99

<210> 12
<211> 1315
<212> DNA
<213> Artificial

<220>
<223> STOP sequence

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atttgtaacc attataagct gcaataaaca agttaacaac aacaattgca ttcattttat 180

gtttcaggtt caggggggagg tgtgggaggt tttttaaagc aagtaaaacc tctacaaatg 240

tggtatggct gattatgatc tctagtcaag gcactataca tcaaatattc cttattaacc 300

cctttacaaa ttaaaaagct aaaggtacac aatttttgag catagttatt aatagcagac 360

actctatgcc tgtgtggagt aagaaaaaac agtatgttat gattataact gttatgccta 420

cttataaagg ttacagaata tttttccata attttcttgt atagcagtgc agctttttcc 480

tttgtggtgt aaatagcaaa gcaagcaaga gttctattac taaacacagc atgactcaaa 540

aaacttagca attctgaagg aaagtccttg gggtcttcta cctttctctt ctttttttgga 600

ggagtagaat gttgagagtc agcagtagcc tcatcatcac tagatggcat ttcttctgag 660

caaaacaggt tttcctcatt aaaggcattc caccactgct cccattcatc agttccatag 720

gttggaatct aaaatacaca aacaattaga atcagtagtt taacacatta tacacttaaa 780

aattttatat ttaccttaga gctttaaatc tctgtaggta gtttgtccaa ttatgtcaca 840

ccacagaagt aaggttcctt cacaaagatc cctcgagaaa aaaaatataa aagagatgga 900

ggaacgggaa aaagttagtt gtggtgatag gtggcaagtg gtattccgta agaacaacaa 960

gaaaagcatt tcatattatg gctgaactga gcgaacaagt gcaaaattta agcatcaacg 1020

acaacaacga gaatggttat gttcctcctc acttaagagg aaaaccaaga agtgccagaa 1080

ataacatgag caactacaat aacaacaacg gcggctacaa cggtggccgt ggcggtggca 1140

gcttctttag caacaaccgt cgtggtggtt acggcaacgg tggtttcttc ggtggaaaca 1200

acggtggcag cagatctaac ggccgttctg gtggtagatg gatcgatggc aaacatgtcc 1260

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<210> 13

<211> 96
<212> DNA
<213> Artificial

<220>
<223> SPBc2 attB site

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atattaatga catgctgcac tcggtgtgaa agggca 96

<210> 14
<211> 99
<212> DNA
<213> Artificial

<220>
<223> SF370.1 attP site

<400> 14
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gttgtagtgc ctaaataatg cttttaaaac ttaaaaata 99

<210> 15
<211> 96
<212> DNA
<213> Artificial

<220>
<223> SF370.1 attB site

<400> 15
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ggtaaaaagg catcttatga tggctcaacc atggtt 96

<210> 16
<211> 52
<212> DNA
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<223> Bxb1 attP site

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<211> 46
<212> DNA
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<220>
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<213> Artificial

<220>
<223> A118 attP site

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agaaacgaga aactaaaatt ataaataaaa agtaaccta 99

<210> 19
<211> 96
<212> DNA
<213> Artificial

<220>
<223> A118 attB site

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gaactaaaca cttaattggt gttacccata agccac 96

<210> 20
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<212> DNA
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<220>
<223> PhiRv1 attP site

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gctgaagaac attccacgcc aggagatcaa ccatgacca 99

<210> 21
<211> 96
<212> DNA
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<220>
<223> PhiRv1 attB site

<400> 21
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