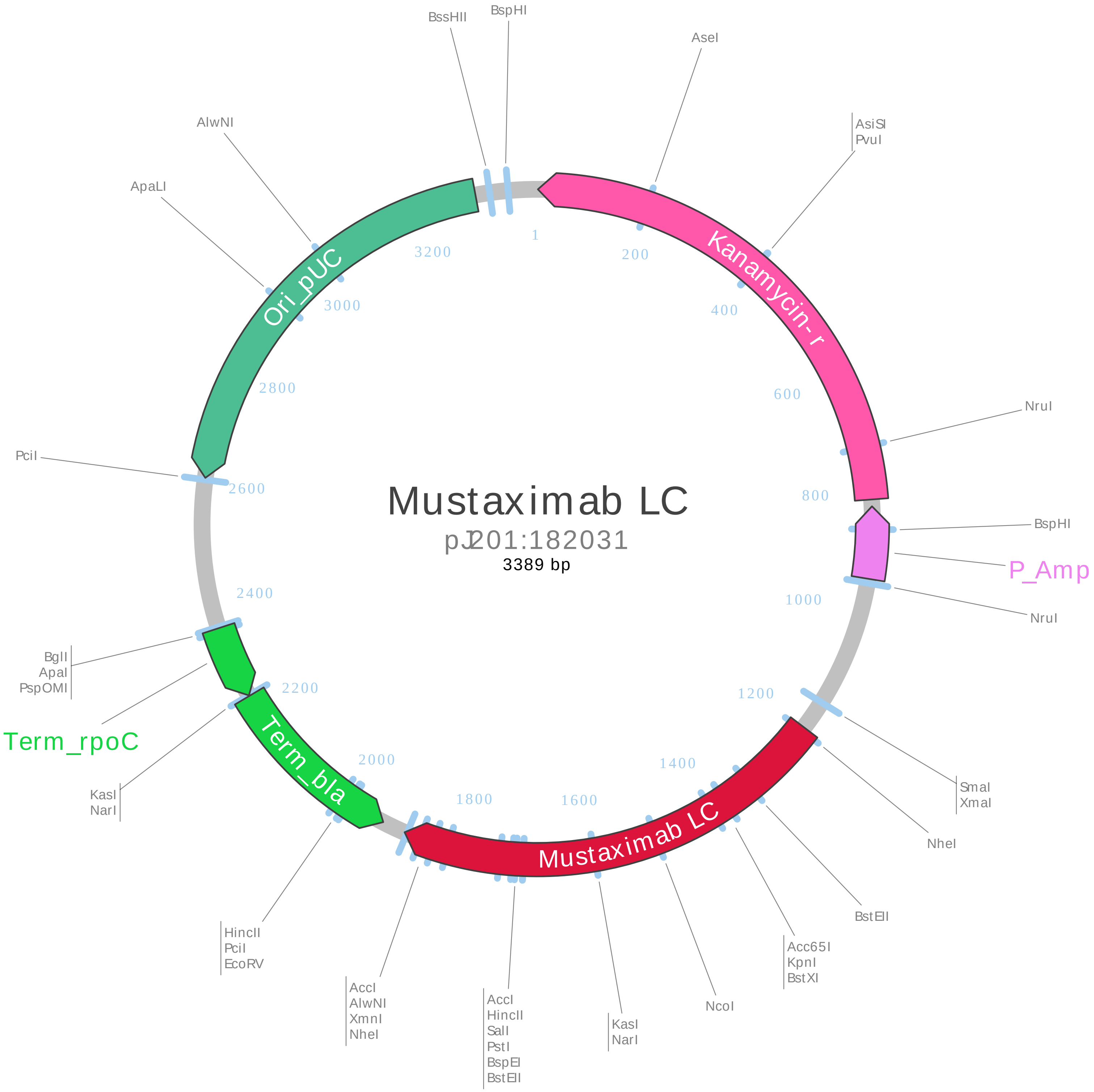
Plasmid Map

pJ201:182031

Only single and double cutters are shown in the map.



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Feature Map

Name	Start	End	Direction
Insert: 182031	1198	1914	Forward
Kanamycin-r	807	1	Reverse
P_Amp	935	818	Reverse
Term_bla	2252	1952	Reverse
Term_rpoC	2372	2253	Reverse
Ori_pUC	3289	2617	Reverse

Restriction Map

Name	Sequence	5' Cut Positions
Acc65I	GGTACC	1373
AccI	GTMKAC	1718, 1841
AlwNI	CAGNNNCTG	1869, 3030
ApaI	GGGCCC	2378
ApaLI	GTGCAC	2928
AseI	ATTAAT	180
AsiSI	GCGATCGC	383
AvaI	CYCGRG	1149, 1455, 2377
BglI	GCCNNNNNGGC	2373
BspEI	TCCGGA	1735
BspHI	TCATGA	855, 3342
BsrBI	CCGCTC	861(C), 1649(C), 2547(C)
BssHII	GCGCGC	3312
BstEII	GGTNACC	1326, 1755
BstXI	CCANNNNNNTGG	1406
BtsI	GCAGTG	435(C), 522, 1240(C), 1714
EcoRV	GATATC	2034
HincII	GTYRAC	1719, 2016
KasI	GGCGCC	1602, 2253
KpnI	GGTACC	1377
NarI	GGCGCC	1603, 2254
NcoI	CCATGG	1499
NheI	GCTAGC	1204, 1910
NruI	TCGCGA	724, 944
NsiI	ATGCAT	269, 535, 1370, 1964
PciI	ACATGT	2018, 2614
PspOMI	GGGCCC	2374
PstI	CTGCAG	1733
PvuI	CGATCG	383
SalI	GTCGAC	1717
SmaI	CCCGGG	1151
SspI	AATATT	456, 824, 2104, 2265
XmaI	CCCGGG	1149
XmnI	GAANNNNTTC	1891
AclI	AACGTT	no cuts

Name	Sequence	5' Cut Positions
AfeI	AGCGCT	no cuts
AgeI	ACCGGT	no cuts
AscI	GGCGCGCC	no cuts
AvrII	CCTAGG	no cuts
BamHI	GGATCC	no cuts
BbsI	GAAGAC	no cuts
BclI	TGATCA	no cuts
BglII	AGATCT	no cuts
BlpI	GCTNAGC	no cuts
BsaI	GGTCTC	no cuts
BsiWI	CGTACG	no cuts
BsmBI	CGTCTC	no cuts
BsrDI	GCAATG	no cuts
BsrGI	TGTACA	no cuts
BstBI	TTCGAA	no cuts
ClaI	ATCGAT	no cuts
EagI	CGGCCG	no cuts
EcoRI	GAATTC	no cuts
FseI	GGCCGGCC	no cuts
HindIII	AAGCTT	no cuts
HpaI	GTTAAC	no cuts
MfeI	CAATTG	no cuts
MluI	ACGCGT	no cuts
MscI	TGGCCA	no cuts
NdeI	CATATG	no cuts
NotI	GCGGCCGC	no cuts
PacI	TTAATTAA	no cuts
PmeI	GTTTAAAC	no cuts
PmlI	CACGTG	no cuts
PpuMI	RGGWCCY	no cuts
PshAI	GACNNNNGTC	no cuts
PspXI	VCTCGAGB	no cuts
PvuII	CAGCTG	no cuts
RsrII	CGGWCCG	no cuts
SacI	GAGCTC	no cuts
SacII	CCGCGG	no cuts
SanDI	GGGWCCC	no cuts
SapI	GCTCTTC	no cuts
SbfI	CCTGCAGG	no cuts
SfiI	GGCCNNNNNGGCC	no cuts
SnaBI	TACGTA	no cuts
SpeI	ACTAGT	no cuts
SphI	GCATGC	no cuts
SwaI	ATTTAAAT	no cuts
XbaI	TCTAGA	no cuts
XhoI	CTCGAG	no cuts

Sequence

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   1 GAAAAACTCA TCGAGCATCA AATGAAACTG CAATTTATTC ATATCAGGAT TATCAATACC
  61 ATATTTTTGA AAAAGCCGTT TCTGTAATGA AGGAGAAAAC TCACCGAGGC AGTTCCATAG
 121 GATGGCAAGA TCCTGGTATC GGTCTGCGAT TCCGACTCGT CCAACATCAA TACAACCTAT
 181 TAATTTCCCC TCGTCAAAAA TAAGGTTATC AAGTGAGAAA TCACCATGAG TGACGACTGA
 241 ATCCGGTGAG AATGGCAAAA GTTTATGCAT TTCTTTCCAG ACTTGTTCAA CAGGCCAGCC
 301 ATTACGCTCG TCATCAAAAT CACTCGCATC AACCAAACCG TTATTCATTC GTGATTGCGC
 361 CTGAGCGAGG CGAAATACGC GATCGCTGTT AAAAGGACAA TTACAAACAG GAATCGAGTG
 421 CAACCGGCGC AGGAACACTG CCAGCGCATC AACAATATTT TCACCTGAAT CAGGATATTC
 481 TTCTAATACC TGGAACGCTG TTTTTCCGGG GATCGCAGTG GTGAGTAACC ATGCATCATC
 541 AGGAGTACGG ATAAAATGCT TGATGGTCGG AAGTGGCATA AATTCCGTCA GCCAGTTTAG
 601 TCTGACCATC TCATCTGTAA CATCATTGGC AACGCTACCT TTGCCATGTT TCAGAAACAA
 661 CTCTGGCGCA TCGGGCTTCC CATACAAGCG ATAGATTGTC GCACCTGATT GCCCGACATT
 721 ATCGCGAGCC CATTTATACC CATATAAATC AGCATCCATG TTGGAATTTA ATCGCGGCCT
 781 CGACGTTTCC CGTTGAATAT GGCTCATATT CTTCCTTTTT CAATATTATT GAAGCATTTA
 841 TCAGGGTTAT TGTCTCATGA GCGGATACAT ATTTGAATGT ATTTAGAAAA ATAAACAAAT
 901 AGGGGTCAGT GTTACAACCA ATTAACCAAT TCTGAACATT ATCGCGAGCC CATTTATACC
 961 TGAATATGGC TCATAACACC CCTTGTTTGC CTGGCGGCAG TAGCGCGGTG GTCCCACCTG
1021 ACCCCATGCC GAACTCAGAA GTGAAACGCC GTAGCGCCGA TGGTAGTGTG GGGACTCCCC
1081 ATGCGAGAGT AGGGAACTGC CAGGCATCAA ATAAAACGAA AGGCTCAGTC GAAAGACTGG
1141 GCCTTTCGCC CGGGCTAATT AGGGGGTGTC GCCCTTTACA CGTACTTAGT CGCTGAAAAG
1201 CTGGCTAGCG CCGCCACCAT GAAATGGGTC ACTTTTATCT CACTGCTTTT CTTGTTCTCC
1261 TCCGCCTACT CCCAAATTGT GCTCACCCAA TCCCCTGCCA TCATGTCCGC CTCCCCCGGC
1321 GAAAAGGTCA CCATGACTTG TTCCGCCTCA TCGTCCGTGT CCTACATGCA TTGGTACCAG
1381 CAGAAGTCAG GCACCTCACC AAAGAGATGG ATCTACGACA CATCGAAGCT GGCCTCCGGC
1441 GTGCCTGCGC GGTTCTCGGG ATCGGGAAGC GGGACCAGCT ACTCCCTGAC TATCTCGTCC
1501 ATGGAAGCCG AGGACGCTGC AACCTATTAC TGCCAACAGT GGTCCAGCAA CCCCTTCACC
1561 TTCGGGTCTG GCACCAAGCT GGAGATTAAG AGGACCGTGG CGGCGCCCTC CGTGTTTATC
1621 TTCCCGCCGA GCGATGAGCA GCTCAAGAGC GGAACTGCAA GCGTGGTCTG CCTGCTCAAC
1681 AATTTCTACC CGCGCGAAGC CAAAGTGCAG TGGAAGGTCG ACAACGCTCT GCAGTCCGGA
1741 AACAGCCAGG AATCGGTGAC CGAACAGGAT TCCAAGGACA GCACCTACTC CCTCTCATCG
1801 ACTCTGACTC TGAGCAAGGC CGACTACGAG AAGCACAAGG TCTACGCCTG CGAAGTGACC
1861 CACCAGGGTC TGTCCAGCCC TGTGACGAAG TCCTTCAACC GGGGAGAGTG CTAGCGTCAA
1921 TCGAGTTCGT ACCTAAGGGC GACACAAAAT TTATTCTAAA TGCATAATAA ATACTGATAA
1981 CATCTTATAG TTTGTATTAT ATTTTGTATT ATCGTTGACA TGTATAATTT TGATATCAAA
2041 AACTGATTTT CCCTTTATTA TTTTCGAGAT TTATTTTCTT AATTCTCTTT AACAAACTAG
2101 AAATATTGTA TATACAAAAA ATCATAAATA ATAGATGAAT AGTTTAATTA TAGGTGTTCA
2161 TCAATCGAAA AAGCAACGTA TCTTATTTAA AGTGCGTTGC TTTTTTCTCA TTTATAAGGT
2221 TAAATAATTC TCATATATCA AGCAAAGTGA CAGGCGCCCT TAAATATTCT GACAAATGCT
2281 CTTTCCCTAA ACTCCCCCCA TAAAAAAACC CGCCGAAGCG GGTTTTTACG TTATTTGCGG
2341 ATTAACGATT ACTCGTTATC AGAACCGCCC AGGGGGCCCG AGCTTAAGAC TGGCCGTCGT
2401 TTTACAACAC AGAAAGAGTT TGTAGAAACG CAAAAAGGCC ATCCGTCAGG GGCCTTCTGC
2461 TTAGTTTGAT GCCTGGCAGT TCCCTACTCT CGCCTTCCGC TTCCTCGCTC ACTGACTCGC
2521 TGCGCTCGGT CGTTCGGCTG CGGCGAGCGG TATCAGCTCA CTCAAAGGCG GTAATACGGT
2581 TATCCACAGA ATCAGGGGAT AACGCAGGAA AGAACATGTG AGCAAAAGGC CAGCAAAAGG
2641 CCAGGAACCG TAAAAAGGCC GCGTTGCTGG CGTTTTTCCA TAGGCTCCGC CCCCCTGACG
2701 AGCATCACAA AAATCGACGC TCAAGTCAGA GGTGGCGAAA CCCGACAGGA CTATAAAGAT
2761 ACCAGGCGTT TCCCCCTGGA AGCTCCCTCG TGCGCTCTCC TGTTCCGACC CTGCCGCTTA
2821 CCGGATACCT GTCCGCCTTT CTCCCTTCGG GAAGCGTGGC GCTTTCTCAT AGCTCACGCT
2881 GTAGGTATCT CAGTTCGGTG TAGGTCGTTC GCTCCAAGCT GGGCTGTGTG CACGAACCCC
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2941 CCGTTCAGCC CGACCGCTGC GCCTTATCCG GTAACTATCG TCTTGAGTCC AACCCGGTAA
3001 GACACGACTT ATCGCCACTG GCAGCAGCCA CTGGTAACAG GATTAGCAGA GCGAGGTATG
3061 TAGGCGGTGC TACAGAGTTC TTGAAGTGGT GGGCTAACTA CGGCTACACT AGAAGAACAG
3121 TATTTGGTAT CTGCGCTCTG CTGAAGCCAG TTACCTTCGG AAAAAGAGTT GGTAGCTCTT
3181 GATCCGGCAA ACAAACCACC GCTGGTAGCG GTGGTTTTTT TGTTTGCAAG CAGCAGATTA
3241 CGCGCAGAAA AAAAGGATCT CAAGAAGATC CTTTGATCTT TTCTACGGGG TCTGACGCTC
3301 AGTGGAACGA CGCGCGCGTA ACTCACGTTA AGGGATTTTG GTCATGAGCT TGCGCCGTCC
3361 CGTCAAGTCA GCGTAATGCT CTGCTTTTA
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Only the synthesized DNA fragment (in red) has been sequence verified. We do not guarantee the vector sequence.