

Comments for pENTR™1A
2717 nucleotides

rrnB T1 transcription termination sequence: bases 106-149

rrnB T2 transcription termination sequence: bases 281-308

attL1: bases 358-457 (complementary strand)

ccdB gene: bases 612-917

attL2: bases 946-1045

Kanamycin resistance gene: bases 1168-1977

pUC origin: bases 2041-2714

atL1

352 GGGCCCCAAA TAATGATTTT ATTTTGACTG ATAGTGACCT GTTCGTTGCA ACAAATTGAT
 CCCGGGGTTT ATTACTAAAA TAAAACTGAC TATCACTGGA CAAGCAACGT TGTTTAACTA

DraI

412 AAG CAA TGC TTT TTT ATA ATG CCA ACT TTG TAC AAA AAA GCA GGC TTT
 TTC GTT ACG AAA AAA TAT TAC GGT TGA AAC ATG TTT TTT CGT CCG AAA

XmnI *SaI* *BamHI* *KpnI* *EcoRI*

460 AAA GGA ACC AAT TCA GTC GAC TGG ATC CGG TAC CGA ATT CGC --- **ccoB gene** ---
 TTT CCT TGG TTA AGT CAG CTG ACC TAG GCC ATG GCT TAA GCG

EcoRI *NotI* *XhoI* *EcoRV*

915 TAG AAT TCG CGG CCG CAC TCG AGA TAT CTA GAC CCA GCT TTC TTG TAC AAA
 ATC TTA AGC GCC GGC GTG AGC TCT ATA GAT CTG GGT CGA AAG AAC ATG TTT

atL2

966 GTTGGCATT TAAGAAAGCA TTGCTTATCA ATTTGTTGCA ACGAACAGGT CACTATCAGT
 CAACCGTAAT ATTCTTTCGT AACGAATAGT TAAACAACGT TGCTTGTCCA GTGATAGTCA

reverse primer binding site

1026 CAAAATAAAA TCATTATTTG CCATCCAGCT GCAGCTCTGG CCCGTGTCTC AAAATCTCTG
 GTTTTATTTT AGTAATAAAC GGTAGGTCGA CGTCGAGACC GGGCACAGAG TTTTAGAGAC

1086 ATGTTACATT
 TACAATGTAA

CTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCTAGCATGGATCTCGGGGACGTCTAA
CTACTAAGCGAGAGTAGGGAAGTCCAGGCATCAAATAAAACGAAAGGCTCAGTCGGAAGACTGGGCCTT
TCGTTTTATCTGTTGTTTGTCTCGGTGAACGCTCTCCTGAGTAGGACAAATCCGCCGGGAGCGGATTTGAAC
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GGGAAGAAGTGGCTGATCTCAGCCACCGCGAAAATGACATCAAAAACGCCATTAACCTGATGTTCTGGGG
AATATAGAATTCGCGGCCGCACTCGAGATATCTAGACCCAGCTTTCTTGTACAAAGTTGGCATTATAAGA
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AAAACAGCATTCCAGGTATTAGAAGAATATCCTGATTCAGGTGAAAATATTGTTGATGCGCTGGCAGTGT
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GTGATTTCTCACTTGATAACCTTATTTTTGACGAGGGGAAATTAATAGGTGTATTTGATGTTGGACGAGT
CGGAATCGCAGACCGATAACCAGGATCTTGCCATCCTATGGA ACTGCCTCGGTGAGTTTTCTCCTTCATTA
CAGAAACGGCTTTTTTCAAAAATATGGTATTGATAATCCTGATATGAATAAATTGCAGTTTCATTTGATGC
TCGATGAGTTTTTTCTAATCAGAATTGGTTAATTGGTTGTAACATTATTCAGATTGGGCCCGTTCCACTG
AGCGTCAGACCCGGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTTCTGCGCGTAATCTGCTGC
TTGCAAAACAAAAAAACCACCGCTACCAGCGGTGGTTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTTC
CGAAGGTA ACTGGCTTCAGCAGAGCGCAGATAACCAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCA
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GCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGG
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TTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGCGGAGCCTATGGAAAAACGC
CAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTT



General Description

DNA Plasmid pENTR™1A

Entire molecule length: 2717 bp

Restriction Map

Enzyme	# of cuts	Positions
AatII	1	67
Acc65I	1	489
AccI	2	477 575
Acil	18	43 191 200(c) 238(c) 251 549(c) 867 924(c) 928 1199 2120 2129(c) 2264 2374(c) 2495(c) 2514(c) 2641(c) 2669(c)
AcsI	4	495 918 1207 1391
AcyI	2	64 247
AfIII	1	344
AfIII	1	2712
AluI	9	349 791 952 1054 1060 2155 2412 2458 2548
Alw44I	2	725 2398
AlwI	9	61 478(c) 491 705(c) 1456(c) 1851 2066(c) 2068 2154
AlwNI	1	2303
ApaI	2	357 2020
ApaLI	2	725 2398
ApoI	4	495 918 1207 1391
AseI	1	1793
AsnI	1	1793
Asp700	1	469
Asp718	1	489
AspHI	2	729 2402
AvaI	4	57 350 694 933
BamHI	1	483
BanI	1	489
BanII	3	357 1249 2020
BbsI	1	135
BbvI	6	1041(c) 1069 2084(c) 2290(c) 2293(c) 2383
Bcgl	1	38(c)
BfaI	4	46 608 943 2219
BfrI	1	344
BmyI	5	357 729 1249 2020 2402
BpuAI	1	135
BsaBI	1	709
BsaHI	2	64 247
BsaI	1	834

BsaJI	5	694 716 1465 1867 2552
BsaWI	4	486 1729 2359 2506
BsiEI	3	928 1594 2378
BsiHKAI	2	729 2402
BsiYI	11	234 701 839 1508 1548 1840 1857 2234 2513 2679 2697
BsII	11	234 701 839 1508 1548 1840 1857 2234 2513 2679 2697
BsmAI	4	753 834 1077 1610
BsmFI	2	75 1525(c)
BsmI	3	617 1478(c) 1555(c)
Bsp120I	2	353 2016
Bsp1286I	5	357 729 1249 2020 2402
BspHI	1	1118
BspWI	6	1063 1306 1338 1552 2094 2666
BsrBI	1	200
BsrDI	3	422 984(c) 1092(c)
BsrFI	2	825 1548
BsrGI	3	441 669 959
BsrI	8	137 485 722(c) 818(c) 1385 2185 2297(c) 2310(c)
BssHII	1	535
Bst1107I	1	576
BstNI	8	97 265 718 1484 1841 2553 2566 2687
BstUI	8	537 869 924 1201 1251 1596 2088 2669
BstXI	1	813
BstYI	5	53 483 1843 2060 2071
CfoI	12	537 539 797 1309 1531 1548 1618 2088 2197 2371 2471 2538
Cfr10I	2	825 1548
Csp6I	5	442 490 670 960 1428
Ddel	8	75 120 176 276 859 1611 2029 2438
DpnI	11	55 485 712 857 1463 1593 1845 2054 2062 2073 2148
DpnII	11	53 483 710 855 1461 1591 1843 2052

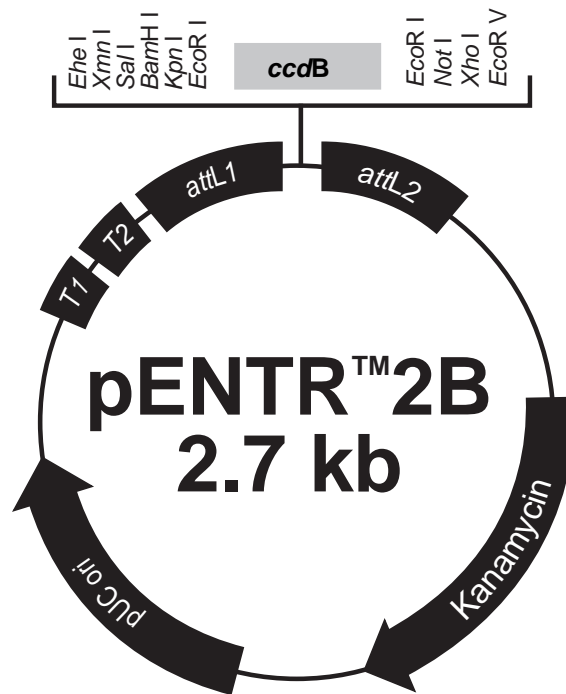
		2060 2071 2146
DraI	1	460
DraII	2	354 2017
DrdI	1	2610
DsaV	16	95 193 226 263 693 694 716 764 1465 1482 1839 2040 2333 2551 2564 2685
EaeI	3	719 815 925
EagI	1	925
EarI	2	330 1407
EclXI	1	925
Eco57I	1	2170(c)
EcoNI	1	1506
EcoO109I	2	354 2017
EcoRI	2	495 918
EcoRII	8	95 263 716 1482 1839 2551 2564 2685
EcoRV	1	940
Esp3I	1	1610
Fnu4HI	11	925 928 1055 1058 1199 2098 2304 2307 2372 2515 2670
FnuDII	8	537 869 924 1201 1251 1596 2088 2669
FokI	7	275(c) 311 679 796 1034(c) 1232 1838(c)
HaeII	1	2472
HaeIII	16	137 226 287 303 355 721 817 927 1066 1198 1681 2018 2238 2672 2690 2701
HgaI	3	255 2022(c) 2600(c)
HgiAI	2	729 2402
HhaI	12	537 539 797 1309 1531 1548 1618 2088 2197 2371 2471 2538
HinP1I	12	535 537 795 1307 1529 1546 1616 2086 2195 2369 2469 2536
HincII	1	478
HindIII	1	478
Hinfl	7	21 1505 1561 1733 1818 1824 2342
HpaII	14	194 228 487 695 766 826 1467 1549 1730 2042 2144 2334

		2360 2507
HphI	6	175 1444(c) 1523 1719(c) 1763 1883
Ital	11	925 928 1055 1058 1199 2098 2304 2307 2372 2515 2670
Kpnl	1	493
Ksp632I	2	330 1407
Mael	4	46 608 943 2219
Maell	4	64 210 729 1190
MaellI	11	339 385 1014 1088 1354 1446 1741 1998 2176 2292 2355
Maml	1	709
Mbol	11	53 483 710 855 1461 1591 1843 2052 2060 2071 2146
Mboll	7	140 317(c) 856 1394(c) 1505 2055(c) 2207(c)
Mcrl	3	928 1594 2378
MluNI	2	721 817
Mnll	9	224(c) 590(c) 1188(c) 1410 1777(c) 1877 2285 2535(c) 2609
MscI	2	721 817
Msel	8	345 459 620 893 1205 1584 1793 1989
MslI	1	811
MspA1I	3	1054 2129 2374
Mspl	14	194 228 487 695 766 826 1467 1549 1730 2042 2144 2334 2360 2507
Mval	8	97 265 718 1484 1841 2553 2566 2687
Mvnl	8	537 869 924 1201 1251 1596 2088 2669
Mwol	6	1063 1306 1338 1552 2094 2666
Ncil	8	195 228 695 696 766 1467 2042 2335
Ndell	11	53 483 710 855 1461 1591 1843 2052 2060 2071 2146
Nhel	1	45
NlaIII	8	53 801 1122 1219 1331 1446 1751 2716

NlaIV	9	355 356 466 485 491 2018 2019 2645 2684
NotI	1	925
NruI	1	1251
NsiI	2	1444 1710
NspI	1	2716
PaeR7I	1	933
PfiMI	1	1857
PleI	2	1826 2336(c)
Ppu10I	2	1440 1706
Psp1406I	1	210
PstI	1	1059
PvuI	1	1594
PvuII	1	1054
RcaI	1	1118
RsaI	5	443 491 671 961 1429
Sall	1	476
Sau3AI	11	53 483 710 855 1461 1591 1843 2052 2060 2071 2146
Sau96I	7	135 225 353 354 1065 2016 2017
ScrFI	16	97 195 228 265 695 696 718 766 1467 1484 1841 2042 2335 2553 2566 2687
SfaNI	9	109 277 1210(c) 1294(c) 1429(c) 1516(c) 1636(c) 1947(c) 2615(c)
Sfcl	3	1055 2256 2447
SmaI	1	696
Snol	2	725 2398
SspBI	3	441 669 959
SspI	1	1519
TaqI	6	477 934 1193 1559 1962 2614
TfiI	5	21 1505 1561 1733 1824
Thal	8	537 869 924 1201 1251 1596 2088 2669
Tru9I	8	345 459 620 893 1205 1584 1793 1989
Tsp509I	12	405 469 495 918 995 1207 1391 1573 1790 1940 1982 1990
Van91I	1	1857
XbaI	2	607 942

XhoI	1	933
XhoII	5	53 483 1843 2060 2071
XmaI	1	694
XmaIII	1	925
XmnI	1	469

No cuts: AatI, AccIII, AgeI, AoiI, AscI, AspEI, AspI, AsuII, AvaII, AviII, AvrII, BbrPI, BclI, BglI, BglII, BlnI, BpmI, Bpu1102I, BsaAI, BseAI, BsgI, BsiWI, BspDI, BspEI, BspMI, BstBI, BstEII, Bsu36I, CclII, ClaI, Csp45I, DraIII, DsaI, Eam1105I, Ecl136II, Eco47III, EspI, FspI, HindIII, HpaI, KasI, KspI, MfeI, MluI, MroI, MunI, NaeI, NarI, NcoI, NdeI, NgoMI, NspV, PacI, PinAI, PmaCI, PmeI, PmlI, PpuMI, RsrII, SacI, SacII, SapI, ScaI, SexAI, SfiI, SfuI, SgrAI, SnaBI, SpeI, SphI, StuI, StyI, SwaI, Tth111I, XcmI



Comments for pENTR™ 2B
2718 nucleotides

rrnB T1 transcription termination sequence: bases 106-149

rrnB T2 transcription termination sequence: bases 281-308

attL1: bases 358-457 (complementary strand)

ccdB gene: bases 613-918

attL2: bases 947-1046

Kanamycin resistance gene: bases 1169-1978

pUC origin: bases 2042-2715

attL1

352 GGGCCCCAAA TAATGATTTT ATTTTGACTG ATAGTGACCT GTTCGTTGCA ACAAATTGAT
 CCCGGGGTTT ATTACTAAAA TAAACTGAC TATCACTGGA CAAGCAACGT TGTTTAACTA

412 AAG CAA TGC TTT TTT ATA ATG CCA ACT TTG TAC AAA AAA GCA GGC TGG
 TTC GTT ACG AAA AAA TAT TAC GGT TGA AAC ATG TTT TTT CGT CCG ACC

*Ehe*I *Xmn*I *Sal*I *Bam*H I *Kpn*I *Eco*R I

460 CGC CGG AAC CAA TTC AGT CGA CTG GAT CCG GTA CCG AAT TCG --- **ccdB gene** ---
 GCG GCC TTG GTT AAG TCA GCT GAC CTA GGC CAT GGC TTA AGC

*Eco*R I *Not*I *Xho*I *Eco*R V

916 TAG AAT TCG CGG CCG CAC TCG AGA TAT CTA GAC CCA GCT TTC TTG TAC AAA
 ATC TTA AGC GCC GGC GTG AGC TCT ATA GAT CTG GGT CGA AAG AAC ATG TTT

attL2

967 GTTGGCATT TAAGAAAGCA TTGCTTATCA ATTTGTTGCA ACGAACAGGT CACTATCAGT
 CAACCGTAAT ATTCTTTCGT AACGAATAGT TAAACAACGT TGCTTGTCCA GTGATAGTCA
reverse primer binding site

1027 CAAAATAAAA TCATTATTTG CCATCCAGCT GCAGCTCTGG CCCGTGTCTC AAAATCTCTG
 GTTTTATTTT AGTAATAAAC GGTAGGTCGA CGTCGAGACC GGCACAGAG TTTTAGAGAC

1087 ATGTTACATT
 TACAATGTAA

CTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCTAGCATGGATCTCGGGGACGTCTAA
CTACTAAGCGAGAGTAGGGAAGTCCAGGCATCAAATAAAACGAAAGGCTCAGTCGGAAGACTGGGCCTT
TCGTTTTATCTGTTGTTTGTGCGGTGAACGCTCTCCTGAGTAGGACAAATCCGCCGGGAGCGGATTTGAAC
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AGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAG
GGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCTGTCTGGG
TTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACG
CCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTT



General Description

DNA Plasmid pENTR™2B

Entire molecule length: 2718 bp

Restriction Map

Enzyme	# of cuts	Positions
AatII	1	67
Acc65I	1	490
AccI	2	478 576
Acil	18	43 191 200(c) 238(c) 251 550(c) 868 925(c) 929 1200 2121 2130(c) 2265 2375(c) 2496(c) 2515(c) 2642(c) 2670(c)
AcsI	4	496 919 1208 1392
AcyI	3	64 247 460
AfIII	1	344
AfIII	1	2713
AluI	9	349 792 953 1055 1061 2156 2413 2459 2549
Alw44I	2	726 2399
AlwI	9	61 479(c) 492 706(c) 1457(c) 1852 2067(c) 2069 2155
AlwNI	1	2304
ApaI	2	357 2021
ApaLI	2	726 2399
ApoI	4	496 919 1208 1392
AseI	1	1794
AsnI	1	1794
Asp700	1	470
Asp718	1	490
AspHI	2	730 2403
AvaI	4	57 350 695 934
BamHI	1	484
BanI	2	459 490
BanII	3	357 1250 2021
BbsI	1	135
BbvI	6	1042(c) 1070 2085(c) 2291(c) 2294(c) 2384
Bcgl	1	38(c)
BfaI	4	46 609 944 2220
BfrI	1	344
BmyI	5	357 730 1250 2021 2403
BpuAI	1	135
BsaBI	1	710
BsaHI	3	64 247 460
BsaI	1	835

BsaJI	5	695 717 1466 1868 2553
BsaWI	4	487 1730 2360 2507
BsiEI	3	929 1595 2379
BsiHKAI	2	730 2403
BsiYI	10	234 702 840 1509 1841 1858 2235 2514 2680 2698
BsII	10	234 702 840 1509 1841 1858 2235 2514 2680 2698
BsmAI	4	754 835 1078 1611
BsmFI	1	75
BsmI	3	618 1479(c) 1556(c)
Bsp120I	2	353 2017
Bsp1286I	5	357 730 1250 2021 2403
BspHI	1	1119
BspWI	6	1064 1307 1339 1553 2095 2667
BsrBI	1	200
BsrDI	3	422 985(c) 1093(c)
BsrFI	2	826 1549
BsrGI	3	441 670 960
BsrI	8	137 486 723(c) 819(c) 1386 2186 2298(c) 2311(c)
BssHII	1	536
Bst1107I	1	577
BstNI	8	97 265 719 1485 1842 2554 2567 2688
BstUI	8	538 870 925 1202 1252 1597 2089 2670
BstXI	1	814
BstYI	5	53 484 1844 2061 2072
CfoI	13	462 538 540 798 1310 1532 1549 1619 2089 2198 2372 2472 2539
Cfr10I	2	826 1549
Csp6I	5	442 491 671 961 1429
Ddel	8	75 120 176 276 860 1612 2030 2439
DpnI	11	55 486 713 858 1464 1594 1846 2055 2063 2074 2149
DpnII	11	53 484 711 856 1462 1592 1844 2053 2061 2072 2147
Drall	2	354 2018

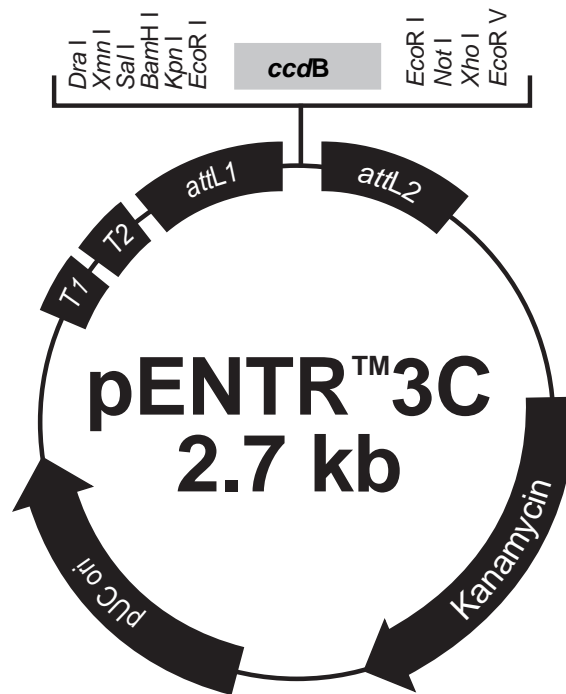
DrdI	1	2611
DsaV	15	95 193 226 263 694 695 717 765 1466 1483 1840 2334 2552 2565 2686
EaeI	3	720 816 926
EagI	1	926
EarI	2	330 1408
EclXI	1	926
Eco57I	1	2171(c)
EcoNI	1	1507
EcoO109I	2	354 2018
EcoRI	2	496 919
EcoRII	8	95 263 717 1483 1840 2552 2565 2686
EcoRV	1	941
Esp3I	1	1611
Fnu4HI	11	926 929 1056 1059 1200 2099 2305 2308 2373 2516 2671
FnuDII	8	538 870 925 1202 1252 1597 2089 2670
FokI	8	275(c) 311 680 718 797 1035(c) 1233 1839(c)
HaeII	2	463 2473
HaeIII	16	137 226 287 303 355 722 818 928 1067 1199 1682 2019 2239 2673 2691 2702
Hgal	3	255 2023(c) 2601(c)
HgiAI	2	730 2403
HhaI	13	462 538 540 798 1310 1532 1549 1619 2089 2198 2372 2472 2539
HinP1I	13	460 536 538 796 1308 1530 1547 1617 2087 2196 2370 2470 2537
HincII	1	479
HindII	1	479
Hinfl	7	21 1506 1562 1734 1819 1825 2343
HpaII	14	194 228 463 488 696 767 827 1468 1550 1731 2145 2335 2361 2508
HphI	7	175 721 1445(c) 1524 1720(c) 1764

		1884
Ital	11	926 929 1056 1059 1200 2099 2305 2308 2373 2516 2671
Kasl	1	459
Kpnl	1	494
Ksp632l	2	330 1408
Mael	4	46 609 944 2220
Maell	4	64 210 730 1191
Maelll	11	339 385 1015 1089 1355 1447 1742 1999 2177 2293 2356
Maml	1	710
Mbol	11	53 484 711 856 1462 1592 1844 2053 2061 2072 2147
Mboll	7	140 317(c) 857 1395(c) 1506 2056(c) 2208(c)
Mcrl	3	929 1595 2379
MluNI	2	722 818
Mnll	9	224(c) 591(c) 1189(c) 1411 1778(c) 1878 2286 2536(c) 2610
MscI	2	722 818
Msel	7	345 621 894 1206 1585 1794 1990
MslI	1	812
MspA1I	3	1055 2130 2375
Mspl	14	194 228 463 488 696 767 827 1468 1550 1731 2145 2335 2361 2508
Mval	8	97 265 719 1485 1842 2554 2567 2688
Mvnl	8	538 870 925 1202 1252 1597 2089 2670
Mwol	6	1064 1307 1339 1553 2095 2667
Narl	1	460
Ncil	7	195 228 696 697 767 1468 2336
Ndell	11	53 484 711 856 1462 1592 1844 2053 2061 2072 2147
Nhel	1	45
NlalI	8	53 802 1123 1220 1332 1447 1752 2717
NlalIV	10	355 356 461 467 486

		492 2019 2020 2646 2685
NotI	1	926
NruI	1	1252
NsiI	2	1445 1711
NspI	1	2717
PaeR7I	1	934
PfiMI	1	1858
PleI	2	1827 2337(c)
Ppu10I	2	1441 1707
Psp1406I	1	210
PstI	1	1060
PvuI	1	1595
PvuII	1	1055
RcaI	1	1119
RsaI	5	443 492 672 962 1430
SalI	1	477
Sau3AI	11	53 484 711 856 1462 1592 1844 2053 2061 2072 2147
Sau96I	7	135 225 353 354 1066 2017 2018
ScrFI	15	97 195 228 265 696 697 719 767 1468 1485 1842 2336 2554 2567 2688
SfaNI	9	109 277 1211(c) 1295(c) 1430(c) 1517(c) 1637(c) 1948(c) 2616(c)
SfiI	3	1056 2257 2448
SmaI	1	697
SnoI	2	726 2399
SspBI	3	441 670 960
SspI	1	1520
TaqI	6	478 935 1194 1560 1963 2615
TfiI	5	21 1506 1562 1734 1825
ThaI	8	538 870 925 1202 1252 1597 2089 2670
Tru9I	7	345 621 894 1206 1585 1794 1990
Tsp509I	12	405 470 496 919 996 1208 1392 1574 1791 1941 1983 1991
Van91I	1	1858
XbaI	2	608 943
XhoI	1	934
XhoII	5	53 484 1844 2061 2072

Xmal	1	695
XmaIII	1	926
XmnI	1	470

No cuts: AatI, AccIII, AgeI, AoiI, AscI, AspEI, AspI, AsuII, AvaII, AviII, AvrII, BbrPI, BclI, BglI, BglII, BlnI, BpmI, Bpu1102I, BsaAI, BseAI, BsgI, BsiWI, BspDI, BspEI, BspMI, BstBI, BstEII, Bsu36I, CclII, ClaI, Csp45I, DraI, DraIII, DsaI, Eam1105I, Ecl136II, Eco47III, EspI, FspI, HindIII, HpaI, KspI, MfeI, MluI, MroI, MunI, NaeI, NcoI, NdeI, NgoMI, NspV, PacI, PinAI, PmaCI, PmeI, PmlI, PpuMI, RsrII, SacI, SacII, SapI, ScaI, SexAI, SfiI, SfuI, SgrAI, SnaBI, SpeI, SphI, StuI, StyI, SwaI, Tth111I, XcmI



Comments for pENTR™3C
2723 nucleotides

rrnB T1 transcription termination sequence: bases 106-149

rrnB T2 transcription termination sequence: bases 281-308

attL1: bases 358-457 (complementary strand)

ccdB gene: bases 618-923

attL2: bases 952-1051

Kanamycin resistance gene: bases 1174-1983

pUC origin: bases 2047-2720

attL1

352 GGGCCCCAAA TAATGATTTT ATTTTGACTG ATAGTGACCT GTTCGTTGCA ACAAATTGAT
 CCCGGGGTTT ATTACTAAAA TAAAACTGAC TATCACTGGA CAAGCAACGT TGTTTAACTA

412 AAG CAA TGC TTT TTT ATA ATG CCA ACT TTG TAC AAA AAA GCA GGC TCT
 TTC GTT ACG AAA AAA TAT TAC GGT TGA AAC ATG TTT TTT CGT CCG AGA

*Dra*I *Xmn*I *Sal*I *Bam*H I *Kpn*I *Eco*R I

460 TTA AAG GAA CCA ATT CAG TCG ACT GGA TCC GGT ACC GAA TTC --- **ccdB gene** ---
 AAT TTC CTT GGT TAA GTC AGC TGA CCT AGG CCA TGG CTT AAG

*Eco*R I *Not*I *Xho*I *Eco*R V

921 TAG AAT TCG CGG CCG CAC TCG AGA TAT CTA GAC CCA GCT TTC TTG TAC AAA
 ATC TTA AGC GCC GGC GTG AGC TCT ATA GAT CTG GGT CGA AAG AAC ATG TTT

attL2

972 GTTGGCATT TAAGAAAGCA TTGCTTATCA ATTTGTTGCA ACGAACAGGT CACTATCAGT
 CAACCGTAAT ATTCTTTCGT AACGAATAGT TAAACAACGT TGCTTGTTCA GTGATAGTCA

reverse primer binding site

1032 CAAAATAAAA TCATTATTTG CCATCCAGCT GCAGCTCTGG CCCGTGTCTC AAAATCTCTG
 GTTTTATTTT AGTAATAAAC GGTAGGTCGA CGTCGAGACC GGGCACAGAG TTTTAGAGAC

1092 ATGTTACATT
 TACAATGTAA

CTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCTAGCATGGATCTCGGGGACGTCTAA
CTACTAAGCGAGAGTAGGGAAGTCCAGGCATCAAATAAAACGAAAGGCTCAGTCGGAAGACTGGGCCTT
TCGTTTATCTGTTGTTTGTTCGGTGAACGCTCTCCTGAGTAGGACAAATCCGCCGGGAGCGGATTTGAAC
GTTGTGAAGCAACGGCCCGGAGGGTGGCGGGCAGGACGCCCGCCATAAACTGCCAGGCATCAAACCTAAGC
AGAAGGCCATCCTGACGGATGGCCTTTTTGCGTTTCTACAAACTCTTCCTGTTAGTTAGTTACTTAAGCT
CGGGCCCCAAATAATGATTTTATTTTGACTGATAGTGACCTGTTTCGTTGCAACAAATTGATAAGCAATGC
TTTTTTATAATGCCAACTTTGTACAAAAAAGCAGGCTCTTTAAAGGAACCAATTCAGTCGACTGGATCCG
GTACCGAATTCGATCGCTTACTAAAAGCCAGATAACAGTATGCGTATTTGCGCGCTGATTTTTGCGGTAT
AAGAATATACTGATATGTATACCCGAAGTATGTCAAAAAGAGGTGTGCTTCTAGAATGCAGTTTAAGG
TTTACACCTATAAAAGAGAGAGCCGTTATCGTCTGTTTGTGGATGTACAGAGTGATATTATTGACACGCC
CGGGCGACGGATGGTGTATCCCCCTGGCCAGTGCACGTCTGCTGTCAGATAAAAGTCTCCCGTGAACTTTAC
CCGGTGGTGCATATCGGGGATGAAAGCTGGCGCATGATGACCACCGATATGGCCAGTGTGCCGGTCTCCG
TTATCGGGGAAGAAGTGGCTGATCTCAGCCACCGCGAAAATGACATCAAAAACGCCATTAACCTGATGTT
CTGGGGAATATAGAATTCGCGGCCGCACTCGAGATATCTAGACCCAGCTTTCTTGTACAAAGTTGGCATT
ATAAGAAAGCATTGCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAAATAAAATCATTATTT
GCCATCCAGCTGCAGCTCTGGCCCCGTGTCTCAAAATCTCTGATGTTACATTGCACAAGATAAAAATATAT
CATCATGAACAATAAACTGTCTGCTTACATAAACAGTAATAACAAGGGGTGTTATGAGCCATATTCAACG
GGAAACGTTCGAGGCCGCGATTAATTCCAACATGGATGCTGATTTATATGGGTATAAATGGGCTCGCGAT
AATGTCGGGCAATCAGGTGCGACAATCTATCGCTTGTATGGGAAGCCCGATGCGCCAGAGTTGTTTCTGA
AACATGGCAAAGGTAGCGTTGCCAATGATGTTACAGATGAGATGGTCAGACTAACTGGCTGACGGAATT
TATGCCTCTTCCGACCATCAAGCATTTTATCCGTAATCCTGATGATGCATGGTTACTCACCCTGCGATC
CCCGGAAAAACAGCATTCCAGGTATTAGAAGAATATCCTGATTCAGGTGAAAATATTGTTGATGCGCTGG
CAGTGTTCTGCGCCGGTTGCATTCGATTCCTGTTTGTAAATTGTCCTTTTAAACAGCGATCGCGTATTTCCG
TCTCGCTCAGGCGCAATCACGAATGAATAACGGTTTGGTTGATGCGAGTGATTTTGATGACGAGCGTAAT
GGCTGGCCTGTTGAACAAGTCTGGAAAGAAATGCATAAACTTTTGCCATTCTCACCGGATTCAGTCGTCA
CTCATGGTGTATTTCTCACTTGATAACCTTATTTTTTGACGAGGGGAAATTAATAGGTTGTATTGATGTTGG
ACGAGTCGGAATCGCAGACCGATAACCAGGATCTTGCCATCCTATGGAACCTGCTCGGTGAGTTTTCTCCT
TCATTACAGAAACGGCTTTTTCAAAAATATGGTATTGATAATCCTGATATGAATAAATTGCAGTTTCATT
TGATGCTCGATGAGTTTTTCTAATCAGAATTGGTTAATTGGTTGTAACATTATTTCAGATTGGGCCCGTT
CCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTTCTGCGCGTAATC
TGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTGTTGCCGGATCAAGAGCTACCAACTC
TTTTTCCGAAGGTAACCTGGCTTCAGCAGAGCGCAGATAACCAATACTGTTCTTCTAGTGTAGCCGTAGTT
AGGCCACCCTTCAAGAAGTCTGTAGCACCGCCTACATACTCCTGCTCTGCTAATCCTGTTACCAGTGGCT
GCTGCCAGTGGCGATAAGTCGTGCTTACCAGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGC
GGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATA
CCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGC
GGCAGGGTTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTG
TCGGGTTTTGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAA
AAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTT



General Description

DNA Plasmid pENTR™3C

Entire molecule length: 2723 bp

Restriction Map

Enzyme	# of cuts	Positions
AatII	1	67
Acc65I	1	491
AccI	2	479 581
Acil	18	43 191 200(c) 238(c) 251 555(c) 873 930(c) 934 1205 2126 2135(c) 2270 2380(c) 2501(c) 2520(c) 2647(c) 2675(c)
AcsI	4	497 924 1213 1397
AcyI	2	64 247
AfIII	1	344
AfIII	1	2718
AluI	9	349 797 958 1060 1066 2161 2418 2464 2554
Alw44I	2	731 2404
AlwI	9	61 480(c) 493 711(c) 1462(c) 1857 2072(c) 2074 2160
AlwNI	1	2309
ApaI	2	357 2026
ApaLI	2	731 2404
ApoI	4	497 924 1213 1397
AseI	1	1799
AsnI	1	1799
Asp700	1	471
Asp718	1	491
AspHI	2	735 2408
AvaI	4	57 350 700 939
BamHI	1	485
BanI	1	491
BanII	3	357 1255 2026
BbsI	1	135
BbvI	6	1047(c) 1075 2090(c) 2296(c) 2299(c) 2389
Bcgl	1	38(c)
BfaI	4	46 614 949 2225
BfrI	1	344
BmyI	5	357 735 1255 2026 2408
BpuAI	1	135
BsaBI	1	715
BsaHI	2	64 247
BsaI	1	840

BsaJI	5	700 722 1471 1873 2558
BsaWI	4	488 1735 2365 2512
BsiEI	4	505 934 1600 2384
BsiHKAI	2	735 2408
BsiYI	10	234 707 845 1514 1846 1863 2240 2519 2685 2703
BsII	10	234 707 845 1514 1846 1863 2240 2519 2685 2703
BsmAI	4	759 840 1083 1616
BsmFI	1	75
BsmI	3	623 1484(c) 1561(c)
Bsp120I	2	353 2022
Bsp1286I	5	357 735 1255 2026 2408
BspHI	1	1124
BspWI	6	1069 1312 1344 1558 2100 2672
BsrBI	1	200
BsrDI	3	422 990(c) 1098(c)
BsrFI	2	831 1554
BsrGI	3	441 675 965
BsrI	8	137 487 728(c) 824(c) 1391 2191 2303(c) 2316(c)
BssHII	1	541
Bst1107I	1	582
BstNI	8	97 265 724 1490 1847 2559 2572 2693
BstUI	8	543 875 930 1207 1257 1602 2094 2675
BstXI	1	819
BstYI	5	53 485 1849 2066 2077
CfoI	12	543 545 803 1315 1537 1554 1624 2094 2203 2377 2477 2544
Cfr10I	2	831 1554
Csp6I	5	442 492 676 966 1434
Ddel	8	75 120 176 276 865 1617 2035 2444
DpnI	12	55 487 504 718 863 1469 1599 1851 2060 2068 2079 2154
DpnII	12	53 485 502 716 861 1467 1597 1849 2058 2066 2077

		2152
DraI	1	462
DraII	2	354 2023
DrdI	1	2616
DsaV	15	95 193 226 263 699 700 722 770 1471 1488 1845 2339 2557 2570 2691
EaeI	3	725 821 931
EagI	1	931
EarI	2	330 1413
EclXI	1	931
Eco57I	1	2176(c)
EcoNI	1	1512
EcoO109I	2	354 2023
EcoRI	2	497 924
EcoRII	8	95 263 722 1488 1845 2557 2570 2691
EcoRV	1	946
Esp3I	1	1616
Fnu4HI	11	931 934 1061 1064 1205 2104 2310 2313 2378 2521 2676
FnuDII	8	543 875 930 1207 1257 1602 2094 2675
FokI	8	275(c) 311 685 723 802 1040(c) 1238 1844(c)
HaeII	1	2478
HaeIII	16	137 226 287 303 355 727 823 933 1072 1204 1687 2024 2244 2678 2696 2707
HgaI	3	255 2028(c) 2606(c)
HgiAI	2	735 2408
HhaI	12	543 545 803 1315 1537 1554 1624 2094 2203 2377 2477 2544
HinP1I	12	541 543 801 1313 1535 1552 1622 2092 2201 2375 2475 2542
HincII	1	480
HindII	1	480
Hinfl	7	21 1511 1567 1739 1824 1830 2348
HpaII	13	194 228 489 701 772 832 1473 1555 1736 2150 2340 2366

		2513
HphI	7	175 726 1450(c) 1529 1725(c) 1769 1889
Ital	11	931 934 1061 1064 1205 2104 2310 2313 2378 2521 2676
Kpnl	1	495
Ksp632I	2	330 1413
MaeI	4	46 614 949 2225
MaeII	4	64 210 735 1196
MaeIII	11	339 385 1020 1094 1360 1452 1747 2004 2182 2298 2361
MamI	1	715
Mbol	12	53 485 502 716 861 1467 1597 1849 2058 2066 2077 2152
MbolI	7	140 317(c) 862 1400(c) 1511 2061(c) 2213(c)
McrI	4	505 934 1600 2384
MluNI	2	727 823
MnII	9	224(c) 596(c) 1194(c) 1416 1783(c) 1883 2291 2541(c) 2615
MscI	2	727 823
MseI	8	345 461 626 899 1211 1590 1799 1995
MslI	1	817
MspA1I	3	1060 2135 2380
MspI	13	194 228 489 701 772 832 1473 1555 1736 2150 2340 2366 2513
MvaI	8	97 265 724 1490 1847 2559 2572 2693
MvnI	8	543 875 930 1207 1257 1602 2094 2675
MwoI	6	1069 1312 1344 1558 2100 2672
NciI	7	195 228 701 702 772 1473 2341
NdeII	12	53 485 502 716 861 1467 1597 1849 2058 2066 2077 2152
NheI	1	45

NlaIII	8	53 807 1128 1225 1337 1452 1757 2722
NlaIV	9	355 356 468 487 493 2024 2025 2651 2690
NotI	1	931
NruI	1	1257
NsiI	2	1450 1716
NspI	1	2722
PaeR7I	1	939
PfiMI	1	1863
PleI	2	1832 2342(c)
Ppu10I	2	1446 1712
Psp1406I	1	210
PstI	1	1065
PvuI	2	505 1600
PvuII	1	1060
RcaI	1	1124
RsaI	5	443 493 677 967 1435
Sall	1	478
Sau3AI	12	53 485 502 716 861 1467 1597 1849 2058 2066 2077 2152
Sau96I	7	135 225 353 354 1071 2022 2023
ScrFI	15	97 195 228 265 701 702 724 772 1473 1490 1847 2341 2559 2572 2693
SfaNI	9	109 277 1216(c) 1300(c) 1435(c) 1522(c) 1642(c) 1953(c) 2621(c)
SfiI	3	1061 2262 2453
SmaI	1	702
SpeI	2	731 2404
SspBI	3	441 675 965
SspI	1	1525
TaqI	7	479 501 940 1199 1565 1968 2620
TfiI	5	21 1511 1567 1739 1830
ThaI	8	543 875 930 1207 1257 1602 2094 2675
Tru9I	8	345 461 626 899 1211 1590 1799 1995
Tsp509I	12	405 471 497 924 1001 1213 1397 1579 1796 1946

		1988	1996
Van91I	1	1863	
XbaI	2	613	948
XhoI	1	939	
XhoII	5	53 485	1849 2066 2077
XmaI	1	700	
XmaIII	1	931	
XmnI	1	471	

No cuts: AatI, AccIII, AgeI, AoiI, AscI, AspEI, AspI, AsuII, AvaII, AviII, AvrII, BbrPI, BclI, BglI, BglII, BlnI, BpmI, Bpu1102I, BsaAI, BseAI, BsgI, BsiWI, BspDI, BspEI, BspMI, BstBI, BstEII, Bsu36I, CclII, ClaI, Csp45I, DraIII, DsaI, Eam1105I, Ecl136II, Eco47III, EspI, FspI, HindIII, HpaI, KasI, KspI, MfeI, MluI, MroI, MunI, NaeI, NarI, NcoI, NdeI, NgoMI, NspV, PacI, PinAI, PmaCI, PmeI, PmlI, PpuMI, RsrII, SacI, SacII, SapI, ScaI, SexAI, SfiI, SfuI, SgrAI, SnaBI, SpeI, SphI, StuI, StyI, SwaI, Tth111I, XcmI