pBeloBAC11

7,507 base pairs
GenBank Accession #: U51113

pBeloBAC11 is available as a transformant of ER2420S (#E4154S) at no charge when shipped with an order or for the cost of shipping if ordered separately.

Feature	Coordinates	Source
T7 promoter	312-329	T7
SP6 promoter	414-398	SP6
*lacZ*α	436-56	–
cat (Cm^R)	1425-766	*Tn9*
repE (*repA*)	2765-3520	F
Ori2 (OriS)	2370-2436	F
sopA	4108-5274	F
sopB	5274-6245	F
sopC	6318-6791	F
cos site	7050-7449	lambda
loxP site	7467-7500	P1

ori = origin of replication
Cm = chloramphenicol

pBeloBAC11 is an *E. coli* plasmid cloning vector designed for the construction of Bacterial Artificial Chromosomes (BACs). It is maintained in single copy, which allows the cloning and stable maintenance of very large DNA fragments (up to 300 kb; 1).

Based on the Ori2 (OriS) replicon of the F (fertility) factor of *E. coli*, the vector encodes the SopAB functions for active partitioning (2). These functions act at SopC to ensure that each daughter cell gets a copy of the plasmid. Initiation factor RepE (also known as RepA) mediates assembly of a replication complex at Ori2 (3-5).

The cloning region includes the following features: unique cloning sites BamHI, SphI and HindIII in a *lacZ*α gene allowing for insert screening by α-complementation; T7 and SP6 phage promoters reading into the cloning sites for generation of RNA probes for blot procedures; several GC-rich restriction sites flanking the cloning segment for removal of the cloned insert; a chloramphenicol selectable marker; a lambda *cos* site for packaging into phage lambda particles if desired and also assuring a unique cleavage site for mapping; and a *loxP* site for specific cleavage by Cre recombinase in the presence of *loxP* oligonucleotide (6).

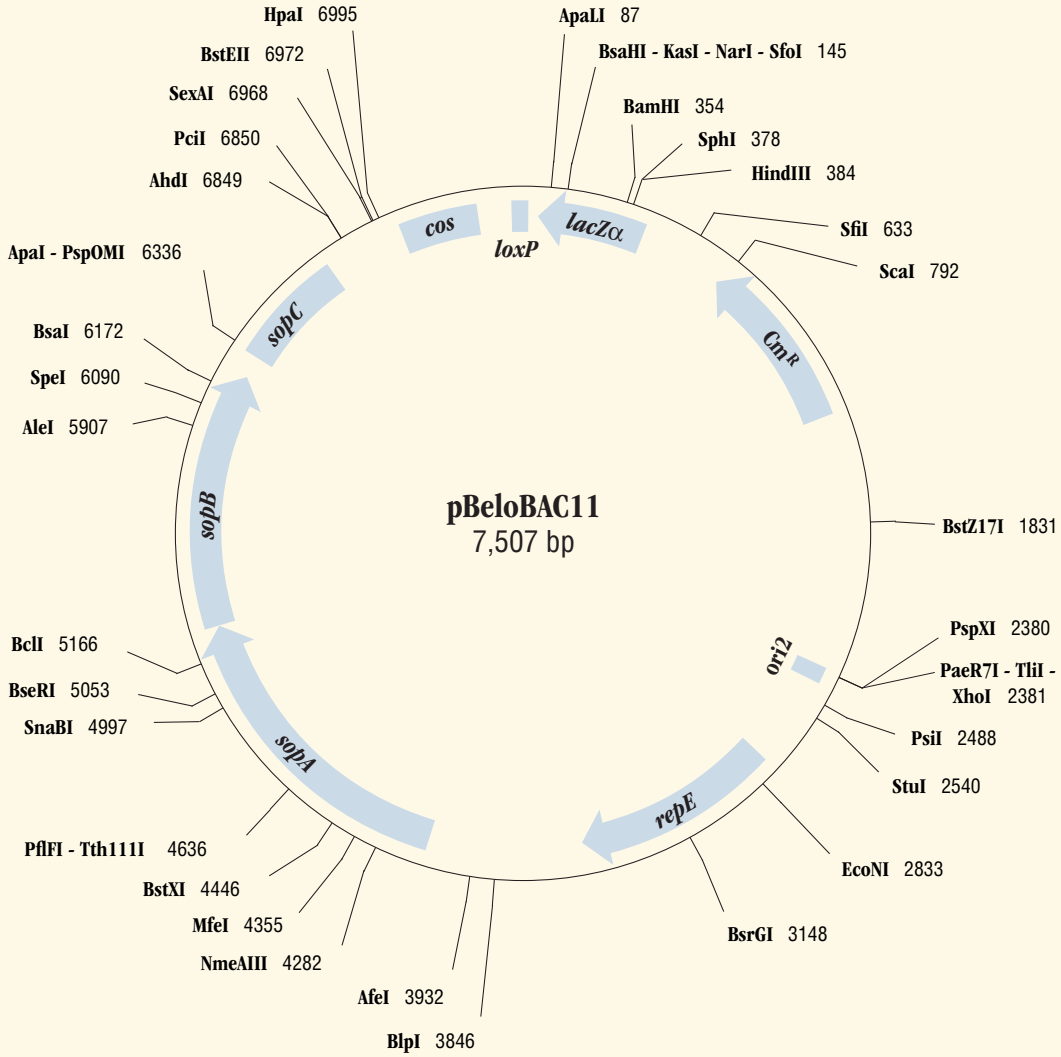
Enzymes with unique restriction sites are shown in **bold** type. Location of sites of all NEB restriction enzymes can be found on the NEB web site (choose Technical Reference > DNA Sequences and Maps). Restriction site coordinates refer to the position of the 5´-most base on the top strand in each recognition sequence.

Open reading frame (ORF) coordinates are in the form "translational start – translational stop"; numbers refer to positions on the top (clockwise) strand, regardless of the direction of transcription and include the start and stop codons.

Lambda *cos* site coordinates are the boundaries of the HincII fragment surrounding the annealed 12 base overhangs.

There are no restriction sites for the following enzymes: AarI(x), AatII, AscI, AsiSI, AvrII, BbvCI, BciVI, BmtI, BsiWI, BspDI, BstBI, Bsu36I, ClaI, FseI, I-CeuI, I-SceI, MluI, NheI, NsiI, PI-PspI, PI-SceI, PacI, PmeI, PmlI, RsrII, SacII, SanDI(x), SwaI, XcmI, ZraI.

(x) = enzyme not available from NEB



References

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4. Disque-Kochem, C. et al. (1986) *Mol. Gen. Genet.* 202, 132–135.
5. Komori, H. et al. (1999) *EMBO J.* 18, 4597–4607.
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