



BLUR8 [pPD8]

79991™

Description

Organism: *Homo sapiens*, human

Clone type: Clone

Shipping information: Rehydrate with TE

Storage Conditions

Product format: Freeze-dried

Intended Use

This product is intended for laboratory research use only. It is not intended for any animal or human therapeutic use, any human or animal consumption, or any diagnostic use.

BSL 1

ATCC determines the biosafety level of a material based on our risk assessment as guided by the current edition of *Biosafety in Microbiological and Biomedical Laboratories (BMBL)*, U.S. Department of Health and Human Services. It is your responsibility to understand the hazards associated with the material per your organization's policies and procedures as well as any other applicable regulations as enforced by your local or national agencies.

Certificate of Analysis

For batch-specific test results, refer to the applicable certificate of analysis that can be found at www.atcc.org.

Insert Information

Insert size (kb): 0.27500000000000002

Type of DNA: genomic

Insert information:

DESCRIPTION OF INSERT COMPONENT:

Genomic copy number: repetitive

Cross references: DNA Seq. Acc.: J00091

Genome: Homo sapiens

Gene name: Alu consensus sequence, repetitive

Gene product: Alu consensus sequence, repetitive

Contains complete coding sequence: Unknown

Insert end: Modification: BamHI linkers

Vector Information

Construct size (kb): 4.639999866485596

Intact vector size: 4.363

Vector name: pBR322

Type of vector: plasmid

Construction: pBR313

Host range: *Escherichia coli*

Vector end: BamHI

Vector information:

Cross references: DNA Seq. Acc.: J01749

Cloning sites: EcoRI; ClaI; HindIII; EcoRV; BamHI; SphI; Sall; XmaIII; NruI; BspMI; BsmI;

StyI; Aval; Ball; BspMII; PvuII; Tth111I; NdeI; AflIII; PpaI; PstI; PvuI; Scal; SspI; AatII

Markers: ampR; tetR

Replicon: pMB1

Notes

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EcoRI--4.7; HindIII--4.7; BamHI--4.4, 0.27; PvuII--4.7; PstI--4.7.

- ATCC staff

Because of the BamHI linkers (CCGGATCCGG), the size of the excised fragment is 275 bp, with 265 bp representing the Alu repeat. Consists of a head to tail dimer of approximately 130 bp with an insert of 31 bp in the right half as compared to the left. There is a 22% mismatch between BLUR8 and the average Alu family sequence (cf. GenBank accession J00092).

- personal communication

Material Citation

If use of this material results in a scientific publication, please cite the material in the following manner: BLUR8 [pPD8] (ATCC 79991)

References

References and other information relating to this material are available at www.atcc.org.

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Contact Information

ATCC

10801 University Boulevard

Manassas, VA 20110-2209

USA

US telephone: 800-638-6597

Worldwide telephone: +1-703-365-2700

Email: tech@atcc.org or contact your local distributor
