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The Beauty of Science is to Make Things Simple

INSTRUCTION MANUAL

EZ-96 DNA Methylation-Lightning™ Kit

Catalog No. **D5032 (Shallow-Well Format)**

Highlights

- Fastest method for *complete*, high-throughput (96-well) bisulfite conversion of DNA for methylation analysis.
- Ready-to-use conversion reagent is added directly to DNA.
- High-yield, converted DNA is ideal for PCR, MSP, array, bisulfite and Next-Gen sequencing.

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Product Contents:

Note: Satisfaction of all Zymo Research products is guaranteed. If you should be dissatisfied with this product please call 1-888-882-9682.

	D5032	Storage Temperature
EZ-96 DNA Methylation-Lightning™ Kit	2 x 96 rxns.	
Lightning Conversion Reagent*	2 bottles	Room Temp.
M-Binding Buffer	125 ml	Room Temp.
M-Wash Buffer**	2 x 36 ml	Room Temp.
L-Desulphonation Buffer	40 ml	Room Temp.
M-Elution Buffer	8 ml	Room Temp.
Silicon-A™ Binding Plates	2 plates	Room Temp.
Conversion Plates w/ Pierceable Cover Film	2 plates/films	Room Temp.
Collection Plates	2 plates	Room Temp.
Elution Plates	2 plates	Room Temp.
Instruction Manual	1	-

Note - Integrity of kit components is guaranteed for one year from date of purchase. Reagents are routinely tested on a lot-to-lot basis to ensure they provide maximal performance and reliability.

* The **Lightning Conversion Reagent** is in a ready-to-use liquid format. The reagent should be stored tightly capped at room temperature with minimum exposure to light.

** Add 144 ml of 100% ethanol to the 36 ml **M-Wash Buffer** concentrate before use.

EZ DNA Methylation-Lightning™ Kit technologies are patent pending.

Use of Methylation Specific PCR (MSP) is protected by US Patents 5,786,146 & 6,017,704 & 6,200,756 & 6,265,171 and International Patent WO 97/46705. No license under these patents to use the MSP process is conveyed expressly or by implication to the purchaser by the purchase of this product.

Note - ™ Trademarks of Zymo Research Corporation. This product is for research use only and should only be used by trained professionals. Some reagents included with this kit are irritants. Wear protective gloves and eye protection. Follow the safety guidelines and rules enacted by your research institution or facility. Freedom EVO® is a registered trademark of Tecan Group Ltd. Pyrosequencing® is a registered trademark of Biotage.

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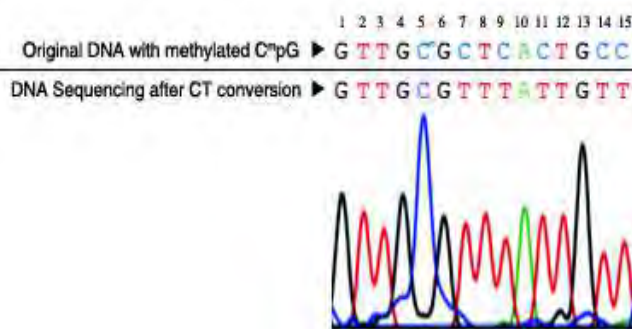
Introduction to DNA Methylation:

Cytosine methylation is a naturally occurring base modification, in both prokaryotic and eukaryotic organisms, consisting of the addition of a methyl group to the fifth carbon position of the cytosine pyrimidine ring via a methyltransferase enzyme (1). In prokaryotes DNA methylation provides a way to protect host DNA from digestion by restriction endonucleases that are designed to eliminate foreign DNA. DNA methylation in higher eukaryotes functions in the regulation/control of gene expression (2).

The majority of DNA methylation in mammals occurs in 5'-CpG-3' dinucleotides, although other patterns do exist. About 80 percent of all 5'-CpG-3' dinucleotides in mammalian genomes are found to be methylated, and the majority of the twenty percent that remain unmethylated are within promoters or in the first exons of genes. It has been demonstrated that aberrant DNA methylation is a widespread phenomenon in cancer and may be among the earliest changes to occur during oncogenesis (3). DNA methylation has also been shown to play a central role in gene imprinting, embryonic development, X-chromosome gene silencing, and cell cycle regulation.

The ability to detect and quantify DNA methylation efficiently and accurately has become essential for the study of cancer, gene expression, genetic diseases, and many other important aspects of biology. To date, a number of methods have been developed to detect/quantify DNA methylation including: high-performance capillary electrophoresis (4) and methylation-sensitive arbitrarily primed PCR (5). However, the most common techniques used today still rely on bisulfite conversion (6).

Treating DNA with bisulfite chemically modifies non-methylated cytosines into uracil, methylated cytosines remain unchanged. Once converted, the methylation profile of the DNA can be determined using the desired downstream application. For single locus analysis, the region of interest is generally amplified following bisulfite conversion (i.e., bisulfite PCR) and then sequenced or processed for Pyrosequencing®. Recent advances in methylation detection also allow the investigation of genome-wide methylation patterns using technologies including array-based methods, reduced representation bisulfite sequencing (RRBS), and whole genome bisulfite sequencing (7).



DNA sequencing results following bisulfite treatment. DNA with methylated C at nucleotide position #5 was processed using the **EZ DNA Methylation™ Kit**. The recovered DNA was amplified by PCR and then sequenced directly. The methylated cytosine at position #5 remains intact while the unmethylated cytosines at positions #7, 9, 11, 14 and 15 are completely converted into uracil following bisulfite treatment (detected as thymine following PCR).

References:

1. Adams RL. *Bioessays*. 1995; 17(2): 139-145.
2. Costello JF, Plass CJ. *Med. Genet.* 2001; 38(5): 285-303.
3. Stirzaker C. *Cancer Res.* 1997; 57(11): 2229-2237.
4. Fraga MF, *et al.* *Electrophoresis*. 2000; 21(14): 2990-2994.
5. Gonzalgo ML. *Cancer Res.* 1997; 57(4): 594-599.
6. Frommer M. *Proc. Natl. Acad. Sci. USA.* 1992; 89(5): 1827-1831.
7. Rakyan VK, *et al.* *Nat. Rev.* 2011, 12(8): 529-541.

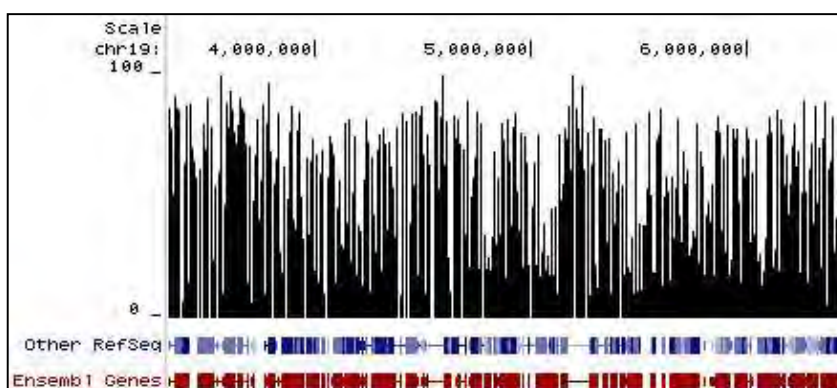
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Product Description:

The **EZ-96 DNA Methylation-Lightning™ Kit** features high-throughput (96-well) bisulfite treatment and conversion of DNA for methylation analysis. Key to the fast workflow is the ready-to-use **Lightning Conversion Reagent**. No preparation is necessary, simply add this unique reagent to a DNA sample, wait about an hour, and let the reaction proceed to completion. DNA denaturation and bisulfite conversion processes are combined with added heat to facilitate rapid denaturation. Desulphonation and clean-up of the converted DNA is performed using a unique 96-well spin-plate. High yield, converted DNA is ideal for PCR, array, bisulfite and next generation sequencing, etc.

Note: Single spin-column formats are available for processing smaller numbers of samples. Also, MagPrep kits are available (p. 8) for adaptation to liquid handling robots (e.g., Tecan – Freedom EVO®) and automated sample prep.



Methylation Plot From Reduced Representation Bisulfite Sequencing (RRBS). Data shows the relative percentage of methylation at individual CpG sites in mouse DNA. Methylation percentage is shown across a ~3 Mb region of mouse chromosome 19. Bisulfite sequencing libraries were prepared using mouse genomic DNA prepped with the **Genomic Clean & Concentrator™** (D4010, D4011 – Zymo Research) and bisulfite converted using **EZ DNA Methylation™** technology prior to Next-Gen sequencing.

Select Citations:

1. Ehrich M, *et al.* Nuc. Acids Res. 2007; 35 (5): e29
2. Kaneda M, *et al.* Nature. 2004; 429: 900-903
3. Zhang F, *et al.* Proc. Natl. Acad. Sci. USA. 2007; 104 (11): 4395-4400.
4. Oda M, *et al.* Genes & Dev. 2006; 20: 3382-3394.
5. England RPM, *et al.* Nature Meth. 2005; 2: 1-2.
6. Berman BP, *et al.* Nature Gen. 2012; 44: 40-46.
7. Leung DC, *et al.* Proc. Natl. Acad. Sci. USA. 2011; 108 (14): 5718-5723.
8. Hesselink AT, *et al.* Clin. Cancer Res. 2011; 17: 2459-2465.
9. Campan M, *et al.* PLoS ONE. 2011, 6 (12): e28141.

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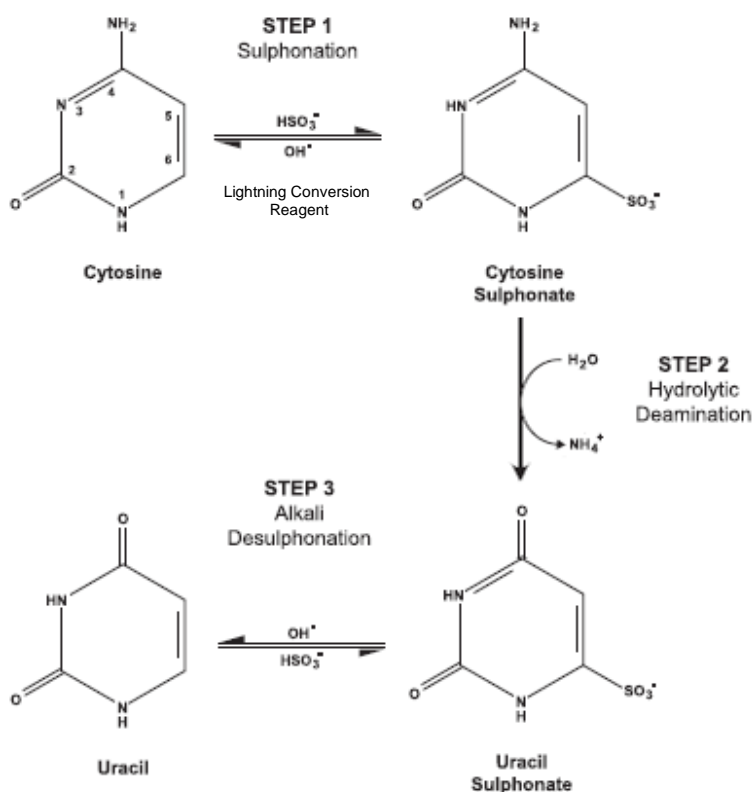
Specifications:

- **DNA Input:** Samples containing between 100 pg to 2 µg of DNA. For optimal results, the amount of input DNA should be from 200 to 500 ng.
- **Conversion Efficiency:** > 99.5% of non-methylated C residues are converted to U; > 99.5% protection of methylated cytosines.
- **DNA Recovery:** > 80%

Reagent Preparation:

- **Preparation of M-Wash Buffer**

Add 144 ml of 100% ethanol to the 36 ml **M-Wash Buffer** concentrate before use.



Overview of Bisulfite Conversion. Steps 1 and 2 occur during bisulfite conversion, while Step 3 is performed as the DNA is bound to the column matrix. For the reaction to proceed to completion, it is essential the DNA be fully denatured.

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Samples >20 µl must be processed using multiple conversion reactions. Replicate reactions can be cleaned using the same well by repeating steps 3-5.

The capacity of each well of the Binding Plate is 600 µl. The capacity of each well of the Collection Plate is 800 µl. Empty the Collection Plate whenever necessary to prevent contamination of the Binding Plate contents by the flow-through.

Alternatively, water or TE (pH ≥ 6.0) can be used for elution if required for your experiments.

Protocol:

1. Add 130 µl of **Lightning Conversion Reagent** to 20 µl of a DNA sample in a **Conversion Plate**. Mix the samples by pipetting up and down.

Note: If the volume of DNA is less than 20 µl, compensate with water.

2. Seal the plate with the provided film. Transfer the **Conversion Plate** to a thermal cycler and perform the following steps:

1. 98°C for 8 minutes
2. 54°C for 60 minutes
3. 4°C storage for up to 20 hours

Note: The 4°C storage step is *optional*.

3. Add 400 µl of **M-Binding Buffer** to the wells of a **Silicon-A™ Binding Plate** mounted on a **Collection Plate**.

4. Transfer the samples from the **Conversion Plate** (Step 2) to the wells of the **Silicon-A™ Binding Plate**. Mix by pipetting up and down.

5. Centrifuge at ≥ 3,000 x g (5,000 x g max.) for 5 minutes. Discard the flow-through.

6. Add 400 µl of **M-Wash Buffer** to each well of the plate. Centrifuge at ≥ 3,000 x g for 5 minutes.

7. Add 200 µl of **L-Desulphonation Buffer** to each well and allow the plate to stand at room temperature (20-30°C) for 15-20 minutes. After the incubation, centrifuge at ≥ 3,000 x g for 5 minutes. Discard the flow-through.

8. Add 400 µl of **M-Wash Buffer** to each well of the plate. Centrifuge at ≥ 3,000 x g for 5 minutes. Discard the flow-through. Add another 400 µl of **M-Wash Buffer** and centrifuge for 10 minutes.

9. Place the **Silicon-A™ Binding Plate** onto an **Elution Plate**. Add 30 µl of **M-Elution Buffer** directly to each well. Wait 5 minutes, then centrifuge at ≥ 3,000 x g for 3 minutes to elute the DNA.

The DNA is ready for immediate analysis or can be stored at or below -20°C for later use. For long term storage, store at or below -70°C. We recommend using 1-4 µl of eluted DNA for each PCR, however, up to 30 µl can be used if necessary. The elution volume can be > 30 µl depending on the requirements of your experiments, but small elution volumes will yield higher DNA concentrations.

Frequently Asked Questions:

Q: Should the input DNA be dissolved in TE, water, or some other buffer prior to its conversion?

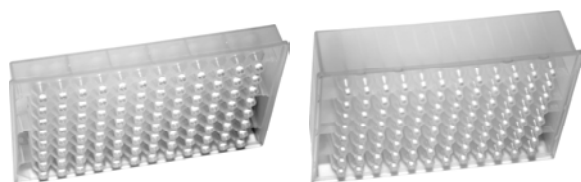
A: *Water, TE or modified TE buffers can be used to dissolve the DNA and do not interfere with the conversion process.*

Q: Which Taq polymerase(s) do you recommend for PCR amplification of converted DNA?

A: *We recommend a "hot start" DNA polymerase (e.g., ZymoTaq™, page 9).*

Q: Why are there two different catalog numbers for the EZ-96 DNA Methylation-Lightning™ Kit?

A: *The two different catalog numbers are used to differentiate between the binding plates that are included in the kit. Deep and shallow-well binding plates are available to accommodate most rotors and microplate carriers. Below is a comparison of the two binding plates.*



Binding Plate	Silicon-A™ Plate	Zymo-Spin™ I-96 Plate
Style	Shallow-Well	Deep-Well
Height of Binding Plate	19 mm (0.75 inches)	35 mm (1.38 inches)
Binding Plate/Collection Plate Assembly	43 mm (1.69 inches)	60 mm (2.36 inches)
Binding Cap./Minimum Elution Volume	5 µg/30 µl	5 µg/15 µl
Catalog Numbers	D5032	D5033

Ordering Information:

Product Description	Catalog No.	Kit Size
EZ DNA Methylation-Lightning™ Kit	D5030	50 rxns.
	D5031	200 rxns.
EZ-96 DNA Methylation-Lightning™ Kit (Shallow-Well)	D5032	2 x 96 rxns.
EZ-96 DNA Methylation-Lightning™ Kit (Deep-Well)	D5033	2 x 96 rxns.
EZ-96 DNA Methylation-Lightning™ MagPrep*	D5046	4 x 96 rxns.
	D5047	8 x 96 rxns.

* **MagPrep** kits are adaptable to liquid handling robots (e.g., Tecan – Freedom EVO®) making them ideal for automated sample prep.

For Individual Sale	Catalog No.	Amount(s)
Lightning Conversion Reagent	D5030-1	1 tube
	D5032-1	1 bottle
M-Binding Buffer	D5005-3	30 ml
	D5006-3	125 ml
	D5040-3	250 ml
M-Wash Buffer	D5001-4	6 ml
	D5002-4	24 ml
	D5007-4	36 ml
	D5040-4	72 ml
L-Desulphonation Buffer	D5030-5	10 ml
	D5031-5	40 ml
	D5046-5	80 ml
M-Elution Buffer	D5001-6	1 ml
	D5002-6	4 ml
	D5007-6	8 ml
	D5041-6	40 ml
Zymo-Spin™ IC Columns (capped)	C1004-50	50 columns
	C1004-250	250 columns
Collection Tubes	C1001-50	50 tubes
	C1001-500	500 tubes
	C1001-1000	1,000 tubes
MagBinding Beads	D4100-2-6	6ml
	D4100-2-8	8 ml
	D4100-2-12	12 ml
	D4100-2-16	16 ml
	D4100-2-24	24 ml
Zymo-Spin™ I-96 Binding Plates	C2004	2 plates
Silicon-A™ Binding Plates	C2001	2 plates
Conversion Plates w/ Pierceable Cover Film	C2005	2 plates/films
Collection Plates	C2002	2 plates
Elution Plates	C2003	2 plates

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