

# diagenode

Innovating Epigenetics Solutions



## CORPORATE GRAPHIC GUIDELINES

# LOGO

The logo features the word "diagenode" in a bold, lowercase, sans-serif font. Above the final two letters, "de", there is a cluster of seven red dots of varying sizes arranged in a curved, upward-pointing pattern, resembling a stylized molecular structure or a cluster of cells.

●	CYAN	18%
	MAGENTA	100%
	YELLOW	80%
	BLACK	5%

R	194
G	33
B	59

PANTONE 187 CVU

WEB # B21329

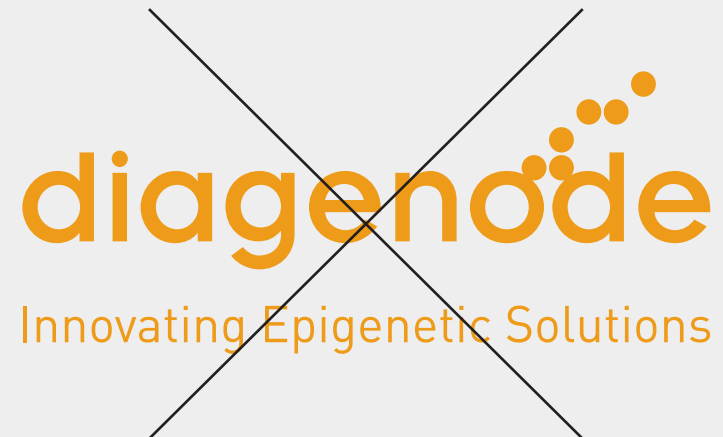
THE LOGO CAN BE USED IN WHITE  
**ONLY** IF THE BACKGROUND  
IS IN A DARK COLOR

LOGO



**DO NOT** CHANGE THE TAGLINE

# LOGO: DON'T





# COLORS



CYAN	14%
MAGENTA	100%
YELLOW	79%
BLACK	42%

R	137
G	10
B	34

WEB	# 8D0E24
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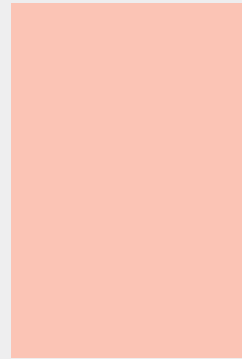


CYAN	18%
MAGENTA	100%
YELLOW	80%
BLACK	5%

R	194
G	33
B	59

WEB	# B21329
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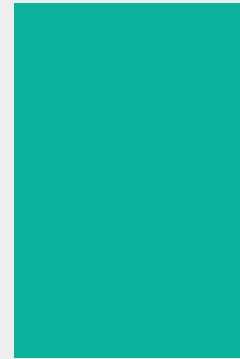
PANTONE	187 CVU
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CYAN	0%
MAGENTA	27%
YELLOW	23%
BLACK	0%

R	248
G	203
B	188

WEB	#F8CBBC
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CYAN	76%
MAGENTA	3%
YELLOW	49%
BLACK	0%

R	99
G	198
B	147

WEB	#13B29C
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CYAN	30%
MAGENTA	7%
YELLOW	20%
BLACK	5%

R	190
G	206
B	199

WEB	# C5D5CF
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# FONT

[PRINT]

DIN

LIGHT  
REGULAR  
MEDIUM  
**BOLD**  
**BLACK**

Usually, the body is in LIGHT, highlighted words are in MEDIUM;  
The big title are in BOLD, title in MEDIUM

If you don't have DIN font on your computer,  
please use CALIBRI.

Maximum size 12 pt for the body of your document.

[WEB & EMAILER]

HELVETICA

THIN  
REGULAR  
**BOLD**

Usually, the titles are in THIN, the paragraphs are in REGULAR and  
highlighted words and titles are in BOLD;

In the css code, **ARIAL** and SANS-SERIF can be mentionned as  
alternative fonts.

# POWERPOINT HEADER



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EPIGENETICS

# DOCUMENTS

This lay-out is used for application notes, protocols, technical data-sheet, contrats, white papers, guidelines, case studies, technical notes, ...

## An automated method for efficient, accurate and reproducible construction of RNA-seq libraries



Maria Tsoimpana, Sujith Vallyaparambil, Jonathan Bard, Brandon Marzullo, Norma Nowak and Michael J. Buck

**Authors' Affiliation:** Department of Biochemistry and Center of Excellence in Bioinformatics and Life Sciences, State University of New York at Buffalo, 701 Ellicott St., Buffalo, NY 14203.

**Corresponding Author:** Maria Tsoimpana, State University of New York at Buffalo, 701 Ellicott St., Buffalo, NY 14203. Phone: 716-881-8046; Fax: 716-849-6655; E-mail: tsoimpana@buffalo.edu

### Introduction

Deciphering the underlying determinants of transcriptional regulation in relation to cell differentiation, functional diversification, environmental signaling, and disease development remains a central question in biology today. Integration of expression data with knowledge on chromatin accessibility, histone modifications, DNA methylation, and transcription factor binding, has been instrumental for the unveiling of cell-specific local and long-range regulatory patterns, facilitating further investigation on the underlying rules of transcription regulation at an individual and allele-specific level. Current interest by large collaborative projects, such as the ENCODE<sup>[1]</sup>, the NIH Roadmap Epigenomics Mapping Consortium<sup>[2,3]</sup>, and the *C. elegans* and *D. melanogaster* modENCODE<sup>[4]</sup>, has been placed on generating genome-wide gene expression maps to locate gene expression changes that accompany important developmental and disease development processes. The pairing of traditional expression assays with high-throughput sequencing (RNA-seq) has allowed the generation of genome-wide gene expression data with unparalleled specificity, throughput, and sensitivity delivering an unbiased representation of the transcriptome.

However, full genome transcriptional gene characterization has been partially limited by the complexity and increased time-requirements of available RNA-seq library construction protocols. Here we report the successful application of the Diagenode IP-Star® Compact System for the easy, rapid, and reproducible RNA-seq library construction of five *Mus musculus* (mouse) samples. Use of the IP-Star® Compact System significantly reduced the hands-on time for RNA-seq library synthesis, adenylation, and adaptor ligation providing with high-quality RNA-seq libraries tailored for Illumina high-throughput next-generation sequencing. Generated data exhibited high technical reproducibility compared to data from RNA-seq libraries synthesized manually for the same samples. Obtained results are consistent regardless the researcher, day of the experiment, and experimental run. Overall, the IP-Star® Compact System proves an efficient and reliable tool for the construction of next-generation RNA-seq libraries, especially for transcriptome-based annotation of larger genomes or genomes with many alternative gene isoforms.

## Sample Submission Guidelines for RRBS

**Contact:** services@diagenode.com

**Website:** <https://www.diagenode.com/categories/rrbs-service>

### 1. Isolation of genomic DNA

- The quality of the DNA to be used in RRBS is very important, we therefore highly recommend the use of Diagenode XL GenDNA extraction module (Cat. No. C03030020) for DNA extraction.
- It is possible to substitute the XL GenDNA extraction kit or an equivalent product that is capable of extracting high molecular weight genomic DNA.
- The XL GenDNA Extraction kit has been optimized for cultured cells. The isolation of genomic DNA from whole blood samples or FFPE material requires specialized kits.
- Do not use Trizol during your DNA extraction as it inhibits the enzymatic digestion.
- Genomic DNA must be free of protein. Regardless the choice of DNA extraction protocol, proteinase K digestion is thus mandatory.
- Do not vortex high molecular weight DNA as this might lead to fragmentation, but mix by pipetting.

### 2. Genomic DNA quantification and preparation

- The concentration of double-stranded DNA must be quantified using a fluorescence-based assay such as Invitrogen's Qubit dsDNA High Sensitivity kit.



Photometric techniques like Nanodrop cannot be used as they tend to overestimate the concentration of double-stranded genomic DNA.

- We recommend to check for genomic degradation by analysis of a small aliquot of each sample on a 0.8 % agarose gel.
- For RRBS, we require at least 400 ng of genomic DNA, quantified in a fluorescence-based assay.**
- The DNA concentration must be higher than 5 ng/μL and the volume higher than 10 μL.**

### 3. Shipment Instructions

- Prepare the samples in 1.5 mL tubes or 96-well plates and label them carefully.
- Ship the samples **overnight** in an insulated container box packed with **3 kg of dry ice**.
- Include the printed list of the samples and their description (name, species, sample type, volume and DNA concentration) in the shipment and send by email an electronic version of it as well.

# BROCHURES



## BIORUPTOR® POWER FOR EVERY APPLICATION



### STATE-OF-THE ART SHEARING DEVICE FOR:

- DNA and RNA shearing
- Chromatin shearing
- FFPE nucleic acid extraction
- Tissue and cell disruption
- Protein, DNA, RNA extraction

The header is white and we use the red logo with the epigenetics tagline

The lay-out will be always the same.


The image is light related to the product (e.g.: on this picture, we used the Bioruptor Pico's texture)

The big title is in Din Medium, subtitle is in Din Light


# BROCHURES



# FLYERS



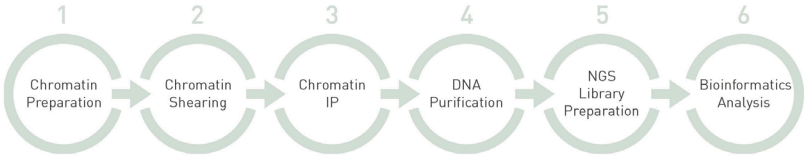
Innovating Epigenetic Solutions

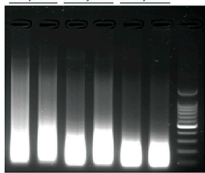


## ChIP-seq Service

Expert services from A to Z

- **Utilize our expertise: 10 years of experience** in ChIP-Seq and official partner of IHEC-BLUEPRINT Epigenome Consortia
- **Customized** support to match your needs
- **Dedicated in-house expert** coordinates your project
- **High quality data** with ENCODE standards
- **Results provided within 6-8 weeks**



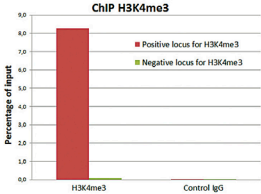


### Chromatin shearing

- Chromatin shearing using Bioruptor® technology
- Isothermal chromatin shearing, preservation of epitopes
- Homogeneous fragment size distribution
- More than 2,000 Bioruptor citations in peer-reviewed publications

### Chromatin Immunoprecipitation

- Choice of 200 ChIP & ChIP-Seq grade antibodies
- Sample automation enables reproducibility
- Inputs from as little as 10,000 cells/IP
- Optimized ChIP protocols maximize signal to noise ratio



Condition	Positive locus for H3K4me3 (%)	Negative locus for H3K4me3 (%)
H3K4me3	~8.5	~0.5
Control IgG	~0.5	~0.5

The header is white and we use the red logo with the epigenetics tagline

The banner is below the logo. We put a lightly image related with the product, if it's not possible the team will choose a graphical and abstract image.

The body of the flyer.

Text is in light, we can use bullets, and highlighted words to be more attractive.

We recommend to put only 2 figures on the recto of the flyer to keep a flat design flyer

# FLYERS





# POSTERS

## DIAGENODE EXOIP™ WORKFLOW : AN EASY AND FAST SOLUTION TO GENERATE HIGH QUALITY EXOSOME PREPARATIONS

Gilles Brocart, Emilia Danilowicz-Luebert, Laurence Barga, Céline Sabatet  
Diagenode ex, Life Science Park, Rue du Bois Saint-Jean 3, 4102 Senargis, Belgium

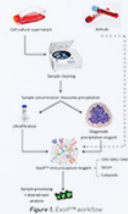


### Introduction

Diagenode dedicates its expertise in immunocapture technology to the field of extracellular vesicles. The ExoIP™ immunocapture reagent is a tool that allows researchers to isolate in an easy and reproducible way, exosomes from cell culture supernatant-based samples as well as most biofluids such as serum and plasma. The sample at the end of the workflow is highly enriched in exosomes and free from common contaminants that easily occur with other purification methods. Exosomes are still functional and can be fully eluted from the magnetic beads without any exosomal damages. ExoIP™ are a range of kits that can lead to highly specific isolation from only subtypes of vesicles bearing particular markers or to a more global isolation from total exosome population in the sample thanks to a mixture of anti-tetraspanins coated beads.

### ExoIP™ workflow : from the starting material to the downstream analysis

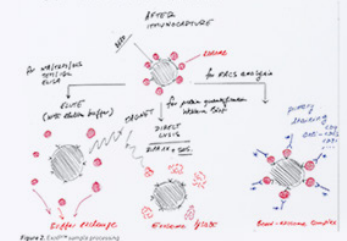
The complete workflow can be accomplished in only two days with an overnight incubation step in between. The ExoIP™ kit can be used directly on biofluids, such as plasma as well as cell culture supernatant. The upcoming Diagenode precipitation reagent ease the way to recover pre-enriched exosome preparations prior to immunocapture. Afterward, ExoIP™ can be used to isolate global or specific exosome population in the sample with high accuracy and little hands-on-time. Finally, recovered exosomes can then be processed in any wanted downstream applications from morphology evaluation to cargo analysis.



### ExoIP™ sample processing : what to do with it

Isolated exosomes can be processed in three different ways:

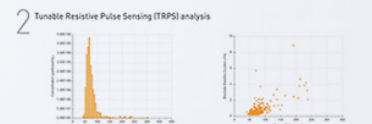
1. An appropriate direct lysis on the beads can be done if the cargo of the exosomes is of interest.
2. The bead-exosomes complex can be maintained for flow cytometry analysis. Indeed, ExoIP™ beads perform excellent in flow cytometry thanks to their high binding capacity resulting in numerous exosomes bound to it and thus leading to strong signal.
3. The ExoIP™ also offers an exclusive elution buffer that gently elutes the exosomes from the beads without any harm, allowing the researchers to perform analysis on highly enriched and intact exosomes preparations.



### Validation data : we talk about highly enriched preparations here

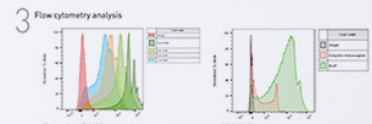
**1 Western Blot**  
Exosomes isolated from HEK293T cell culture supernatant. Common and well-accepted proteins enriched in exosomes are detected in ExoIP™ preparations.

Figure 3: Western blot data set

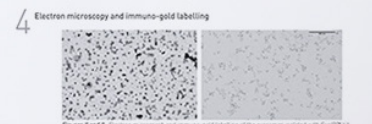


Figures 4 and 5: TRPS analysis of the exosome preparations using qNano system (DION)

Exosomes isolated from HEK293T cell culture supernatant. Measured nanoparticles fall into the exosome theoretical size range: 30-100 nm. Moreover, the results displayed on the right show that all measured nanoparticles are between 30 and 100 nm with few exceptions meaning that ExoIP™ preparations are indeed highly enriched in exosomes.



Exosomes isolated from HEK293T cell culture supernatant. A significant FACS signal can already be obtained with only 1 ml of CCM (anti-CD81) meaning that the ExoIP™ has high binding capacity and is especially suited for efficient isolation even from low occurring targets. On the right, the picture clearly shows that in the same exact experimental conditions, ExoIP™ beads capture more exosomes than a competitor's kit.



Exosomes isolated from HEK293T cell culture supernatant. Intact exosomes are eluted from the beads and are still functional. Left: transmission electron microscopy. Right: immuno-gold labelling with 10 nm gold particles coated with anti-CD81 antibody.

### Conclusion

ExoIP™ kit from Diagenode is a complete solution for thorough exosome isolation, simple and straightforward. Validation data clearly show that high quality preparations generated in only two days without the need for special and expensive equipments.

# STAND, BOOTH AND EVENTS

## EUROPE

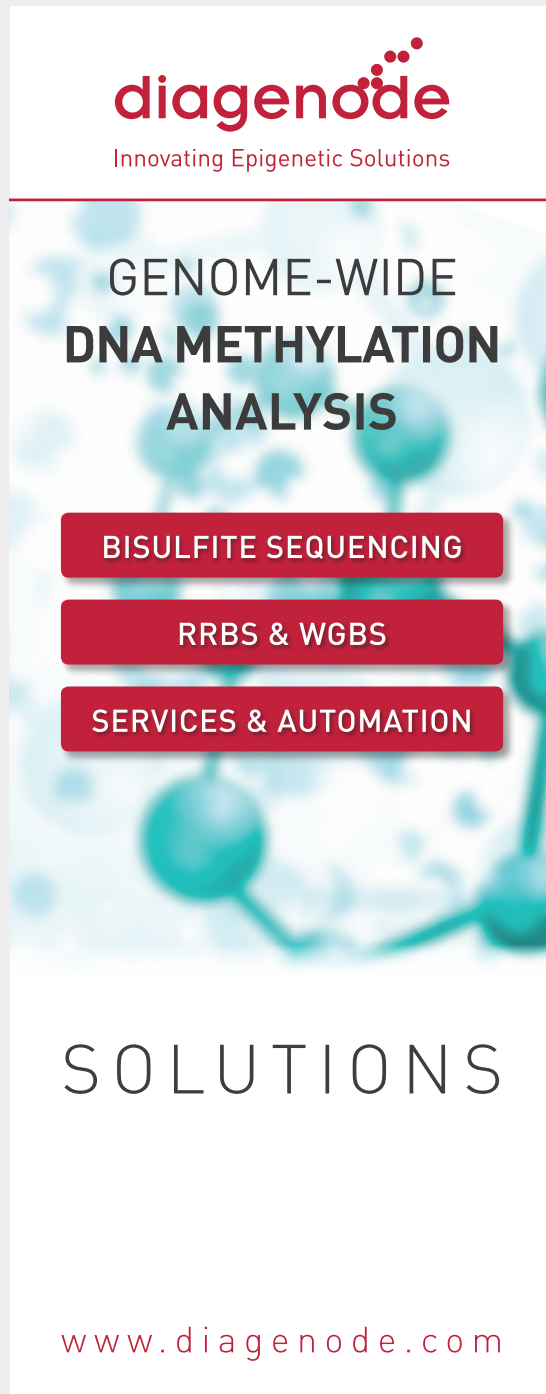


# STAND, BOOTH AND EVENTS

## EUROPE



# EU ROLL-UP'S



The header is white and we use the red logo with the epigenetics tagline.

We put a lightly image related with the product with a blue/green hue.

This image is blur.

The title is in dark grey. It's a short and clear message in maximum 3 lines.

The body is display like bullets.



# STAND, BOOTH AND EVENTS

USA



# STAND, BOOTH AND EVENTS

## USA

**diagenode**

Innovating Epigenetic Solutions

### ACCOMPLISH ROBUST CHIP-SEQ WITH EASE

#### CHIP-SEQ SOLUTIONS

- Low input ChIP-seq down to 10,000 cells
- Validated histone or transcription factor ChIP-seq solutions
- ChIP-seq validated antibodies



[www.diagenode.com](http://www.diagenode.com)

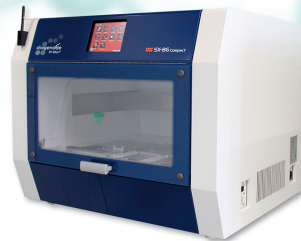
**diagenode**

Innovating Epigenetic Solutions

### AUTOMATE EPIGENETICS AND NGS LIBRARIES

#### IP-STAR®

- Automate ChIP-seq, MeDIP, hMeDIP, MethylCap, and NGS library prep
- Achieve unmatched reproducibility
- Simplify optimization of difficult assays including transcription factor ChIP



[www.diagenode.com](http://www.diagenode.com)

**diagenode**

Innovating Epigenetic Solutions

### RELIABLY SHEAR DNA FROM 3KB TO 75KB

#### MEGARUPTOR®

- High-quality fragmentation for long-read sequencing
- Automated walk-away processing
- Tight fragment distribution



[www.diagenode.com](http://www.diagenode.com)

**diagenode**

Innovating Epigenetic Solutions

### SHEAR DNA CHROMATIN, AND RNA RELIABLY


#### BIORUPTOR® PICO

- Next-gen seq: DNA and RNA shearing (5µl-100µl)
- Chromatin shearing (10µl - 2ml)
- Process 12 samples in parallel



[www.diagenode.com](http://www.diagenode.com)

# US ROLL-UP'S



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**AUTOMATE  
EPIGENETICS AND  
NGS LIBRARIES**

**IP-STAR®**

- Automate ChIP-seq, MeDIP, hMeDIP, MethylCap, and NGS library prep
- Achieve unmatched reproducibility
- Simplify optimization of difficult assays including transcription factor ChIP



[www.diagenode.com](http://www.diagenode.com)

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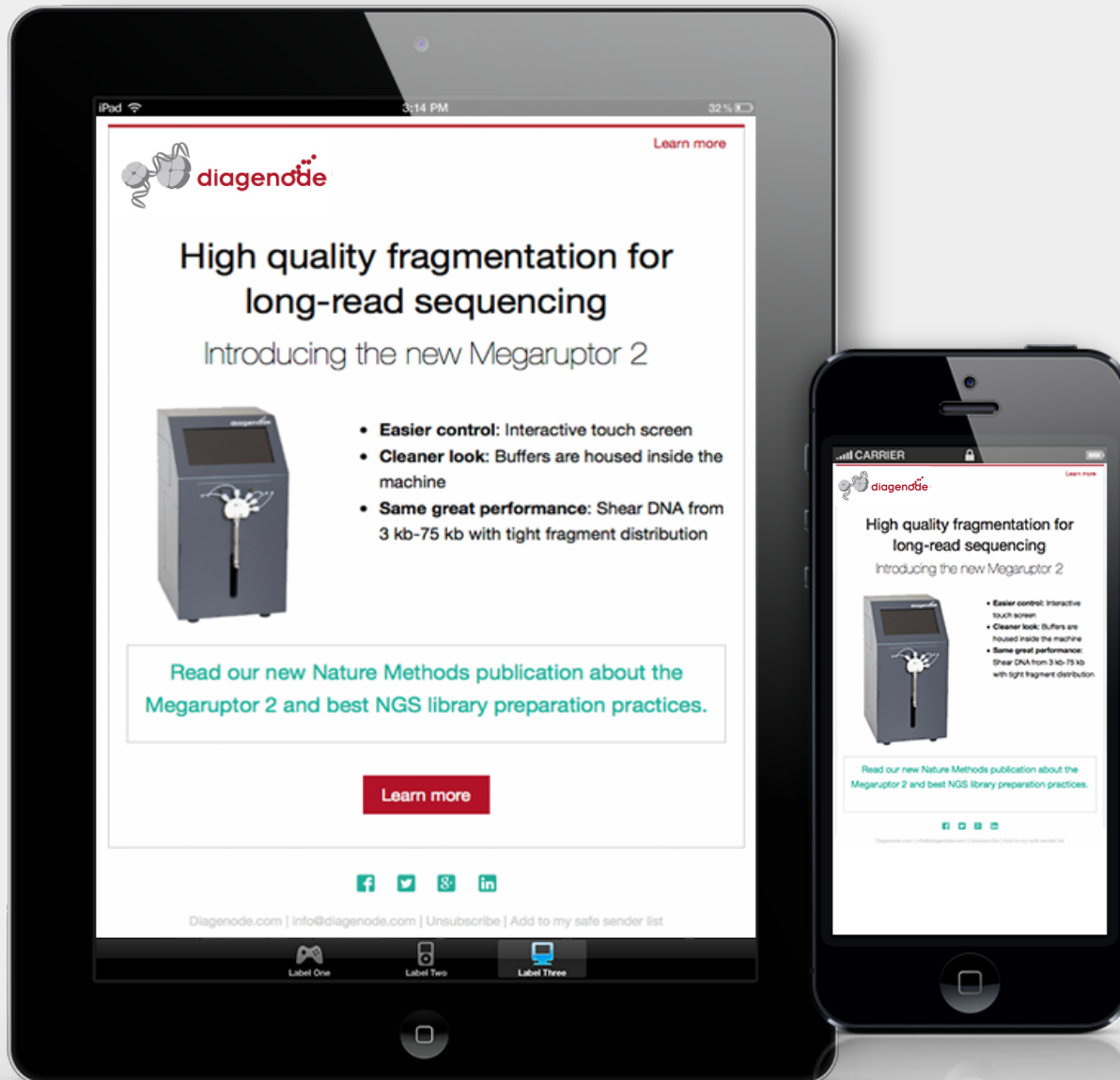
This image is blur.

The title is in dark grey. It's a short and clear message in maximum 3 lines.

Subtitle in blue/green

The body is display like bullets.

# EMAILERS



The emailer is responsive and create with Foudation 6.

The max-width is 580 pixels.

The general background of the emailer is white.

You can use a picture to illustrate your message as long as it is consistent with the subject.

The links are written in red.

Text can be highlited in color, bold and put into a frame to put it in evidence.

The action button is written in white with a red background.

The footer contains:

- Social icons in green
- Website link
- Email address
- Add to my safer sender list



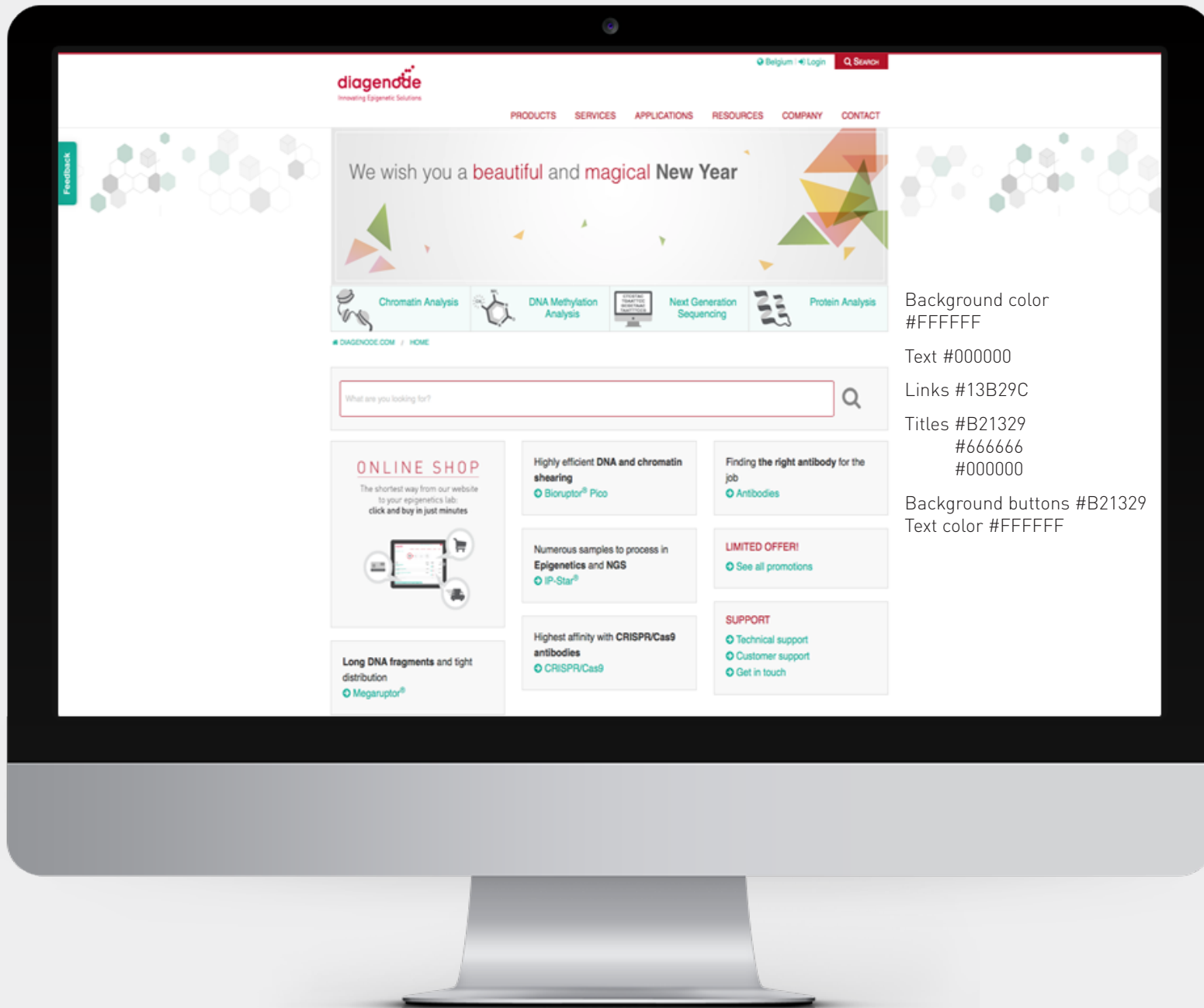
# BANNER HEADER



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The icon left to the logo must always be the one here above.

# WEBSITE



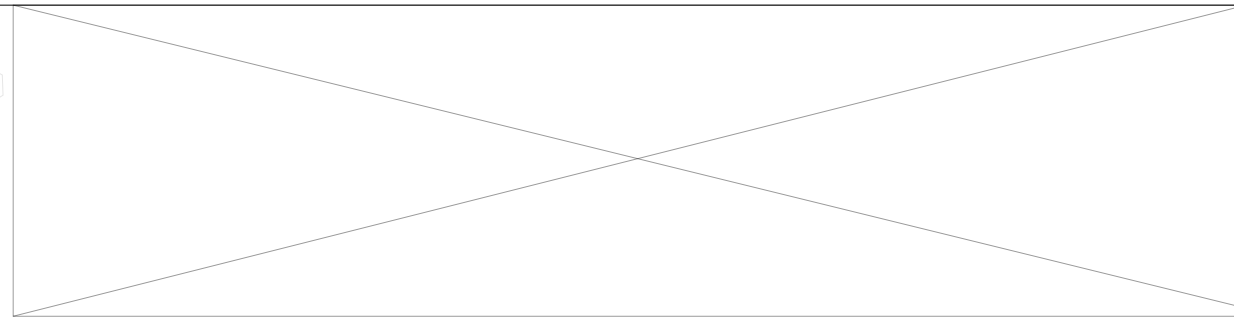
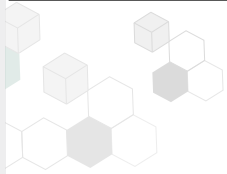
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Text #000000

Links #13B29C

Titles #B21329  
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Background buttons #B21329  
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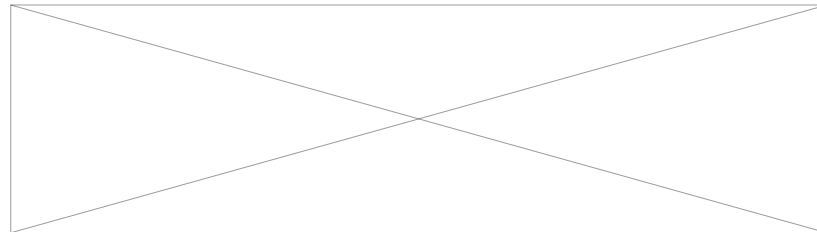
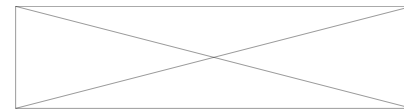
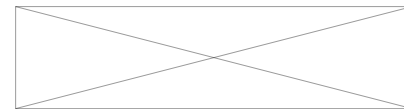
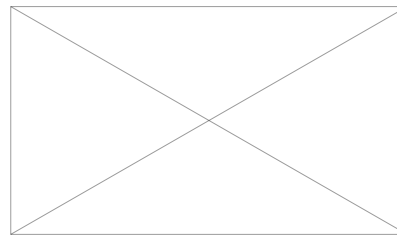
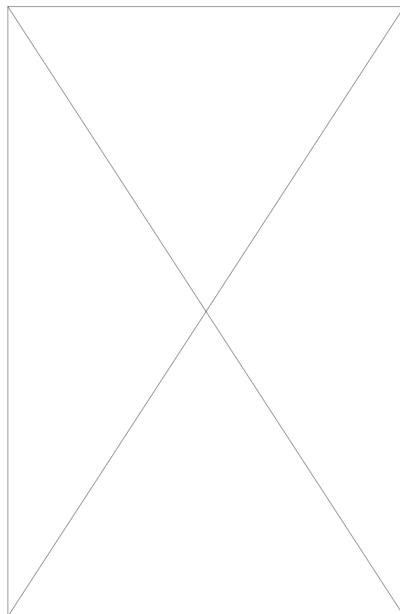
241 PX

970 PX

303 PX

303 PX

303 PX



303 PX

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303 PX

# PRODUCT PAGE

## Bioruptor® Pico sonication device



### BUYBACK PROGRAM

Personalised trade in offer for your  
Bioruptor model

Temperature-controlled

Easy to use

All-in-one solution

Processing of 6-12 samples

Sample size 5 µl – 2 ml

No soundproof box

**SelectScience®**  
The Fastest Way to Expert Opinion™

**Bioruptor® Pico**



"Once setup the unit was easy to use and very reproducible. Once we got past the learning c..."

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CATALOG NUMBER  
B01060001

FORMAT  
1 unit

The Bioruptor® Pico is the latest innovation in shearing and represents a new breakthrough as an all-in-one shearing system optimized for shearing micro-volumes of 5 µl to larger volumes of up to 2 ml. The built-in cooling system (water cooler and Single Cycle Valve) ensures high precision temperature control resulting in higher quality samples.

- All-in-one shearing solution
- Simultaneous sonication of 6-12 samples
- Small, light, and easy to use
- Temperature-controlled

#### Ideal for

- DNA shearing for Next-Generation-Sequencing (5 - 100 µl)
- Chromatin shearing (10 µl - 2 ml)
- RNA shearing
- Protein extraction from tissues and cells
- FFPE DNA extraction

#### TESTIMONIAL

My group is mostly focused on epigenetic reprogramming and I have been using Diagenode products for the last 5 years. My experience with both [antibodies](#), [ChIP-Kits](#) and the [Bioruptor](#) is nothing but positive. Diagenode products are unique for reproducibility, and this has always been a great plus for the success of my experiments.

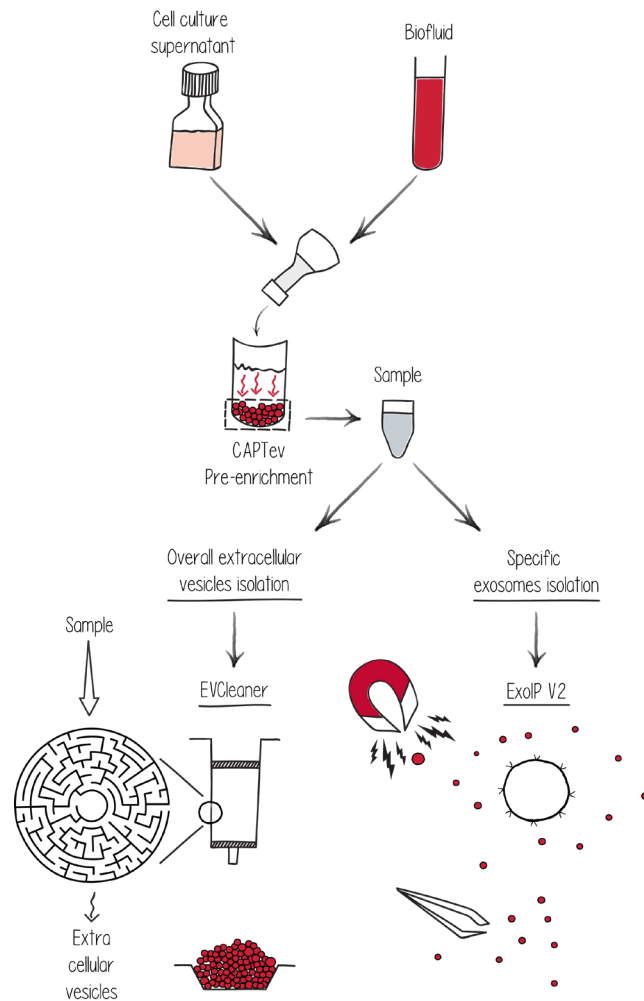
— Dr. Raffaele Teperino - Environmental Epigenetic Group - Institute of Experimental Genetics, Helmholtz Zentrum Muenchen GmbH, Germany

# ICON STYLES



This is a non-exhaustive list

# MEDIAS



Exosome enrichment level

Drawings are usually used on the website but it also can be photos with approval of the graphic design team.

Videos and animations about the products may also be published on the website.