iDeal ChIP-seq kit for Transcription Factors

Cat. No. C01010054 (10 rxns)
    C01010055 (24 rxns)
    C01010170 (100 rxns)
Please read this manual carefully before starting your experiment
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Introduction

Association between proteins and DNA has a major influence on gene transcription, epigenetic silencing and other nuclear processes which control many vital cellular functions. It is crucial to understand these interactions and the mechanisms by which they control and guide gene regulation pathways and cellular proliferation. Chromatin immunoprecipitation (ChIP) is a technique to analyze the association of proteins with specific genomic regions in intact cells. ChIP can be used to study changes in epigenetic signatures, chromatin remodeling and transcription regulator recruitment to specific genomic sites.

The iDeal ChIP-seq kit for Transcription Factors provides a robust ChIP protocol suitable for investigation of transcriptional factors associated with chromatin from cells and tissues. The protocol involves protein-DNA cross-linking with formaldehyde, followed by cell lysis and fragmentation of the cross-linked chromatin. The subsequent immunoprecipitation of chromatin is performed with an antibody (user supplied) specific to a target protein. Protein A magnetic beads are used to isolate the protein-DNA complexes of interest. The immunoprecipitated DNA is eluted and purified using unique IPure magnetic beads. The eluted DNA is ideal for qPCR analysis and ChIP-seq library preparation. Additionally, the kit includes a negative (IgG) and a positive (CTCF) control antibody and primer pairs amplifying CTCF positive and negative loci.

The iDeal ChIP-seq kit for Transcription Factors offers unique benefits:

- Highly optimized protocol for ChIP-seq from cells and tissues
- Most complete kit available (covers all steps, including the control antibodies and primers)
- Validated for ChIP-seq with multiple transcription factors and non-histone targets
- Magnetic beads make ChIP easy, fast and more reproducible
- Combination with Diagenode ChIP-seq antibodies provides high yields with excellent specificity and sensitivity
- Eluted DNA suitable for any downstream application
- Easy-to-follow protocol
## Kit method overview & time table

<table>
<thead>
<tr>
<th>STEP</th>
<th>Description</th>
<th>Time needed</th>
<th>Day</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Cell or tissue collection and DNA-protein cross-linking</td>
<td>30 minutes</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>Cell lysis and chromatin shearing</td>
<td>1 to 2 hours</td>
<td>1</td>
</tr>
<tr>
<td>3</td>
<td>Magnetic immunoprecipitation</td>
<td>Overnight</td>
<td>1-2</td>
</tr>
<tr>
<td>4</td>
<td>Elution, decross-linking and DNA purification</td>
<td>5 hours</td>
<td>2</td>
</tr>
<tr>
<td>5</td>
<td>Quantitative PCR and data analysis preparation prior to library preparation and Next-Generation Sequencing</td>
<td>2 to 3 hours</td>
<td>2</td>
</tr>
</tbody>
</table>

**LEGEND**

- **Protein of interest**
- **DNA**
- **Magnetic bead**
- **Other protein**
- **Antibody**
- **Magnet**
Kit materials

The iDeal ChIP-seq kit for Transcription Factors contains enough reagents to perform the number of chromatin preparations, chromatin immunoprecipitations and DNA purifications, as described in Table 1. Reagents for chromatin size assessment of each batch of chromatin are also included.

Table 1. Number of reactions included in the different references of the iDeal ChIP-seq kit for Transcription Factors

<table>
<thead>
<tr>
<th>Kit reference</th>
<th>Number of chromatin preparations</th>
<th>Number of ChIP reactions</th>
<th>Number of DNA purifications</th>
</tr>
</thead>
<tbody>
<tr>
<td>C01010054</td>
<td>2</td>
<td>10</td>
<td>14</td>
</tr>
<tr>
<td>C01010055</td>
<td>4</td>
<td>24</td>
<td>32</td>
</tr>
<tr>
<td>C01010170</td>
<td>17</td>
<td>100</td>
<td>134</td>
</tr>
</tbody>
</table>

The kit content is described in Table 2. Upon receipt, store the components at the indicated temperatures.

Table 2. Components supplied with the iDeal ChIP-seq kit for Transcription Factors

<table>
<thead>
<tr>
<th>Description</th>
<th>Qty (x10)</th>
<th>Qty (x24)</th>
<th>Qty (x100)</th>
<th>Storage</th>
</tr>
</thead>
<tbody>
<tr>
<td>Protease inhibitor cocktail</td>
<td>38 µl</td>
<td>76.52 µl</td>
<td>325 µl</td>
<td>-20°C</td>
</tr>
<tr>
<td>5% BSA (DNA free)</td>
<td>380 µl</td>
<td>784 µl</td>
<td>3.25 ml</td>
<td>-20°C</td>
</tr>
<tr>
<td>Rabbit IgG</td>
<td>4 µg</td>
<td>8 µg</td>
<td>35 µg</td>
<td>-20°C</td>
</tr>
<tr>
<td>ChIP-seq grade CTCF antibody</td>
<td>4 µg</td>
<td>8 µg</td>
<td>35 µg</td>
<td>-20°C</td>
</tr>
<tr>
<td>ChIP-seq grade H19 imprinting control region primer pair</td>
<td>42 µl</td>
<td>96 µl</td>
<td>400 µl</td>
<td>-20°C</td>
</tr>
<tr>
<td>ChIP-seq grade Myoglobin exon 2 primer pair</td>
<td>42 µl</td>
<td>96 µl</td>
<td>400 µl</td>
<td>-20°C</td>
</tr>
<tr>
<td>Carrier</td>
<td>32 µl</td>
<td>64 µl</td>
<td>270 µl</td>
<td>-20°C</td>
</tr>
<tr>
<td>Glycine</td>
<td>4.4 ml</td>
<td>8.8 ml</td>
<td>38 ml</td>
<td>4°C</td>
</tr>
<tr>
<td>Shearing Buffer iS1b</td>
<td>3.4 ml</td>
<td>6.64 ml</td>
<td>31 ml</td>
<td>4°C</td>
</tr>
</tbody>
</table>
DiaMag protein A-coated magnetic beads | 300 µl | 720 µl | 3 ml | 4°C
--- | --- | --- | --- | ---
Wash buffer iW1 | 3.5 ml | 8.4 ml | 42 ml | 4°C
Wash buffer iW2 | 3.5 ml | 8.4 ml | 42 ml | 4°C
Wash buffer iW3 | 3.5 ml | 8.4 ml | 42 ml | 4°C
Wash buffer iW4 | 3.5 ml | 8.4 ml | 42 ml | 4°C
ChIP-seq grade water | 14 ml | 26.6 ml | 110 ml | 4°C
Elution Buffer iE2 | 64 µl | 144 µl | 600 µl | 4°C
Fixation buffer | 4 ml | 5.6 ml | 26 ml | 4°C
Wash buffer 1 w/o iso-propanol | 900 µl | 2 ml | 8 ml | 4°C
Wash buffer 2 w/o iso-propanol | 900 µl | 2 ml | 8 ml | 4°C
Buffer C | 700 µl | 1.6 ml | 6.7 ml | 4°C
IPure Beads v2 | 180 µl | 385 µl | 1.33 ml | 4°C
Elution Buffer iE1 | 1.5 ml | 3.4 ml | 16 ml | 4°C
5x ChIP Buffer iC1b | 3.4 ml | 6.88 ml | 32 ml | 4°C
Lysis Buffer iL1b | 50 ml | 110 ml | 425 ml | 4°C
Lysis Buffer iL2 | 30 ml | 60 ml | 255 ml | 4°C

**Required materials not provided**

**Materials and Reagents**

- Gloves to wear at all steps
- RNase/DNase-free 1.5 ml tubes
- Formaldehyde, 37%, Molecular Grade
- Phosphate buffered saline (PBS) buffer
- 100% isopropanol
- qPCR SYBR® Green Mastermix
- ChIP/ ChIP-seq grade antibodies – www.diagenode.com
- Fluorescence-based assay for DNA concentration measurement, e.g. the Qubit High Sensitivity assay (Life Technologies #Q32851)
• Cell culture scraper (for adherent cells)

Additional supplies for tissue protocol:
• Protease inhibitor cocktail (Diagenode, Cat. No. C12010011 or C12010012) (100 µl per chromatin preparation)
• Dounce homogenizer with loose and tight pestles (2 ml)
• Scalpel blades
• Petri dishes

Equipment
• DiaMag 1.5 magnetic rack (Diagenode, Cat. No. B04000003)
• Bioruptor® sonication device and the associated microtubes:
  • Bioruptor® Plus (Diagenode, Cat. No. B01020001) and 1.5 ml TPX Microtubes (Cat. No. C30010010) or
  • Bioruptor® Pico (Diagenode, Cat. No. B01060001) and 1.5 ml Bioruptor® Microtubes with Caps (Cat. No. C30010016)
• Refrigerated centrifuge for 1.5 ml, 15 ml and 50 ml tubes
• DiaMag Rotator (Rotating wheel) (Diagenode, Cat. No. B05000001)
• Vortex
• Thermomixer
• Qubit® Fluorometer (ThermoFisher Scientific)
• qPCR cycler

Optional supplies
• Chromatin Shearing Optimization kit - Low SDS (iDeal Kit for TFs) (Diagenode, Cat. No. C01020013)
• 1M Sodium butyrate (NaBu) (Diagenode, Cat. No. C12020010)
• ChIP Cross-link Gold (Diagenode, Cat. No. C01019027)
• RNase cocktail (e.g. Ambion, AM2286A), required for chromatin shearing assessment
• MicroPlex Library Preparation™ kit v2 (Diagenode, Cat. No. C05010012, Cat. No. C05010013, Cat. No. C05010014) or
• iDeal Library Preparation Kit x24 (incl. Index Primer Set 1) (Diagenode, Cat. No. C05010020)
Remarks before starting

1. Cell number

The protocol describes the preparation of a batch of chromatin from approximately 25 million cells which is sufficient for 6 IP reactions, 1 input sample and 1 sample for chromatin shearing assessment. Approximately 4 million cells per IP reaction are used in this standard protocol. The protocol is optimized for the use of 250 µl of sheared chromatin in a total volume of ChIP reaction equal to 350 µl. It is crucial to keep these volumes consistent for optimal results.

Please note that the described protocol uses a prompt direct fixation in a cell culture plate. Fixed and scraped cells cannot be accurately counted. This means that for adherent cells you need to use an approximate estimation of cell number per plate. Alternatively, an additional parallel plate for counting can be prepared. Suspension cells can be counted before the fixation.

Depending on the abundance of the target, the specificity of the antibody, and the amount of cells available, it may be possible to scale up and down the amount of cells per IP and/or start with a smaller or a bigger batch of cells.

For using lower amounts of cells per IP, you can start with a batch of 25 millions of cells (as for a standard protocol) and follow the protocol up to the chromatin shearing step. Then simply dilute the sheared chromatin in shearing buffer iS1b before adding it to the IP reaction. The final volume of diluted chromatin containing the desired amount of cells should be 250 µl per IP reaction.

If starting with an amount of cells different from the standard protocol or if you want to use a higher amount of cells per IP, first determine the number of cells that you will use per IP and the total number of IPs. Fix cells as described in the standard protocol. For cell collection and lysis, scale up or down the volume of iL1b and iL2 buffers using 1 ml of iL1b and 0.6 ml of iL2b per 1 million cells. Define the volume of shearing buffer
iS1b taking into account that you will need:

- 250 µl of sheared chromatin (containing a desired amount of cells) per IP reaction
- 2.5 µl of sheared chromatin per input
- 50 µl of sheared chromatin for chromatin shearing assessment
- Add 5% excess of iS1b

Resuspend the cells in the required volume of shearing buffer iS1b and follow the standard protocol.

Please note that an increased or decreased cell concentration in the shearing buffer may impact the shearing efficiency and an additional optimization of the shearing conditions may be required.

### 2. Tissue amount

The protocol describes the preparation of a batch of chromatin from approximately 200 mg of tissue which is sufficient for 6 IP reactions, 1 input sample and 1 sample for chromatin shearing assessment. Approximately 30 mg of tissue per IP reaction are used in this standard protocol. The protocol is optimized for use of 250 µl of sheared chromatin in a total volume of ChIP reaction equal to 350 µl. It is crucial to keep these volumes constant for optimal results.

Depending on the abundance of the target, the specificity of the antibody and the amount of tissue available, it may be possible to scale up and down the amount of tissue per IP and/or start with a smaller or a bigger batch of tissue.

For using lower amounts of tissue per IP, start with 200 mg of tissue (as for a standard protocol) and follow the protocol up to the chromatin shearing. Then simply dilute the sheared chromatin in shearing buffer iS1b before adding it to the IP reaction. The final volume of diluted chromatin containing a desired amount of tissue should be 250 µl per IP reaction.

If starting with a tissue amount different from the standard protocol or if you want to use a higher amount of tissue per IP, first determine the amount of tissue that you will use per IP and the total number of IPs.
Fix the cells as described in the standard protocol. Follow the standard protocol for tissue fixation, collection and lysis. Do not scale lysis buffers iL1b and iL2. Define the volume of shearing buffer iS1b taking into account that you will need:

- 250 µl of sheared chromatin (containing the desired amount of tissue) per IP reaction
- 2.5 µl of sheared chromatin per input
- 50 µl of sheared chromatin for chromatin shearing assessment
- Add 5% excess of iS1b

Resuspend the tissue in the required volume of shearing buffer iS1b and follow the standard protocol.

Please note that the increased cell concentration in the shearing buffer may impact the shearing efficiency and an additional optimization of the shearing conditions may be required.

When harvesting cross-linked chromatin from tissue samples, the yield of chromatin can vary significantly between tissue types. Usually, the amount of chromatin to be used per IP is 3-10 µg. We recommend performing a pilot experiment to determine the optimal amount of tissue. Once determined, it should be kept consistent between experiments.

3. Fixation optimization

Formaldehyde is the most commonly used cross-linking reagent ideal for two molecules which interact directly. The fixation time can depend on your target of interest and might require an additional optimization (usually between 10 and 20 minutes). Please note that a longer fixation may lead to chromatin resistant to sonication.

However, for higher order and/or dynamic interactions, other cross-linkers should be considered for efficient protein-protein fixation, e.g. Diagenode ChIP Cross-link Gold, an innovative dual cross-linking ChIP fixation reagent (Diagenode, Cat. No. C01019027).
4. Shearing optimization

Chromatin shearing is one of the most critical steps for a successful ChIP experiment. Chromatin fragments between 100-600 bp are ideal for ChIP experiments. The optimal time of sonication depends on many factors, like cell type, cell density, sample volume, fixation time, etc. Hence it is important to optimize the sonication conditions for each new ChIP project. For optimization of the shearing conditions, we recommend using the Chromatin Shearing Optimization kit - Low SDS (iDeal Kit for TFs) (Cat. No. C01020013) which contains all buffers needed for chromatin preparation compatible with the iDeal ChIP-seq kit for TF. The reagents included in this kit allow preparing chromatin using already optimized shearing settings only; it does not contain sufficient reagents for optimization of chromatin shearing.


Choose the shortest sonication time resulting in an efficient chromatin shearing. Avoid over-sonication, as it may lead to a drop in efficiency in ChIP experiments, especially when non-histone proteins are to be evaluated by ChIP.

5. Magnetic beads

This kit includes DiaMag Protein A-coated magnetic beads and IPure beads v2. Make sure the beads do not dry during the procedure as this will result in reduced performance. Keep the beads homogenously in suspension at all times when pipetting. Variation in the amount of beads
will decrease reproducibility. Do not freeze the beads.

DiaMag Protein A-coated magnetic beads are suitable for immunoprecipitation of rabbit polyclonal antibodies, mouse IgG2a, IgG2b and IgA, guinea pig IgG, dog IgG, pig IgG.

6. ChIP/ChIP-seq grade antibodies

The quality of antibodies used in ChIP/ChIP-seq is essential for success. It is recommended to use only validated antibodies, specifically recognizing the target. Diagenode offers extensively validated and high-performance antibodies, confirmed for their specificity in ChIP/ChIP-seq. Each batch is validated, and batch-specific data are available on the website www.diagenode.com

7. Input

The input sample corresponds to whole DNA which went through the full ChIP procedure without any immunoselection. The input sample is used as a reference to calculate the recovery at the end of the ChIP procedure. It is also used by most of the bioinformatics tools for analysis of ChIP-seq data where it serves to determine the bias which may result from experimental conditions. We recommend including one input for each chromatin preparation.

8. Negative and positive controls

The kit contains a negative (IgG) and a positive (CTCF) control antibody to monitor the efficiency of the IP on the same chromatin as the one used with the antibody of interest. We recommend including one negative IgG control in each series of ChIP reactions. We also recommend using the positive control ChIP-seq grade CTCF antibody at least once.

The kit also contains qPCR primer pairs for amplification of a positive and negative control target for CTCF in Human (H19 imprinting control region and Myoglobin exon 2, respectively).
9. Quantification

After the ChIP, determine the concentration of the IP’d DNA with a highly sensitive method such as the dsDNA HS Assay Kit on the Qubit® system from ThermoFisher Scientific. PicoGreen® is also suitable but UV spectrophotometric methods such as the NanoDrop are usually not sufficiently sensitive. In most cases it is sufficient to use approximately 10% of the IP’d material for quantification. The DNA yield will be dependent on different factors such as cell type, quality of the antibody used and antibody target. The expected DNA yield obtained with the positive control CTCF antibody on 4,000,000 HeLa cells is approximately 20 ng.

10. Quantitative PCR analysis

Prior to the sequencing, we recommend analysing the input and immunoprecipitated samples by SYBR® Green qPCR using at least 1 positive and 1 negative control region to determine the enrichment. The kit contains two primer pairs targeting two regions which are positive (H19 imprinting control region) and negative (Myoglobin Exon 2) for the control antibody provided in the kit (CTCF ChIP-seq grade antibody). Each specific antibody will require specific control primers designed by the user. For each primer pair, run the input DNA alongside the immunoprecipitated samples. In order to have sufficient DNA left for sequencing, we recommend not using more than 10% of the total IP’d DNA for qPCR. You can dilute the DNA (1/10 or more) to perform sufficient PCR reactions. PCR reactions should be performed at least in duplicate although performing in triplicate is recommended to be able to identify potential outliers.
STEP 1 - Cell collection and DNA-protein cross-linking from cultured cells  
STEP 2 - Cell lysis and chromatin shearing from cells  
STEP 1 - Tissue disaggregation and DNA-protein cross-linking  
STEP 2 - Cell lysis and chromatin shearing derived from tissue samples  
STEP 3 - Magnetic immunoprecipitation  
STEP 4 - Elution, decross-linking and DNA purification  
STEP 5 - Quantitative PCR analysis
Protocol

The iDeal ChIP-seq kit for transcription factors is suitable for chromatin preparation and immunoprecipitation from cells and tissues. The protocol for Step 1 "DNA-protein cross-linking" and Step 2 "Cell lysis and chromatin shearing" differs for cells and tissues. Please refer to the corresponding section. Starting from Step 3 "Magnetic immunoprecipitation", the protocol is identical for both sample types.

The protocol below describes the chromatin preparation (formaldehyde cross-linking, cell collection, lysis and chromatin shearing) from a batch of approximately 25 million cells or 200 mg of tissue. This will be sufficient for 6 ChIP reactions (using approximately 4 million cells or 30 mg of tissue per IP), 1 input and 1 sample for chromatin shearing assessment.

Please note that the described protocol uses a prompt direct fixation in a cell culture plate. Fixed and scraped cells cannot be accurately counted. This means that for adherent cells you need to use an approximate estimation of cells number per plate. Alternatively, an additional parallel plate for counting can be prepared. Suspension cells can be counted before the fixation.

If using a different amount of starting material and/or different amount of material per IP, please refer to "Remarks before starting".
STEP 1

Cell collection and DNA-protein cross-linking from cultured cells

FOR CULTURED CELLS

1.1. Equilibrate the Fixation Buffer to room temperature before use.

1.2. Prepare the cross-linking solution in a fume hood by adding formaldehyde to the Fixation Buffer to a final concentration of 11% (e.g. add 0.596 ml of 37% formaldehyde to 1.407 ml of Fixation Buffer). Add the diluted formaldehyde directly to the cell culture medium in a proportion of 1:10. For a 20 ml cell culture you will need 2 ml of cross-linking solution.

1.3. Incubate the cells for 15 minutes at room temperature with gentle shaking.

**NOTE:** The fixation time might require an additional optimization. Please refer to the “Remarks before starting”.

1.4. Add Glycine to the cell culture medium in a proportion of 1:10 to stop the fixation. Incubate for 5 minutes at room temperature with gentle shaking. Proceed to the next step immediately.

**NOTE:** We strongly recommend using freshly fixed cells for preparation of sheared chromatin prior to ChIP. If not possible, the fixed cells can be stored at -80°C for up to 4 months. To freeze the cells, remove the medium, wash the cells once with 20 ml of PBS. Add another 5 ml of PBS, collect the cells by scrapping and/or centrifugation at 500 x g for 5 minutes and 4°C and discard the supernatant. Store the cell pellet at -80°C.
STEP 2

Cell lysis and chromatin shearing from cells

FOR CULTURED CELLS

For adherent cells:

2.1. Remove the medium and wash the cells once with 20 ml of PBS. Discard the PBS. Keep everything at 4°C or on ice from now on.

2.2. Add 5 ml of cold Lysis buffer iL1b to the plate. Collect the cells by scraping and transfer them into a 50 ml tube.

2.3. Rinse the flask with 20 ml of Lysis buffer iL1b and add this to the 50 ml tube. The total volume of Lysis buffer iL1b should be 25 ml per 25 million cells (for up or down scaling use 1 ml of buffer iL1b per million of cells). Proceed immediately with step 2.4.

For suspension cells:

2.1. Transfer cells into a 50 ml tube. Pellet the cells by centrifugation at 500 x g and 4°C for 5 minutes. Discard the cell culture medium.

2.2. Resuspend the cells in 20 ml of ice-cold PBS, centrifuge at 500 x g and 4°C for 5 minutes and gently discard the supernatant. Keep everything at 4°C or on ice from now on.
2.3. Resuspend the cells in 1 ml of ice-cold lysis buffer iL1b by pipetting up and down several times. Add 24 ml of buffer iL1b to obtain a total volume of 25 ml per 25 million cells (for up or down scaling use 1 ml of iL1b per 1 million cells). Proceed immediately with step 2.4.

2.4. Incubate at 4°C for 20 minutes with gentle mixing on a DiaMag Rotator. Pellet the cells by centrifugation at 500 x g and 4°C for 5 minutes and discard the supernatant. Resuspend the cell pellet in 1 ml of ice-cold Lysis buffer iL2 by pipetting up and down several times. Add 14 ml of buffer iL2 and incubate for 10 minutes at 4°C with gentle mixing on a DiaMag Rotator (for up or down scaling, use 600 µl of buffer iL2 per 1 million of cells).

2.5. Pellet the cells again by centrifugation for 5 minutes at 500 x g and 4°C and discard supernatant.

2.6. Add 8.4 µl of 200x protease inhibitor cocktail to 1.67 ml of Shearing Buffer iS1b. This is a complete Shearing buffer needed for 25 million cells. Keep on ice.

2.7. Add the complete Shearing buffer iS1b to the cell pellet. The cell concentration in the shearing buffer should be 1.5 million of cells per 100 µl of iS1b. Resuspend the cells by pipetting up and down several times and incubate on ice for 10 minutes. Split the cell suspension into aliquots of maximum 300 µl by transferring it to the appropriate sonication microtubes:

- When using the Bioruptor® Plus use 1.5 ml TPX Microtubes (Cat. No. C30010010)
- When using the Bioruptor® Pico use 1.5 ml Bioruptor® Microtubes with Caps (Cat. No. C30010016)

**NOTE:** The maximum volume for shearing with the Bioruptor® is 300 µl per 1.5 ml Microtube. The use of correct type of microtubes is essential for the efficiency of sonication.

2.8. Shear the chromatin by sonication using the Bioruptor®. Choose the protocol which is adapted to your device:

- When using the Bioruptor® Standard or Plus, shear for 10 to 30
cycles [30 seconds “ON”, 30 seconds “OFF”] each at High power setting.

- When using the Bioruptor® Pico shear for 5 to 12 cycles [30 seconds “ON”, 30 seconds “OFF”].

**NOTE:** We recommend performing pilot experiments for each new sample type using the Chromatin Shearing Optimization kit - Low SDS (iDeal Kit for TFs) (Cat. No. C01020013).

2.9. Briefly spin down the liquid in the samples for 15 seconds. Transfer samples to new 1.5 ml tubes and centrifuge at 16,000 x g at 4°C for 10 minutes. Pool the supernatants which contain the sheared chromatin.

2.10. Take an aliquot of 50 µl of sheared chromatin for the shearing assessment. The protocol is described in a separate section “Protocol for chromatin shearing analysis”.

**NOTE:** We recommend analysing the shearing for each batch of chromatin. This step can be omitted when optimal sonication settings for given experimental conditions (cell type, cell number and fixation) have been optimised previously. The analysis of chromatin shearing can be done in parallel with the following steps of the protocol or can be included in the main workflow starting from Step 4.2 (decross-linking). Store the chromatin aliquot at -20°C until analysis.

2.11. Use the chromatin for immunoprecipitation (Step 3 Magnetic immunoprecipitation) or store it at -80°C for up to 2 months.
STEP 1
Tissue disaggregation and DNA-protein cross-linking

NOTE: An additional amount of fixation buffer is required when working with tissues (available separately at Diagenode).

1.1. Equilibrate the Fixation Buffer to room temperature before use.

1.2. Prepare the cross-linking solution in a fume hood by adding **54 µl of 37% formaldehyde** to **2 ml of Fixation buffer** to a final concentration of 1%. Use 2 ml of Fixation buffer for one chromatin preparation.

1.3. Put 200 mg of fresh or frozen tissue in a petri dish on ice. Keep samples on ice at all times and minimize the time of manipulation to prevent sample degradation.

1.4. Chop the tissue into small pieces (between 1-3 mm³) using a scalpel blade and transfer it into a Dounce homogenizer. Add **1 ml of formaldehyde diluted in Fixation buffer**.

1.5. Immediately disaggregate the tissue using a Dounce homogenizer (loose fitting pestle) to get a homogeneous suspension. Set the timer for a total fixation time of **15 minutes** and start deducting the fixation time from this point.

FOR TISSUES

Day 1
30 minutes
1.6. Transfer the tissue suspension into a 15 ml tube. Rinse the Dounce homogenizer with an additional 1 ml of diluted formaldehyde and pool with the sample in the same 15 ml tube.

1.7. Incubate for a total time of \textbf{15 minutes} (starting at step 1.5) at room temperature with gentle rotation on a DiaMag Rotator.

\textit{NOTE}: The fixation time might require an additional optimization. Please refer to the “Remarks before starting”.

1.8. Add \textbf{200 µl} of \textbf{Glycine} to the tissue suspension to stop the fixation. Incubate for 5 minutes at room temperature with gentle mixing on a DiaMag Rotator. Proceed to the next step immediately.

\textit{NOTE}: We strongly recommend using freshly fixed tissue for preparation of sheared chromatin prior to ChIP. If not possible, the fixed tissue can be stored at -80°C for up to 4 months. To freeze the tissue, remove the medium and wash the tissue once with 2 ml of PBS. Store the tissue pellet at -80°C.
STEP 2
Cell lysis and chromatin shearing derived from tissue samples

FOR TISSUES

**NOTE**: An additional 100 µl of protease inhibitors cocktail is required per chromatin preparation – available separately from Diagenode

2.1. Centrifuge samples at 850 x g for 5 minutes at 4°C. Gently discard the supernatant and keep the pellet.

2.2. Wash the pellet with 10 ml of ice-cold PBS and centrifuge samples at 850 x g for 5 minutes at 4°C. Gently discard the supernatant. Keep everything at 4°C or on ice from now on.

2.3. Add 50 µl of 200x protease inhibitor cocktail to 10 ml of ice-cold Lysis buffer iL1b. This is a complete lysis buffer iL1b needed for 200 mg of tissue.

2.4. Add 1 ml of ice-cold complete Lysis buffer iL1b to the pellet and resuspend by pipetting up and down several times. Add the remaining amount of complete buffer iL1b.

2.5. Incubate at 4°C for 20 minutes with gentle mixing on a DiaMag Rotator.

2.6. Pellet the cells by centrifugation at 850 x g for 5 minutes at 4°C and discard the supernatant.

1 Day 1
1 to 2 hours
2.7. Add 50 µl of 200x protease inhibitor cocktail to 10 ml of ice-cold Lysis buffer iL2. This is a complete Lysis buffer iL2 needed for 200 mg of tissue. Add 1 ml of ice-cold complete Lysis buffer iL2 to the cell pellet and resuspend the cells by pipetting up and down several times. Add the remaining amount of complete buffer iL2.

2.8. Incubate at 4°C with gentle mixing on a DiaMag Rotator for 10 minutes.

2.9. Pellet the cells again by centrifugation at 850 x g for 5 minutes at 4°C and discard supernatant.

2.10. Add 8.4 µl of 200x protease inhibitor cocktail to 1.67 ml of Shearing buffer iS1b. This is a complete Shearing buffer needed for 200 mg cells. Keep on ice.

2.11. Add the complete Shearing buffer iS1b to the pellet. Resuspend the cells by pipetting up and down several times and homogenize using a dounce homogenizer (tight pestle). Incubate for 10 minutes on ice.

2.12. Split the cell suspension into aliquots of maximum 300 µl by transferring it to the appropriate 1.5 ml microtubes:

   a. When using the Bioruptor® Plus use 1.5 ml TPX Microtubes (Cat. No. C30010010)

   b. When using the Bioruptor® Pico use 1.5 ml Bioruptor® Microtubes with Caps (Cat. No. C30010016)

   **NOTE**: The maximum volume for shearing with the Bioruptor® is 300 µl per 1.5 ml Microtube. The use of correct type of microtubes is essential for the efficiency of sonication.

2.13. Shear the chromatin by sonication using the Bioruptor®. Choose the protocol which is adapted to your device:

   • When using the Bioruptor® Standard or Plus, shear for 10 to 30 cycles [30 seconds “ON”, 30 seconds “OFF”] each at High power setting.

   • When using the Bioruptor® Pico shear for 5 to 12 cycles [30 seconds “ON”, 30 seconds “OFF”].
**NOTE**: We recommend performing pilot experiments for each new sample type using the Chromatin Shearing Optimization kit - Low SDS (iDeal Kit for TFs) (Cat. No. C01020013).

2.14. Briefly spin down the liquid in the samples for 15 seconds. Transfer samples to new 1.5 ml tubes and centrifuge at 16,000 x g at 4°C for 10 minutes. Pool the supernatants which contain the sheared chromatin.

2.15. Take an aliquot of 50 µl of sheared chromatin for the shearing assessment. The protocol for chromatin shearing analysis is described in a separate section “Protocol for chromatin shearing analysis”.

**NOTE**: We recommend analysing the shearing for each batch of chromatin. This step can be omitted when optimal sonication settings for given experimental conditions (cell type, cell number and fixation) have been optimised previously. The analysis of chromatin shearing can be done in parallel with the following steps of the protocol or can be included in the main workflow starting from Step 4.2 (decross-linking). Store the chromatin aliquot at -20°C until analysis.

2.16. Use the chromatin in immunoprecipitation (Step 3 Magnetic immunoprecipitation) or store it at -80°C for up to 2 months.
STEP 3
Magnetic immunoprecipitation

FOR CELLS AND TISSUES

3.1. Determine the amount of IP reactions to be run including the positive and negative control IPs. Take the required amount of DiaMag Protein A-coated magnetic beads and transfer it to a clean 1.5 ml tube. **30 µl of beads** are needed per IP.

3.2. Prepare **4 ml of 1x ChIP buffer iC1b** by mixing the following reagents:
- 3.2 ml ChIP-seq grade water
- 0.8 ml 5x ChIP buffer iC1b
- 80 µl of 5% BSA

Keep the diluted ChIP buffer iC1b on ice.

3.3. Wash the beads 3 times with **1 ml of ice-cold 1x ChIP buffer iC1b**. To wash the beads, add 1 ml of 1x ChIP buffer iC1b directly to the beads suspension, resuspend the beads by pipetting up and down several times and incubate at 4°C with gentle shaking for **5 minutes**. Spin the tubes and place them in the 1.5 ml Diagenode magnetic rack (DiaMag1.5). Wait for one minute to allow the beads to be captured by the magnet and remove the supernatant. Repeat this 2 times.

3.4. After the last wash, resuspend the beads in **1x ChIP buffer iC1b** adding the original volume of beads (this means 30 µl per IP).

3.5. Take the required number of 1.5 ml tubes (one tube per IP) and add
30 µl of the washed beads to each tube.

3.6. Prepare the ChIP reaction mix as described below for 1 IP. Scale according to the number of IPs including a small excess (0.5 extra reaction).

**NOTE:** Proceed separately with reaction mixes to be used with different antibodies

- 6 µl of BSA
- 1.8 µl 200x protease inhibitor cocktail
- 20 µl 5x iC1b buffer
- (42.2 µl –x µl) ChIP-seq grade water
- Add x µl of ChIP-seq grade antibody

The total volume of the ChIP reaction mix per IP is 70 µl

**NOTE:** The required amount of antibody per IP varies. Check the supplier’s recommendation or perform a titration curve using different amounts of antibody.

Use 1 µg of IgG (negative control antibody) for the negative control IP. If a positive control IP is included in the experiment, use 1 µg of the CTCF positive control antibody.

If required, NaBu (20 mM final concentration) or other inhibitors can be added.

3.7. Add 70 µl of ChIP reaction mix to the individual tubes containing 30 µl of washed Protein A-coated magnetic beads. Incubate the tubes for 2-4 hours at 4°C under constant rotation on the DiaMag Rotator.

3.8. Briefly spin the tubes containing the ChIP reaction mix and add 250 µl of sheared chromatin. Keep aside 2.5 µl of the sheared chromatin at 4°C to be used as an INPUT starting from step 4.2. Incubate the tubes overnight at 4°C under constant rotation on the DiaMag Rotator.

3.9. Perform the washes as follows: briefly spin the tubes and place them in the DiaMag1.5. Wait for one minute and remove the supernatant. Add 350 µl of Wash buffer iW1: gently shake the tubes to resuspend the beads and incubate for 5 minutes on the DiaMag Rotator at 4°C.

3.10. Repeat the washing step as described above once with Wash buffer iW2, iW3 and iW4, respectively.
STEP 4
Elution, decross-linking and DNA purification

FOR CELLS AND TISSUES

**NOTE**: Before the first use of the kit, prepare Wash buffer 1 and Wash buffer 2 by adding an equal volume of isopropanol. Wash buffers 1 and 2 should be stored at 4°C. Never leave the bottle open during storage to avoid evaporation.

4.1. After removing the last wash buffer, add **100 µl of Elution buffer iE1** to the beads, resuspend the beads pellet and incubate for **30 minutes** on the DiaMag Rotator at room temperature.

**NOTE**: If a precipitation is observed in Elution buffer iE1, warm it at 37°C until it becomes clear. This will not impair the reaction.

4.2. Briefly spin the tubes and place them into the DiaMag1.5 magnetic rack. Wait for one minute, transfer the supernatant to a new 1.5 ml tube and add **4 µl of Elution buffer iE2**. At the same time add **97.5 µl buffer iE1** and **4 µl of buffer iE2** to the **2.5 µl INPUT** sample. Incubate for **4 hours** or **overnight** at 65°C with shaking.

**NOTE**: if desired, include a chromatin sample for shearing assessment (from step 2.10 for cells or from step 2.15 for tissues) at this step. Perform decross-linking and DNA purification in parallel with the IP and input samples. Please follow the instructions described in a separate section “Protocol for chromatin shearing analysis”
4.3. Add 2 µl of carrier to each IP and INPUT sample.

4.4. Add 100 µl of 100% isopropanol to each IP and INPUT sample.

   **NOTE:** Following the addition of isopropanol the solution may become cloudy. This is not detrimental to your experiment and will not influence the quality or quantity of your purified DNA.

4.5. Resuspend the IPure beads v2 by vortexing and transfer 10 µl to each IP and INPUT sample.

4.6. Incubate the IP and INPUT samples for 10 minutes at room temperature on the DiaMag Rotator.

4.7. Briefly spin the tubes, place in the DiaMag1.5 magnetic rack, wait 1 minute and discard the buffer.

4.8. Add 100 µl of Wash buffer 1 per tube. Close the tubes and vortex well until the beads pellet is completely resuspended. Incubate for 30 seconds at room temperature. Briefly spin the tubes, place in the DiaMag1.5 magnetic rack, wait 1 minute and discard the buffer.

4.9. Add 100 µl of Wash buffer 2 per tube. Close the tubes and vortex well until the beads pellet is completely resuspended. Incubate for 30 seconds at room temperature. Briefly spin the tubes and place them into the DiaMag 1.5 magnetic rack, wait 1 minute and discard the buffer.

4.10. Spin the tubes again and place them on the DiaMag1.5. Discard the remaining Wash buffer 2 if necessary. Resuspend the beads pellet in 25 µl of Buffer C. Incubate at room temperature for 15 minutes on the DiaMag Rotator.

   **NOTE:** Buffer C is compatible with down-stream applications such as qPCR analysis and library preparation for Next-Generation sequencing.

4.11. Spin the tubes and place them into the DiaMag1.5, wait 1 minute and transfer the supernatant containing the immunoprecipitated DNA into a new labelled 1.5 ml tubes. Discard the beads.
4.12. Place the DNA on ice and take 2 µl of IP’d DNA to determine the concentration with Qubit® dsDNA HS Assay Kit or a similar method.

4.13. Determine the total number of regions to be analyzed by qPCR for each sample. Take the required volume of INPUT and immunoprecipitated samples for qPCR analysis. Take into account that these samples will be diluted 1/10 and 5 µl will be used per PCR reaction.

   **NOTE:** The dilution of samples and the volume per PCR may vary depending on a sensitivity of a Master Mix and qPCR cycler used.

4.14. Store the remaining DNA at -20°C until further use.
STEP 5
Quantitative PCR analysis

FOR CELLS AND TISSUES

NOTE: For each primer pair, run the INPUT DNA alongside the immunoprecipitated samples and negative IgG control.

5.1. Take an aliquot of immunoprecipitated DNA and a corresponding INPUT (step 4.13) and dilute them 1/10 using ChIP-seq grade water.

5.2. Prepare the qPCR mix as follows (20 µl reaction volume using the provided control primer pairs):
- 10 µl of a 2x SYBR® Green qPCR master mix
- 1 µl of primer pair
- 4 µl of water
- 5 µl of diluted IP’d or INPUT DNA

5.3. Use the following PCR program:

NOTE: These conditions may require optimization depending on the type of Master Mix, qPCR system used and user provided primer pair.

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<th>Temperature</th>
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<td>3-10 min*</td>
<td>95°C</td>
</tr>
<tr>
<td>2. Amplification</td>
<td>30 seconds</td>
<td>95°C</td>
</tr>
<tr>
<td></td>
<td>30 seconds</td>
<td>60°C</td>
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<tr>
<td></td>
<td>30 seconds</td>
<td>72°C [acquire fluorescence data]</td>
</tr>
<tr>
<td>3. Melting curve**</td>
<td>Follow qPCR instrument manufacturer recommendations</td>
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</tbody>
</table>

* Please check carefully supplier’s recommendations about Taq polymerase activation time
Include and inspect the melting curves based on the protocols recommended by the qPCR instrument manufacturer to ensure that primer pairs amplify only a single specific product.

5.4. Record the threshold cycles (Ct values) from the exponential phase of the qPCR for the IP’d DNA sample and input for each primer pair.

5.5. Calculate the relative amount of immunoprecipitated DNA compared to INPUT DNA for the control regions (% of recovery) using the following formula:

\[
\text{% recovery} = 2^{(\text{Ct}_{\text{input}} - 6.64) - \text{Ct}_{\text{sample}}} \times 100%
\]

- \(\text{Ct}_{\text{sample}}\) and \(\text{Ct}_{\text{input}}\) are the threshold cycles from the exponential phase of the qPCR for the IP’d DNA sample and INPUT, respectively.
- 2 is the amplification efficiency
- 6.64 is a compensatory factor to correct the input dilution

**NOTE:** This equation assumes that the PCR is 100% efficient (amplification efficiency = 2). For accurate results, the amplification efficiency with given primer pair has to be close to 100% meaning that for each cycle the amount of product is doubles \(E=2\). The real amplification efficiency, if known, should be used. The formula takes into account that 1% of INPUT was used as suggested in the protocol (2.5 μl INPUT vs 250 μl of chromatin per IP). If the amount of INPUT used is different from 1%, an introduction of a compensatory factor in the formula is required to correct the input dilution \(x\) as follows:

\[
\text{% recovery} = 2^{[(\text{Ct}_{\text{input}} - \log_2(X\%) - \text{Ct}_{\text{sample}})]} \times 100%
\]

Where: \(\log_2(x)\) accounts for the INPUT dilution

**Example:** If you use an INPUT of 5 μl from 250 μl of chromatin used per IP, it corresponds to 50 X dilution. The compensatory factor is equal to \(\log_2(50)=5.64\) and the formula to calculate the recovery will be as follows: \%recovery = \(2^{[(\text{Ct}_{\text{input}}-5.64 - \text{Ct}_{\text{sample}})]} \times 100\%\).

5.6. If an expected enrichment over positive loci with a low background is observed, proceed to the library preparation using an appropriate protocol (not supplied with iDeal TF kit).
Library preparation and Sequencing recommendations

The iDeal ChIP-seq for TF protocol has been validated for ChIP-seq on an Illumina®HiSeq Next-Gen sequencer. However, other sequencing systems such as the Illumina®MiSeq or the Life Technologies SOLiD™ systems can also be used.

For library preparation compatible with Illumina® sequencers, we highly recommend using Diagenode kits: MicroPlex Library Preparation Kit v2 (Cat. No. C05010012, 12 indices; C05010014, 48 indices) or iDeal Library Preparation Kit x24 (incl. Index Primer Set 1) (Cat. No. C05010020).

Please, do not hesitate to contact our customer support team if you have any questions about the design of your ChIP-seq experiment or the bioinformatics data analysis.

Contact for Europe, Asia, Oceania and Africa: custsupport@diagenode.com
Contact for North and South America: custsupport.na@diagenode.com
ChIP-seq data analysis recommendations from our bioinformaticians

ChIP-seq data analysis workflow

In the following chapter we will guide you through the basics of ChIP-seq data analysis. We will also provide some examples of software tools suitable for each step. We cite numerous analysis tools, including free and commercial softwares.

1. (Optional step) Trimming: use trimming to get rid of low quality bases and artefacts in the readset, such as adapter contaminations
   a. Cutadapt
   b. Trim Galore!
   c. Trimmomatic

2. Alignment: in this step you will map the reads against a known reference sequence
   a. ELAND
   b. Tmap
   c. BWA
   d. Bowtie2

3. (Optional step) Quality control: you can check the general quality of the sequencing and the alignment
   a. FastQC
   b. Picard Tools

4. Peak calling: during peak calling the software will detect sites of enrichment along the genome
   a. MACS2
   b. SICER
c. ZINBA  
d. PeakRanger  
e. Pyicoteo  
f. MUSIC  
g. SPP  
h. hiddenDomains

After above described basic analysis, the peaks can be analyzed further to get answers to our biological questions. There are countless ways and tools for further analyses, the project goals determine which ones we should pick. Just as in the case of basic analysis, we recommend to thoroughly study the manual of the chosen software tool to understand its purpose and its function. Below we will list a few common analysis types to further process the peaks, along with example tools again.

5. Visualization: the peaks, the reads, and other data (e.g. gene positions) can be displayed in a suitable genome browser  
   a. IGV  
   b. IGB  
   c. USCS Genome Browser

6. Descriptive statistics: the peaks can be described in various useful ways, like how many reads fall into them, what is their number, mean size and significance etc.; these figures are also very useful when you compare datasets  
   a. Peak callers usually provide per peak and/or summary statistics after peak detection  
   b. HOMER  
   c. GREAT  
   d. BEDTools

7. Motif search: especially in the case of TF data peaks frequently occur at specific motifs; therefore identifying these motifs and checking enrichments over them is essential for TF data analysis  
   a. HOMER  
   b. MEME Suit
8. Annotation, Gene Ontology, Pathway analysis: after annotation/GO/Pathway analysis you will get a clear picture about which genomic features or pathways your peaks are associated to, providing an important information about disease mechanisms, the role of DNA binding proteins, or treatment effects
   a. HOMER
   b. GREAT
   c. BEDTools
   d. ReactomePA

9. Comparative analysis: this type of analysis is the obvious choice when you have several datasets from comparable conditions [e.g. treated and untreated cells] or when you want to check the performance of your ChIP-seq by comparing it to a reference; there are many different ways to compare peaks, including checking the overlaps, the correlation of enrichment sizes and performing statistical tests on the peaksets
   a. HOMER
   b. BEDTools
   c. DiffBind

Figure 1. ChIP-seq data analysis workflow
Example of results

Figure 2. Successful chromatin shearing using the Bioruptor® Pico and the iDeal-ChIP-seq for TF.

HeLa cells were fixed with formaldehyde and chromatin was prepared accordingly to the iDeal-ChIP-seq for TF protocol. Samples were sonicated for 8 cycles of 30” ON/30” OFF using the Bioruptor® Pico. A 100 bp ladder was loaded as size standard. Panel A: Fragment size assessment by an agarose gel electrophoresis. Panel B: Fragment size assessment using a Fragment Analyzer (Advanced Analytical).

Figure 3. Chromatin immunoprecipitation analysis using control CTCF antibody

ChIP was performed on human HeLa cells using the control antibodies from the iDeal ChIP-seq kit for Transcription Factors. Sheared chromatin from 4 million cells, 1 µg of the positive control antibody and 1 µg of the negative IgG control were used per IP. Quantitative PCR was performed with
the positive control H19 imprinting control region and the negative control Myoglobin exon 2 primer sets from the kit. The figure shows the recovery, expressed as a % of input (the relative amount of immunoprecipitated DNA compared to input DNA after qPCR analysis).

For the positive control antibody (CTCF) the recovery of the positive control target (H19 imprinting control region) is expected to be approximately 5% although this will depend on the cell type used. The recovery of the negative control target (Myoglobin exon 2 locus) should be below 0.5% as shown in Figure 3.

![Figure 3](image.png)

**Figure 4. ChIP-seq results obtained with the Diagenode antibody directed against CTCF**

ChIP was performed on sheared chromatin from 4,000,000 HeLa cells using the iDeal ChIP-seq kit for Transcription Factors and 1 µg of the CTCF positive control antibody. The IP’d DNA was subsequently analysed on an Illumina HiSeq 2000. Library preparation, cluster generation and sequencing were performed according to the manufacturer’s instructions. The 50 bp tags were aligned to the human genome using the BWA algorithm. Figure 4 shows the peak distribution in a genomic region surrounding the H19 imprinting control region.
Protocol for chromatin shearing analysis

General remarks
We recommend using an agarose gel analysis or the Fragment Analyzer (Advanced Analytical) for the size assessment.

For accurate size determination of the chromatin fragments, reverse crosslinking, including RNase treatment followed by DNA purification, is advised. Size estimation of chromatin fragments without reverse cross-linking is not precise. The presence of the crosslinks retards electrophoretic migration resulting in a misinterpretation of fragment size. RNase treatment significantly reduces background caused by degraded RNA and improves visual assessment of shearing.

Workflow for analysis of sheared chromatin:
- RNase treatment (1h, optional but highly recommended for an accurate size assessment)
- Reverse cross-linking (4h or overnight)
- DNA purification using IPure beads (v.2) (30 minutes)
- Fragment size assessment (agarose gel or Fragment Analyzer) (1 h)

RNase treatment

**NOTE**: RNase cocktail (e.g. Ambion, AM2286A) is not supplied with iDeal TF kit.

1. Take 50 µl of sheared chromatin (step 2.10 for cells or step 2.15 for tissues in the protocol) and transfer to a 1.5 ml microtube.

2. Dilute 1 µl of RNase cocktail (e.g. Ambion, AM2286A) in 150 µl of ChIP-seq grade water.

3. Add 2 µl of diluted RNase cocktail to the aliquot of sheared chromatin.

4. Incubate for 1 hour at 37°C.
Reverse cross-linking

5. Add 50 µl of Elution buffer iE1.

6. Add 4 µl of Elution buffer iE2, mix thoroughly.

7. Incubate samples at 65°C for 4 hours (or overnight).

DNA purification

**NOTE:** The protocol below describes DNA purification using the IPure magnetic beads included in the kit. Other methods of DNA purification (columns-based DNA clean-up, e.g. DiaPure columns from Diagenode or a phenol–chloroform extraction followed by ethanol precipitation) can be used also.

**NOTE:** Before the first use of the kit, prepare Wash buffer 1 and Wash buffer 2 by adding an equal volume of isopropanol. Wash buffers 1 and 2 should be stored at 4°C. Never leave the bottle open during storage to avoid evaporation.

8. Add 2 µl of carrier to the sample.

9. Add 108 µl of 100% isopropanol to the samples.

**NOTE:** Following the addition of isopropanol the solution may become cloudy. This is not detrimental to your experiment and will not influence the quality or quantity of your purified DNA.

10. Resuspend the IPure beads v2 by vortexing and add 20 µl to the sample.

11. Incubate samples for 10 minutes at room temperature on the DiaMag Rotator.

12. Briefly spin the tubes, place in the DiaMag1.5 magnetic rack, wait 1 minute and discard the buffer.

13. Add 100 µl of Wash buffer 1 per tube. Close the tubes and vortex well until the beads pellet is completely resuspended. Incubate for 30 seconds at room temperature. Briefly spin the tubes, place in the DiaMag1.5 magnetic rack, wait 1 minute and discard the buffer.

14. Add 100 µl of Wash buffer 2 per tube. Close the tubes and vortex
well until the beads pellet is completely resuspended. Incubate for 30 seconds at room temperature. Briefly spin the tubes and place them into the DiaMag 1.5 magnetic rack, wait 1 minute and discard the buffer.

15. Spin the tubes again and place them on the DiaMag1.5. Discard the remaining Wash buffer 2 if necessary. Resuspend the beads pellet in 25 µl of buffer C. Incubate at room temperature for 15 minutes on the DiaMag Rotator.

16. Spin the tubes and place them into the DiaMag 1.5, wait 1 minute and transfer the supernatants into a new 1.5 ml tube. Discard the beads.

Fragment size assessment

Analyze the purified DNA on a 1.5% agarose gel. Load around 300 ng of DNA for an optimal separation and visualization. Alternatively, you can use a Fragment Analyzer (Standard Sensitivity NGS Fragment Analysis Kit [DNF-473]).
FAQs

What is the amount of DNA I can precipitate after IP?

The amount of DNA you precipitate largely depends on the antibody and cell type used. With the CTCF control antibody the amount is ~20 ng from 4 million HeLa cells. A typical yield for a transcription factor will be in the range of 1-5 ng.

Can I use iDeal ChIP-seq kit for proteins other than transcriptional factors?

The iDeal ChIP-seq kit for transcription factors is intended for all non-histone proteins, including transcription factors, histone modifying enzymes and other chromatin associated proteins.

Is the included control CTCF antibody compatible with mouse?

The included control CTCF antibody has been raised in rabbit against human CTCF, but it is compatible with mouse and rat.

Are the included controls primers compatible with mouse?

The included control primers are specific for human DNA sequences and will not perform on DNA from other species.

How much antibody is needed per IP?

The amount of antibody needed depends on different factors of which the antibody itself is the most important. Most of Diagenode ChIP-grade antibodies have been tested at different concentrations to determine the optimal amount and the suggested amount of antibody is given in the data sheet. Please note, however, that this can be assay dependent and might need to be optimized for each experimental setting. If the antibodies come from other companies, please refer to the corresponding technical data sheet. If no required amount of antibody is given, we suggest performing a titration experiment. For ChIP-seq it is important to select the amount of antibody which gives the lowest background signal.
What is the binding capacity of DiaMag Protein A-coated magnetic beads?

30 µl of DiaMag Protein A-coated magnetic beads can bind 10 µg of antibody.

What is the specificity of protein A-coated magnetic beads?

Ideal TF ChIP kit contains DiaMag Protein A-coated magnetic beads which allow an efficient capture of rabbit, guinea pig, dog and pig polyclonal and monoclonal Abs, mouse IgG2a, IgG2b and IgA and human IgG1, IgG2 and IgG4. If the antibody of interests belongs to a different class of immunoglobulins (mouse IgG1 and IgG3, rat or goat polyclonal Abs, and human IgG3), DiaMag Protein G-coated magnetic beads should be used instead of protein A coated beads. These beads are available separately (C03010021).

Can I use a monoclonal antibody in ChIP experiment?

ChIP can be performed using either monoclonal or polyclonal antibodies. In general, polyclonal antibody populations will recognize a number of different epitopes, in contrast to monoclonal antibodies, which recognize a single epitope. Because monoclonals recognize a single epitope on a target protein, they often provide a high level of specificity, low non-specific binding, and low background signals. The major disadvantage of a monoclonal antibody is its recognition of only one epitope, which can be masked by cross-linking, decreasing the efficiency of immunoprecipitation.

Why do I observe a different DNA size on agarose gel and Bioanalyzer for sheared chromatin?

We recommend using agarose gel or Fragment analyzer (Advanced Analytical) for an accurate size assessment of sheared chromatin.

Although Agilent BioAnalyzer 2100 is widely used for size assessment of DNA fragments before library preparation for NGS, this technology is less optimal for analysis of sheared chromatin. For example, some inconsistencies between agarose gel and BioAnalyzer 2100 profiles have been documented. It may be linked to a higher sensitivity of microfluidics chips to residual contaminants (ions, SDS, proteins, carrier used for DNA
precipitation, etc.), overloading and to conformation/spacial structure of DNA molecules which might be affected by fixation and not fully relieved by de-crosslinking.

Moreover, BioAnalyzer 2100 traces are log-based, so a large distribution of higher molecular weight fragments are compacted into a much smaller area of the trace as compared to the smaller size fragments leading to a visual misinterpretation of fragment distribution.

Another key point is about quantitation of BioAnalyzer 2100 peaks. If each region is calculated using molarity which represent number of molecules in a particular range, a significantly higher level of molecules are found in low molecular weight region (fig. below).

Figure 5. Size assessment of sheared chromatin using an agarose gel and the BioAnalyzer.

HeLa cells were fixed with formaldehyde and chromatin was prepared according to Diagenode’s protocol. Samples were sonicated for 10 cycles of 30” ON/30” OFF with the Bioruptor® Pico using 1.5 ml Bioruptor®
microtubes with caps (C30010016) and analyzed by agarose gel (panel A) or by BioAnalyzer, High sens Agilent DNA kit (panel B). Fragment content below and above 500 bp was calculated as percentage of total surface (panel C). Panel D shows fragment content calculated as molarity (BioAnalyzer trace only).

**What is the composition of buffers included in the kit?**

The composition of the buffers is proprietary.
Related products

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Validated antibodies – check out the complete list at www.diagenode.com

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