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TECH TIPS FOR SUCCESSFUL ChIP EXPERIMENTS

New to ChIP or just want to improve? Our tech tips will help you achieve successful ChIP experiments.





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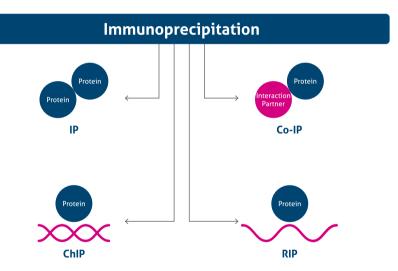




IMMUNOPRECIPITATION TYPES

There are several types of immunoprecipitation:

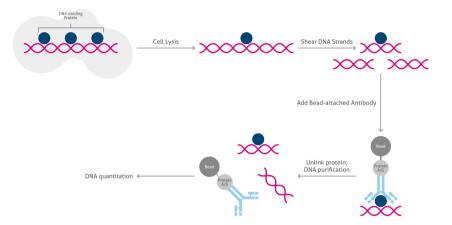
- IP used to isolate a single protein
- Co-Immunoprecipitation (Co-IP)
- Chromatin Immunoprecipitation (ChIP)
- RNA Immunoprecipitation (RIP)





ChIP OVERVIEW

- ChIP provides a live cell picture of the native chromatin structure and factors bound to genes in different functional states.
- ChIP methodology involves protein –DNA cross-linking.
- Isolated, crude chromatin is sonicated to small fragments, usually with an average size of 300–1000 bp.
- Protein-specific antibodies are used to immunoprecipitate fragments of chromatin.





ChIP Tip 1:

Always keep cells/tissue on ice

Temperature is critical. Perform cell lysis at 4°C.
Keep the samples ice-cold and use ice-cold buffers.

ChIP Tip 2:

Under/over cross-linking

Please note: When using paraformaldehyde, ensure that it is freshly prepared (final concentration of 1%–1.5%).

- Under cross-linking can prevent the disassociation of protein–DNA complexes and result in poor yield.
- Over cross-linking can mask epitope sites crucial for antibody binding, prevent chromatin shearing, and inhibit the successful uncross-linking of the protein–DNA complex.



ChIP Tip 3:

Chromatin shearing and sonication

- Avoid large fragments in the tissue suspension.
- Pipette with cut tips for better homogenization.
- Ensure the sonicator probe is not in contact with the tube wall.
- Increase the number of sonication steps; however, avoid increasing the time (or the power) of each step as this may overheat the sample and lead to loss of antigenicity.
- Add ice to the sonicator to avoid the sample overheating.



ChIP Tip 4:

Bead and primary antibody choice (Beads)

- Always fully resuspend beads by vortexing before pipetting. _
- Always store at 4°C and never allow beads to dry out.
- Check the subclass of your antibody is compatible with _ Protein A/G.

| Affinity of human | Species | Subclass | Protein A | Protein G | Binding Capacity: ++++ Strong Binding | |
|---|---------|--|--|---------------------------------|---|--|
| immunoglobulins to Protein A and G The full table of human, mouse, rat and guinea pig immunoglobins can be found in our technical guide "Overview & Technical Tips: Immunoprecipitation". To download click <u>here</u> | Human | IgA IgD IgE IgG ₁ IgG ₂ IgG ₃ IgG ₄ IgM | Variable + + +++++ ++++ - ++++ Variable | - - +++++ ++++ ++++ | +++/++ Medium Binding Variable/- Weak or No Binding | |



ChIP Tip 4:

Bead and primary antibody choice (Antibody)

- Verify your antibody of interest is ChIP validated.
- Insufficient amount of antibody can result in not enough material for successful PCR analysis.
- Too much antibody can increase PCR background.

Negative ChIP controls

- Use non-immune IgG in the IP incubation mix from the same species the antibodies were produced in.
- Incubate IP fraction with beads (without antibody coating).



ChIP Tip 5:

IP efficiency in reverse cross-linking IP

Usually, a 15-minute incubation at 95°C is sufficient.
Some samples require Proteinase K treatment for four or more hours at 65°C.

ChIP Tip 6:

DNA elution and purification

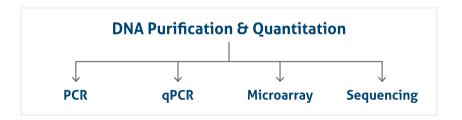
- Use different washing buffers (low & high salt, LiCl nd TE buffers).
- While using a commercial purification column, check the column is completely dry after the wash step as any leftover moisture will inhibit elution.
- Make sure the elution buffer is placed directly onto the silica membrane and allowed to adsorb for at least one minute.



ChIP Tip 7:

Analysis on Immunoprecipitated DNA

- To avoid variations between replicates, add the same amount of protein G/A-agarose or magnetic beads for all samples. Ensure beads are well suspended while pipetting.
- Complete the elution of chromatin from protein G/A beads. Elution is optimal at 65°C with frequent mixing to keep beads suspended in solution (~10 minutes).



Please note: A weak PCR signal or no DNA amplification shown in the samples may be due to an inadequate primer result in the PCR amplified region spanning the nucleosome-free region.

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