ChIP-seq (Chromatin Immunoprecipitation Sequencing)
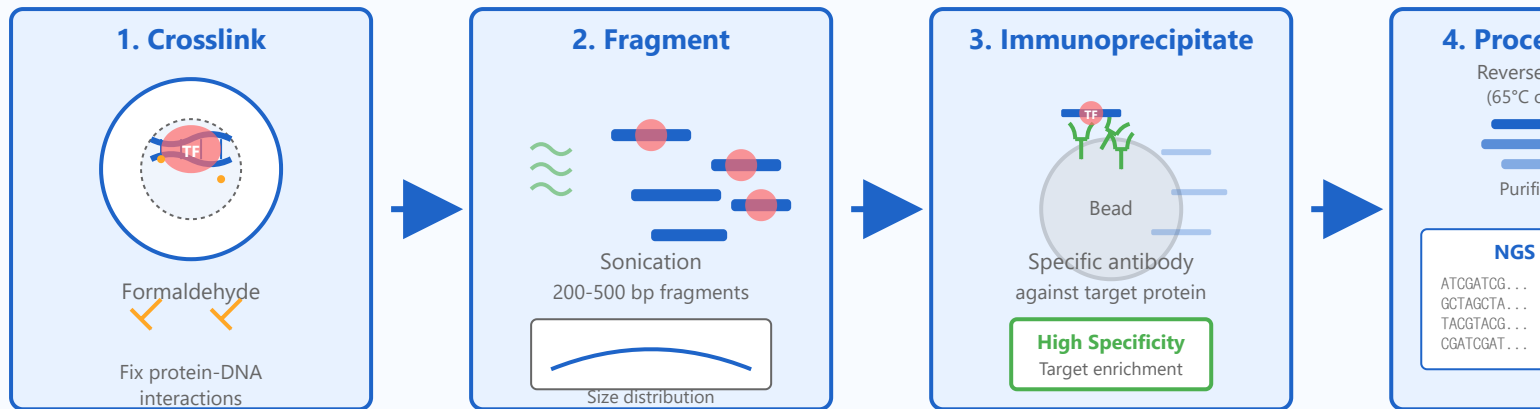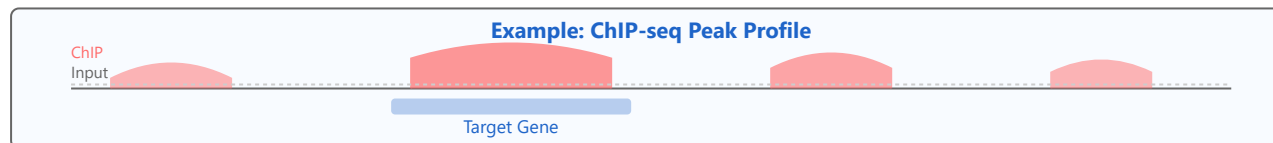
ChIP-seq Mechanism and Workflow

ChIP-seq: Mapping Protein-DNA Interactions

1. Crosslink

TF

Formaldehyde

Fix protein-DNA interactions

2. Fragment

Sonication
200-500 bp fragments

Size distribution

3. Immunoprecipitate

TF

Bead

Specific antibody against target protein

High Specificity
Target enrichment

4. Proce

Reverse
(65°C o

Purifie

NGS
ATCGATCG...
GCTAGCTA...
TACGTACG...
CGATCGAT...

ChIP-seq Data Analysis Pipeline

Read Alignment
Map to genome
(BWA, Bowtie2)

→

Peak Calling
Find enriched regions
(MACS2, SICER)

→

Annotation
Assign to genes
(ChIPseeker)

→

Motif Analysis
Find binding motifs
(HOMER, MEME)

→

Visualization
Browser tracks
(IGV, deepTools)

Example: ChIP-seq Peak Profile

ChIP
Input

Target Gene

Common Targets

• Transcription factors (TFs)
• H3K4me3 (active promoters)
• H3K27ac (active enhancers)
• H3K27me3 (repression)

Critical Controls

• Input DNA (no IP)
• IgG control (non-specific)
• Biological replicates
• Technical validation

Requires high-quality antibodies and proper controls for reliable results