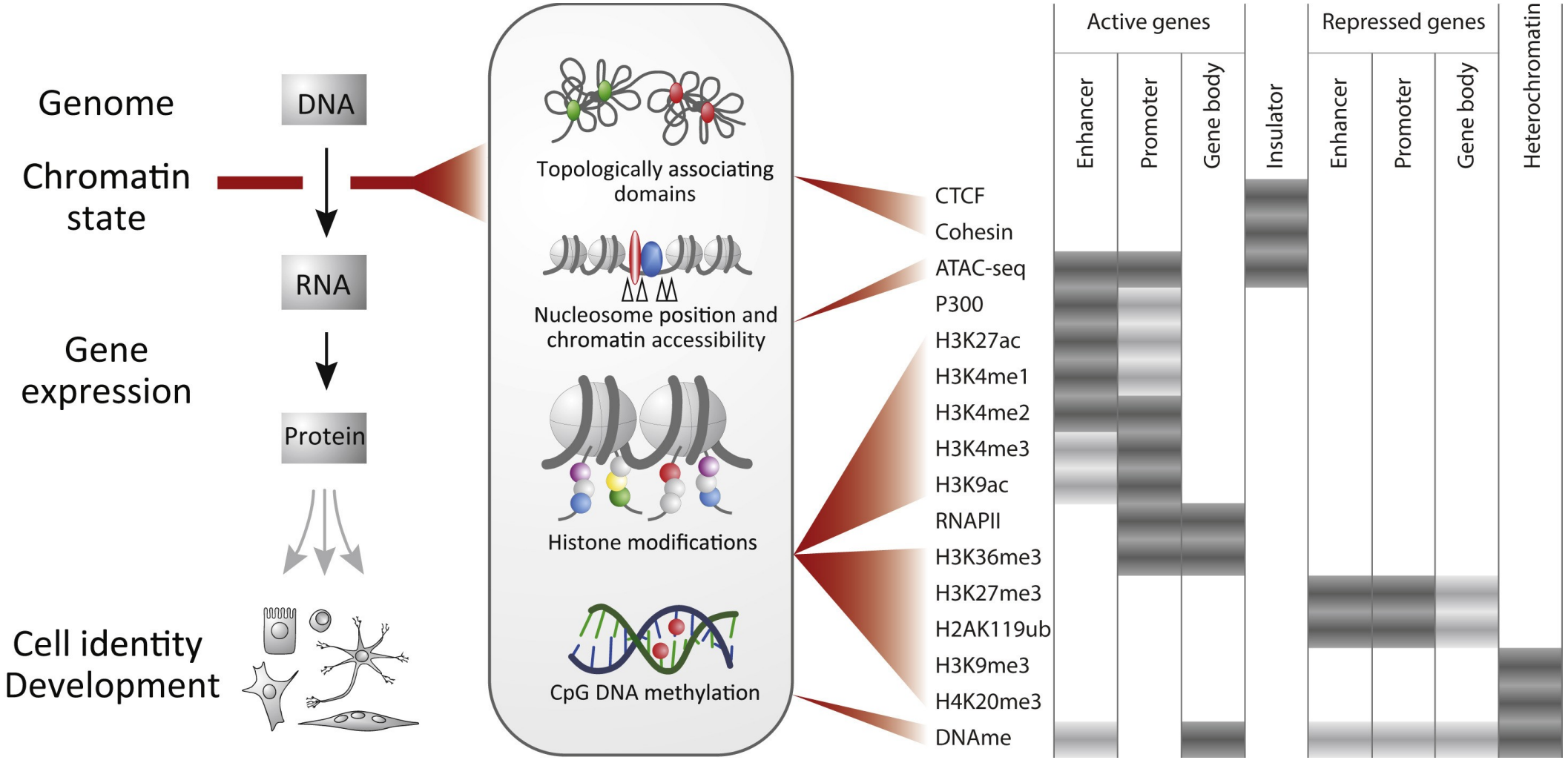

The role of chromatin as a filter for genomic information in gene expression and the determination of cell identity

Chromatin acts at various scales of size, from top:

- Topological organization of chromatin (different colors represent A and B compartments)
- Chromatin accessibility (triangles represent chromatin accessibility, gray spheres represent nucleosomes)
- Histone modifications (colored spheres represent modified histone H3 residues)
- DNA methylation (methyl-cytosine indicated in red)

Chromatin modifications and binding of different factors.

- CTCF and Cohesin are involved in the organization of chromosomal loops
- ATAC sequencing (indicated) and DNase I sequencing (not shown) can be used to assess chromatin accessibility
- The p300 coactivator protein acetylates H3K27 and is mainly found at enhancers. RNAPII causes deposition of H3K36me3 in actively transcribed genes.

Lighter gray shades indicate a lower or variable degree of factor binding, histone-tail modification or DNA methylation (DNAme). For DNAme, light gray indicates that the sequence could be either methylated or unmethylated depending on the example considered. H3K27me3-repressed genes tend to be unmethylated. Active promoters tend to be unmethylated unless they have a low CpG density.

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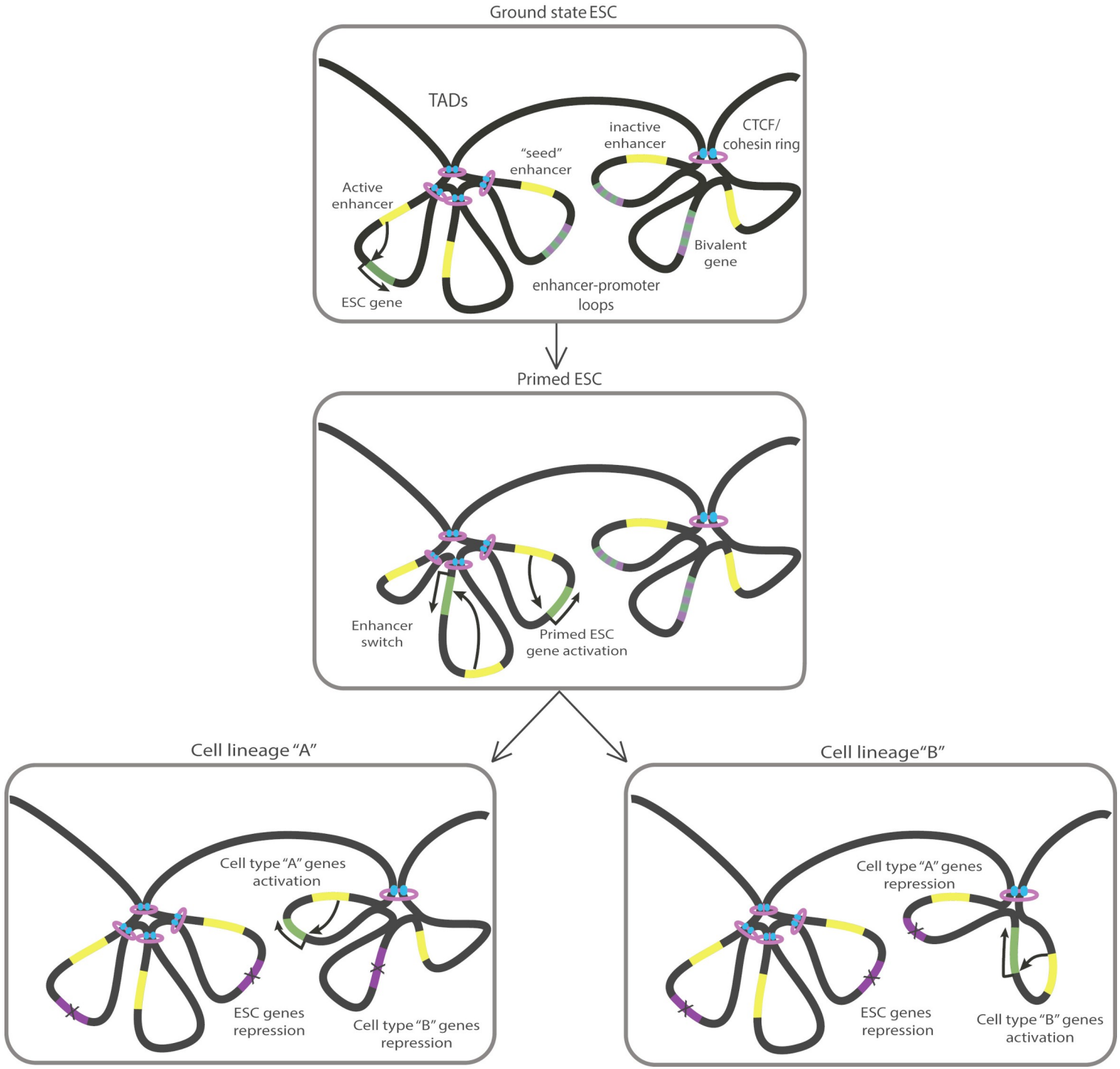

Enhancer usage during ESC differentiation

"Ground-state" ESCs achieve expression (green) of pluripotency genes through specific enhancer clusters or super-enhancers (yellow), while differentiation genes are repressed or in a bivalent state (green and purple). The blue dots and purple ring represent CTCF and Cohesin holding the chromatin loop together.

In primed ESC genes, expression of pluripotency-associated genes is often achieved via a switch in enhancer usage, which also may involve local loop rearrangement. Additional primed ESC genes may also start to be expressed.

Upon cell-fate determination, lineage-specific genes are activated while pluripotency-associated and alternative-fate genes lose active marks and acquire a repressive chromatin environment (purple genes with black cross).

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