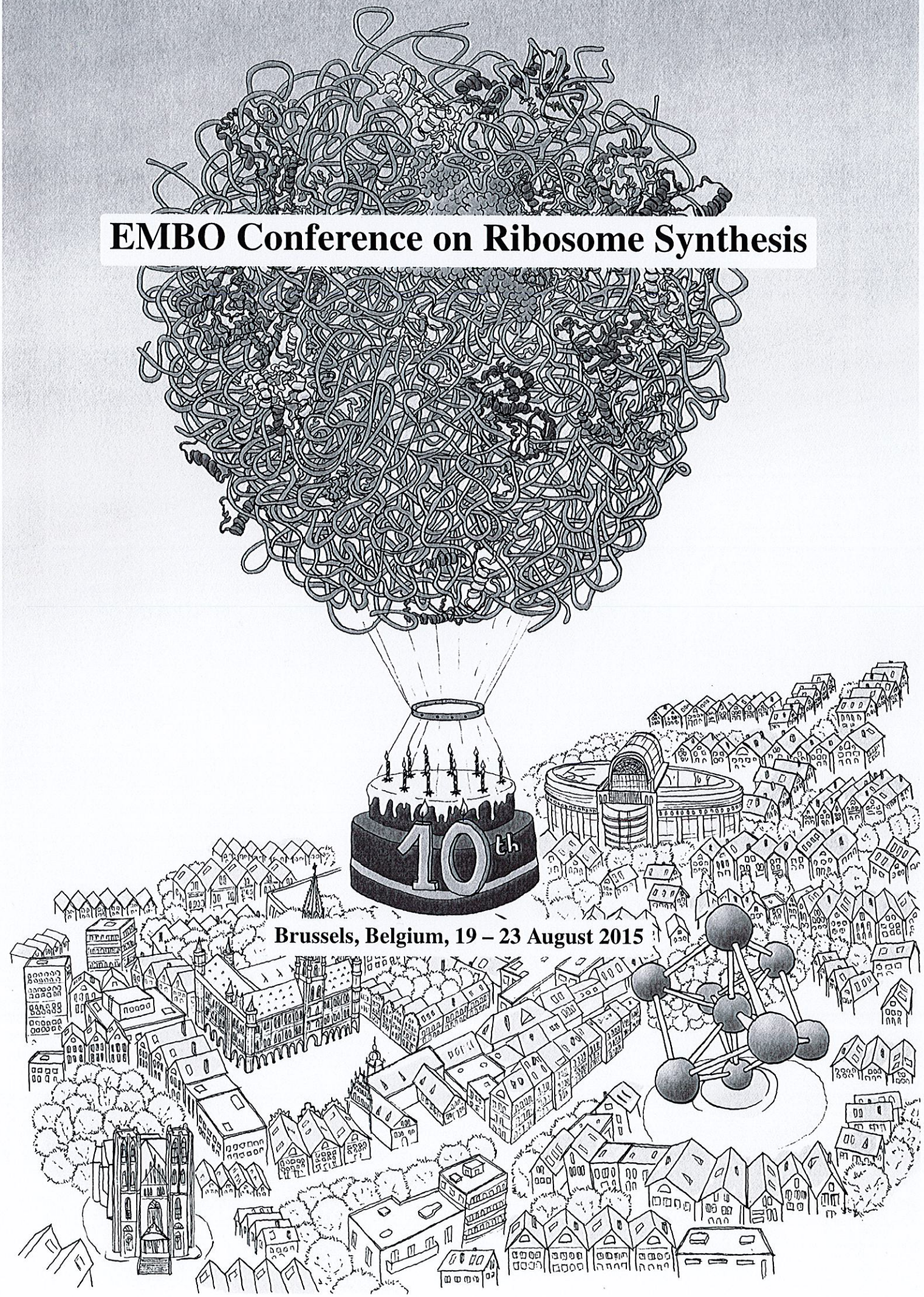
EMBO Conference on Ribosome Synthesis



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105. **Link between organization and transcription of Ribosomal RNA genes in mouse growing oocytes and at the very beginning of embryonic development.**

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During the final stages of mouse oogenesis, large-scale modifications occur in the nucleus of fully-grown oocytes and are correlated with transcriptional silencing. Indeed, while oocytes with un-condensed chromatin (NSN) are able to synthetize rRNA, more advanced oocytes with dense chromatin around the nucleolus (SN) are transcriptionally silent. Conversely, transcription of ribosomal genes (rDNA) is switched off in 1-cell stage embryos and then rRNA synthesis starts at the end of the 2-cell stage. In this context, we have investigated the organization of rDNA with 3D-FISH (Fluorescent In Situ Hybridization on 3D-preserved nuclei) approaches. We have also examined the relative position of these genes with regards to pericentromeric heterochromatin domains. We observed that in SN oocytes, in 1-cell and early 2-cell stages embryos (when rDNAs are not transcribed), the ribosomal sequences are clustered in highly condensed foci and juxtaposed to major satellite sequences which formed a discontinuous ring around nucleolus-like structures. On the other hand, in NSN oocytes, at the late 2-cell stage and further stages of embryonic development (when rRNA are transcribed), ribosomal sequences form necklace structures and are less in contact with pericentromeric regions. These results suggest a close link between the spatial organization (relaxed or clustered) of ribosomal genes sequences and their transcriptionnal states (active or silent).