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## Regulatory Networks in Gene Expression: From the Genome to the Organism

<b>Status</b>	Past
<b>Competition</b>	Competition II
<b>Sector</b>	Health
<b>Genome Centre</b>	Genome Quebec
<b>Project Leaders</b>	Benoit Coulombe

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### Project Description

At the onset of this research program in 2002, the scientific community was entering the post-genomics era armed with a wealth of information on the sequence of the human genome that encodes the information required for RNA and protein synthesis. However, little was known about the regulatory information necessary to specify what sets of genes and proteins are expressed under specific conditions during growth and development – not only in normal development, but in processes leading to disease states.

The main objective of this program was to develop and use expertise and technologies for uncovering the regulatory potential of the human genome and deciphering the networks of protein-DNA and protein-protein interactions that regulate cell growth and differentiation.

Our unique approach has generated a wealth of information on the regulatory networks involved in gene transcription in normal development and in processes leading to diseases such as prostate cancer and HIV infection. Many novel proteins have been identified and future experiments are being planned to characterize their role in processes leading to disease.

Through the course of this project, we've developed a wealth of information, know-how, and tools including protocols, methodologies, microarrays, and bioinformatics algorithms and databases. In particular, our microarrays have generated a significant amount of interest within the scientific community and we are evaluating their commercial potential.

Our discoveries and advances in science and technology have added a tremendous amount of knowledge to the field of transcriptional regulation, and have accelerated research in genomics, proteomics and bioinformatics. The identification of novel therapeutic targets is anticipated to translate into social benefit and commercial and economic development through drug discovery.

## **Fast Facts**

**Highlighted outcome:** wealth of information on the regulatory networks involved in gene transcription in normal development, and in processes leading to diseases such as prostate cancer and HIV infection

**Number of research personnel employed by the project:** 58

**Number of peer reviewed publications published:** 25 papers and 111 invited presentations

**Resources generated for drug discovery:**

- set of regulatory models represents the best available repertoire of human regulatory sequences
- first to define novel modes of action and physiological functions for nuclear receptors
- definitions of novel interfacing partners in protein complexes and novel proteins

**Co-Funders:** Province of Quebec