

Stephen QUAKE

Head of Science at the Chan Zuckerberg Initiative and Lee Otterson Professor at Stanford University

Understanding the mysteries of the cell

12 & 26 May 2025

COLLÈGE DE FRANCE **Thomas Römer** Administrateur du Collège de France 11, place Marcelin-Berthelot, 75005 Paris www.college-de-france.fr

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Hosts: Edith Heard, Thomas Lecuit and Hugues de Thé

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12 May 2025

Amphithéâtre Maurice Halbwachs, 17h-18h

Understanding the mysteries of the cell: how do many cell types arise from one genome?

Although the genome is often called the blueprint of an organism, it is perhaps more accurate to describe it as a parts list composed of the various genes that may or may not be used in the different cell types of a multicellular organism. Although nearly every cell in the body has essentially the same genome, each cell type makes different use of that genome and expresses a subset of all possible genes. This has motivated efforts to characterize the molecular composition of various cell types within humans and multiple model organisms, both by transcriptional and proteomic approaches. We used single cell transcriptomics to create a human reference atlas comprising more than one million cells from 24 different tissues and organs, many from the same donor. This atlas enabled molecular characterization of more than 400 cell types, their distribution across tissues, and tissue-specific variation in gene expression, and provides an experimental basis to understand the cell type diversity which can be generated from a single genome.

26 May 2025

Amphithéâtre Maurice Halbwachs, 17h-18h

Understanding the mysteries of the cell: how do mutations arise in our bodies?

The question of how heritable mutations arise is one of long-standing interest in biology. In the case of bacteria, there was a debate about whether mutations arise as a consequence of adaptation to selective pressure from the environment, or whether they are pre-existing in populations even in the absence of such selective pressure. This was famously resolved as the latter by Luria and Delbruck. Genomic technologies now allow us to ask similar questions in humans. How is genetic diversity generated and what are the consequences? How do mutations acquired during the course of our life sometimes lead to cancer, and can we understand the evolutionary history of a tumor? My lecture will discuss these issues and illustrate how we have used single cell genomics to provide answers to some of these questions.