

# PROF. HENRIK KAESMANN

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<b>PROJECT TYPE</b>	ERC Starting Grant (FP7)
<b>TITLE</b>	Sex-biased genome and transcriptome evolution in mammals
<b>ACRONYM</b>	SexGenTransEvolution
<b>DURATION</b>	01.02.2010 – 31.01.2015
<b>BUDGET</b>	1 901 522 €

Gene expression changes may underlie much of phenotypic evolution. The development of high-throughput RNA sequencing protocols has opened the door to unprecedented large-scale and cross-species transcriptome comparisons by allowing accurate and sensitive assessments of transcript sequences and expression levels.

In the framework of our ERC Starting Grant-funded projects, in which we produced unprecedented cross-mammalian transcriptome datasets for various organs using state-of-the-art RNA sequencing protocols, we have unveiled commonalities and differences in the dynamics of gene expression evolution for various types of coding and non-coding genes across mammalian lineages, organs, chromosomes and sexes.

Our work has thus also provided intriguing new clues to the regulatory basis and phenotypic implications of evolutionary gene expression changes.