



SFB1425 - Heterocellular Nature of Cardiac Lesions: Identities, Interactions, Implications

# P01: Post-doc Project

based at the

## MPI of Immunobiology and Epigenetics

### *Tracking Spatio-Temporal Dynamics of Scar Formation at Single-Cell Resolution*

#### Background

Understanding the process of cardiac lesion development requires detailed knowledge of the constituent cell types of the healthy heart, as well as of the cell types from intra- and extra-cardiac sources that contribute to scar formation. To develop therapeutic approaches targeting scar properties to minimise perturbations of cardiac function, the identification and characterisation of cellular constituents of scar tissue, their spatial interrelation, and the dynamics of lesion remodelling over time are fundamental prerequisites.

#### Project Description

The first goal of this project is the establishment of a large-scale spatial cell type atlas of the healthy adult mouse heart. This will be achieved by integrating single-cell RNA-seq with high-resolution spatial gene expression analysis using multiplexed single-molecule fluorescence in situ hybridisation (seqFISH). By applying bioinformatic analysis, co-localisation and putative interactions of cell types will be deciphered. This resource will serve as the reference for investigating peculiarities of cell types and cellular states during lesion development in mouse heart damage models.

#### Qualifications and Requirements

- High motivation to work on a state-of-the-art research topic in a highly dynamic, interdisciplinary and supportive environment
- Solid background in molecular biology, tissue handling, next generation sequencing and/or tissue imaging
- Prior experience in bioinformatics is a plus
- Excellent PhD in a field relevant for the proposed study
- English language proficiency at level B2 or higher

#### Research Areas

Single-cell RNA-seq, single-cell resolution tissue imaging, bioinformatics

#### Experimental Tasks

- Single-cell RNA-seq of healthy and damaged heart tissue
- In situ analysis of tissue composition by multiplexed single-molecule FISH (seqFISH)
- Integration of single-cell RNA-seq and seqFISH imaging data to decipher cell type co-localisation and inter-cellular crosstalk.

#### Background

Molecular Biology, Next generation sequencing, Tissue Imaging, Bioinformatics

#### Starting Date

from 01/07-2020

#### Advisor

Dominic Grün, Max Planck Institute of Immunobiology and Epigenetics  
[gruen@ie-freiburg.mpg.de](mailto:gruen@ie-freiburg.mpg.de)

#### Contact

[info@sfb1425.uni-freiburg.de](mailto:info@sfb1425.uni-freiburg.de)

#### Applications via

[info@sfb1425.uni-freiburg.de](mailto:info@sfb1425.uni-freiburg.de)