Introduction
Cellular therapies are increasingly relevant for personalized medicine, requiring resources informing about the complex characteristics of cells. Large amounts of research data on stem cells are already available, but these are scattered, derived by diverse technologies, not standardized and are not available at the necessary integration level for cellome modelling. Consequently, the selection of cells, e.g. for therapeutic applications, is based on rather incomplete information.

CellFinder aims at mapping stem cell information to lift the cellome to an even level with the other ‘omics’ fields to provide a basis for global understanding of cells, increase comparability of data and relate cells to more complex systems. One major aim of CellFinder is to be able to collect data on cell development and to organize it into the developmental tree of the organism (Figure 1).

Methodology
To organize the data stored in CellFinder we have developed a novel ontology, the CellFinder Ontology (CFO, Figure 2). The CFO core ontology links other existing ontologies like the Cell Ontology, Foundational Model of Anatomy (FMA), Gene Ontology (GO), BioTop Ontology and others. The design of the CFO core includes a multi-species concept (human, rodent, fish…), the multi-layer concept (in vivo / in vitro) and the multi-domain concept (stem cell biology, genetics, medicine…).

It allows annotation of data from the organ down to single cell level in relation to their respective development stages and mapping of homologous entities between species. This way it is able to map developmental data like cell lineage differentiation (Figure 2).

Future development includes community and scientific networking applications that will allow users to store and analyse their own data and to explore cells and their interactions on singular and complex resolution levels.

Outlook
Current work concentrates on the integration of existing cell biology datasets to assimilate the diverse dimensions of data spanning molecular, functional, anatomical and cyto-histological, as well as auxiliary levels. The CellFinder repository will aid standardization and comparability of complex datasets for each cell and organize these in a cellome environment by ontological description and technical implementation. Future development includes community and scientific networking applications that will allow users to store and analyse their own data and to explore cells and their interactions on singular and complex resolution levels.

http://www.Cell-Finder.org