



**Project Summary:** The overall aim of this platform is to support various translational aspects of the CRC128. In particular, we pursue the following approaches:

- Provide a platform for „proof-of-concept“ clinical studies (association with project A08)
- Present a translational platform for support of single scientific projects in order to strengthen their translational aspects (examples are A01, A08, A09, B03, B07)
- Provide a service platform in terms of infrastructure as well as biomaterial collection for use in individual scientific projects (examples are A08, A09, A10, B01, B08)

**Methods and approaches:**

One key technique of this platform is highly standardized multi-parameter flow-cytometry based profiling, which can even be performed with frozen PBMC specimen to allow for a standardized analysis of samples in a longitudinal fashion. Besides conventional analysis techniques, we apply unbiased high dimensional analysis of flow cytometry data using different algorithms including tSNE and SPADE, respectively.

To allow for further functional characterization of immune cell subtypes, cytokine profiles as well as cytolytic as well as phagocytic functions and respiratory burst can be assessed. Furthermore, a detailed metabolic analysis of immune cells encompassing mitochondrial respiratory activity, glycolytic function, fatty acid oxidation can be measured in different immune cell subpopulations employing Seahorse technology.

In both CD4 and CD8 T cells, detailed characterization of the T cell receptor repertoire evaluating changes in repertoire diversity, clonality, entropy as well as single clone tracking over time or in different tissues can be provided. Finally, sequencing-based analysis of the transcriptome in cell populations and on a single cell level can be performed (deep immune sequencing).

Besides analysis of peripheral blood-derived immune cell specimen, analysis of CSF material as well as stool (for evaluation of gut microbiome composition) is performed as part of individual projects.

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