

PERSIMUNE SCIENTIFIC ANNUAL REPORT 2022

Annual highlights

2022 was another productive year for PERSIMUNE. A total of 59 papers were published across the fields outlined in the research plan from 2019, 21 of which in high-impact journals (IF>8).

PERSIMUNE was markedly affected by the SARS-CoV-2 pandemic on multiple fronts. In 2022, we worked diligently to return to a less crisis-directed workflow. Additionally, attempts were made to normalize the atmosphere allowing for social interactions, which were suppressed in the preceding two years. Although the pandemic obviously has affected our 2019 research plan, in 2022 we could conclude that the center is actually on track across the many fields we have embraced on. This is a testament to the dedication, motivation and professionalism of the staff affiliated with the center. Below are some highlights:

- PERSIMUNE is developing novel immune tracers. These are radiolabeled peptides binding to specific cellular proteins, that are infused and where cell binding can be visualized on imaging. It is critical to identify the most optimal peptides pre-clinically, and the team has developed a novel screening methodology to identify peptides binding to the CD4 protein. It is expected that this process will be finalized in 2023, so the tracer can be tested in humans in 2024.
- The center has focused on the development of novel analytic methodologies using machine learning. A prototype of a pipeline that allows for large-scale analysis of diverse datasets has been finalized and the first projects published.
- A version 1 of a data catalogue of data within the PERSIMUNE data lake entered the public domain in the end 2022. This feature was required to scale research output across diverse areas of the center's project portfolio, in addition to the ongoing work related to data harmonization and enrichment.
- Expansion of antimicrobial resistance is a major public health concern. At PERSIMUNE, we are focused on how antibacterial medications affect the expression of bacterial resistance genes in the gut microbiome (the resistome). This work is based on the creation of a large biobank and deep phenotyping of the cohort. A bioinformatics pipeline has been developed to highlight functionality of the gut microbiome. At this point, our research focuses on patients undergoing human stem cell transplantation, as such patients receive extensive antibiotic therapy, in part to reduce risk of bacterial infection derived from the transplant. The 13 most frequently used antibiotics were significantly associated with 154 (40% of tested associations) microbiome features. We see a rapid expansion of the project scope within this field to address additional research questions and to other groups of patients.
- Immune and viral deep phenotype profiling of patients hospitalized with COVID-19 identified that the degree of viral replication (using a viral antigen in plasma as a proxy hereof) varied markedly across this population, and prognosis was markedly affected by the degree of viral replication. This insight assisted in rationalizing further research efforts of interventions to improve prognosis, and further developed a precision-medicine approach framework.

Besides the scientific outputs, PERSIMUNE members have engaged in several other activities, such as teaching in the precision medicine MSc program, explaining ongoing research via short videos shared in social media and organizing colloquia where people with interest in personalized medicine can meet, discuss, strengthen collaborations and get inspiration for current and future projects.