

## Summary

Studying the immune system broadens our understanding of the underlying mechanisms contributing to health and disease. Recently, single-cell RNA sequencing (scRNA-seq) has provided an alternative unbiased approach to study gene expression on a single cell-level and has emerged as one of the leading techniques to uncover the immune system's complex networks. It has allowed researchers to discover rare cell types and novel cell states in the immune system and has provided a comprehensive overview of the novel insights in immune cell characteristics, temporal, and spatial distribution as well as cellular function. Here, a review summarizing the current state of research of single-cell transcriptomics is provided, focusing on hematopoietic origin, novel immune cell types in thymus organogenesis, as well as the developing and the adult immune system. Moreover, we highlight the limitations inherent to the scRNA-seq experimental pipeline that propose challenges in advancing our knowledge of the comprehensive immune cell landscape.