

## Abstract

Leukemia is a cancer of hematopoietic cells affecting the whole organism. Currently, there are many treatment options for all disease types, but it is still not always possible to fully cure the patient. The single-cell RNA sequencing method offers a new insight into the heterogeneity of both cancerous and non-cancerous cells in the leukemic environment. This thesis aims to briefly present the method and its history and to highlight current findings about leukemia obtained with the help of it.

## Keywords

leukemia (AML, CML, ALL, CLL), sequencing, scRNA-seq, cells, transcriptome, treatment

Okomentoval(a): [o1]: To the reader se v odborné literatuře moc nepoužívá