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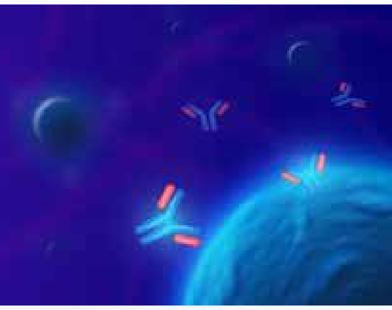
Where data means more

CASE STUDY

Custom annotation of public single-cell data offers opportunities for target identification



Client

Industry
Partner Research Organization

Location
Europe

Specification

The client wanted to uncover and characterize microglia phenotypes for therapeutic target discovery

Our approach

Integrated 6 public single-cell RNAseq datasets followed by clustering, marker gene identification, and differential gene expression analysis to identify transcriptional differences between microglia phenotypes

Results

We provided the client with the identification and characterization of rare phenotypes that were not identified earlier and also the new potential therapeutic targets

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