



# Identifying subpopulations for a personalized treatment

**Armed with the right insights, this company was able to successfully progress personalized treatment strategies for its innovative immune-oncology therapy.**

## Challenge

**Understanding the molecular events of a drug to decide which asset to move forward in a clinical program.**

A medium-sized pharmaceutical company had a multi-layered

need within its immune-oncology research team. Firstly, it wanted to identify immune cell populations with an increased expression level of a particular target. Secondly, it needed to identify patient subpopulations in which its drug may overcome resistance to checkpoint inhibitor therapy.

This information was integral to its research programs by contributing to the development of its personalized

treatment strategies and improving the patient outcomes of those taking its immunotherapy drugs, ultimately leading to healthier patients and commercial gains.

The company, who already had an ongoing relationship with Clarivate™, engaged with the bioinformatics consulting team to put in place several methods to address both aims.

## Solution

### Single-cell RNA sequencing data analysis.

The bioinformatics team used its MetaBase™ and MetaCore™ solutions to study the effects of monotherapy or a combination of drugs the client was developing. It worked to understand molecular events with that drug, for example the upstream triggers that produce the gene expression changes observed in the model. This understanding was facilitated by two techniques; single-cell RNA sequencing (scRNA-seq) and CITE-sequencing analysis.

The scRNA-seq pre-processing and analysis of tumor immune

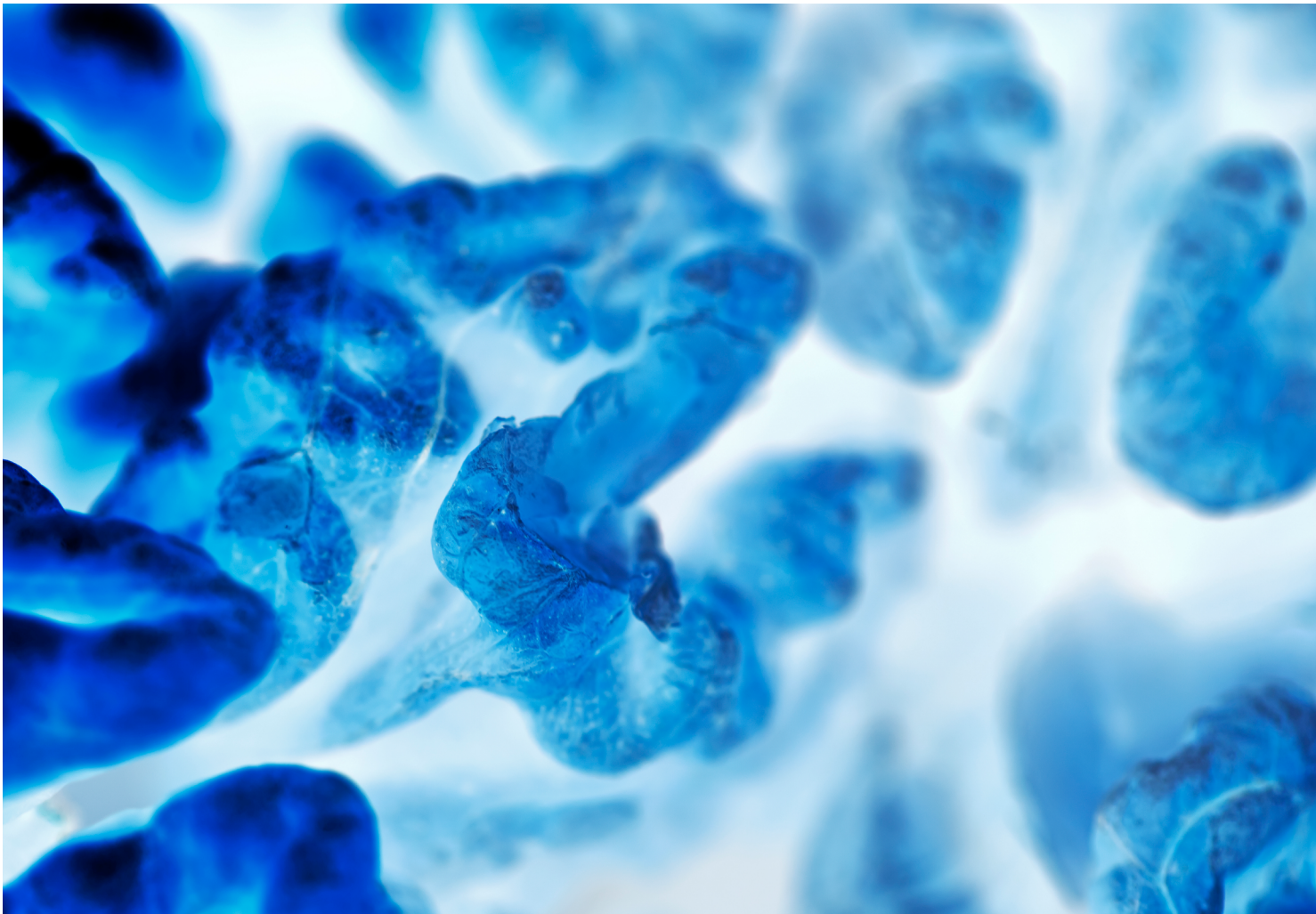
cells from treated mice found changes in proportions of cell types with monotherapy and drug combinations, as well as potential regulators driving transcriptome remodeling mediated by monotherapy and combination therapy.

The client was provided with insights on target expression levels in various immune cell subpopulations within relevant tumor types in addition to hypotheses on the client's drug cell-based mechanism and its interplay with checkpoint inhibitor therapies.

The CITE-seq analysis on tumor samples obtained from human patients undergoing treatment allowed the client to see increased cell annotation accuracy because of the combined protein/RNA approach, the identification of cell clusters enriched or reduced in

patients that experience adverse events, and identified genes transcriptionally enriched or reduced in these cell clusters of interest.

Clarivate also tapped into its analytics expertise, Computational Biology Methods for Drug Discovery (CBDD) and Algorithm Benchmarking Consortium (ABC) groups that bring together industry leaders and innovators to collaborate on the development and implementation of state-of-the-art approaches for network and pathway analyses. These help the client to standardize algorithms, and to benchmark different algorithms in trending topics that are of future interest for its R&D programs. This allows internal resources from bioinformatics divisions to redirect their time on to strategy and innovation.



## Outcome

### Data-driven decisions to progress R&D programs.

The client requested a way to visualize and browse the complex data in a handy way. The Clarivate bioinformatics consulting team provided interactive shinyApps for the visualization of scRNA-seq data, in addition to a comprehensive set

of results to the pharmaceutical company, several Excel tables showing all results and asset prioritization, slides describing the results as an overview, and detailed interactive html reports.

Armed with the insights provided by Clarivate, the pharmaceutical company was able to stratify patients within its clinical trials programs, allowing the study to reflect the population that would benefit the most from an innovative therapy.

**"The data provided has allowed a better understanding of the disease and how the drug works, which has assisted us in prioritizing which drug to move forward to the next steps in our development pipeline, or to know better what combination of drugs holds the best synergistic effects."**

Head of Bioinformatics

The Clarivate MetaBase data repository includes:



**3.7M+**

molecular interactions



**1.1K+**

molecular networks



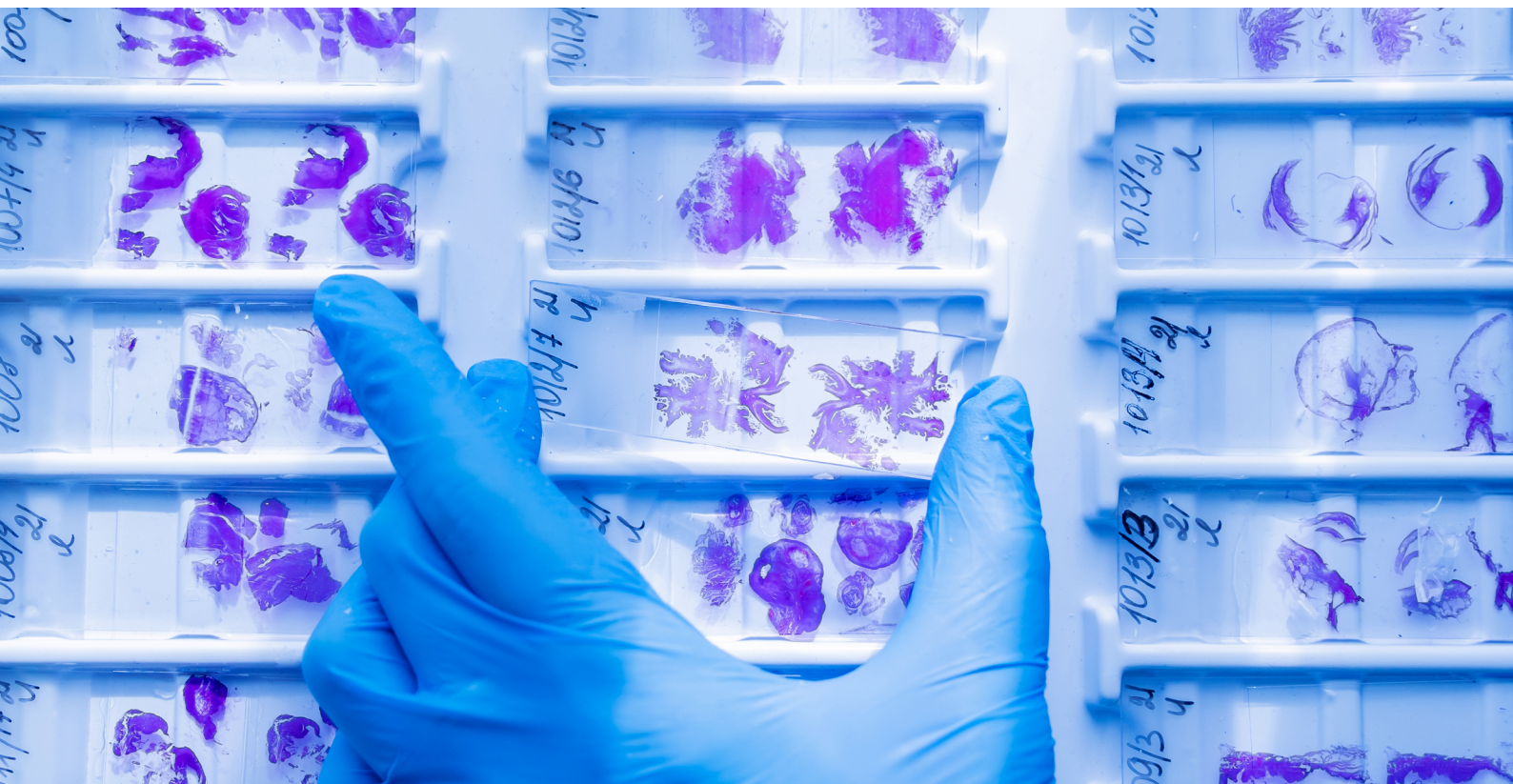
**1.5K+**

molecular pathways



**3.9M+**

publication references



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