# Multi-omic data driven drug discovery and indication prioritisation platform in oncology

## Reporting

Project Information

**mCUBE**

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10.3030/190185351

Project closed

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The European Innovation Council (EIC)

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**Investment in EU policy priorities**

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|---|---|---|---|
| Digital agenda | ○ | Clean air | ○ |
| Artificial Intelligence | ○ | Climate action | ○ |
| Biodiversity | ○ | | |

**Coordinated by**
EPIGENE LABS SAS
France

# Periodic Reporting for period 2 - mCUBE (Multi-omic data driven drug discovery and indication prioritisation platform in oncology)

**Reporting period:** 2023-05-01 to 2024-07-31

## Summary of the context and overall objectives of the project

The attrition rate in oncology drug discovery is among the highest, causing a real societal challenge. Most cancers remain unmet clinical needs and only 1 in 5 patients respond to their treatment. Drug development takes an average of 10 to 15 years and requires more than €2bn in investment to bring an efficient compound from the bench to the bedside. In 2020, 80% of clinical trials were focusing on cancer and a third of them were testing anticancer drugs. Accumulating evidence suggests that drug candidates validated through molecular analysis ("omics" analysis) are twice as likely to succeed in clinical studies. However, with data growing by about 25 petabytes year on year and the lack of adequate tools for data aggregation and analysis, cancer scientists battle to leverage this rich data for the prioritisation of drug discovery programs. They need an efficient and user-friendly solution to support their daily work.

## Work performed from the beginning of the project to the end of the period covered by the report and main results achieved so far

The project has focused on further developing mCUBE, integrating more data and implementing more analysis modules.
More specifically, our team carried out the following activities:
- Development of AI-augmented pipelines for the data mapping and integration,
- Development of multi-omic data analysis pipelines for target discovery, biomarker discovery, patient selection and preclinical model selection,
- Integration and harmonization of omic data at scale,
- Implementation of a subset of these tools into a user-friendly cloud-based platform and deployment of the solution for our industrial partners, and
- Generation of scientific results using the different tools and pipelines developed with our academic partners.

## Progress beyond the state of the art and expected potential impact (including the socio-economic impact and the wider societal implications of the project so far)

No performant multi-omic data aggregation and analysis tool is currently available on the market and cancer scientists are thus unable to leverage this valuable data for the prioritisation of drug discovery programs. With limited data skills, they can only rely on often disappointing collaborations with teams of bioinformaticians, with whom communication can be difficult, or on the use of suboptimal data science software. While the available solutions are generally based on relevant mathematical frameworks, they are poorly designed, non-user friendly and require computer programming skills. Moreover, available tools do not use AI to assist the user in the harmonisation of clinical data, a very time-consuming step in data aggregation.

We are developing mCUBE, an Artificial Intelligence (AI)-augmented cloud-based precision oncology

platform for multi-omic, multi-cancer and multi-source data identification, aggregation and analysis. mCUBE encapsulates Epigene Labs' deep expertise in oncology, data science, and bioinformatics into a user-friendly solution that will make a difference for cancer patients. Our solution delivers 3 main gains:
- increased productivity for our users (cancer scientists),
- increased profitability for our customers (biopharma companies), and
- improved care for cancer patients ultimately.

The conventional timeline for discovering a new target for a specific indication is 2 years. At Epigene, in the context of our first partnership with the Eyquem's lab at UCSF, we not only rediscovered known antigens but also prioritised a list of promising targets for relapsed/refractory multiple myeloma in only 6 months. A few months later, in a second program focusing on colorectal and gastric cancer, this same task took only 3 months. Soon, thanks to the support of the EIC Accelerator, we will be able to tackle a new indication in only a few weeks.


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