



## Accelerating Life-Saving Cellular Therapy Discovery with the Next Generation of Software Solutions

### Integrated, Organized, Searchable Bioinformatics Data Will Release Time for High-Value Research

Cell therapies have demonstrated huge therapeutic benefit for patient outcomes in recent years. For example, several CAR-T therapeutics have shown excellent clinical efficacy against CD19+ blood-borne cancers. This success has encouraged both well-established and start-up entrants to vigorously pursue new and challenging research projects, for example treating solid tumors and creating allogenic cell therapies. Research at these new frontiers is an extraordinarily data-intensive activity, yet often the underlying support processes continue to rely on a fragmented information infrastructure. For lean teams, working with paper notebooks and a small pool of shared files can be satisfactory. Keeping track of project progress and data often starts with spreadsheets, which are quick and easy to create and share, and personal recollection of resource and file locations can work well at this scale. But spreadsheet software was not purpose-built for R&D bioinformatics, and projects soon run up against multiple drawbacks: no searchability across the organization, difficulties with document version control, problems with external linked data, and more.

For example, while researchers may find it easy to locate data from recent projects, finding data from work older than six months typically involves laborious manual searches – assuming the data can be found at all.

As projects grow and scale, with greater team numbers and more data, the lack of searchability and the poor control of external sources can generate significant challenges. Sequence characterizations and cloning data soon becomes stored in multiple places, and maintaining valid links to public data sources can become extraordinarily difficult as document and spreadsheet copies are emailed within the organization. Similarly, users spend time copying and pasting into spreadsheets in multiple formats, making it difficult to search, compare, and share. To address the lack of integration, teams with technical knowhow may attempt to build a custom solution. But developing and maintaining technical infrastructure that may only be used on a single project is a poor use of time and budget, and may not offer sufficient scale and capacity for larger research programs.



### Moving to Integrated Bioinformatics

Moving successfully to a new platform that offers shared, integrated, searchable data depends on making the transition easy for users, delivering benefits quickly, and providing clear return on investment.

The Signals Research Suite consists of Signals Notebook, Signals VitroVivo, and Signals Inventa, built to resolve searchability, management, and integration challenges. Searchability is a key feature of the Signals Research Suite, combined with standardized analysis, sequence intelligence, and secure collaboration. The solution provides fully integrated tools that eliminate manual administration work, enable team collaboration, and provide key workflow and data management capabilities.

Signals Notebook is the hub of the Signals Research Suite solution, offering structured data capture with APIs and interfaces for integration with instruments, in-house systems, and databases. Signals Notebook provides a comprehensive set of scientific use cases, spanning biology, chemistry, formulations, analysis, and more. With an intuitive drag-and-drop app interface, almost no training is needed, and users can get up and running in a matter of hours. Inside Signals Notebook, scientists can track receptor candidate progress from sequence design and registration to functional assays such as antigen affinity and off-target interactions. The solution captures the full experimental context, with the receptor candidate lineage being fully traceable from physical sample back to initial in silico design. Given the blurring lines between R & D and process

development in this space, capturing context and relevant documentation in a single platform is invaluable for accelerating work from the bench to the clinic.

For lab data management and preparation, Signals VitroVivo unites assay development, low- and ultra-high-throughput production assays, high content screening, and in-vivo studies, enabling users to search across all assays and screening data within a single platform. All raw data, from experiment to results, are captured and analyzed in context from bacterial growth and clone picking to cell line proliferation and expression optimization. Signals VitroVivo is the data processing engine, from single data points to outlier detection and curve fitting, ensuring that no information is lost along the way, and data is always documented, and processes are repeatable. Signals VitroVivo adapts to the need of the scientists regardless of the type of assay related to DNA, proteins, cells, and even in vivo animals.

Signals Inventa delivers next-generation analysis of scientific results, throughout the research and development lifecycle. Signals Inventa offers chemical and biological analytics functionality, providing advanced query and data management capabilities without any manual data wrangling and reformatting.

The Signals Research Suite solution provide reusable templates and standardized workflows that enable processes to be replicated from project to project, removing the reliance on personal recollection. Pre-built apps can be combined to create workflows, and results can be analyzed, published, and shared. And when viewing results,

