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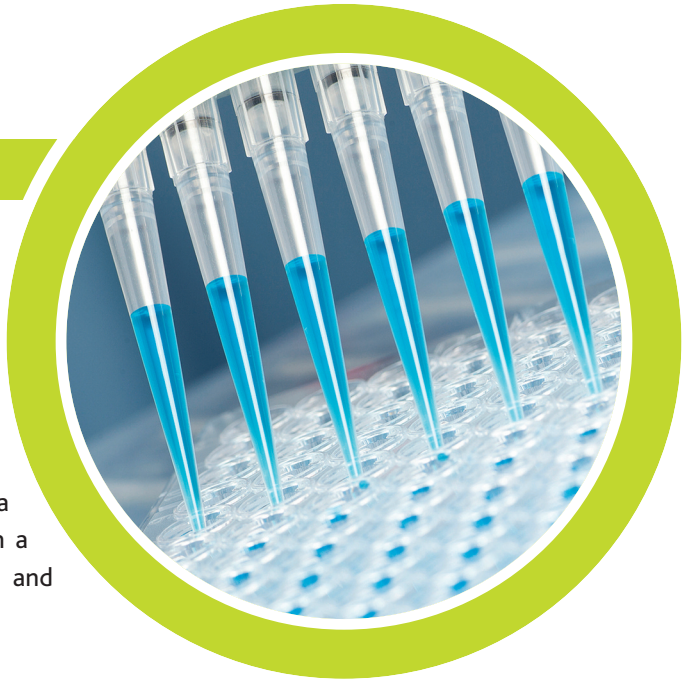
Multi-Assay Omics Data Model

The Multi-assay Omics Data Model is a structured representation of data elements, relationships, and rules designed to facilitate the ingestion and management of DNA & RNA sequencing and Immunohistochemistry (IHC) data. It is designed to enable accurate and efficient management of multi-omics data, containing study-, subject-, and sample-level metadata. The model includes information on sample treatment, analysis platform, and results, offering a standardized approach to multi-omics data management.

WHAT IS IT USED FOR



The Multi-assay Omics Data Model facilitates integration and analysis of multi-omics data, such as DNA & RNA sequencing and IHC data, from various sources. It allows researchers to easily access and analyze internal and external public resources, such as Gene Expression Omnibus (GEO), genome annotations, and pathway databases. With customizable features, the model can accommodate new assays, experimental designs, and data types, offering a versatile tool for researchers to gain a comprehensive understanding of biological processes and disease mechanisms.

SUPPORTED USE CASES

FUNCTIONALITY

- Collaborative Ontology Management
- Templates
- Data Curation
- F.A.I.R Data
- Data Catalogues
- Data Tagging
- Machine Learning & AI
- Knowledge Graphs
- Data Stewardship

USE CASES

- Clinical Data Search
- Biomarker Search
- Enterprise Search
- Pharmacovigilance
- Portfolio Analytics
- Asset Management

VALUE

The Multi-assay Omics Data Model provides a standardized and efficient approach to manage and integrate multi-omics data, facilitating analysis and enabling researchers to gain new insights into biological processes and disease mechanisms. Its customizable features and ability to integrate internal and external public resources make it a versatile tool for researchers across various fields.

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