Data Alliances: A collaborative opportunity for FAIR and AI-ready data

Rancho bio • sciences

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Problem statement

Public biomedical data is abundant but rarely analysis-ready. Fragmented formats, inconsistent annotations, and accessibility barriers prevent researchers from leveraging this resource at scale. Our Alliances provide a collaborative framework to harmonize data by domain and disease type, delivering FAIR, AI-ready datasets that accelerate research.

Disease Agnostic
- Access to high-quality data across diseases and cell types
- Customizable to your needs

Flexible and Compatible
- Interoperable, FAIR
- Use any tools, workflows and pipelines with the data
- Platform-agnostic

Standardized Data
- Consistent standards across datasets
- Ready for immediate analysis
- Processed, harmonized, AI/ML machine readable

Maximize ROI
- Minimal membership fees
- NO cost to maintain access
- Shared investment across members

01 Harmonized data: unified model, aligned values

02 All data processed uniformly and with modern algorithms

03 Control over content & portable formats

04 Keep your data forever

Single Cell data alliance

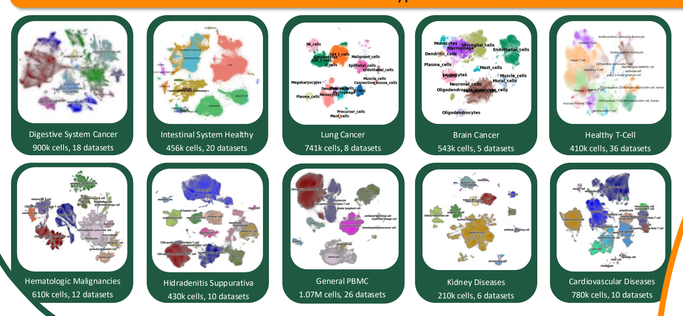
Description

Supporting a collaborative community of biomedical researchers with AI-ready **single-cell** data, governance, and inspiration
- Mining public data: 9,000+ public single cell datasets available, member request process
- Rich, harmonized metadata: comprehensive study, dataset, donor, sample, cell-level annotations, version-controlled ontologies
- Advanced processing pipeline: uniform mapping and quantification, standardized QC, multi-modal data support
- Flexible data delivery: h5ad, Seurat, TileDB, optimized for downstream analysis

Data

112 million Reprocessed, and annotated single-cells	37,851 Batch-corrected samples	17,854 Biological donors	1,154 Analysis-ready datasets for Seurat and Scanpy
100% Cell-types annotated	48% of datasets include author-provided annotations	48% Cells are from diseased samples	

14
Number of cell type atlases delivered



Oncology data alliance

Description

A collaborative initiative aimed at generating large-scale, disease-specific content across multiple datasets. The content will be integrated, re-analyzable, harmonized, and portable. The goal is to extract value from vast amounts of disparate public domain oncology data.
- Metadata is harmonized using an interoperable data model that is used among the alliances
- Standardized processing workflow customized for data type and flexible for various raw data types
- Delivered directly to client and platform independent

Data

Bulk RNA-seq

TCGA 33 cancer types	GTeX Healthy	GEO 8 cancer types

As **healthy** counterpart to TCGA

Next steps

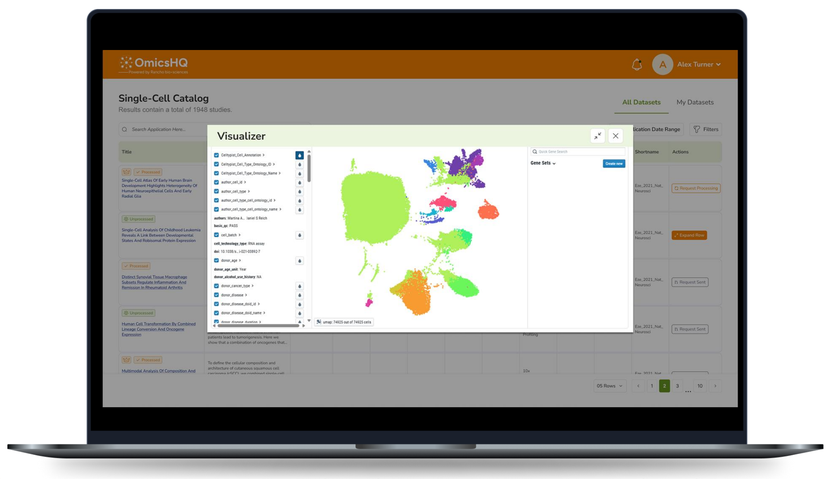
Flexibility to choose any **oncology** data of interest, including various cancer types and data types.

Transcriptomic · Gene variants · Phenotypical · Proteomics · Epigenetics

OmicsHQ

Description

Advance discovery through a comprehensive, high-quality, and standardized multi-omics data platform from public and proprietary sources, accessible to every scientist.



Catalog · Visualize · Request · Curation

Spatial data alliance

Description

To accelerate **spatial biology** research by creating standardized, interoperable, and AI-ready transcriptomics datasets, faster and more cost effectively than any single organization
- Aggregate and harmonize spatial transcriptomics datasets across platforms and tissue types
- Establish a coherent spatial data model based on Rancho's ontology and curation framework
- Enable cross-platform benchmarking and reproducibility
- Provide access to ready-to-use, quality-controlled datasets for analysis and AI applications

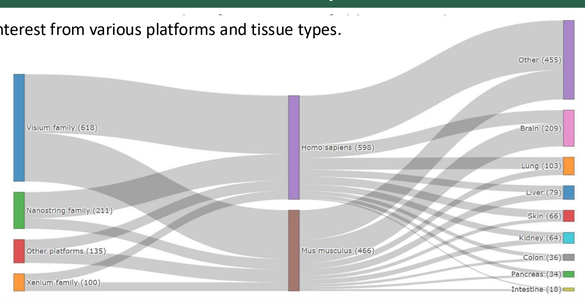
Data

33 Total Datasets (26 studies)	21 Human 12 Mouse	13 Diseased 10 both 8 Healthy	25 10x Visium v1/2** 6 GeoMx 1 CosMx 1 MerFish	17 Oncology 8 Healthy 4 Immunology 2 Liver Disease 2 NeuroDegen. 4 Brain · 6 Colon 3 Lung · 6 Liver 5 Kidney · 3 Skin

**cell deconvolution completed for all Visium v1/2 datasets

Next steps

Flexibility to choose ten datasets of interest from various platforms and tissue types.



Perturb-Seq data alliance

Description

Perturb-seq and related assays refer to the combination of genetic- (CRISPR, siRNA, shRNA) or chemical-based (small molecule) perturbations with gene expression sequencing e individual cell level
- Causal relationships: Perturb-Seq provides direct perturbation data (knockdowns, knockouts) that reveal cause-and-effect relationships between genes, rather than just correlational patterns in observational data
- Functional annotations: Each perturbation creates a controlled experiment, helping models learn gene function and regulatory networksalone
- Counterfactual learning: Models can learn "what happens if" scenarios, which is valuable for prediction and intervention designatlas data alone
- Richer training signal: The combination of perturbation identity + cellular response provides more structured supervision than unlabeled atlas data alone

Next steps

As of Feb. 2026, there are over 180 publicly available studies to choose from, including:
- Tahoe-100M (> 100 million cells target with 1,100 small-molecules)