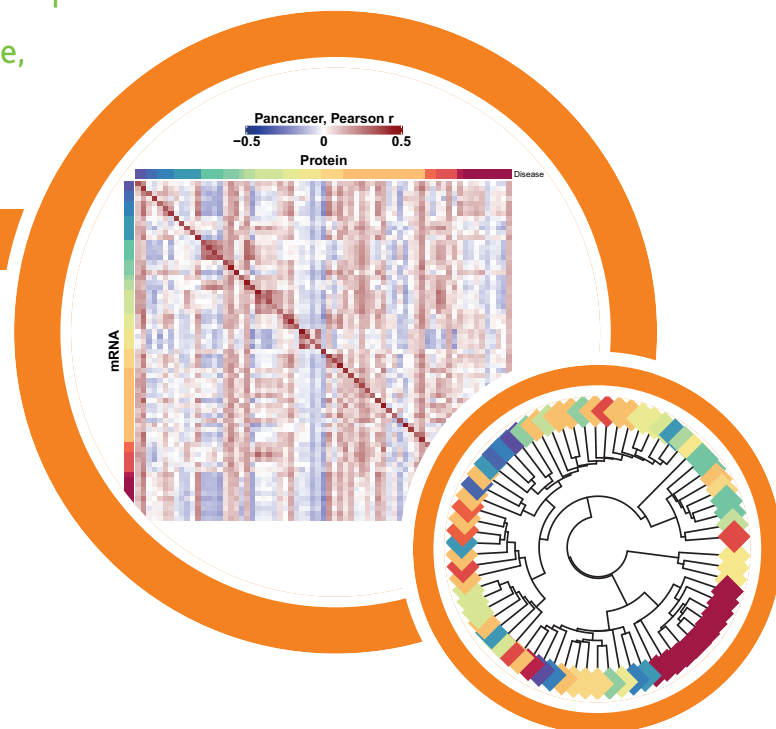# Rancho
biosciences

Proteomics Analysis & Support

Rancho Biosciences is an international Data Curation, Bioinformatics, and Data Science company. Our translational sciences team is composed of experienced Ph.D. and MD scientists and biostatisticians that deliver high quality work on time and on budget. Our goal is to support the life science community by providing analytical support across the spectrum of experimental proteomic modalities, including spectrometry, fluorescence, and tagging.

RANCHO PROTEOMICS SERVICES

- Peptide identification & quantification
- Proteomics data ingestion (PRIDE, CPTAC)
- Differential proteomics (QMS, LC-MS/MS)
- Cellular proteomics & abundance analysis (CyTOF, CITE-Seq)
- Protein interaction analysis (Co-IP, Phage display)
- Protein network &receptor/ligand analysis
- Homology, domain, cellular expression mining (HPA, UniProt)
- Spatial proteomics (HMIF, VizGen, SMT)

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PROCESS

Rancho Biosciences has PhD and MD scientists with domain knowledge and expertise in quantitative and comparative proteomics.

Our process is designed to alleviate the workload and stress of projects. Our team will meet with you to define your project scope and then prepare a proposal covering the project deliverables, timelines, risks, expectations, and costs. Your feedback is incorporated, and the proposal document is turned into an actionable document – a SOW (statement of work) for processing. Our Project Managers schedule kick-off meetings with you at the start of the project to discuss deliverables, timelines, and to establish a communication
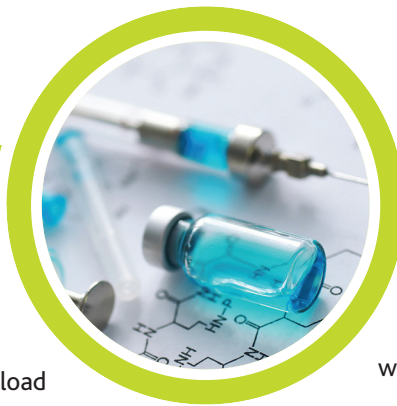
cadence that works best for you, and to ensure that project progress is always available to you, when needed. For projects that require Rancho to access your infrastructure, we will work with you to onboard our scientists.

When your project is complete, we will host a final project wrap-up meeting to exhibit the major results, review all deliverables, transfer all project materials, and to answer any of your questions.

PROTEOMICS SERVICES

Our scientists have deep expertise across the range of proteomic study designs. We provide data-to-insight services across the range of proteomics modalities such as:

Peptide inference & quantification pipelines

We can create pipelines that determine protein abundances from quantitative mass-spec data, including data from ProteomeXchange, to identify proteins and their abundance levels or (for Co-IP/Co-fragmentation) protein interactions.

Single-cell proteomic solutions

Cellular abundance changes by CyTOF or CITE-seq are key strategies for identifying cellular targets. Rancho can identify key cell populations and (for CITE-seq) expression profiles using state-of-the-art informatic methods.

Optical proteomics

Fluorescent staining, including high-throughput spatial Visum assays, enable spatial profiling and quantification of protein abundance. Rancho can build scalable pipelines for processing, integrating, and analyzing in-situ proteomics modalities.

Data modeling and ingestion

Mining of external data resources and databases for protein structural and functional information can be advantageous to drug discovery. Rancho can develop automated scripts to integrate
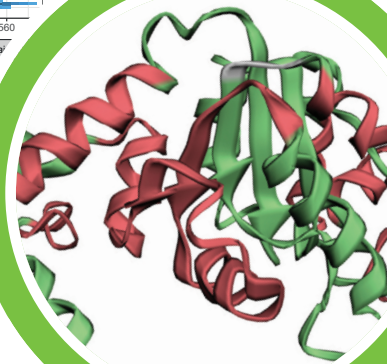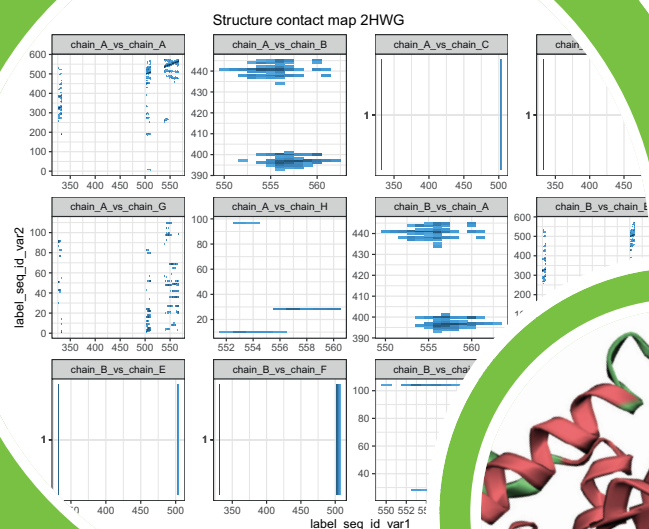
proteomics data with public resources such as UniProt, RefSeq, PDB, KEGG, InWEB, BioGRID, Human Protein Atlas, or CPTAC, and further curated to a specific data model for ingestion.

Differential proteomics

Understanding protein abundance differences in tissues or single cells can reveal major mechanisms of diseases or treatments. Rancho's experienced biostatisticans can analyzed and interpret these data, at both protein and mRNA level, to infer critical factors at the level of single proteins, complexes, receptor/ligand interactions, or pathways.