Open cytokine response data and tools from the Allen Institute for Immunology and the Human Immune System Explorer platform

Poster No. PB042

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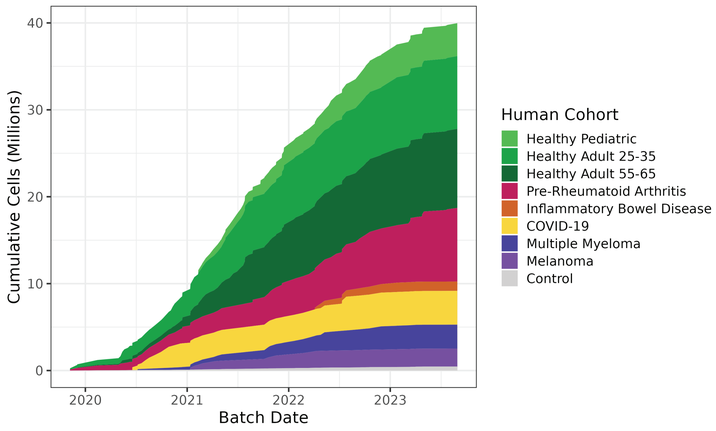
We have *a lot* of data from human cohorts

We developed high throughput, high quality, multimodal pipelines to deeply profile the peripheral immune system. Over the last 5 years, we've brought this scale and quality to 8 human health and disease cohorts.



Totals from our scRNA-seq Pipelines as of August 22, 2024:

460 subjects **2,302 samples** **55,519,418 single cells**

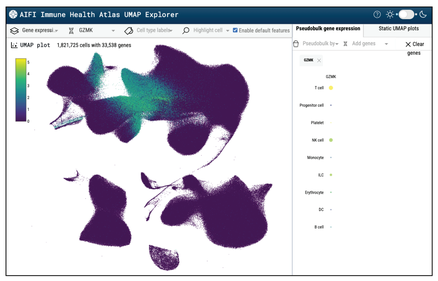
Now, we're completing initial studies and working towards releasing this trove of high quality data to the scientific community.

A suite of rich exploration tools

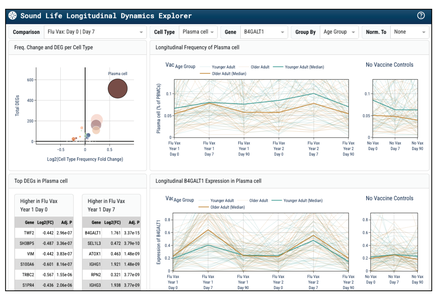
To support the release of our ***Immune Health Atlas***, we built tools to enable scientists to refer to and explore this resource generated from 108 healthy subjects from 11 to 65 years old.

Quickly see which PMBC populations express a gene with our **Gene Expression Reference**.

Explore cell type annotations and gene expression with our dynamic **UMAP Explorer** which interactively displays **> 1.8 million single cells**.



Our ***Dynamics of Immune Health and Age*** project explores how age, CMV infection, and flu vaccine responses alter our peripheral immune cells. To elucidate these dynamic changes over time, we developed visualization tools that chart longitudinal and pairwise changes found in our dataset from 96 healthy adults, with 868 samples and **> 13.7 million single cells**.

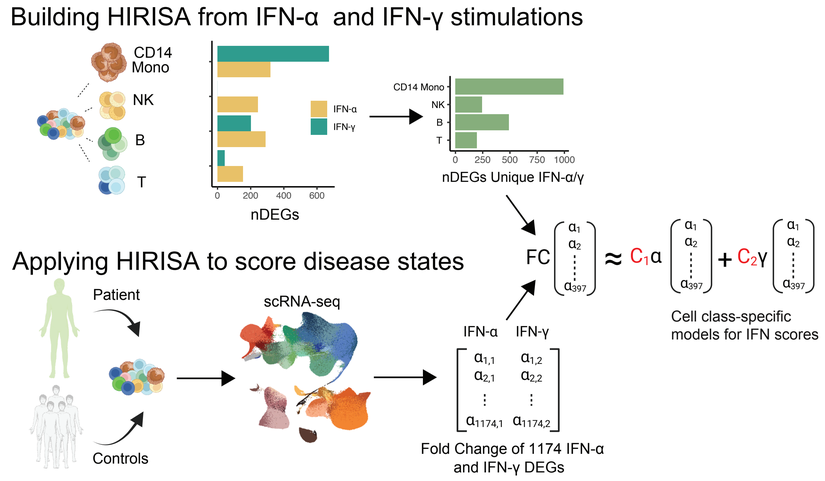


Longitudinal Dynamics Viewer enables visualization of changes to population frequency and gene expression over time and in response to flu vaccination.

Differential Gene Explorer displays specific comparisons related to CMV infection status, age group, and biological sex, and enables exploration of changes to specific genes.

A new atlas of Interferon responses in PBMC types

To understand cell type specific immune responses in human peripheral blood cells (PBMCs), we isolated specific classes of PBMCs and separately treated them with interferons: IFN-α, IFN-β, IFN-γ, and IFN-λ1. We profiled changes in expression induced by each IFN in each type to build a new resource: **The Human Interferon Response in Immune Subsets Atlas (HIRISA).**

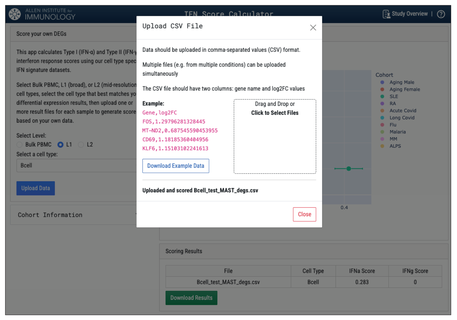


HIRISA enabled us to deconvolute signatures of Type I and Type II IFN responses in multiple cell types, and develop a scoring algorithm to identify IFN responses in differentially expressed genes.

We then applied our scoring algorithm to a broad panel of immune diseases.

Tools to put your IFN responses in context

We want to enable anyone studying IFN responses to use our algorithms for response scoring, and to see where their own DEG panels lie with respect to various immunological diseases. To assist with these goals, we developed new open, interactive tools.

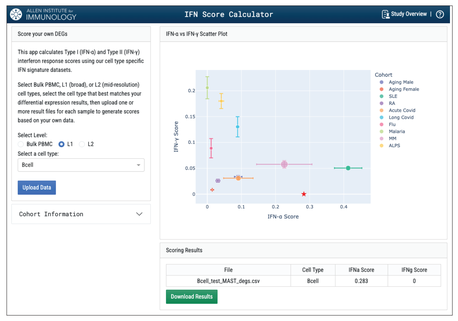


Our IFN Score Calculator app allows users to upload their own DEG results.

IFN-α and IFN-γ scores are computed from your DEGs.

After scoring, your results will be put in context using pre-computed values from Aging, Lupus, Rheumatoid Arthritis, Flu, COVID-19, Malaria, Multiple Myeloma, and Autoimmune Lymphoproliferative Syndrome (ALPS) studies.

In this case, the user-submitted values are highlighted with a red star.



More at Cytokines 2025 and our website

For more information about the HIRISA project, see:

Poster PB055
presented by
Emma Kuan

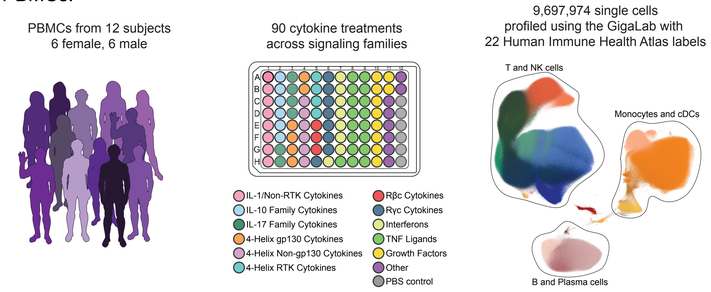
Poster PB065
presented by
Erik Layton

See all 9 posters from the Allen Institute for Immunology and ***links to our online IFN tools*** at:

https://tinyurl.com/aifi-cyto-2025

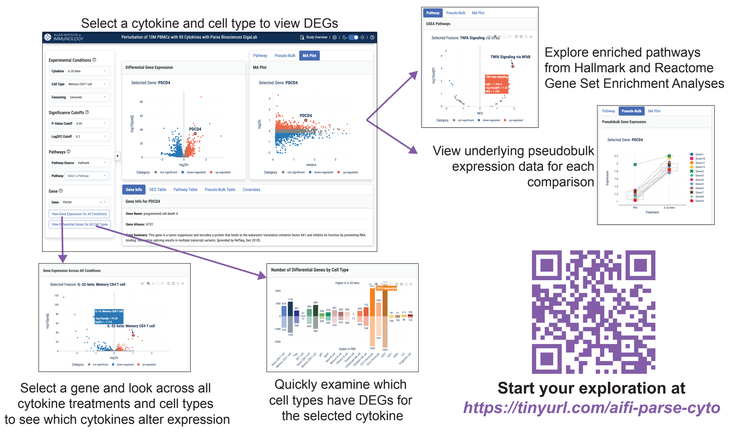
Tools to interrogate 90 cytokine treatments

Parse Biosciences utilized their **GigaLab platform** to profile 90 cytokine treatments in peripheral blood mononuclear cells (PBMCs) from 12 human donors. After sequencing, data assembly, and quality control with the Parse Analysis Pipeline, the resulting dataset consists of transcriptomic profiles from ~10 million PBMCs.



Parse Biosciences openly released this dataset to demonstrate the scale and quality of their GigaLab platform. We downloaded this dataset, annotated cell types based on our Human Immune Health Atlas, and performed differential expression analyses for each cytokine vs. the PBS control.

To make these results accessible to other researchers, we developed an interactive DEG Explorer, available for free on our website.

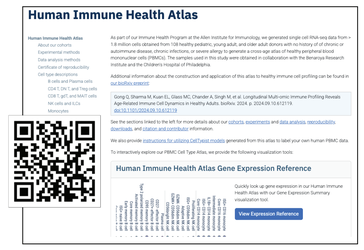


Start your exploration at
https://tinyurl.com/aifi-parse-cyto

To learn more about how the dataset was generated and download the complete original dataset, see:
10 Million Human PBMCs in a Single Experiment, https://www.parsebiosciences.com/datasets/10-million-human-pbmcs-in-a-single-experiment/; Parse Biosciences.

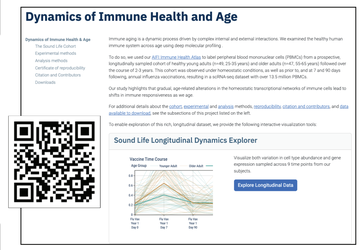
Human cohort data available now

Our first HISE Data Apps are available now. These focus on the release of deeply characterized and longitudinally profiled healthy peripheral immune cells and progression to rheumatoid arthritis:

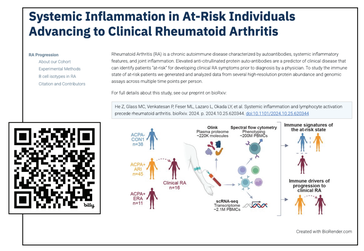


An atlas of PBMC populations from 108 pediatric, young adult, and older adult healthy subjects

Interactive tools and cell type labeling models



Longitudinal profiling and extensive analyses of changes over time and across age, sex, and CMV infection in healthy subjects



Subjects at-risk for rheumatoid arthritis (RA) were longitudinally profiled over two years.

~30% of subjects developed clinical symptoms of RA. Comparisons between subjects with progressive RA to non-progressive at-risk subjects, early RA, and healthy controls characterize progression in at-risk patients.

In total, we've released scRNA-seq data from **~16 million** peripheral blood mononuclear cells, along with extensive documentation and visualizations.

Watch us grow at ***explore.allenimmunology.org***