We would like to highlight a new community resource: the Immunological Proteome Resource (ImmPRes; http://immprres.co.uk/). ImmPRes aims to provide an in-depth high-quality map of the immune cell proteomes. It is an initiative inspired by resources such as ImmGen, in which systematic analyses of RNA expression in immune cells have yielded invaluable biological insights about lymphocyte populations. ImmPRes maps the proteomes of immune cells rather than the transcriptome, which is important because changes in rates of protein synthesis and degradation mean that mRNA levels are not always effective predictors of cellular protein abundance. There are thus clear examples of discordance between mRNA and protein abundance in T cells that reflect the ability of post-transcriptional mechanisms to control T cell proteomes. Because proteins are the molecules that structure cells and control almost all metabolic processes and regulatory mechanisms, there is enormous value in the characterization of cellular proteomes to understand lymphocyte identity. Fortunately, technological advances in high-resolution mass spectrometry have made it feasible to characterize cell proteomes quantitatively. The technology can be used to explore how immune cells remodel their proteomes when they respond to immune or environmental stimuli or when key signaling networks are disrupted. Proteomic data can provide extensive information about the cellular repertoires of proteins to create an objective understanding of cell ‘identity’. For example, knowledge of the abundance of metabolic enzymes, nutrient transporters, ribosomes, and translational enhancers and repressors enables the assessment of the metabolic capacity of different lymphocyte populations.

To leverage value from proteomic datasets, an easily interrogated online resource that enables rapid exploration of the protein landscape of key immune cells is vital. There is a resource focused on subsets of peripheral blood-derived human leukocytes; however, no current mouse equivalent exists. We have therefore developed ImmPRes as a resource to integrate data derived from high-resolution mass spectrometry analysis of mouse hematopoietic populations. ImmPRes displays proteomic data of T cell subsets from lymph nodes, spleen, gut and liver, plus T cell populations activated in vitro with antigen and/or inflammatory cytokines. It includes datasets that map how the triggering of antigen receptors remodels the proteomes of naïve CD4+ and CD8+ T cells. It enables a comparison of the proteomes of different in vitro-generated CD4+ T effector populations and shows how cytokines differentially affect the proteomes of cytotoxic T cells. The resource also shows how inhibition of key signaling pathways or the loss of important transcription factors or changes in environmental conditions shapes T cell proteomes. Furthermore, the major splenic and lymph node B cell populations are characterized, and the effect on B cell proteomes of B cell activation in vitro via antigen receptors, co-stimulators, cytokines and innate stimuli is examined. The resource also includes proteomes of innate immune cells with datasets from natural killer (NK) cells, neutrophils and bone marrow-derived mast cells and macrophages.

Data reproducibility and integrity are a priority, so the resource has a protocols section that documents in detail how each sample is prepared. The raw mass spectrometry files for the different ImmPRes populations are uploaded and stored in the Proteomics Identifications Database (PRIDE), which is part of the ProteomeXchange consortium. PRIDE is a vital resource that excels at the storage of raw files, therefore ImmPRes integrates direct links to PRIDE for access to the raw mass spectrometry data. The mass spectrometry-based datasets in ImmPRes have been acquired using both data-dependent acquisition and more recently data-independent acquisition. The objectives across all datasets have been to obtain in-depth coverage of cellular proteomes while using a rigorous false discovery rate, no ‘match-between-runs’ between heterogeneous populations and no data imputation to maximize the data quality.

The proteomic data on ImmPRes are quantified using the ‘proteomic ruler’ method, which uses the mass spectrometry-based signal of histones as a standard to estimate protein copy numbers per cell. These estimated protein copy numbers provide an important biological context to the mass spectrometry-derived data that is easily understood by immunologists. ImmPRes enables access to the estimated protein copy number per cell as well as protein concentration data for thousands of proteins across all datasets via a simple graphical interface that displays interactive plots facilitating data exploration for non-expert users. These automatic plots enable users to easily search for the quantities of individual proteins within different populations, and perform broader comparisons of how cells vary in terms of expression of protein families such as kinases, phosphatases, E3 ligases, and metabolic proteins. The availability of protein copy number data enables assessments of the stoichiometry of crucial protein complexes in lymphocytes, including key repressor proteins.

We believe that the proteomic data of the different mouse immune cells will expand our understanding of immune cell identity and functional capacity and will lead to new and exciting biological discoveries. As such, ImmPRes aims to make the exploration and visualization of proteomic data easily accessible to non-mass spectrometrists and hence become a valuable resource for immunologists.

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Competing interests
The authors declare no competing interests.