

Hyperion Imaging System

A comprehensive solution for high-parameter tissue imaging



The Hyperion™ Imaging System is a transformative imaging solution that enables comprehensive analysis of cellular phenotypes and their interrelationships using Imaging Mass Cytometry™. Bringing together high-parameter CyTOF® technology with imaging capability, the Hyperion Imaging System enables you to visualize 4 to 37 protein markers in the spatial context of the tissue microenvironment, surpassing the capabilities of fluorescent immunohistochemistry (IHC). With the ability to utilize up to 135 channels to detect additional parameters, the Hyperion Imaging System is ideal to meet your needs today and well into the future.

The Hyperion Imaging System is accompanied by a pathologist-verified Maxpar® imaging antibody portfolio, a software suite for image acquisition and data analysis, and experienced Fluidigm service and support. Delivering a comprehensive view from one scan, the Hyperion Imaging System can enable you to deeply profile precious FFPE or frozen tissues at subcellular resolution to power your next breakthrough.

Highlights

Comprehensive—Highly multiplexed IHC enables simultaneous analysis of 4 to 37 protein markers.

Contextual—Get subcellular resolution while preserving tissue architecture and cellular morphology.

Powerful—Preserve precious samples and reduce variability by eliminating the dependency on serial sections.

The Imaging Mass Cytometry workflow

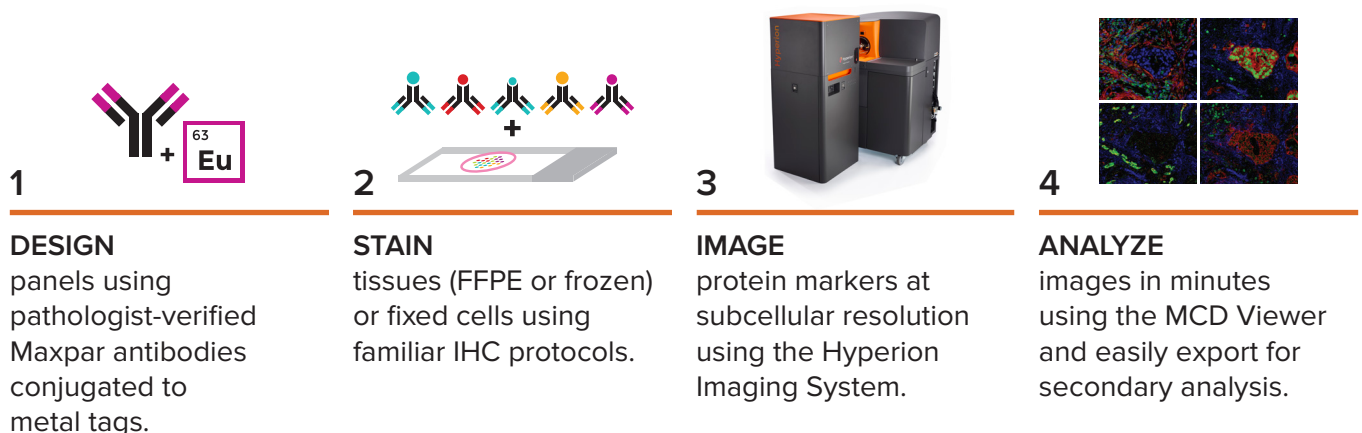
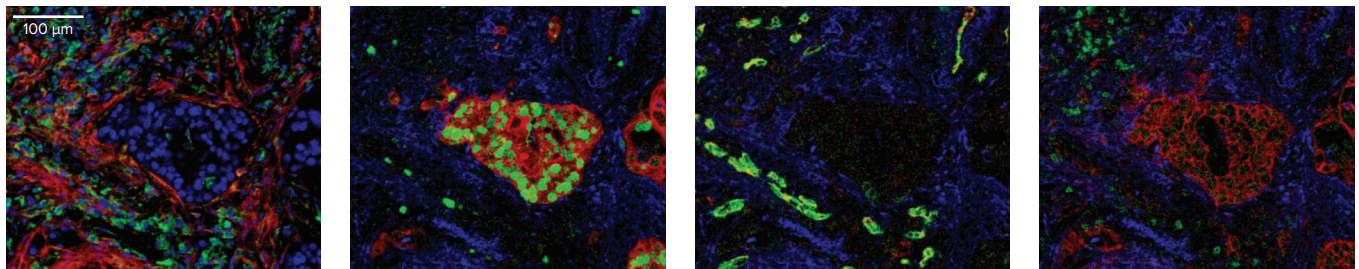


Figure 1. The Imaging Mass Cytometry workflow. A simple four-step workflow to deliver highly multiplexed imaging.

Simplify multiplex panel design with pathologist-verified Maxpar antibodies

Metal-tagged pathologist-verified Maxpar antibodies for Imaging Mass Cytometry are designed and optimized for use with the Hyperion Imaging System. These antibodies can be combined using a protocol that provides a common antigen retrieval step to simplify panel design for use with formalin-fixed, paraffin-embedded (FFPE) human tissue sections. Flexibly customize panels using your own antibodies with custom conjugation options.

Simultaneously interrogate multiple protein biomarkers. All from a single slide.



Alpha smooth muscle actin, vimentin, histone H3

HMWK, Ki-67, collagen I

CD31, CD34, collagen I

beta-catenin, CD3, collagen I

Figure 2. Protein biomarkers in human lung tissue are visualized at subcellular resolution following precise metal-tag capture from a user-defined tissue location and detection at 1 Da spectral resolution using proven CyTOF technology. Markers used with a human lung FFPE tissue sample include alpha-smooth muscle actin (^{141}Pr), high-molecular-weight keratin (^{144}Nd), CD31 (^{145}Nd), beta-catenin (^{147}Sm), vimentin (^{143}Nd), Ki-67 (^{168}Er), CD34 (^{158}Gd), CD3 (^{170}Er), histone H3 (^{176}Yb), and collagen I (^{169}Tm).

Visualize spatial context of multiplex data in minutes

The MCD Viewer software that accompanies the Hyperion Imaging System precisely converts the scanned cells and tissues into TIFF images of publication quality. Each image can be spectrally separated to display the expression of each protein. Data for each region of interest (ROI) can be exported for third-party analysis on software such as histoCAT™.

Maximize system performance with Fluidigm service, support and training

With the Fluidigm service plan, you can boost productivity, control costs and minimize downtime. Service plan options are attractively priced and include regularly scheduled maintenance visits to ensure that your Hyperion Imaging System is kept in peak operating condition. Fluidigm Field Application Specialists provide you with a selection of training programs to help you get started so you can begin asking new questions in your own research with the Hyperion Imaging System.

Learn more at

fluidigm.com/hyperionimaging

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Now that we can measure so many markers simultaneously, we for the first time have the ability to determine which cell types are present in the tissue, and especially in the tumors, and also how they are spatially arranged.”

Bernd Bodenmiller, PhD
Assistant Professor
Institute of Molecular Life Sciences
University of Zurich

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