

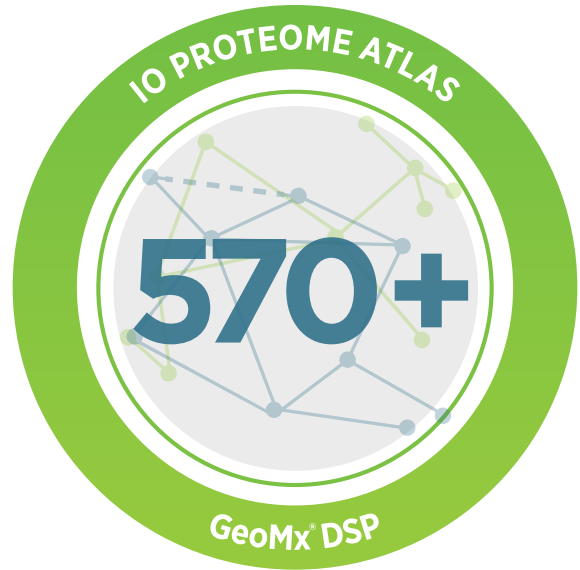
The main title of the factsheet, "NanoString GeoMx<sup>®</sup> IO Proteome Atlas Spatial Proteomics Redefined", is displayed in large, bold, white sans-serif font. The background behind the text is a detailed, colorful microscopic image of tissue, showing various cellular structures and patterns in shades of purple, blue, and pink.

**NanoString GeoMx<sup>®</sup>  
IO Proteome Atlas  
Spatial Proteomics Redefined**

Comprising nearly all Abcam's immunohistochemistry (IHC)-validated human antibodies for immuno-oncology (IO) research, the GeoMx IO Proteome Atlas (IPA) is the highest-plex panel available for spatial proteomics of Formalin-Fixed Paraffin-Embedded (FFPE) and fresh frozen tissue sections and enables broad biomarker discovery for translational research. Rapidly discover new protein biomarkers and drug targets by non-destructively profiling over 570 proteins in different tissue compartments such as the tumor, microenvironment, and the immune infiltrate.

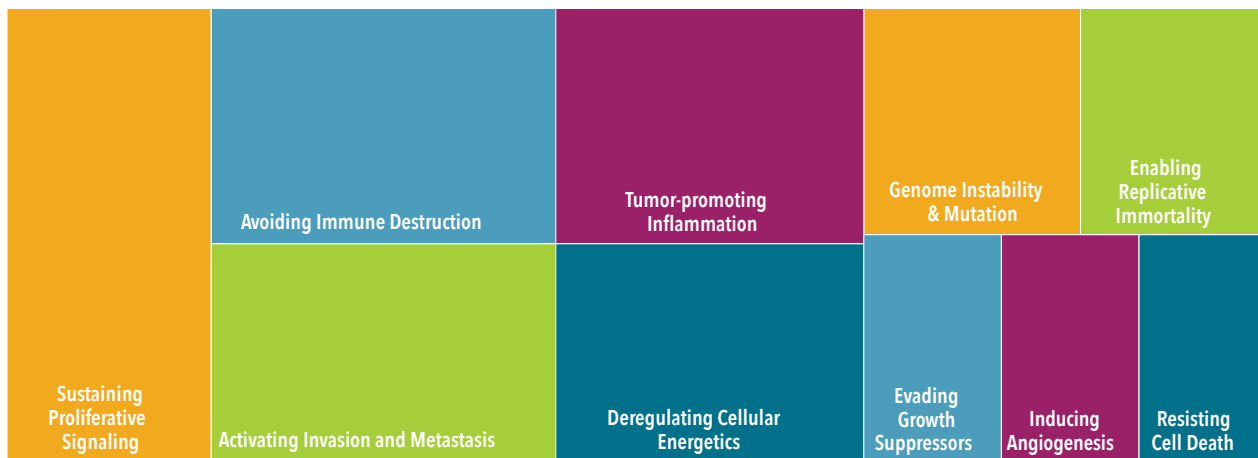
**Product Highlights**

- Find the next blockbuster IO drug target
- Be the first to discover new multiomic biomarkers utilizing spatial proteogenomics with the GeoMx® Whole Transcriptome Atlas (WTA)
- Screen the world's largest catalog of IHC-validated antibodies on a single slide
- Customize with up to 40 additional protein targets of your choice



**Abcam's IO Catalog at your Fingertips**

Find the next blockbuster IO spatial biomarker by profiling the expression of 570+ human protein targets on one slide. Take advantage of the open-source clone information from Abcam for downstream validation. Although the content is ideal for immuno-oncology research with comprehensive coverage of all 10 Hallmarks of Cancer, the GeoMx IO Proteome Atlas has broad applicability for other research areas such as autoimmunity, infectious disease, and organ transplant..



Content breakdown as distributed across the 10 Hallmarks of Cancer



## Flex your Protein Muscles. All 570+ of Them

Rapidly discover new protein biomarkers and drug targets from human samples with unrivaled plex, getting more comprehensive biological information per slide than traditional IHC or Immunofluorescence (IF) assays. Screen multiple samples per slide with whole slide scanning or maximize the number of samples per slide with a Tissue Microarray (TMA). Work with a variety of sample types, including whole tissue sections and organoids. Take advantage of next-generation sequencing (NGS) readout and use higher capacity Illumina sequencers such as the NovaSeq or NextSeq series with the GeoMx IPA.

### Panel Annotations

Content in the GeoMx IPA can be divided into 77 annotated pathways across 556 genes and includes coverage of 60+ phosphorylated targets.

Pathway	# of Targets
AMPK Signaling	33
Androgen Signaling	28
Apoptosis	82
Autophagy	51
Cancer Antigens	2
Cell Adhesion and Motility	102
Cell Cycle	92
Chemokine Signaling	56
Complement System	11
Cytotoxicity	3
Differentiation	125
DNA Damage Repair	36
Drug Resistance	1
EGFR Signaling	8
EMT	95
Endocytosis	38
Epigenetic Modification	82
ERBB2 Signaling	16
Estrogen Signaling	62
FGFR Signaling	13
FoxO Signaling	57

Pathway	# of Targets
Glutamine Metabolism	1
Glycolysis & Glucose Transport	9
Hedgehog Signaling	12
HIF1 Signaling	56
Hippo Signaling	5
IDH1/2	6
IL-1 Signaling	37
IL-17 Signaling	28
IL-2 Signaling	23
IL-6 Signaling	7
Immortality & Stemness	24
Insulin Signaling	43
Interferon Response Genes	10
JAK-STAT Signaling	49
Lipid Metabolism	22
Lymphocyte Regulation	36
Lymphocyte Trafficking	27
Lysosome	9
MAPK Signaling	108
Matrix Remodeling and Metastasis	18
MET Signaling	14



Pathway	# of Targets
MHC Class I Antigen Presentation	24
MHC Class II Antigen Presentation	6
Mitochondrial Metabolism / TCA	15
mTOR Signaling	61
Myc	14
Myeloid Inflammation	43
NF-kB Signaling	45
NO Signaling	7
Notch Signaling	53
NRF2 Signaling	15
Other Interleukin Signaling	112
Oxidative Stress	99
p53 Signaling	58
PDGF Signaling	20
PI3K-Akt Signaling	119
PPAR Signaling	4
Prostaglandin Inflammation	4

Pathway	# of Targets
Proteotoxic Stress	9
Purinergic Signaling	1
RAGE Signaling	9
Senescence	111
T Cell Exhaustion	11
T Cell Checkpoints	18
TCR Signaling	62
TGF-beta Signaling	40
TH1 Differentiation	12
TH17 Differentiation	24
TH2 Differentiation	14
TLR Signaling	74
TNF Signaling	54
Treg Differentiation	13
Type I Interferon Signaling	16
Type II Interferon Signaling	24
VEGF Signaling	40
Wnt Signaling	60

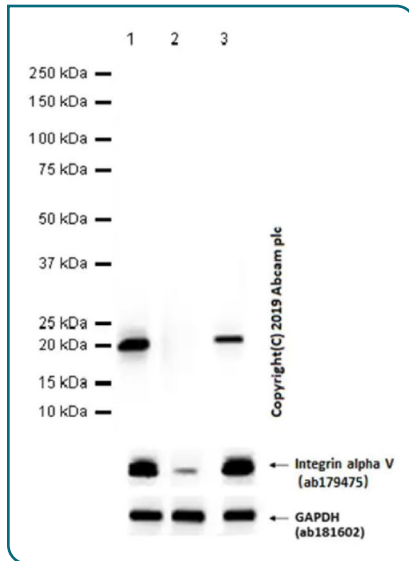


## Functional Validation

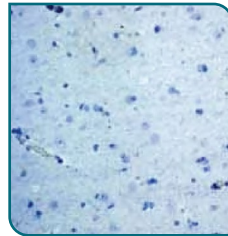
All antibodies in the GeoMx IPA have been validated with IHC and a host of other orthogonal single plex methods by Abcam, as well as in multiplex by NanoString, to ensure that every antibody has appropriate specificity, sensitivity, and performance. Multiplex validation was completed using FDA-approved TMAs across 77 normal human cores representing 29 tissue types and 54 tumor human cores representing 26 tissue types. All panel antibodies were additionally validated in multiplex across 90+ human cell lines for specificity and sensitivity.

### Single plex IHC validation by Abcam

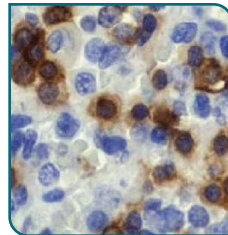
CD3e (Clone ID: EP449E)



Western Blot



Positive IHC staining in normal spleen tissue



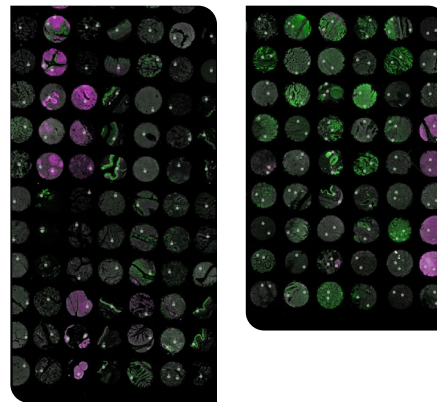
Negative IHC staining in normal brain tissue

### Multiplex validation by NSTG

Measured on 90 pellet CPA and FDA-approved screening arrays TMA with tumor and normal tissues.

Assessed:

- Clear positive signal in positive control cells and tissues
- Clear negative signal in negative control cells and tissues
- Phospho-specific antibodies also validated using established models, including phosphatase inhibitor treatment prior to fixation

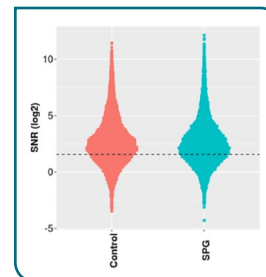


GeoMx images of FDA-approved tissue microarrays (TMAs) used for functional validation of the GeoMx IPA

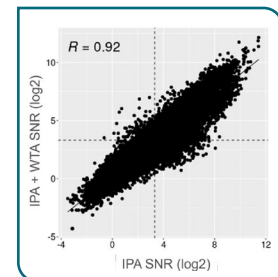
## Enable Spatial Proteogenomics

Be the first to discover new biology and novel multiomic biomarkers by utilizing our Spatial Proteogenomics workflow to run the GeoMx IO Proteome Atlas and the GeoMx Human Whole Transcriptome Atlas (WTA) simultaneously on the same tissue section. Updated probe chemistry for GeoMx IPA enables same-slide co-detection of RNA and protein at the same sequencing depth and cost as separate detections of RNA and protein from serial sections.

Performance Remains Consistent from IPA alone to IPA+WTA:



Iar SNR Distribution Pattern



Great Concordance

To view the annotated protein target list for the GeoMx<sup>®</sup> IO Proteome Atlas visit [nanosttring.com/products/geomx-digital-spatial-profiler/io-proteome-atlas](https://nanosttring.com/products/geomx-digital-spatial-profiler/io-proteome-atlas)

## Get in touch



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