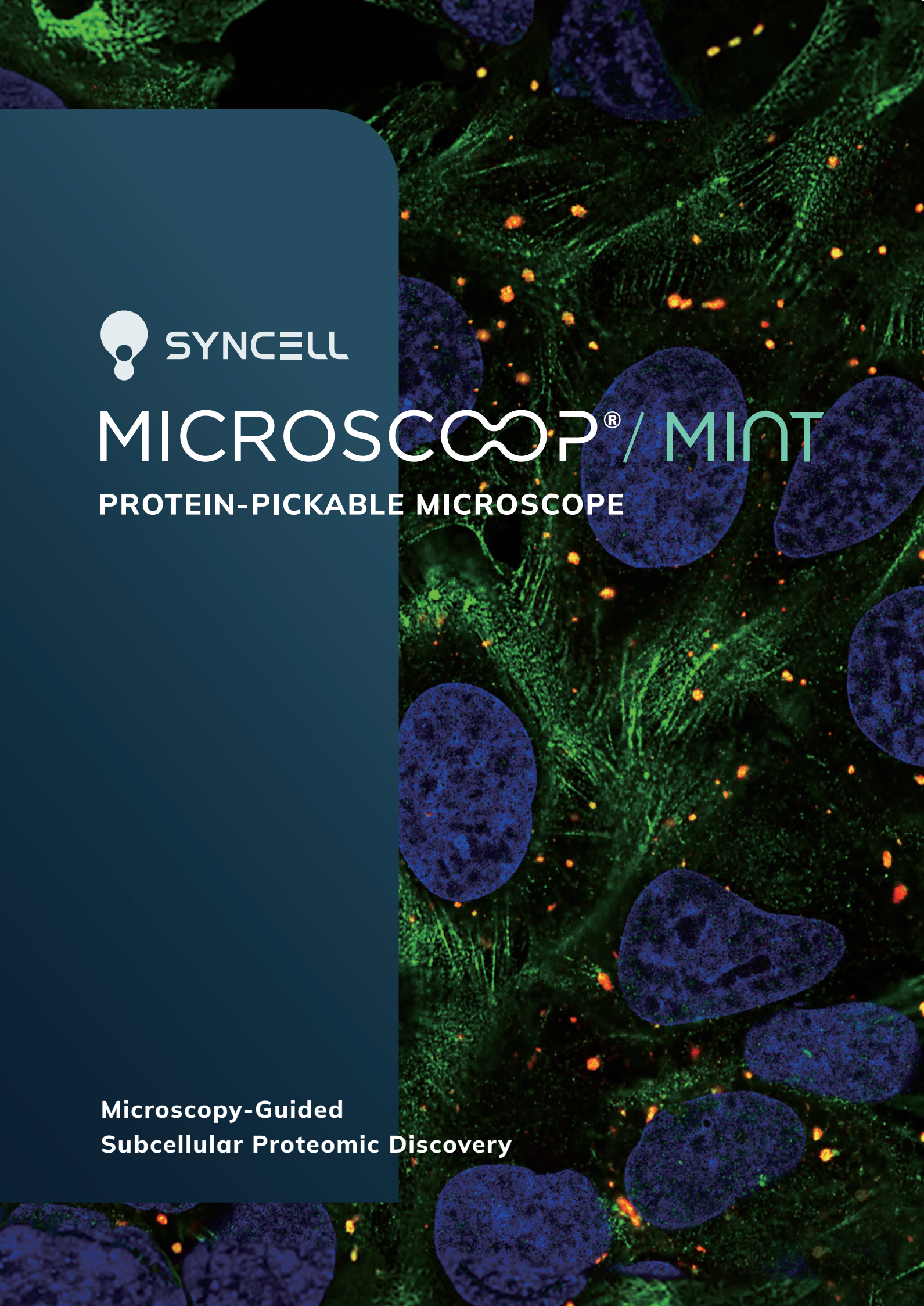


SYNCELL

MICROSCOOP® / MINT

PROTEIN-PICKABLE MICROSCOPE

Microscopy-Guided
Subcellular Proteomic Discovery

AI MICROSCOPY-GUIDED PHOTO-BIOTINYLATION

Revealing novel protein constituents at the TDP-43 aggregates of a postmortem FFPE brain section from an amyotrophic lateral sclerosis (ALS) patient. Sample provided by the Rossoll lab, Mayo Clinic.

TARGETED SCOOPING TO DISCOVER INVISIBLE PROTEINS

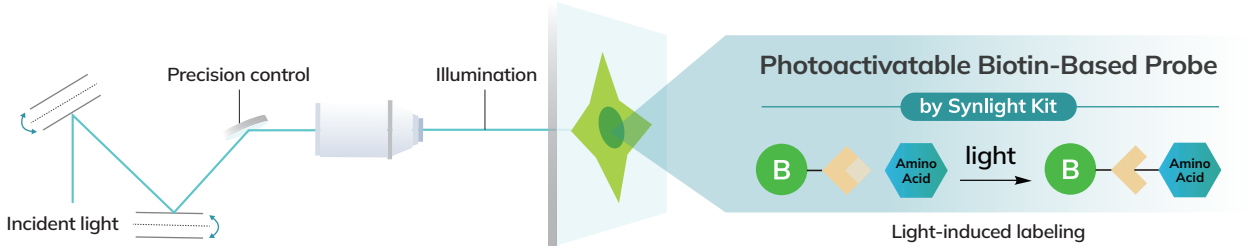
Microscoop Mint is a groundbreaking spatial proteomics platform that has been used to reveal novel protein constituents at specific subcellular regions of interest for many biological problems. Microscoop Mint performs microscopic scooping, i.e. automated ultra-content microscopy-guided photo-biotinylation to photolabel and isolate/pick engugh subcellular proteins for mass spectrometry-based proteomic discovery. It is an unprecedented spatial pulldown technology that enables unbiased subcellular proteomic identification in high resolution, high sensitivity, and high specificity.

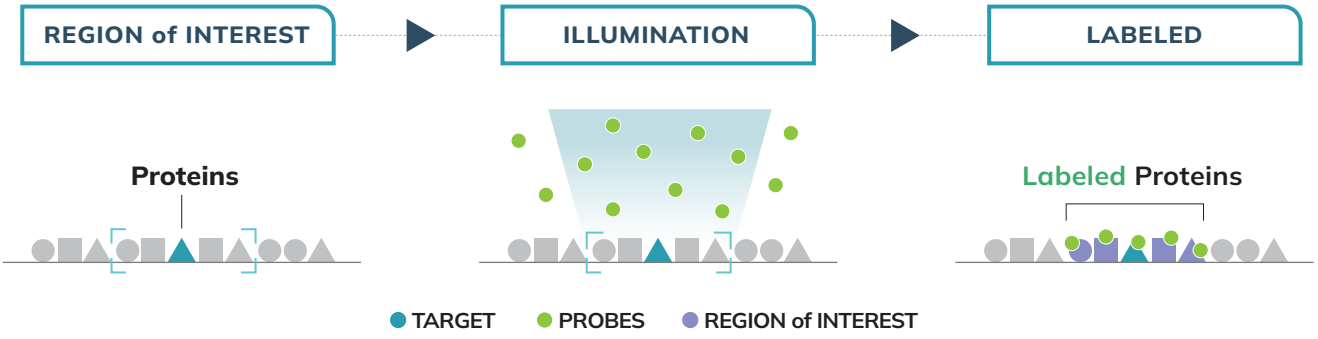
HOW MICROSCOOP® WORKS?

PHOTOCHEMISTRY

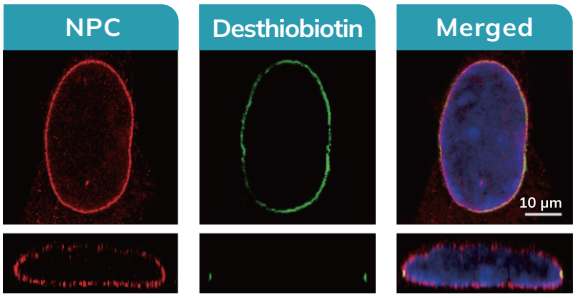
Submicron spatial photo-biotinylation

Photolabeling is achieved by utilizing two-photon illumination to trigger a photochemical reaction with a photocatalyst, which drives redox reactions of molecules that are composed of biotin and a photoactivable amino acid linker to form covalent bonds with, or biotinylate, amino acids within the illuminated focal spot at the submicron labeling resolution. Duration of each illumination spot is in the millisecond or sub-millisecond range to allow fast biotinylation for the entire sample.

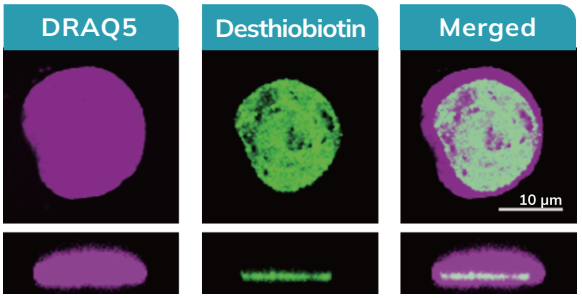




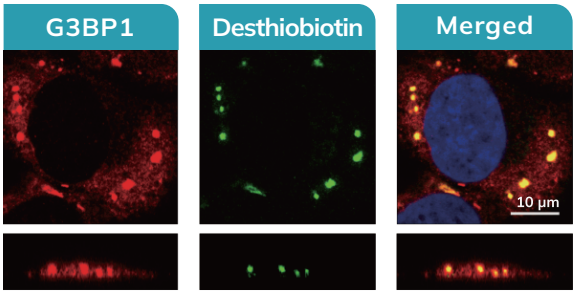
PHOTOLABELING IMAGING



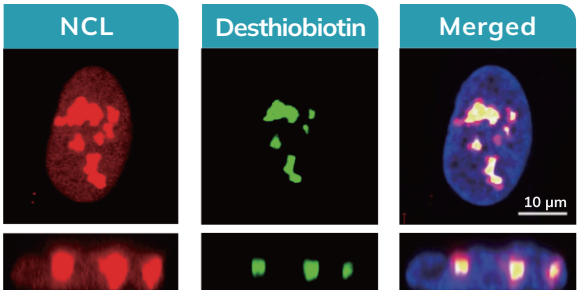
Nuclear pore complex



Nucleus

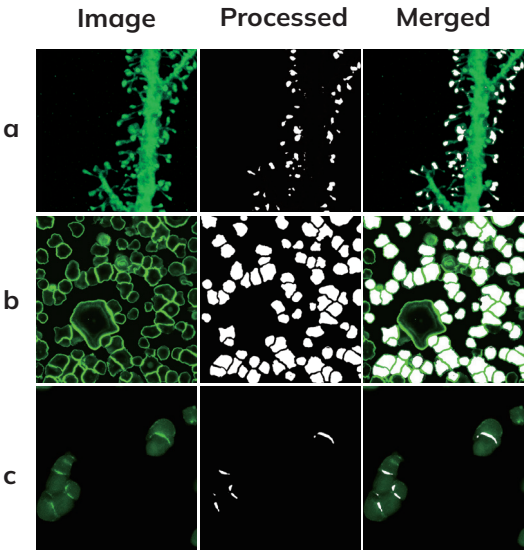


Stress granules



Nucleoli

ON-THE-FLY AI



AI-Guided Targeted Photolabeling

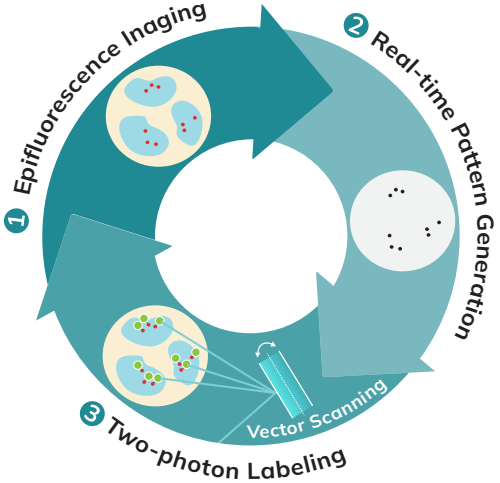
The Autoscoop AI functionality is based on computer vision designed for target recognition. The models are trained externally and then integrated into Autoscoop to generate pixel-level masks from microscopy images, enabling automated identification of regions of interest (ROIs) for downstream pattern generation and photolabeling. The system operates under a set of defined constraints—including fixed image resolutions (800×800 or 1600×1600), channel-last input formatting, normalized pixel values, and single-channel binary outputs—ensuring consistency and robustness in a production environment. Functionally, this AI does not perform biological interpretation but instead serves as a precision targeting tool within the workflow, translating imaging data into spatially resolved masks that guide high-specificity proteomic sampling.

MECHATRONICS

Synchronized Automation

The hardware-firmware-software intergrated mechatronic system enables accurate and fast control of scan systems, lasers, microscope, camera, epi-illumination light source, and peropheral devices in real time. The automated process was optimized by synchronizing steps from imaging to intelligent labeling with sub-millisecond temporal percisioin through this intergrated system to allow high-speed, hight-resolution spatial photolabeling.

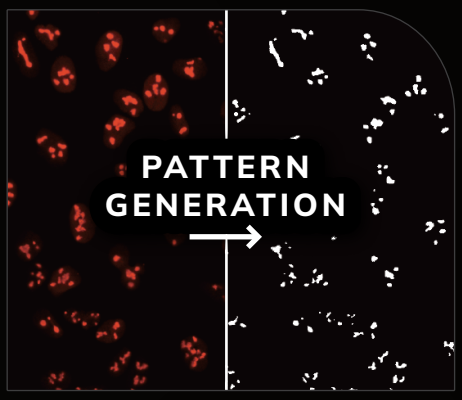
THOUSAND CYCLES OF REPEATS



Ultra-Content

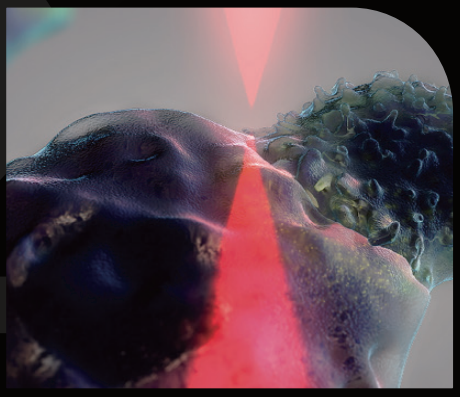
Proteins collected from the regions of interest of one FOV are not enough for mass spectrometer's sensitivity to reveal low abundant proteins. To address the protein amplification problem, Microscoop achieves protein accumulation by performing automated targeted photolabeling at ~10,000 or more FOVs to biotinylate enough proteins for mass spectrometry. The three steps of imaging-pattern generation-photolabeling are repeated for all FOVs. The speed of each step is optimized so that the entire photolabeling process can be finished overnight.

WORKFLOW



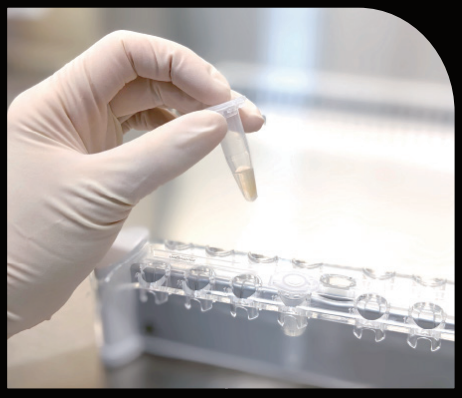
STEP 1
REAL-TIME IMAGE ANALYSIS

Photolabeling kit (i.e. Synlight-Rich Kit) is first added to a cell or tissue sample for a photochemical reaction. After the sample is loaded onto the stage, Microscoop takes an image (or images of multiple colors) of the sample at one field of view (FOV) at a time. The image or images are analyzed in real time by Microscoop's software Autoscoop, which executes traditional image processing or AI deep learning to segment the user's region of interest. Pre- or post-processing can be included to enhance segmentation accuracy.



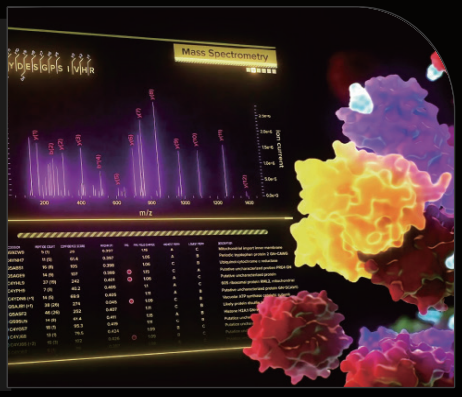
STEP 2
PATTERNED PHOTO-BIOTINYLATION

A femtosecond light source is controlled to illuminate the segmented region of interest one point at a time. This patterned illumination triggers targeted protein photo-biotinlyation in high spatial precision through the reactions of light-sensitive probes of Synlight-Rich Kit. This patterned photolabeling is repeated for thousands of FOVs automatically to assure that enough proteins are biotinlyated for later proteomics analysis using mass spectrometry.



STEP 3
PROTEIN EXTRACTION

Photolabeled cells or tissues are scraped from the slide or chamber. Materials from multiple slides or chambers can be pooled together to increase the total protein contents. The scraped sample is then treated with reagents of protein extraction kit (i.e. Synpull Kit) to lyse the sample, enrich the proteins by immunoprecipitation, and digest them into peptides for proteomics analysis.



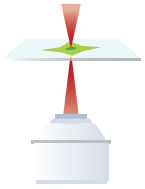
STEP 4
PROTEOMIC IDENTIFICATION

The collected peptides are sent to a mass spectrometer to perform LC-MS/MS analysis. Proteomes of both the photo-labeled and unlabeled (CTL) samples are obtained. By comparing the control and photolabeled proteomes, a location-specific proteome at the region of interest is obtained in high sensitivity, high specificity, and high spatial precision. Validation can be done by colocalization of immunostaining or additional functional assays.

REAGENT KITS FOR MICROSCOOP® / MINT

Syncell offers optimized reagent kits for Microscoop Mint. Synlight Kits are the proprietary kits that contain photochemical probes and other needed reagents for photolabeling. Synlight-Rich Kit is suitable for features larger than ~350nm with high labeling efficiency. Synpull Kit contains a large group of reagents optimized for low-volume pulldown and mass spectrometry-ready preparation suitable for both cell and tissue samples.

PHOTOLABELING KIT



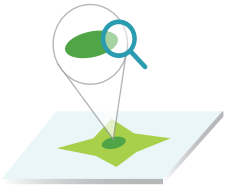
Targeted photolabeling by MICROSCOOP

NAME	QUANTITY
Synlight-Rich Kit	**Up to 6 reactions** (1-3 rounds of LC-MS/MS)
Synlight-Pure Cell Kit	**Up to 6 reactions** (1-3 rounds of LC-MS/MS)

- 350 nm precision for broad, unbiased discovery
- High sensitivity optimized for organelles, cell populations, and tissue compartments
- Ideal for exploratory studies and comparative profiling

- 25 nm labeling precision for subcellular structures and high-precision ROI definition
- Optimized for studying direct and indirect interacting proteins
- Designed for pharma discovery, trafficking, and mechanistic studies

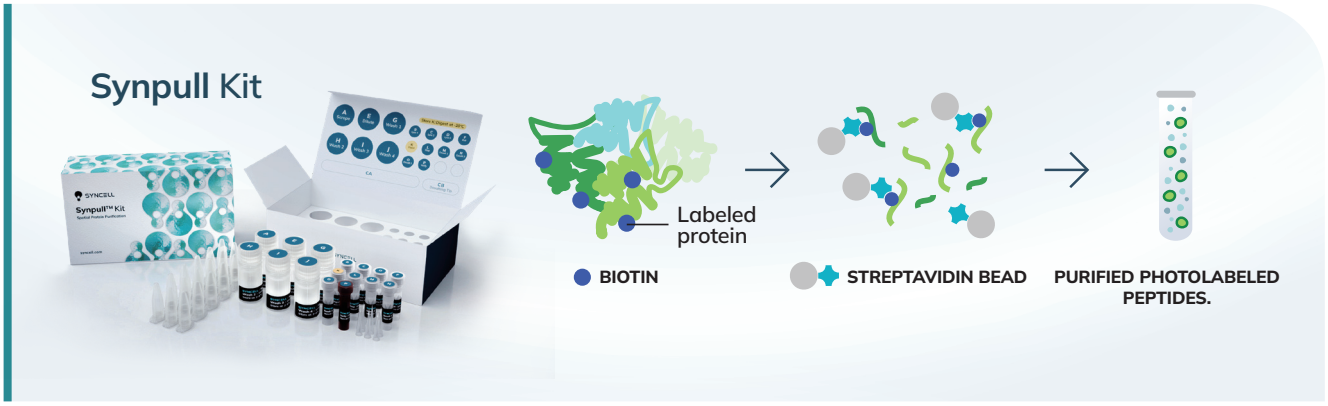
PROTEIN EXTRACTION KIT



Extraction and processing of photolabeled samples for MS-based proteomics

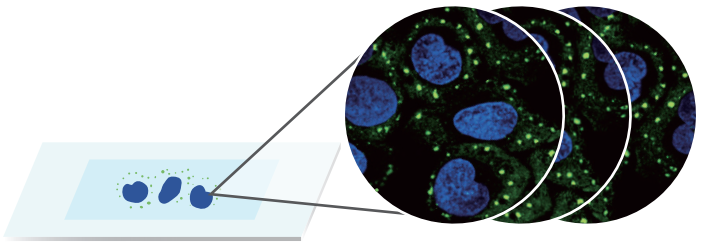
NAME	QUANTITY
Synpull Kit	**Up to 6 reactions** (3 rounds** of LC-MS/MS)

**1 round=1 test group+1 control group



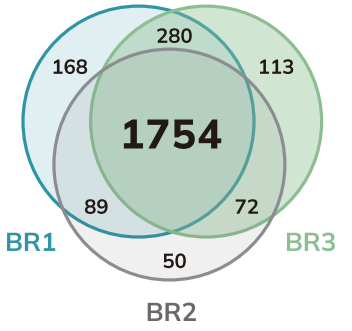
SUBCELLULAR SPATIAL PROTEOMIC DISCOVERY

INPUT

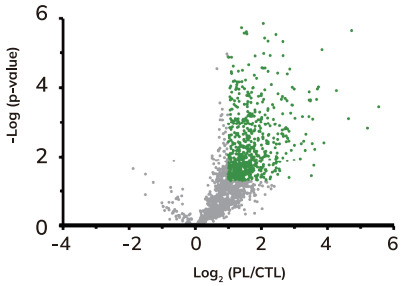


MICROSCOOP®
+
Mass Spectrometry

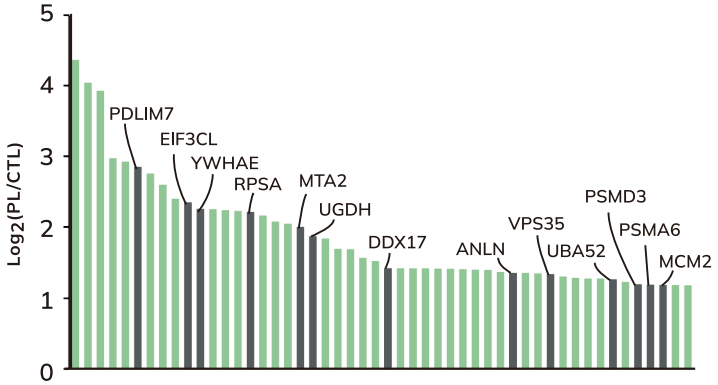
OUTPUT



Venn diagram of the stress granule proteins spatially isolated by Microscoop and analyzed by mass spectrometry.



Volcano plot of relative protein levels in photolabeled (PL) samples to control (CTL) samples in log_2 sccale. Over-represemrd (enriched) proteins are shown in green.



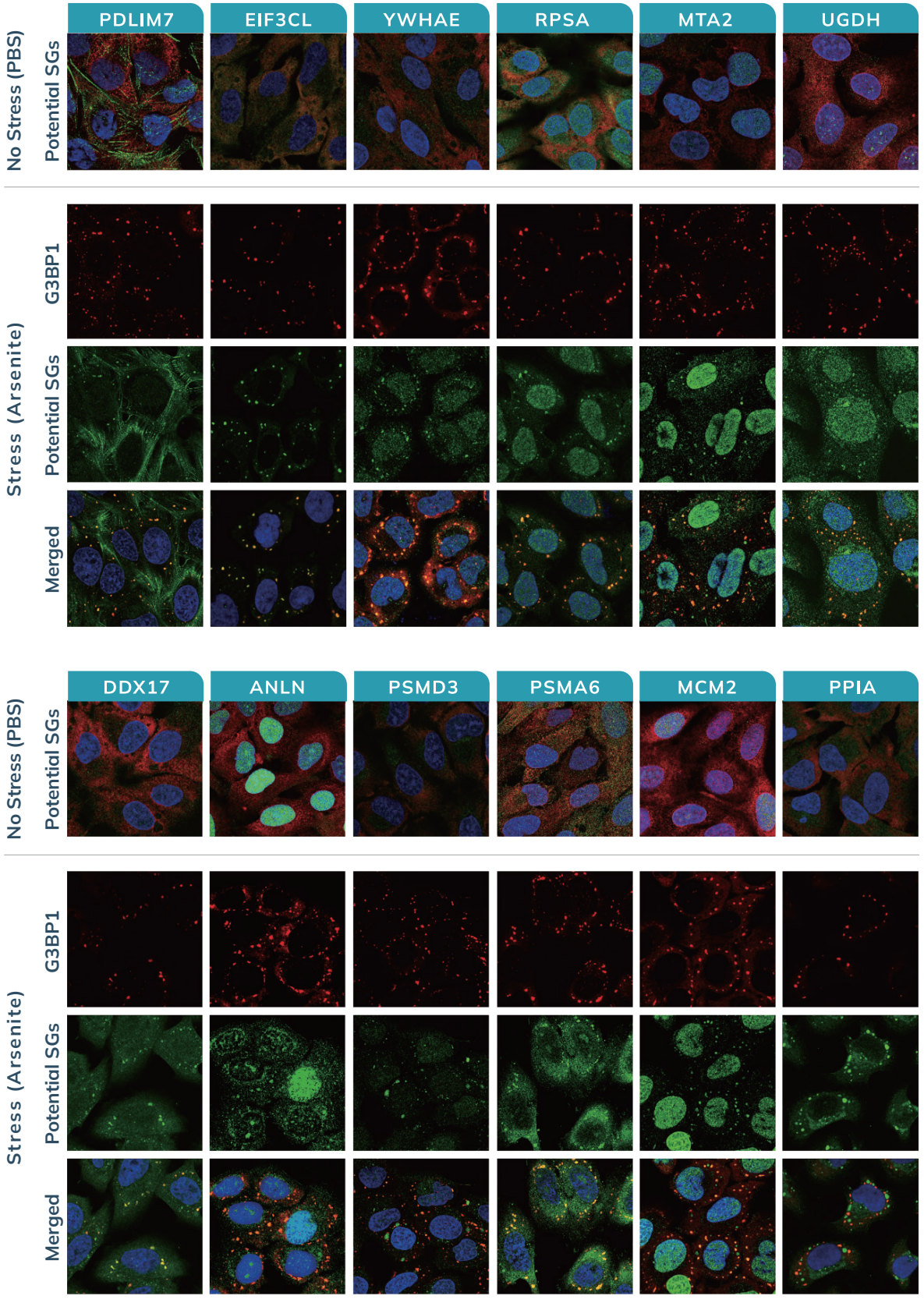
Top 50 spatially enriched proteins by Microsccop include many known stress granule proteins (green) and others without clear prior annotation as stress granule proteins (gray).

Protein ● Known ● Novel	Log_2 (PL/CTL)
PALLD	4.37
HNRNPK	4.04
CSDE1	3.92
VCL	2.97
GSPT1	2.92
PDLIM7	2.83
PABPC1	2.74
GARS1	2.60
HNRNPH1	2.39
EIF3CL	2.34
YWHAE	2.25
TARDBP	2.24
FXR1	2.23
EIF3E	2.22
RPSA	2.21
MOV10	2.16
HDLBP	2.07
HNRNPL	2.04
MTA2	1.99
UGDH	1.86
PCBP1	1.83
SYNCRIP	1.69
VCP	1.68
PABPC4	1.56
DPYSL2	1.52
DDX17	1.42
DDX50	1.42
EEF1D	1.42
CPNE3	1.42

A List of Proteins at the Targets

COLOCALIZATION VALIDATION

Proteins without clear prior annotation as stree granule proteinc were checked by co-immunostaining with stress granule marker G3BP1 one at a time. The colocalization result shows high specificity of the Microscoop technology. Novel protein constituents of stree granules were identified in bulk.



Colocalization validation of novel protein components of stress granules identified by the Microscoop technology. Confocal micrographs depict stress granule formation in U-2OS cells with or without an arsenite stress. Twelve proteins without clear prior annotation as stress granule proteins are highly colocalized with stress granule marker G3BP1. Green: proteins identified by Microscoop; Red: G3BP1; Blue: DAPI.

BROAD DISCOVERY APPLICATIONS

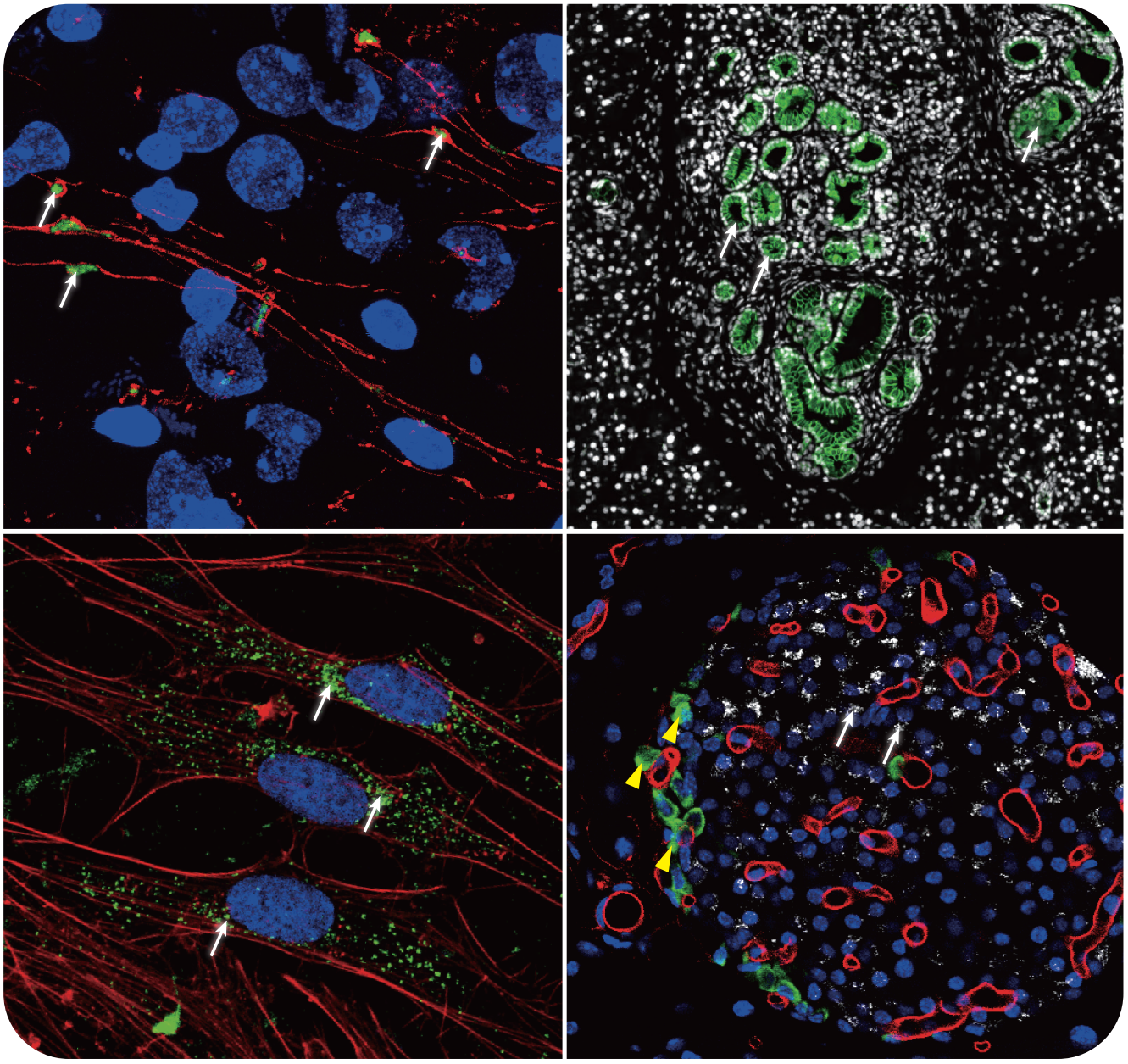
Neuroscience
Cancer Biology
Cell Biology
Immunology
Developmental Biology
Infectious Diseases
Aging
Metabolic Diseases
Inflammatory Diseases
Stem Cell Research
Immuno-Oncology
Pathology
Druggable Target Discovery
Biomarker Discovery
..... more

NEUROSCIENCE

Microscopy-recognizable structures such as β amyloids, reelin positive neurons at medial entorhinal layer II, or dendritic spines can be studied using Microscoop-enabled spatial enrichment.
Here is an example of hippocampal mossy fiber boutons photo-biotinylated by Microscoop (Alexa488-neutravidin, green) for subsequent protein pulldown and proteome discovery.

CANCER BIOLOGY

Problems such as identifying E-cadherin-associated proteins of metastatic cells, proteins at the cancer cell-T cell interface, and the proteome of Ki67+ cells in triple negative breast cancer can be addressed by Microscoop-enabled spatial enrichment and the subsequent proteomics analysis. Here is an example of the early-stage cancer marker cytokeratin19 around lesions in mouse pancreatic cancer.



CELL BIOLOGY

Proteomes of subcellular features such as larger extracellular vesicles, stress granules, filopodia tips, focal adhesion, or ER-mitochondria interface can be identified using Microscoop and mass spectrometry. Here shows an example of peroxisomes (PEX14, green) that can be photo-biotinylated using Microscoop for subcellular spatial isolation and proteomics analysis.

METABOLIC BIOLOGY

Microscoop-enabled proteomic discovery can be performed on other biological problems in immunology, metabolic diseases, developmental biology, infectious diseases, etc. Here is an image of pancreatic islet, where one can isolate α cells (glucagon, green), β-cells (insulin, white), or blood vessels (WGA, red) and identify novel protein constituents.

About SYNCELL

Syncell is a life science technology company at the forefront of developing tools for next-generation proteomics. Our pioneering Microscoop technology enables the discovery of spatial protein constituents, making de novo subcellular spatial proteomics feasible for the first time. This groundbreaking technology can be applied to a broad range of biological problems, aiding in the understanding of molecular mechanisms, identifying novel disease biomarkers, and revealing new drug targets.

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AVOID EYE OR SKIN EXPOSURE TO DIRECT OR SCATTERED RADIATION
CLASS 4 LASER PRODUCT
IEC 60825-1:2014 EN 60825-1:2014/A11:2021
WAVELENGTH: 780nm
AVERAGE POWER: <5 W
PULSE DURATION: <150 fs

COMPLIES WITH FDA PERFORMANCE STANDARDS FOR LASER PRODUCTS EXCEPT FOR CONFORMANCE WITH IEC 60825-1 ED. 3., AS DESCRIBED IN LASER NOTICE NO. 56, DATED MAY 8, 2019.