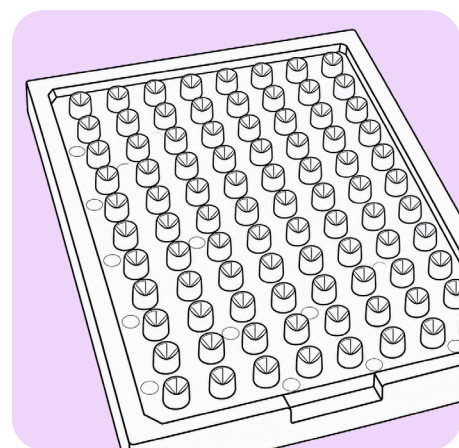
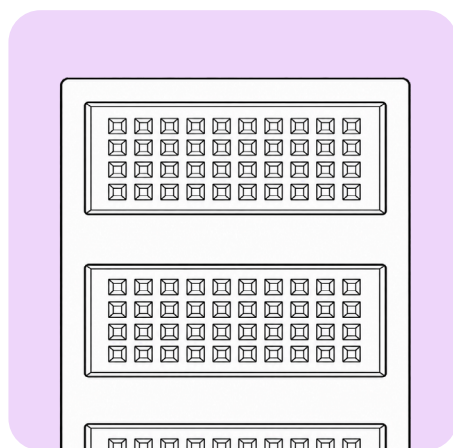
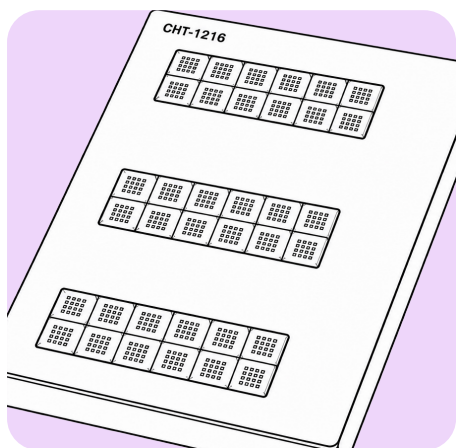
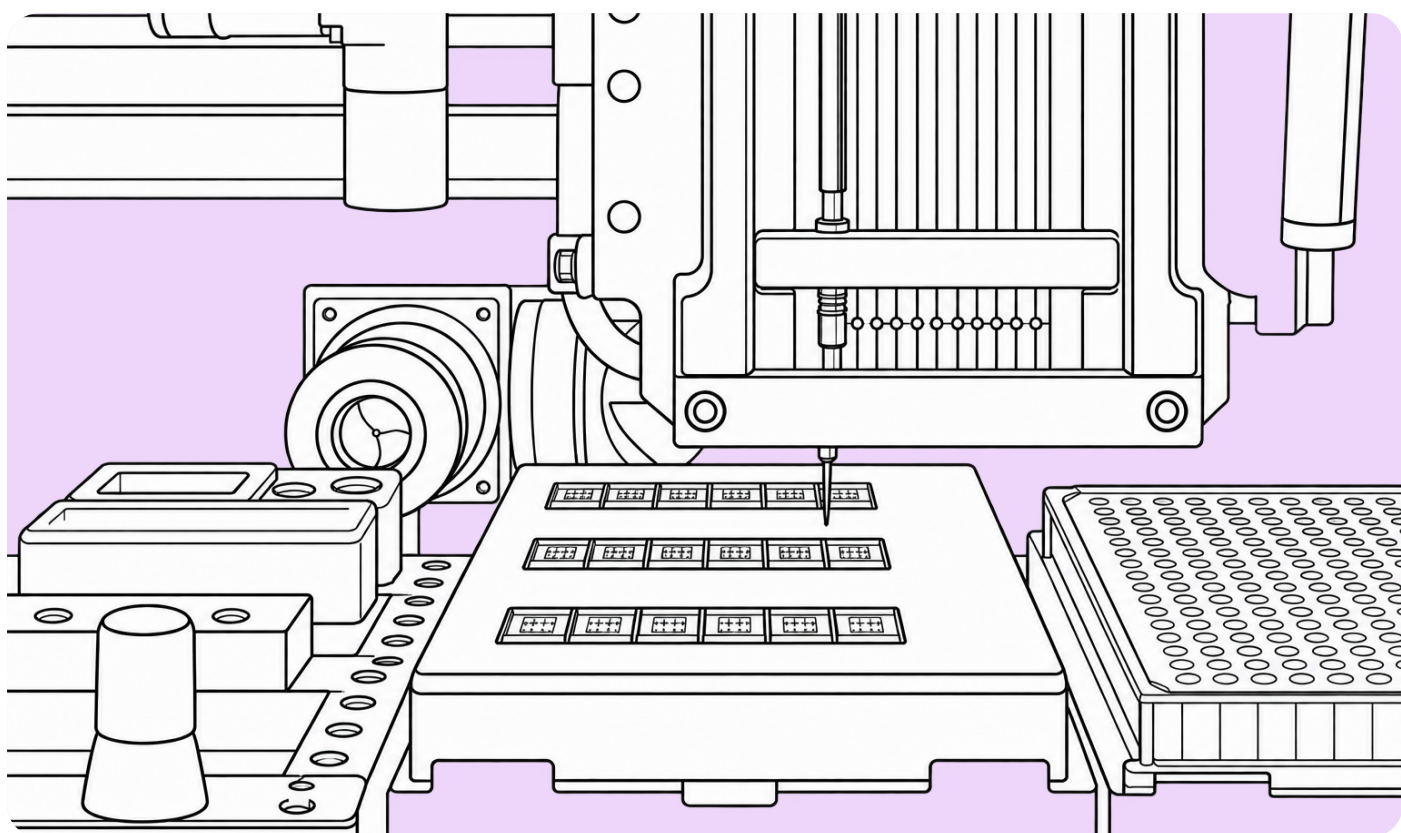


PROTEOCHIP

PRODUCT LINE

ONE PROTEOCHIP® RANGE. THREE FORMATS. ONE STREAMLINED PATH FROM SINGLE CELL TO LC-MS.



Explore the proteoCHIP® range for sensitive, scalable single-cell and spatial proteomics — from label-free workflows to high-throughput multiplexed analysis.

Why proteoCHIP?

Proteins can't be amplified. In single-cell and spatial proteomics, that means every molecule lost during sample prep is lost for good, and even small losses can compromise sensitivity. Every transfer, every manual step, is a point where a non-amplifiable protein can be lost. proteoCHIP is engineered to remove that risk at each stage, from isolation to LC-MS.



MINIATURIZED

Nanoliter-scale reactions reduce sample and reagent consumption while supporting sensitive proteomic analysis.



LOSS-MINIMIZED

Designed to reduce transfers, manual handling and sample loss throughout sample preparation.



AUTOMATED

Integrates with the cellenONE® platform for automated single-cell isolation and precision dispensing.



SCALABLE

Choose the format that fits your experimental scale — from exploratory label-free studies to high-throughput multiplexed workflows.



LC-MS READY

Designed for streamlined sample recovery and direct interfacing with downstream LC-MS workflows, so the sample reaches the instrument without an extra manual handoff.



REPRODUCIBLE

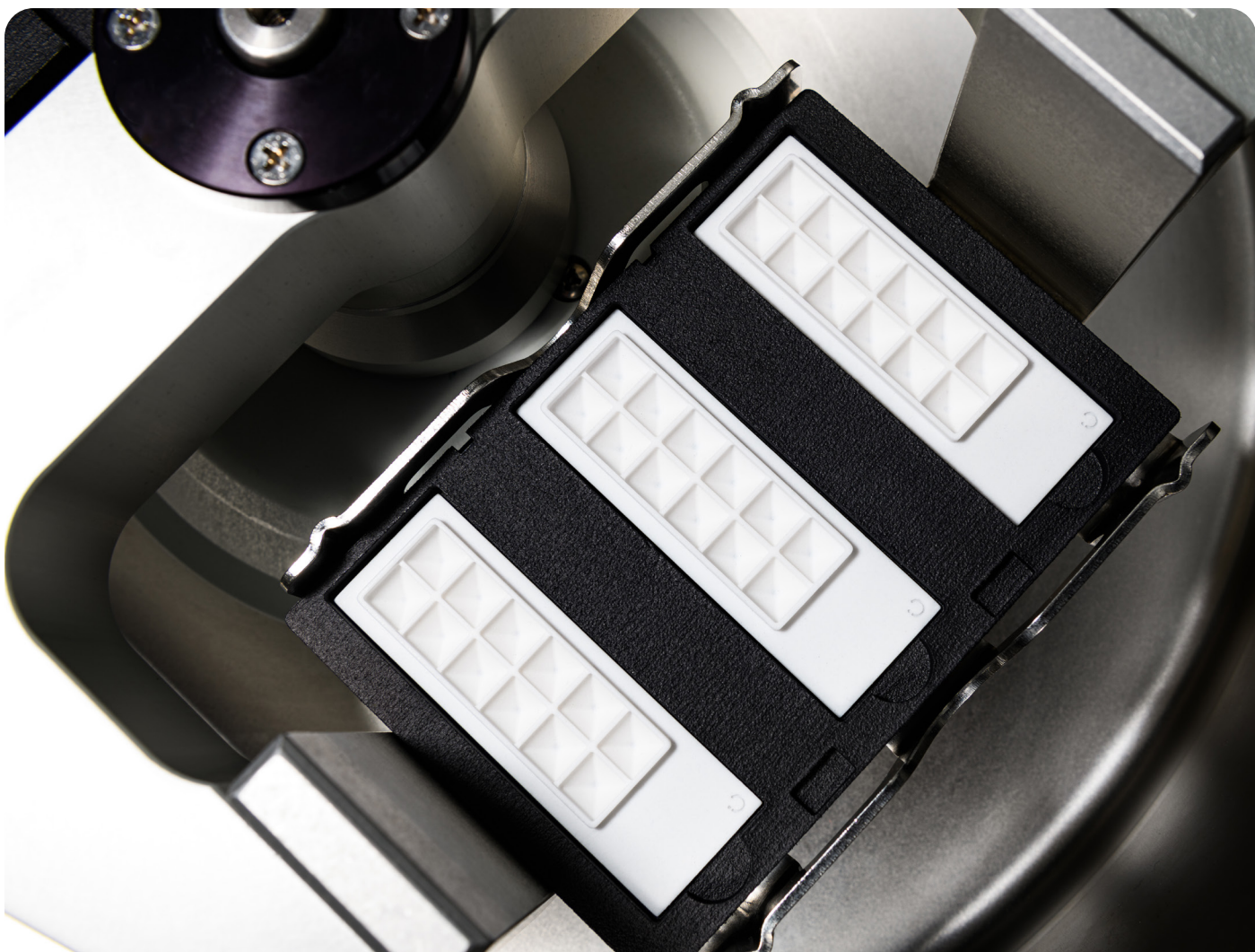
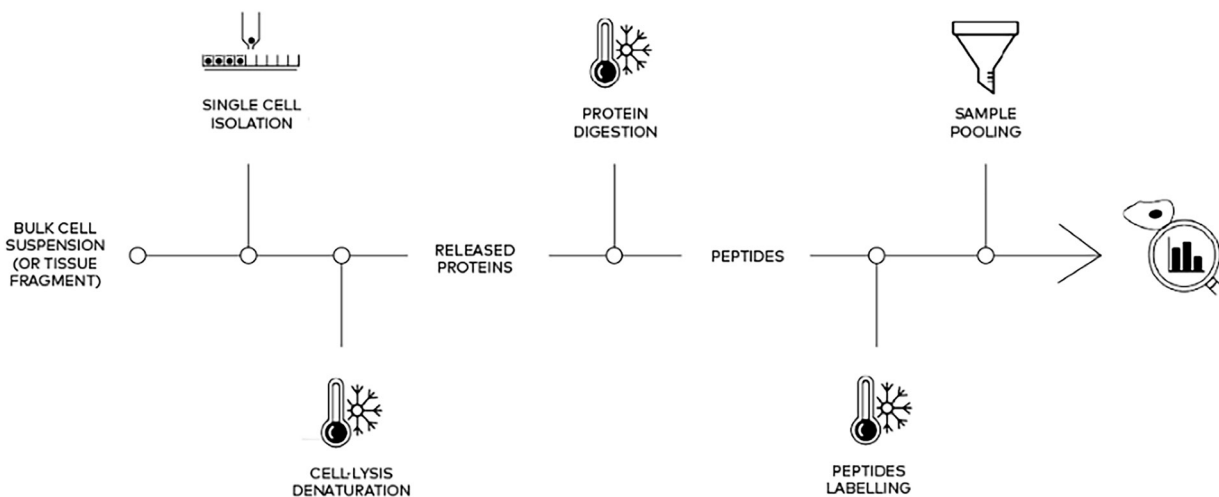
Automation and standardized workflows help reduce variability and improve consistency across experiments.



The workflow

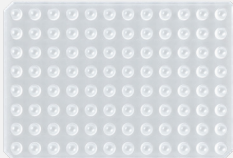
A streamlined workflow from single-cell isolation to mass spectrometry.

The proteoCHIP is designed to work with cellenONE for image-based single-cell isolation and pico/nanoliter dispensing, with downstream sample recovery and LC-MS interfacing.



The range

One range. Three ways to scale your single-cell proteomics.

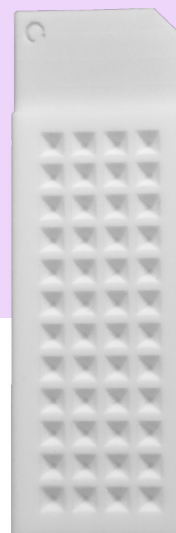
			
PRODUCT REFERENCE	C-PLF-48-3 and C-PLF480F-3 (oil-free)	C-PEVO-96-10	CPK-1216
SCP APPROACH	L A B E L F R E E		Multiplexed (TMTpro™)
CELLS PER RUN	Up to 144	Up to 192	Up to 576
PERFORMANCE	Up to 5,000 proteins/cell on the latest generation MS systems		Up to 1,400 proteins per cell
WORKFLOW TIME	< 3 hours		4-5 hours
SAMPLE INTERFACE	Direct transfer to LC-MS/MS through autosampler or manual pipetting	Direct transfer to Evtips through centrifugation for simultaneous sample clean-up and transfer	Centrifugal pooling followed by direct transfer to LC-MS/MS through autosampler or manual pipetting
IDEAL FOR	Interfacing with Bruker nanoElute® systems, sensible samples	Seamless interfacing with Evosep One, unprecedented reproducibility, spatial proteomics	High throughput, good signal-to-noise ratio even with low or no carrier. Interfacing with Thermo Scientific™ Vanquish™ Neo UHPLC autosampler

proteoCHIP 12*16

Multiplex more cells. Get more from every LC-MS run.

The **proteoCHIP® 12×16** is designed for high-throughput, multiplexed single-cell proteomics, enabling analysis of up to 576 single cells per run.

Its **12 × 16** well format supports TMTpro-based multiplexing, allowing samples to be combined for parallel LC-MS/MS analysis. Automated isolation, dispensing, labeling, pooling and transfer on the cellenONE® platform streamline the workflow from individual cells to multiplexed samples.



Up to 576 cells per run

Increase experimental scale and statistical power for population-level studies.



16-plex TMTpro workflow

Multiplex samples for efficient comparative analysis.



Automated end-to-end preparation

Reduce manual handling across cell isolation, reagent dispensing, labeling and pooling.



Low-adsorption polymer

Designed to minimize sample loss during low-volume processing.



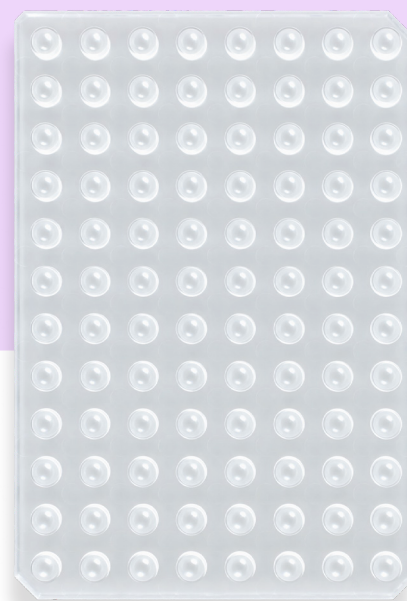
Efficient sample recovery

Pooling funnels support recovery by centrifugation.

FIELD PROVEN

In this study, we explored the possibility of applying the single-cell proteomics technology to a single-protoplast proteomic analysis and identified about a thousand of proteins from single protoplasts."
— Vu, H.M., Lee, J.Y., Kim, Y. et al. Journal of Journal of Analytical Science and Technology

proteoCHIP EVO 96

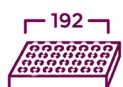


Scale your single-cell proteomics. Simplify your workflow.

The **proteoCHIP® EVO 96** brings speed, scale and streamlined sample transfer to label-free single-cell proteomics.

With 96 wells per chip and up to 192 samples per run, **EVO 96** enables preparation of hundreds of single-cell samples in under three hours.

Its integrated transfer workflow enables direct recovery into Evotips by centrifugation, simplifying sample handling and providing a streamlined path to the Evosep One LC system.



High-throughput processing

Prepare up to 192 single-cell samples per run.



Fast workflow

Complete sample preparation in under three hours.



Direct-to-Evotip transfer

Transfer samples directly to Evotips by centrifugation, minimizing handling and potential sample loss.



Low-loss sample preparation

Miniaturized reactions and streamlined recovery help preserve precious peptides.



Built for reproducibility

Automation reduces manual steps and variability across large experiments.

FIELD PROVEN

Our workflow sets a benchmark in SCP for sensitivity and throughput, with broad applications in basic biology and biomedicine for identification of cell type-specific markers and therapeutic targets." Ye, Z., Sabatier, P., van der Hoeven, L. et al. Nature Methods 22, 499–509 (2025)

proteoCHIP LF48



Reliable and sensitive. Built for exploratory single-cell proteomics.

The **proteoCHIP® LF 48** is designed for sensitive, label-free single-cell proteomics where robustness and reproducibility are critical. Its optimized well geometry and evaporation control support reliable sample preparation while minimizing sample loss.

With up to 144 single-cell samples per run, **LF 48** provides a practical solution for exploratory studies and challenging or precious cell types.



Up to 144 cells per run

Process 48 wells per chip across three chips for parallel single-cell sample preparation.



Controlled evaporation

Oil-sealed wells help maintain reaction volumes and minimize evaporation. An oil-free option is also available.



Low-volume reactions

Miniaturized reactions reduce reagent consumption while supporting sensitive peptide recovery.



Easy recovery

Sloped wells facilitate pipetting and sample recovery.



Automated workflow

From single-cell isolation to sample preparation, LF 48 integrates with the cellenONE® platform to reduce manual handling.

FIELD PROVEN

Our workflow enables us to distinguish between in vitro analogs of two human blastocyst lineages: naive human pluripotent stem cells (epiblast) and trophectoderm-like cells." — Bubis, J.A., Arrey, T.N., Damoc, E. et al. Nature Methods 22, 510–519 (2025)



PROTEO CHIP

Reliable single-cell and spatial proteomics data, at any scale, supports discovery in basic biology, drug development, and precision medicine.

12*16

High-throughput multiplexed single-cell proteomics

LF48

Robust label-free sample preparation

EVO 96

Scalable label-free workflows with direct Evotip transfer

READY TO SCALE
YOUR SINGLE-CELL
PROTEOMICS?

TALK TO OUR
APPLICATION EXPERTS.



CONTACT US

SCIENION GmbH

Wagner-Régeny-Str. 15
12489 Berlin, Germany
Fon +49 (0)30 6392 1700
Fax +49 (0)30 6392 1701
support@scienion.com
www.scienion.com

SCIENION US, Inc

1231 W. Warner Road, Ste. 103
Tempe, AZ 85284
United States
Tel: +1 (888) 988-3842
USsalesupport@scienion.com

SCIENION (UK) Ltd

2000, Lakeside North Harbour
Western Road, Portsmouth
PO6 3EN
United Kingdom
+44 (0)7483 388 271
+44 (0)23 9323 3603
support@scienion.com

SCIENION China

Room 1106B Building 3
No.391 Guiping Road Xuhui
District, Shanghai
Phone: +86 186 2170 9292
support@scienion.com
www.scienion.com