

Efficient Peptide Fractionation, Designed for Reproducible Proteomics

Spin Tips for Peptide

GL-Tip SCX and GL-Tip SDB-SCX

**Less Redundancy.
More Identifications.**



Product Concept & Background

Why Fractionation Matters

In large-scale proteomics, reducing sample complexity prior to LC–MS/MS analysis is essential for improving peptide identification depth. Strong cation-exchange (SCX)–based fractionation is widely adopted; however, conventional salt-gradient methods often suffer from peptide redundancy across fractions, resulting in inefficient use of MS acquisition time.

GL-Tip Concept

The GL-Tip Series was developed to address these limitations by combining optimized polymeric media with a centrifuge-based workflow that ensures reproducible fractionation with minimal operational complexity. The series supports both conventional SCX fractionation and an advanced TFA gradient elution strategy, offering improved orthogonality between fractions.



Improved Peptide Fractionation Efficiency Using TFA Gradient Elution
DLD-1 human colorectal cancer cell–derived phosphopeptides

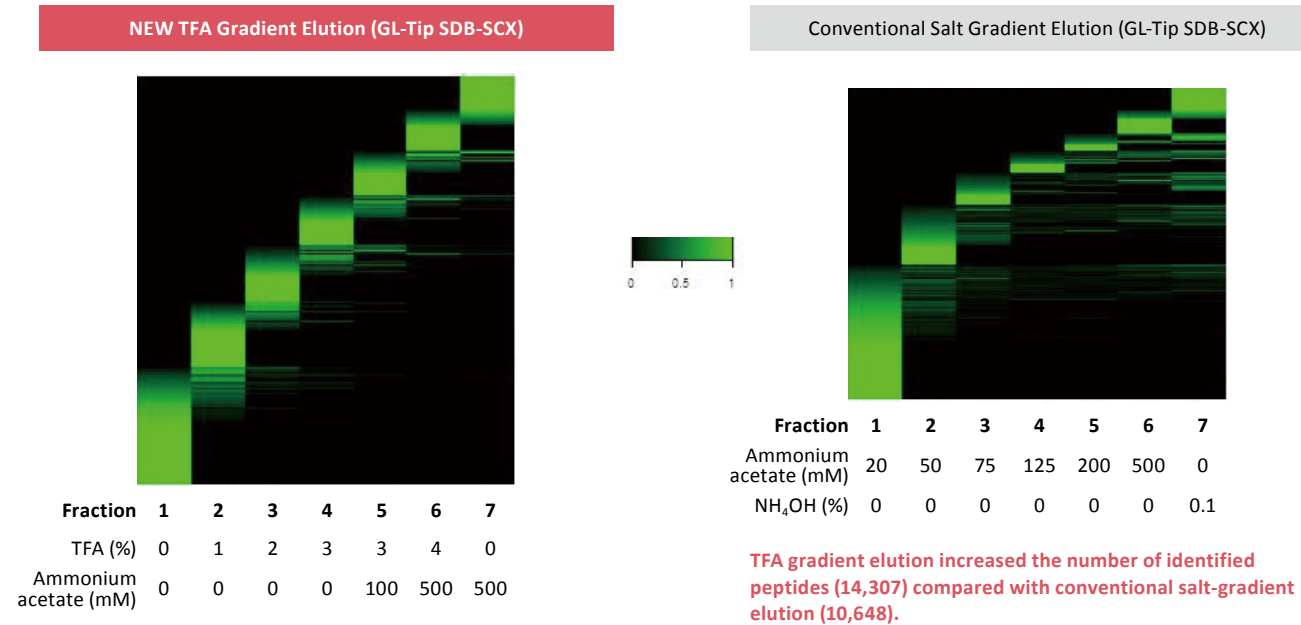


Figure. Comparison of peptide fractionation efficiency between TFA gradient elution and conventional salt-gradient elution using GL-Tip SDB-SCX. The TFA gradient method reduced peptide overlap between fractions and increased the total number of identified non-redundant phosphopeptides. Data provided by the National Institute of Biomedical Innovation (Dr. Jun Adachi).

Products & Performance

GL-Tip SCX

GL-Tip SCX is packed with a strong cation-exchange polymer optimized for peptide fractionation from desalted samples. It provides consistent fractionation performance suitable for routine and comparative proteomics studies.

GL-Tip SDB-SCX

GL-Tip SDB-SCX employs a dual-layer configuration consisting of a styrene divinylbenzene (SDB) polymer layer for on-tip desalting and an SCX layer for fractionation. This design allows direct loading of non-desalted peptide samples, reducing sample handling steps.

Performance Highlights

- Reduced peptide redundancy across fractions
- Increased total number of identified peptides using TFA gradient elution
- Improved fraction orthogonality compared with traditional salt-gradient methods

Principle of Peptide Fractionation

Strong cation-exchange (SCX) fractionation is widely used in shotgun proteomics to reduce sample complexity prior to LC–MS/MS analysis. In conventional salt-gradient elution, however, identical peptides are often distributed across multiple fractions, leading to redundancy and inefficient use of MS acquisition time.

The GL-Tip SDB-SCX supports a newly developed TFA gradient elution method (patent applied) that modulates peptide elution strength through changes in acidity rather than salt concentration. This approach:

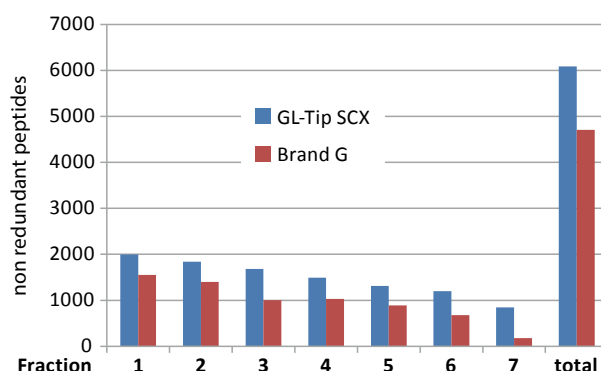
- Reduces peptide overlap between adjacent fractions
- Improves the effective depth of peptide identification
- Preserves a simple and reproducible experimental workflow

GL-Tip SCX Increases the Number of Identified Non-Redundant Peptides

GL-Tip SCX recovered a higher number of non-redundant peptides than a commercially available SCX tip column (Brand G). The use of the optimized TFA gradient elution method reduced peptide overlap between fractions, resulting in improved identification efficiency across the entire fraction set.

Sample and analytical conditions

Sample: Trypsin-digested HeLa cell lysate (25 µg)
 Fractionation: GL-Tip SCX
 LC–MS: LTQ-Orbitrap XL
 LC gradient: 45 min
 Data analysis: MaxQuant v1.5.1.2, UniProt human database
 Identification: 40% of recovered peptides analyzed



Number of Identified Non-Redundant Peptides

Fraction	1	2	3	4	5	6	7	Total
GL-Tip SCX	1996	1839	1684	1491	1311	1196	847	6085
Brand G	1552	1397	1004	1032	890	676	179	4704

Figure. Comparison of the number of identified non-redundant peptides obtained using GL-Tip SCX and a commercially available SCX tip column (Brand G). GL-Tip SCX consistently yielded higher peptide counts across all fractions, resulting in improved overall identification efficiency.

Data provided by the National Institute of Biomedical Innovation (Dr. Jun Adachi).

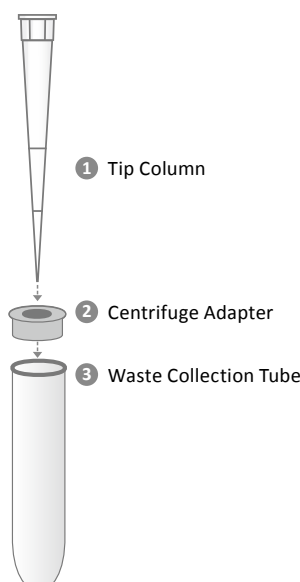
Workflow & Specifications

Typical Workflow

1. Condition the GL-Tip with appropriate solvents
2. Load peptide sample
3. Centrifuge at approximately 3,000 × g
4. Wash to remove residual salts
5. Elute peptides using stepwise or gradient buffers
6. Collect fractions for LC–MS/MS analysis

Key Specifications

- Tip volume: 200 µL
- Typical sample loading capacity: 60 µg (Angiotensin II)
- Compatible with standard laboratory centrifuges



Specification



Item	GL-Tip SCX	GL-Tip SDB-SCX
Tip volume	200 μ L	200 μ L
Test compound	Angiotensin II	Angiotensin II
Typical sample loading capacity*	$\sim$ 60 μ g	$\sim$ 60 μ g

* Capacity is shown as an approximate value and may vary depending on sample composition.

Ordering Information

Description	Cat. No.
GL-Tip SDB-SCX, 96 pcs/pack	7510-11202
GL-Tip SCX, 96 pcs/pack	7510-11203
Centrifuge Adapter, 24 pcs/pack	5010-21514
Centrifuge Adapter for 96-well plate, 1 pc	5010-21341
Centrifuge Adapter for 96-well plate, 2 pcs	5010-21343

*A centrifuge adapter (24 pcs/pack) is required for the use of GL-Tip spin tips and needs to be purchased only once.

*The centrifuge adapter is reusable.

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