

Resource Summary Report

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Skyline

RRID:SCR_014080

Type: Tool

Proper Citation

Skyline (RRID:SCR_014080)

Resource Information

URL: <https://skyline.gs.washington.edu/labkey/project/home/software/Skyline/begin.view>

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Description: Software tool as Windows client application for targeted proteomics method creation and quantitative data analysis. Open source document editor for creating and analyzing targeted proteomics experiments. Used for large scale quantitative mass spectrometry studies in life sciences.

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: [PMID:20147306](#)

Keywords: Proteomics, SRM, MRM, DDA, DIA, shotgun, mass, spectrometry, data, analysis, quantitative

Funding: NCI U24 CA126479;
NCRR P41 RR011823;
NHLBI R01 HL082747;
NIA P30 AG013280;
NIDDK R01 DK069386

Availability: Free, Available for download, Freely available

Resource Name: Skyline

Resource ID: SCR_014080

License: Apache 2.0

Record Creation Time: 20220129T080318+0000

Record Last Update: 20260905T132742+0000

Ratings and Alerts

No rating or validation information has been found for Skyline.

No alerts have been found for Skyline.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3040 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Nayak S, et al. (2026) Discovery of BMS-986365, a First-in-Class Dual Androgen Receptor Ligand-Directed Degradar and Antagonist, for the Treatment of Advanced Prostate Cancer. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(1), 224.

Kochanova NY, et al. (2026) A time-resolved atlas of histone modifications during mitotic entry. *Molecular cell*, 86(9), 1653.

Savoca A, et al. (2026) Preclinical to Clinical Translation of Pharmacokinetic-Pharmacodynamic Relationship in EGFR Exon20Ins Mutations: A Modeling Framework for Irreversible Inhibitors. *Molecular cancer therapeutics*, 25(7), 1157.

Martín A, et al. (2026) Targeted KRASG12V Degradation in vivo Elicits Lung Adenocarcinoma Regression with Subsequent Relapse from Dysregulated Proteolysis. *Cancer research*.

Osman ST, et al. (2026) Repurposing SGLT2 and DPP-4 inhibitors for mild cognitive impairment in type 2 diabetes mellitus: Insights from proteomics, target prediction and molecular docking. *British journal of pharmacology*, 183(10), 2533.

Ravazza D, et al. (2026) Quantitative Mass Spectrometry-Based Biodistribution of Monoclonal Antibodies: An Alternative to Radio-Biodistribution. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(38), e20265.

Veeckmans G, et al. (2026) Ferroptosis inhibition enhances liver and lung graft function. *Cell*, 189(13), 3991.

Mitra T, et al. (2026) MEK-dependent bioenergetic demand drives terminal CD8+ T cell exhaustion. *Immunity*.

Röhr PT, et al. (2026) Deciphering the Molecular Bittercode in Potato Protein Hydrolysates through a Sensoproteomics Approach. *Journal of agricultural and food chemistry*, 74(1), 1357.

- Schmitt F, et al. (2026) Metabolic Profiling of the EmDia Cohort by LC-MS Reveals Empagliflozin-Intake Associated Regulation of 1,5-anhydroglucitol and Urate. *Proteomics*, 26(1), 44.
- Xiang H, et al. (2026) Predominant mutated non-canonical tumor-specific antigens identified by proteogenomics demonstrate immunogenicity and tumor suppression in CRC. *Cell genomics*, 6(1), 101062.
- Liu X, et al. (2026) A high-throughput N-glycan analysis strategy with targeted mass spectrometry (HTnGQs-target) for liver disease diagnosis. *Chemical science*, 17(1), 364.
- Chai M, et al. (2026) Mass spectrometry footprinting reveals microsomal CYP2A6 structural changes induced by interaction with its reductase flavin mononucleotide domain. *Drug metabolism and disposition: the biological fate of chemicals*, 54(1), 100210.
- Lu S, et al. (2026) *Lactiplantibacillus plantarum* GUANKE ameliorates influenza a virus-induced inflammation and lung barrier dysfunction through enhancing mitophagy and improving oxidative phosphorylation. *Cellular and molecular life sciences : CMLS*, 83(1), 107.
- Alhamad DW, et al. (2026) Tryptophan metabolites 3-hydroxykynurenine (3HK) and 3-hydroxyanthranilic acid (3HAA) increase oxidative stress and impair osteoblastic bone formation. *The Journal of biological chemistry*, 302(4), 111174.
- Zhang Y, et al. (2026) Microbiota-derived IPA protects against colitis by regulating intestinal HMGCS2-mediated ketogenesis to facilitate mucosal healing. *Nature communications*, 17(1).
- Chan HJ, et al. (2026) IsoPS-DIA: Dual Functionality of Absolute Targeted Quantification and Global Proteome Profiling. *Analytical chemistry*, 98(7), 5227.
- Thomann G, et al. (2026) Application of Proteomic Workflows for the Identification of Biomarkers for the Retrospective Verification of Sulfur Mustard Intoxication. *Analytical chemistry*, 98(14), 10550.
- Robbins JM, et al. (2026) Blood Biochemical Responses to Acute Exercise: Findings from the Molecular Transducers of Physical Activity Consortium (MoTrPAC). *bioRxiv : the preprint server for biology*.
- Najib N, et al. (2026) Plasma proteomics implicates NOX-driven redox imbalance in degenerative cervical myelopathy: findings from the Australian MYelopathy Natural History Registry [AO Spine RECODE-DCM research priority number 5]. *Redox report : communications in free radical research*, 31(1), 2649669.