

Resource Summary Report

Generated by ASWG on Sep 18, 2026

Lunenfeld-Tanenbaum Research Institute Network Biology Collaborative Centre Proteomics Core Facility

RRID:SCR_025375

Type: Tool

Proper Citation

Lunenfeld-Tanenbaum Research Institute Network Biology Collaborative Centre
Proteomics Core Facility (RRID:SCR_025375)

Resource Information

URL: <https://nbcc.lunenfeld.ca/facilities/proteomics>

Proper Citation: Lunenfeld-Tanenbaum Research Institute Network Biology Collaborative
Centre Proteomics Core Facility (RRID:SCR_025375)

Description: Provides mass-spectrometry based identification and quantification of proteins. Facility specializes in functional proteomics with focus on protein proximity and protein interaction mapping. Services include access to reagents, plasmids, sample preparation, mass spectrometry, and data analysis. Applications include: proximity-dependent biotinylation mapping to identify neighboring proteins in cells ,protein-protein interaction mapping,post-translational modification identification (with a focus on phosphorylation),differential protein abundance,chemical proteomics (identifying on- and off-target binding to small molecules or biologics)., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Synonyms: Lunenfeld-Tanenbaum Research Institute Network Biology Collaborative
Centre Proteomics, Network Biology Collaborative Centre Proteomics

Resource Type: access service resource, core facility, service resource

Keywords: ABRF, functional proteomics, protein proximity and protein interaction
mapping, mass spectrometry service, data analysis service,

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Lunenfeld-Tanenbaum Research Institute Network Biology
Collaborative Centre Proteomics Core Facility

Resource ID: SCR_025375

Alternate IDs: ABRF_2798

Alternate URLs: <https://coremarketplace.org/?FacilityID=2798&citation=1>

Record Creation Time: 20240525T053230+0000

Record Last Update: 20260912T200443+0000

Ratings and Alerts

No rating or validation information has been found for Lunenfeld-Tanenbaum Research Institute Network Biology Collaborative Centre Proteomics Core Facility.

No alerts have been found for Lunenfeld-Tanenbaum Research Institute Network Biology Collaborative Centre Proteomics Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Wu R, et al. (2026) KRAS-dependent glycolytic reprogramming of endothelial cells in sporadic arteriovenous malformations. EMBO molecular medicine, 18(3), 1091.

Xiong Y, et al. (2026) Molecular and Chromatin Accessibility Programs Underlying Epithelial Injury and Impaired Regeneration in Neonatal Necrotizing Enterocolitis. Cellular and molecular gastroenterology and hepatology, 20(6), 101730.

Tessier TM, et al. (2026) Identification of E3 ligase substrates and PROTAC-induced ubiquitylation sites using proximity-based identification of ubiquitin sites (PrIUS). Communications biology, 9(1).

Medak KD, et al. (2026) Semaglutide reduces murine blood pressure through the vascular smooth muscle GLP-1 receptor. JCI insight, 11(8).

Chana CK, et al. (2026) The molecular glue CLEO4-88 inhibits the ACAA1 thiolase by induced binding to GID4. Nature chemical biology.

Kumar N, et al. (2026) HSV-1 hijacks the DNA repair protein RAD51 at gene promoters to drive viral transcription. bioRxiv : the preprint server for biology.

Bradley CA, et al. (2026) An X-linked long non-coding RNA, PTCHD1-AS, and the core features of autism. Nature, 655(8122), 418.

Gonzalez-Rellan MJ, et al. (2026) The weight-loss-independent hepatoprotective benefits of semaglutide are orchestrated by intrahepatic sinusoidal endothelial GLP-1 receptors. *Cell metabolism*, 38(7), 1334.

Evdokimova V, et al. (2026) Proinflammatory signaling in Ewing sarcoma is driven by retroelement activity and counteracted by reverse transcriptase inhibitors. *Cell reports*, 45(7), 117708.

Park T, et al. (2025) Long AKAP18 isoforms anchor ubiquitin specific proteinases and coordinate calcium reuptake at the sarcoplasmic reticulum. *The Journal of biological chemistry*, 301(7), 110317.

Fu C, et al. (2025) Expansion of the functional genomics GRACE library reveals genes relevant for temperature-dependent fitness in *Candida albicans*. *PLoS biology*, 23(10), e3003409.

Park T, et al. (2025) Proximity-dependent proteomics and network analysis of adenylyl cyclase isoforms 5, 6, and 9 in cardiomyocytes. *The Journal of biological chemistry*, 301(9), 110539.

Xiong EH, et al. (2025) Identification and characterization of components of the *Candida albicans* inner kinetochore. *Genetics*, 231(3).

Kitaygorodsky J, et al. (2025) Optimizing Proximity Proteomics on the EvoSep-timsTOF LC-MS System. *Proteomics*, 25(15), 58.

Feng MY, et al. (2025) Molecular cartography of the human down syndrome and trisomic mouse brain. *Nature communications*, 16(1), 8689.