

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 1, 2026

[SRMAtlas](#)

RRID:SCR_016996

Type: Tool

Proper Citation

SRMAtlas (RRID:SCR_016996)

Resource Information

URL: <http://www.mrmatlas.org/>

Proper Citation: SRMAtlas (RRID:SCR_016996)

Description: Resource of targeted proteomics assays to detect and quantify proteins in complex proteome digests by mass spectrometry. Used to quantify the complete human proteome.

Abbreviations: SRM Atlas, SRMAtlas

Resource Type: atlas, data or information resource, database

Defining Citation: [PMID:27453469](#)

Keywords: collection, proteomic, assay, detect, quantify, protein, mass, spectrometry, peptide

Funding: American Recovery and Reinvestment Act ;
NHGRI RC2 HG005805;
NIGMS R01 GM087221;
NCRR S10 RR027584;
NIGMS P50 GM076547;
Luxembourg Centre for Systems Biomedicine University Luxembourg ;
European Research Council ;
Swiss National Science Foundation

Availability: Publicly available, Registration required

Resource Name: SRMAtlas

Resource ID: SCR_016996

Record Creation Time: 20220129T080333+0000

Record Last Update: 20260801T042807+0000

Ratings and Alerts

No rating or validation information has been found for SRMATlas.

No alerts have been found for SRMATlas.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Owusu M, et al. (2019) Mapping the Human Kinome in Response to DNA Damage. Cell reports, 26(3), 555.

Rezeli M, et al. (2011) MRM assay for quantitation of complement components in human blood plasma - a feasibility study on multiple sclerosis. Journal of proteomics, 75(1), 211.

Fendt SM, et al. (2010) Unraveling condition-dependent networks of transcription factors that control metabolic pathway activity in yeast. Molecular systems biology, 6, 432.