

# Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

## Center for Computational Mass Spectrometry

RRID:SCR\_008161

Type: Tool

---

### Proper Citation

Center for Computational Mass Spectrometry (RRID:SCR\_008161)

---

### Resource Information

**URL:** <http://proteomics.ucsd.edu/>

**Proper Citation:** Center for Computational Mass Spectrometry (RRID:SCR\_008161)

**Description:** Biomedical technology research center that focuses on the computational bottlenecks that impair the interpretation of data, bringing modern algorithmic approaches to mass spectrometry and building a new generation of reliable, open-access software tools to support both new mass spectrometry instrumentation and emerging applications.

**Abbreviations:** CCMS

**Synonyms:** UCSD Center for Computational Mass Spectrometry

**Resource Type:** biomedical technology research center, training resource

**Keywords:** systems biology technology center, mass spectrometry, algorithm, computational proteomics, proteomics

**Funding:** NCRR ;  
NIGMS

**Resource Name:** Center for Computational Mass Spectrometry

**Resource ID:** SCR\_008161

**Alternate IDs:** nlx\_152677

**Alternate URLs:** <https://api.datacite.org/doi/prefix=10.25345>

**Record Creation Time:** 20220129T080245+0000

**Record Last Update:** 20260905T133328+0000

---

### Ratings and Alerts

No rating or validation information has been found for Center for Computational Mass Spectrometry.

No alerts have been found for Center for Computational Mass Spectrometry.

---

## Data and Source Information

**Source:** [SciCrunch Registry](#)

---

## Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Sanyal A, et al. (2019) Alpha-Synuclein Is a Target of Fic-Mediated Adenylation/AMPylation: Possible Implications for Parkinson's Disease. *Journal of molecular biology*, 431(12), 2266.

Okada H, et al. (2019) Sex-dependent and sex-independent regulatory systems of size variation in natural populations. *Molecular systems biology*, 15(11), e9012.

Nakatsuji T, et al. (2018) A commensal strain of *Staphylococcus epidermidis* protects against skin neoplasia. *Science advances*, 4(2), eaao4502.

Okada H, et al. (2016) Proteome-wide association studies identify biochemical modules associated with a wing-size phenotype in *Drosophila melanogaster*. *Nature communications*, 7, 12649.

Lynch DC, et al. (2014) Disrupted auto-regulation of the spliceosomal gene SNRPB causes cerebro-costo-mandibular syndrome. *Nature communications*, 5, 4483.

Tovchigrechko A, et al. (2014) PGP: parallel prokaryotic proteogenomics pipeline for MPI clusters, high-throughput batch clusters and multicore workstations. *Bioinformatics (Oxford, England)*, 30(10), 1469.

Kim S, et al. (2014) MS-GF+ makes progress towards a universal database search tool for proteomics. *Nature communications*, 5, 5277.