

# Resource Summary Report

Generated by [nidm-terms](#) on Jul 29, 2026

## Loom

RRID:SCR\_028253

Type: Tool

### Proper Citation

Loom (RRID:SCR\_028253)

### Resource Information

**URL:** <https://linnarssonlab.org/loompy/format/index.html>

**Proper Citation:** Loom (RRID:SCR\_028253)

**Description:** Loom is an efficient HDF5-based file format for storing large, high-dimensional single-cell genomics datasets, including data, metadata, and clustering results. Loom file format is designed to efficiently hold large omics datasets. Typically, such data takes the form of a large matrix of numbers, along with metadata for the rows and columns. Loom files (.loom) are created in the HDF5 file format, which supports an internal collection of numerical multidimensional datasets. HDF5 is supported by many computer languages, including Python, R, MATLAB, Mathematica, C, C++, Java, and Ruby.

**Synonyms:** , .loom, Loom File Format

**Resource Type:** data or information resource, narrative resource, standard specification

**Keywords:** HDF5-based file format, hold large omics datasets, large matrix of numbers, metadata for rows and columns,

**Availability:** Free, Freely available,

**Resource Name:** Loom

**Resource ID:** SCR\_028253

**Record Creation Time:** 20260404T065920+0000

**Record Last Update:** 20260729T044721+0000

### Ratings and Alerts

No rating or validation information has been found for Loom.

No alerts have been found for Loom.

---

## Data and Source Information

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

---

## Usage and Citation Metrics

We have not found any literature mentions for this resource.